UNIVERSIDAD DE EXTREMADURA

TESIS DOCTORAL

CONTROL DE MOHOS TOXIGÉNICOS MEDIANTE LA PROTEÍNA PgAFP. INFLUENCIA EN EL METABOLISMO, PROTEOMA Y SÍNTESIS DE MICOTOXINAS

JOSUÉ DELGADO PERÓN

Departamento de Producción Animal y Ciencia de los Alimentos
IPROCAR (Instituto Universitario de Investigación de Carne y Productos Cárnicos)

Conformidad de los Directores:

Fdo: Miguel Ángel Asensio Pérez **Fdo:** Félix Núñez Breña

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DEPARTAMENTO DE PRODUCCIÓN ANIMAL
Y CIENCIA DE LOS ALIMENTOS

Campus Universitario
Avenida de la Universidad, s/n
E-10071 – CÁCERES
Teléfonos: +34 (9) 27 25 71 00
Fax: +34 (9) 27 25 71 10

Miguel Ángel Asensio Pérez, Doctor en Veterinaria y Catedrático de Universidad del área de Nutrición y Bromatología en la Facultad de Veterinaria de la Universidad de Extremadura,

INFORMA:

Que la Tesis Doctoral titulada ¨**Control de mohos toxigénicos mediante la proteína PgAFP. Influencia en el metabolismo, proteoma y síntesis de micotoxinas**¨, de la que es autor el Licenciado en Veterinaria D. Josué Delgado Perón, ha sido realizada en el Instituto Universitario de Investigación de Carne y Productos Cárnicos bajo mi dirección y cumple las condiciones exigidas para optar al grado de Doctor.

Cáceres, 18 de diciembre de 2015

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Fax: +34 (9) 27 25 71 10

Félix Núñez Breña, Doctor en Veterinaria y Profesor Titular de Universidad del área de Nutrición y Bromatología en la Facultad de Veterinaria de la Universidad de Extremadura,

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Si no conozco una cosa, la investigaré.

Louis Pasteur

íNDICE

I. INTRODUCCIÓN

I.1. Población fúngica en derivados cárnicos curado-madurados

Existe una gran diversidad de grupos microbianos capaces de desarrollarse y multiplicarse en alimentos, debido a su ubicuidad y a la gran diversidad fisiológica, y tolerancia a condiciones ambientales diversas (McMeekin et al. 1997). Los factores que determinan qué tipo de microorganismo prolifera en los alimentos viene determinado en gran medida por las características físico-químicas del alimento, tales como: pH, actividad de agua (a_w), concentración de NaCl, temperatura de conservación, presencia o ausencia de oxígeno, etc. En líneas generales, las bacterias suelen predominar en alimentos con una a_w elevada, (>0,90). Sin embargo, en alimentos con valores de a_w inferiores las bacterias no pueden competir por el sustrato, y son los mohos y levaduras los que constituyen la población mayoritaria (Pitt and Hocking 1997).

La contaminación inicial de los derivados cárnicos curado-madurados proviene de la piel y del contenido intestinal de los animales sacrificados, de ingredientes como la sal (Sonjak et al. 2011), que puede estar contaminada por microorganismos halófilos y esporas de mohos y del ambiente en que se manipulan las piezas, incluyendo el aire, utensilios y paredes de las salas donde se manipulan (Asefa et al. 2011).

Las condiciones ambientales tanto externas (temperatura y humedad relativa) como propias del producto (a_w, pH) durante el procesado de los derivados cárnicos curado-madurados no permiten el desarrollo de la mayoría de los microorganismos que pueden haber llegado a la carne. En las primeras etapas esta población microbiana se controla manteniendo los productos a temperaturas bajas. Sin embargo, las temperaturas que se alcanzan durante el secado y la maduración en piezas cárnicas o durante el estufaje en embutidos (15-30 °C) permitirían un rápido desarrollo microbiano, que es controlado por los restantes factores ecológicos. Uno de los factores más importantes es la pérdida de agua, que junto a la incorporación y difusión de la sal provoca una reducción progresiva de la a_w. Este parámetro disminuye en los jamones desde niveles de aproximadamente 0,96, al final de post-salado, cuando se inicia el ascenso de la temperatura en fases tempranas hasta valores que oscilan entre 0,81 y 0,87 en el producto final (Rodríguez et al. 1994).

Estos cambios en las condiciones ambientales durante el procesado provocan una evolución de la población microbiana que se traduce en cambios de los grupos microbianos mayoritarios (Figura I1). Durante el post-salado predominan los estafilococos, que van disminuyendo paulatinamente a lo largo de todo el procesado, aunque aún se mantienen en el producto final (Rodríguez et al. 1994). Por su parte los lactobacilos mantienen su población en los primeros 80 días aproximadamente, para descender drásticamente una vez las piezas

comienzan la etapa en secadero. La población de mohos y levaduras se mantiene relativamente estable a lo largo del procesado, convirtiéndose en dominantes después de la etapa de secadero (Rodríguez et al. 2001), donde las condiciones ambientales y del producto hacen que estos microorganismos compitan más fácilmente que los demás, principalmente por su mayor tolerancia a bajas a_w. El crecimiento de mohos en carne fresca es muy poco importante en comparación con las bacterias, ya que debido a la alta a_w de este producto las bacterias tienen ventajas competitivas y se desarrollan más rápidamente, aunque en algunos casos en carne fresca pueden desarrollarse mohos de crecimiento rápido, bien adaptados a valores de a_w elevados, encuadrados en el Orden Mucorales, como *Mucor*, *Thamnidium*, *Rhizopus*, etc. (Hawker and Linton 1971). En la superficie de derivados cárnicos curado-madurados, como embutidos y jamones, donde los valores de a_w son menores, es donde cobran mayor importancia, ya que la competencia de los mohos frente a otros microorganismos es mucho más eficiente. Las especies más frecuentes en estos alimentos pertenecen a los géneros *Penicillium*, *Aspergillus* y *Eurotium* (Hernández and Huerta 1993; Núñez et al. 1996a) que llegan a representar más del 98% de los mohos aislados, ya que están más adaptados a las condiciones ecológicas, principalmente de humedad, que se alcanzan. Los mohos incrementan su proporción y su diversidad a medida que avanza el procesado del producto (Núñez et al. 1996a). Por otra parte, se suelen observar diferencias en cuanto a la distribución de los citados géneros a lo largo del procesado. Así, en las fases en las que la a_w aún no se ha reducido excesivamente, y se mantiene la temperatura en valores relativamente bajos (<20 °C), como sucede en las etapas de post-salado del jamón, predominan los mohos del género *Penicillium*. Consecuentemente, este género es el mayoritario durante todo el procesado en la mayor parte de los embutidos y en jamones de maduración corta. Sin embargo, en jamones con maduración prolongada, como el ibérico, a medida que se incrementa la temperatura y disminuye la a_w al final del proceso, los integrantes del género *Aspergillus* y su teleomorfo *Eurotium* se convierten en los mayoritarios (Asensio et al. 2004; Núñez et al. 1996a), lo que sucede cuando se alcanzan en la superficie valores de a_w 0,88-0,79 (Rodríguez et al. 2001).

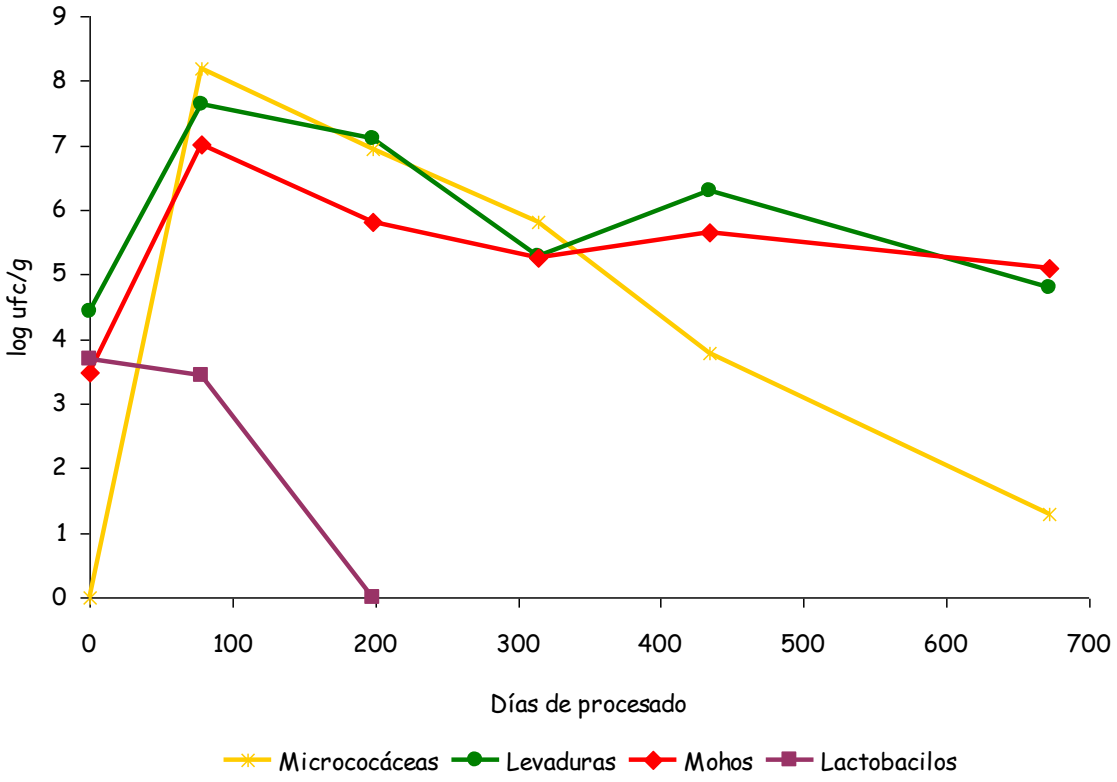


Figura I1. Evolución de la población microbiana en la superficie del jamón (Rodríguez et al. 2001)

I.2. Efectos del desarrollo de mohos en derivados cárnicos curado-madurados

La población fúngica presente en la superficie de los derivados cárnicos curado-madurados durante su maduración puede tener efectos tanto positivos como negativos en relación con la calidad y la seguridad del producto final.

Entre los efectos beneficiosos atribuidos a los mohos durante la maduración de los derivados cárnicos curado-madurados destaca su contribución a los cambios proteolíticos y lipolíticos que se producen durante la maduración (Martín et al. 2002; Martín et al. 2004). Como consecuencia de esta actividad producen un aumento de la concentración de aminoácidos y ácidos grasos libres, precursores de compuestos volátiles deseables en derivados cárnicos curado-madurados (Bruna et al. 2001; Martín et al. 2003). Por otra parte, constituyen una barrera antioxidante por su producción de enzimas como la catalasa (Núñez et al. 1998) sumado a la acción sinérgica del consumo de O_2 y protección frente a la luz, a los que se considera agentes prooxidantes (Boselli et al. 2009; Ferioli et al. 2008). Estas acciones tienen como resultado la formación de una cantidad menor de compuestos volátiles relacionados con la oxidación lipídica y un incremento de compuestos derivados de aminoácidos libres (Martín et al. 2002), asociados de forma positiva a las características sensoriales deseables en los derivados

cárnicos curado-madurados (Ruiz et al. 1999; Martín et al. 2006). En conjunto se relaciona a los mohos con una disminución del enranciamiento, lo que influye positivamente a nivel sensorial (Bruna et al. 2001).

Sin embargo, se han descrito diversos problemas asociados al crecimiento incontrolado de mohos en la superficie del jamón. Por una parte pueden provocar la aparición de defectos o alteraciones sensoriales (Comi et al. 2014; Lozano-Ojalvo et al. 2014; Poma 1998), y por otra parte, lo que es más preocupante desde el punto de vista de la seguridad alimentaria, pueden desarrollarse mohos productores de micotoxinas (Núñez et al. 2000; López-Díaz et al. 2001; Sosa et al. 2002; Núñez et al. 2007; Rodríguez et al. 2012e).

En este sentido, la mayor parte de los mohos aislados de embutidos y jamón curado pertenecientes a los géneros *Penicillium* y *Aspergillus* son potencialmente toxigénicos (Núñez et al. 1996b; López-Díaz et al. 2001), e incluso se ha demostrado la capacidad de producción de micotoxinas de varias especies toxigénicas pertenecientes a estos dos géneros cuando se desarrollan en la superficie de jamón curado (Núñez et al. 2007; Rodríguez et al. 2012e). Debido al peligro potencial que representa la presencia de mohos toxigénicos en alimentos, existe una creciente preocupación por parte de las autoridades sanitarias. Así, en los últimos años se ha producido un incremento paulatino en la normativa legal de la Unión Europea fijándose tanto el contenido máximo de estos contaminantes en una cada vez mayor variedad de alimentos, como métodos de muestreo y de análisis para el control oficial de dicho contenido. Se han establecido límites para aflatoxinas (Ministerio de Sanidad y Consumo 2001; Comisión Europea 2010a), ocratoxina A (OTA) (Ministerio de Sanidad y Consumo 2003; Comisión Europea 2010b), patulina (Ministerio de Sanidad y Consumo 2004; Comisión Europea 2006) y toxinas de *Fusarium* (Comisión Europea 2005; Comisión Europea 2007). Teniendo en cuenta esta evolución legislativa es previsible que se amplíe el número de micotoxinas y de alimentos para los que se establezca un límite máximo en un futuro próximo, entre los que podrían incluirse derivados cárnicos curado-madurados. En este sentido, en algunos países como Italia se ha establecido en 1 ppm el contenido máximo permitido de OTA para carne de cerdo y productos derivados (Ministerio della Sanità 1999).

Por último, la producción de estas toxinas no se limita exclusivamente a productos cárnicos curado-madurados, sino que también se ha demostrado una alta capacidad de producción de estos metabolitos por mohos en otros alimentos de humedad intermedia como quesos son susceptibles de desarrollo de mohos (Lie and Marth 1967; Taniwaki et al. 2001; Crowley et al. 2013)

I.2.1. Aflatoxinas

Las aflatoxinas son metabolitos secundarios producidas por mohos del género *Aspergillus*, siendo las dos principales especies productoras *Aspergillus flavus* y *Aspergillus parasiticus* (Reverberi et al. 2005), aunque también se ha descrito su producción por otros mohos de los géneros *Aspergillus*, *Emericella*, *Penicillium* y *Rhizopus* (Varga et al. 2009; Rodríguez et al. 2012c). Químicamente son policétidos altamente oxigenados (Fig. I2) (Jayashree and Subramanyan 2000), y, debido a sus características químicas, son muy estables frente a tratamientos térmicos y reacciones químicas. Son necesarios tratamientos a temperaturas superiores a 150 °C para reducir la concentración de micotoxinas (Bullerman and Bianchini 2007). Las aflatoxinas más importantes y estudiadas se han clasificado en los tipos: B_1, B_2, G_1 y G_2 según su fluorescencia de color azul o verde en presencia de luz ultravioleta a 365 nm (Liang et al. 1996). Estas micotoxinas se caracterizan por su alto potencial hepatotóxico, inmunosupresor, carcinogénico, teratogénico y mutagénico (Cigić and Prosen 2009), encuadrándose dentro del grupo A según la clasificación de la Agencia Internacional de Investigación sobre el Cáncer (IARC). Las especies productoras están ampliamente distribuidas y tienen capacidad de producir aflatoxinas en un amplio rango de condiciones de temperatura y humedad, así como en diversos sustratos. Entre esta variedad de sustratos, debido a sus características físico-químicas, a las condiciones ambientales y al largo proceso de maduración, se encuentran los derivados cárnicos curado-madurados (Rodríguez et al. 2012e; Bernáldez et al. 2014). Este hecho supone un riesgo para la salud de los consumidores, así como una barrera comercial que podría frenar las exportaciones de estos productos, siendo un factor negativo para la economía de las industrias.

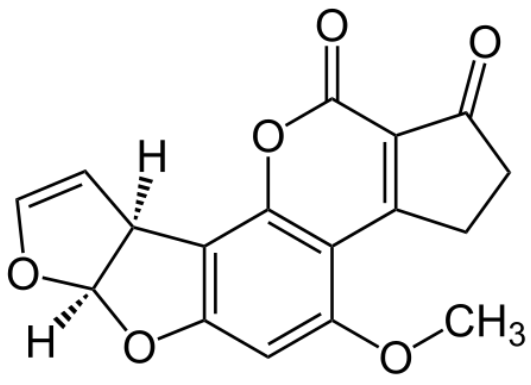


Figura I2. Estructura química de la aflatoxina B_1.

I.2.2. Ocratoxinas

Estas toxinas se constituyen por un pentaquétido cíclico que contienen una porción de dihidroisocumarina clorada ligada a una L-fenilalanina a través de un grupo carboxilo mediante un enlace amida (Fig. I3). *Aspergillus alliaceus*, *Aspergillus auricomus*, *Aspergillus carbonarius*, *Aspergillus glaucus*, *Aspergillus meleus* and *Aspergillus niger*, así como *Penicillium nordicum* y *Penicillium verrucosum*, son productores de OTA (Bezerra da Rocha et al. 2014). La OTA es la más tóxica de las ocratoxinas producidas por mohos, ya que su consumo crónico produce nefropatía intersticial, siendo también teratogénica, hepatotóxica, neurotóxica e inmunotóxica (Soriano del Castillo 2007). Además, está clasificada por la IARC como posible carcinógeno humano de clase 2B.

La OTA es una de las micotoxinas que se encuentran de forma más frecuente en derivados cárnicos curado-madurados, debido a residuos procedentes no solo de la alimentación de los animales, sino también al crecimiento en dichos productos de mohos ocratoxigénicos (Rodríguez et al. 2012d; Bertuzzi et al. 2013). Este peligro ha llevado a autoridades sanitarias de algunos países como Italia a fijar un contenido máximo de residuos en productos cárnicos, como se ha indicado anteriormente.

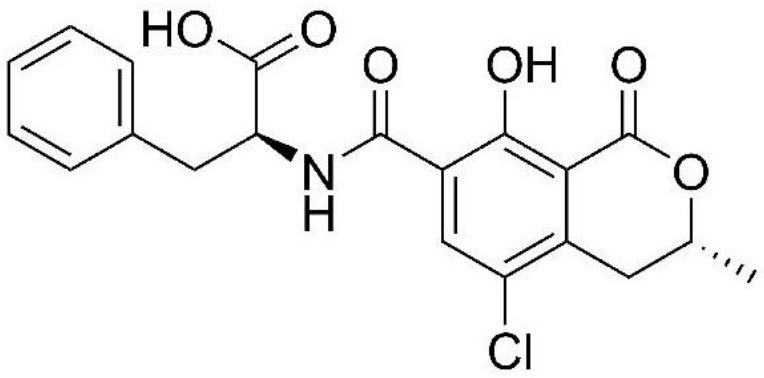


Figura I3. Estructura química de la ocratoxina A.

I.3. Métodos de control de mohos en derivados cárnicos curado-madurados

Debido al peligro que representa la producción de micotoxinas, es necesario establecer estrategias viables para evitar su síntesis durante el procesado de los derivados cárnicos curado-madurados. Existen distintos procedimientos efectivos para controlar este peligro en diferentes alimentos, entre los que se pueden citar métodos físicos (tratamientos térmicos, radiaciones ionizantes o altas presiones) o químicos (atmósferas controladas, ácidos orgánicos, aceites esenciales o peróxido de hidrógeno). Sin embargo, muchos de estos tratamientos no son

aplicables durante el procesado de productos cárnicos curado-madurados ya que impedirían el correcto desarrollo del proceso de maduración. En otros casos, el gran volumen de los secaderos y bodegas que albergan a los productos y el difícil manejo de una gran cantidad de piezas dificultan la aplicación de tratamientos físicos. Para controlar el desarrollo de los mohos se pueden utilizar diversos conservantes químicos. El ácido sórbico y el propiónico limitan la capacidad de los mohos para adaptarse a factores ambientales adversos (Sergeeva et al. 2009), inhibiendo el desarrollo de mohos toxigénicos (Lennox and McElroy 1984), pero no son totalmente eficaces, salvo a valores de pH ácidos o con altas concentraciones de sal (Razavi-Rohani and Griffiths 1999). Además, algunas especies de *Penicillium* o de *Aspergillus* crecen en presencia de altas concentraciones de ácido propiónico o de sorbatos (Bullerman 1984; Mann and Beuchat 2008), e incluso algunos *Penicillium* y *Debaryomyces* decarboxilan el sorbato para producir 1,3 pentadieno de olor a petróleo (Casas et al. 2004). Por ello se ha propuesto la aplicación combinada de distintos compuestos antimicóticos (Mann and Beuchat 2008). Sin embargo, la demanda creciente de alimentos libres de aditivos, y especialmente de conservantes, hace necesario explorar nuevas alternativas para controlar el desarrollo de mohos toxigénicos durante la maduración de los alimentos que evite la utilización de estos conservantes químicos.

Por una parte, se podrían introducir variaciones en las condiciones de maduración que eviten o disminuyan la población fúngica, pero pueden originar problemas tecnológicos en el procesado que impedirían una maduración adecuada y que finalmente radicarían en una merma importante en la calidad sensorial del producto final. Las medidas higiénicas para evitar la contaminación se ven desbordadas en secaderos y bodegas, donde resulta imposible eliminar totalmente la contaminación ambiental. Por tanto, el abanico de posibilidades que la industria puede barajar incluye algunas que resultan poco prácticas y, en muchos casos, imposibles de llevar a cabo. Del mismo modo, es necesario tener en cuenta los requerimientos de fabricantes de otros productos en los cuales no se desea la presencia de moho, como es el caso de algunos embutidos o quesos. Para satisfacer las necesidades del sector en este aspecto, sería necesario ofrecer alternativas que impidan o limiten al máximo el desarrollo de mohos, siendo recomendable que se basen en estrategias que no supongan la adición de aditivos artificiales, de acuerdo a las demandas de los consumidores y además deben descartarse los tratamientos inespecíficos que impidan el desarrollo de la población fúngica deseable en el alimento madurado.

Una de las posibilidades con mejores perspectivas se basa en el empleo de cultivos de cepas no toxigénicas que contribuyan a la maduración del producto donde se inoculan. Para ello,

el uso de la propia microbiota presente de forma habitual durante la maduración de productos presenta grandes ventajas. Por una parte, la adición de estos microorganismos como cultivo protector no supone una ruptura con la microbiota habitual en estos productos, por lo que se reduce al mínimo el riesgo de alteraciones sensoriales derivadas de la adición de estos cultivos protectores. Además, la capacidad de estos microorganismos para implantarse y ejercer su efecto será mejor si se trata de cepas aisladas de productos curados, dada su adecuación a esas condiciones ecológicas particulares. Así desde hace años se han utilizado cultivos iniciadores y, de forma más específica, cultivos protectores para mejorar la seguridad de los alimentos (Holzapfel et al. 1995). Por último, esta estrategia sería adecuada en relación a las demandas de los consumidores con respecto a la minimización del empleo de aditivos artificiales. De los microorganismos presentes en este tipo de productos que pueden interferir con el desarrollo de mohos toxigénicos o con la formación de micotoxinas destacan las bacterias ácido-lácticas (BAL), las levaduras y los mohos productores de proteínas antifúngicas.

I.3.1. Bacterias acidolácticas

Las bacterias acidolácticas (BAL) son habituales en productos crudos curados, especialmente en embutidos y en las primeras etapas de la maduración de jamones. Algunos de estos microorganismos, principalmente de los géneros *Lactococcus* y *Lactobacillus* y, en menor medida, *Pediococcus* y *Leuconostoc*, tienen capacidad de inhibición del crecimiento de mohos toxigénicos y de la producción de micotoxinas (Dalié et al. 2010). La actividad antifúngica de las BAL se ha relacionado principalmente con la producción de compuestos antifúngicos de bajo peso molecular, incluyendo ácidos orgánicos, ácidos grasos, reuterina, peróxido de hidrógeno, compuestos fenólicos, lactonas, dipéptidos cíclicos y compuestos proteicos, que no sólo pueden afectar al desarrollo de mohos sino a la capacidad de producir micotoxinas (Dalié et al. 2010; Crowley et al. 2013; Li et al. 2014; Ryu et al. 2014). Además tampoco puede descartarse el efecto inhibidor debido a la competencia por el sustrato. De acuerdo con las preferencias de los consumidores, las BAL son buenas candidatas a biocontrol de mohos toxigénicos ya que tienen la consideración americana de GRAS (Generalmente Reconocidas como Seguras) y la europea QPS (Presunción Cualificada de Seguridad), y se les considera que poseen propiedades probióticas saludables. Sin embargo, debido su limitada resistencia a los valores intermedios de actividad de agua los hace inadecuados para productos de larga maduración, en particular cuando no se añade azúcar. Consecuentemente, sería necesario optimizar el momento de inoculación así como posibles reinoculaciones o establecer pequeñas modificaciones en los parámetros de la maduración con el objetivo de maximizar su presencia a lo largo del proceso de maduración.

I.3.2. Lactobacilos

Diferentes levaduras muestran actividad antifúngica o capacidad para disminuir la acumulación de micotoxinas en alimentos (Asensio et al. 2014). En consecuencia, algunas cepas han sido propuestas como cultivos protectores, especialmente en alimentos de origen vegetal con el objetivo de reducir el uso de fungicidas sintéticos para el control de enfermedades de post-cosecha y reducir el crecimiento de mohos, incluyendo algunos toxigénicos (Petersson et al. 1998; Qin et al. 2004; Ponsone et al. 2012; Armando et al. 2013; Spadaro et al. 2013).

En los derivados cárnicos curado-madurados las levaduras predominantes pertenecen a la especie *Debaryomyces hansenii*, llegando a constituir el 99% de los aislados en la fase de bodega de jamones (Núñez et al. 1996b), probablemente debido a ser moderadamente halófila (Breuer and Harms 2006), siendo capaz de desarrollarse con hasta un 15% de NaCl (Asefa et al. 2009). Además, *D. hansenii* es una levadura con importantes aplicaciones biotecnológicas en alimentos debido a sus propiedades metabólicas características (Breuer and Harms 2006). Por lo tanto, su utilización como cultivos protectores podría asegurar su presencia a lo largo de todo el procesado. En los productos cárnicos esta levadura contribuye de manera notable en la textura final gracias a fenómenos de proteólisis (Rodríguez et al. 1998; Martín et al. 2002), así como la generación de compuestos volátiles formados durante la maduración de productos curados (Martín et al. 2003; Martín et al. 2006; Andrade et al. 2009).

En cuanto a su capacidad antifúngica, cepas de *D. hansenii* se han mostrado eficaces para inhibir el crecimiento y la esporulación de mohos de los géneros *Penicillium*, *Aspergillus* y *Eurotium* en diferentes alimentos, por lo que se han propuesto como agentes de control biológico contra mohos en frutas (Chalutz and Wilson 1990; Hernández-Montiel et al. 2010), el yogur y queso (Liu and Tsao 2009). En este sentido, también se ha probado en productos cárnicos la eficacia de cepas de *D. hansenii* autóctonas para reducir el desarrollo y la producción de toxinas de mohos toxigénicos frecuentes en estos productos (Virgili et al. 2012; Andrade et al. 2014; Simoncini et al. 2014; Núñez et al. 2015).

También otras especies de levaduras aisladas de productos cárnicos, como *Candida zeylanoides*, *Candida famata* y *Endomyces fibuliger* son capaces de inhibir el crecimiento de mohos ocratoxinógenos como *A. niger*, *A. ochraceus*, *P. nordicum*, *P. verrucosum*, y en consecuencia la producción de OTA en la superficie de jamón curado (Virgili et al. 2012; Comi and Iacumin 2013). Sin embargo, estas levaduras se encuentran a niveles bajos en los productos cárnicos curado-madurados (Núñez et al. 1996b; Simoncini et al. 2007; Asefa et al. 2009) por lo

que su adaptación a estos alimentos en menor que *D. hansenii* y serían potencialmente menos útiles.

Diferentes mecanismos de acción pueden explicar el efecto antifúngico de estas levaduras, como la competencia por nutrientes y espacio (Druvefors et al. 2005; Coelho et al. 2007), la producción de toxinas killer (Marquina et al. 2001; Hernández et al. 2008), la producción de compuestos volátiles (Masoud et al. 2005), el parasitismo (Wisniewski et al. 1991), la resistencia inducida (El-Ghaouth et al. 1998), y la producción de enzimas hidrolíticas de pared celular (Masih and Paul 2002). En algunas cepas de *D. hansenii* aisladas de productos cárnicos pueden estar implicados varios de estos mecanismos (Andrade et al. 2014; Núñez et al. 2015).

Además, las levaduras pueden disminuir el contenido de micotoxinas por adsorción (Var et al. 2009), su degradación (Patharajan et al. 2011) o por impedir su síntesis mediante el bloqueo de cualquier paso en la ruta biosintética de las micotoxinas. En este sentido, *D. hansenii* es capaz de reducir la concentración de OTA en cultivos mixtos con *A. westerdijkiae* debido a una reducción en la expresión de genes biosintéticos de OTA (Gil-Serna et al. 2011).

I.3.3. Mohos

Algunas cepas de mohos aisladas de productos cárnicos curado-madurados no toxigénicos y con una actividad metabólica adecuada pueden limitar por competición el desarrollo de otros mohos indeseables. No obstante, la evolución de las condiciones ecológicas durante la maduración hace poco probable que una sola cepa seleccionada pueda limitar el crecimiento de todas las especies toxigénicas habituales en todo el rango de temperaturas y de a_w que se alcanzan durante la maduración (Núñez et al. 2000; Sosa et al. 2002). El éxito de esta estrategia sería más probable en el caso de utilizar mohos con capacidad de producir metabolitos, como pueden ser proteínas con actividad antifúngica que pueden inhibir o frenar el desarrollo de determinados mohos toxigénicos, lo que le otorgaría una ventaja competitiva para el control de estos mohos indeseables (Acosta et al. 2009). Para la evaluación de la capacidad antifúngica de estos metabolitos se han diseñado diversas estrategias. Algunas basadas en inhibición en placas de agar (Geisen 2000) y otras en placas microtiter (Broekaert et al. 1990).

I.3.3.1. Proteínas antifúngicas de origen microbiano

En los últimos años se ha producido un incremento importante en la investigación de agentes antifúngicos debido a la aparición de resistencias frente a agentes antimicóticos

empleados habitualmente para el tratamiento de micosis en humanos y en plantas. Entre las distintas opciones, destaca la caracterización de nuevas proteínas con actividad antifúngica (Wang and Ng 2002). Se han purificado y caracterizado proteínas con efecto antifúngico a partir de diferentes organismos tales como plantas (Chu et al. 2003), bacterias (Yang et al. 2002) o mohos (Marx 2004; Acosta et al. 2009). Existe una amplia variabilidad en la composición, estructura secundaria y terciaria de estas proteínas, aunque la mayoría se caracterizan por poseer una carga neta positiva y numerosos residuos de cisteína envueltos en la formación de puentes bisulfuro (Leiter et al. 2005).

Dentro de estos compuestos, se han descubierto varias proteínas antifúngicas producidas por mohos que se caracterizan por ser de naturaleza catiónicas, ricas en cisteína y de bajo peso molecular (Tabla I1).

Tabla I1. Proteínas antifúngicas producidas por mohos

Nombre	Moho productor	pI	Pm (Da)	Referencia
AcAFP	*Aspergillus clavatus*	-	5773	(Skouri-Gargouri and Gargouri 2008)
AcAMP	*Aspergillus clavatus*	9.066	5777	(Hajji et al. 2010)
AFP	*Aspergillus giganteus*	8.8	5800	(Nakaya et al. 1990)
AFP_{NN5353}	*Aspergillus giganteus*	9.3	-	(Binder et al. 2011)
Anafp	*Aspergillus niger*	7.14	6583	(Gun Lee et al. 1999)
FPAP	*Fusarium polyphilaidicum*	6.3	-	(Galgóczy et al. 2013)
NAF	*Penicillium nalgiovense*	8.93	6300	(Geisen 2000)
NFAP	*Neosartorya fischeri*	8.93	6625	(Kovács et al. 2011)
PAF	*Penicillium chrysogenum*	8.93	6250	(Marx et al. 1995)
Pc-Arctin	*Penicillium chrysogenum*	-	7000	(Chen et al. 2013)
PgAFP	*Penicillium chrysogenum*	9.22	6494	(Rodríguez-Martín et al. 2010)

I.3.3.2. Características de PgAFP producida por Penicillium chrysogenum

La proteína PgAFP es producida por la cepa de *Penicillium chrysogenum* CECT 20922 (previamente nombrada RP42C), aislada de jamón curado (Acosta et al. 2009; Rodríguez-Martín et al. 2010). Esta proteína mostró capacidad de inhibición frente a mohos toxigénicos frecuentes en derivados cárnicos curado-madurados, pertenecientes a los géneros *Penicillium* y *Aspergillus* (Acosta et al. 2009). El peso molecular de la proteína madura es de 6494 Da y su punto isoeléctrico 9.2 (Rodríguez-Martín et al. 2010). Se sintetiza como una pre-pro-proteína de 92

aminoácidos y después de la eliminación de las secuencias N-terminal pre- y pro- (18+16 aminoácidos) la proteína madura se libera en el medio de cultivo (58 aminoácidos). Las prosecuencias son de una importancia crucial para impedir el plegamiento adecuado y la actividad biológica completa (Marx et al. 2005) siendo todas éstas, características comunes de las proteínas antifúngicas.

La secuencia que codifica la PgAFP consiste en una región de codificación de 279 pares de bases interrumpido por dos intrones de 63 y 62 pares de bases. La secuencia de aminoácidos deducida de la matriz de la proteína madura muestra un 79% de identidad con Anafp de *Aspergillus niger*, mientras que con PAF muestra un 34% y con AFP un 33% de identidad (Rodríguez-Martín et al. 2010).

P. chrysogenum produce compuestos considerados como seguros (GRAS) según la Food and Drug Administration de EEUU. Este hecho junto a que PgAFP no mostró toxicidad frente a células de mamíferos (Rodríguez 2009) y que es sensible al tratamiento con enzimas como tripsina, pepsina y lisozima (Acosta 2006), permite ser optimistas respecto a su uso en alimentos ya que puede ser degradada en el tracto intestinal.

Aunque se desconoce el mecanismo de acción de PgAFP, debido a las homologías con otras proteínas antifúngicas, se podría presumir que algunos de los mecanismos de acción descritos para estas proteínas podrían explicar la actividad antifúngica de la PgAFP. El conocimiento de dicho mecanismo aportaría una información muy valiosa, tanto para caracterizar mejor a esta proteína, como para establecer condiciones de aplicación de la proteína o del moho productor para obtener la mayor eficacia posible frente a mohos toxigénicos en derivados cárnicos curado-madurados.

I.3.3.3. Efecto de las proteínas antifúngicas sobre mohos sensibles

Los mecanismos de acción de las proteínas que inhiben el desarrollo de los mohos son muy variados. Algunos atraviesan la membrana e interfieren en la síntesis de ADN, ARN o proteínas, inhiben la cadena respiratoria celular (Cociancich et al. 1993) o interaccionan con enzimas ATP-dependientes (Hilpert et al. 2010). En todos ellos la permeabilidad de la membrana parece jugar un papel decisivo en el mecanismo de acción.

Las proteínas antifúngicas de mayor utilidad son las que presentan mecanismos de acción específicos para la cubierta externa de los hongos (Groll et al. 1998), ya que suelen ser poco tóxicas para las células de los mamíferos. En la interacción de la proteína con la membrana juega un papel destacado la carga (Hoover et al. 2003) y el carácter catiónico o hidrofóbico del compuesto (Friedrich et al. 1999). La hidrofobicidad y la estructura en α-hélice se correlacionan

con la toxicidad para las células de mamíferos, mientras que la carga positiva se relaciona con la actividad antimicrobiana (Hong et al. 2001). Se asume que la actividad antifúngica de estas proteínas está relacionada con la capacidad de interaccionar con fosfolípidos aniónicos, que forman parte de la membrana de mohos y bacterias, lo que permite la unión de la proteína y su posterior acción (Lacadena et al. 1995). Sin embargo parece poco probable que se trate de una unión inespecífica, ya que la membrana externa de bacterias está principalmente compuesta también por fosfolípidos aniónicos y no se ven afectadas por AFP. En las células de eucariotas superiores al carecer de dichos fosfolípidos o al estar confinados en la cara interna de la membrana plasmática, y no estar en contacto con el medio extracelular se puede descartar este tipo de interacción (Rivas and Andreu 2003; Theis and Stahl 2004).

Del mismo modo, se han descrito diversos efectos de este tipo de proteínas sobre los mohos tratados, tales como reducción del metabolismo celular, cambios drásticos en la morfología de las hifas, incremento en el flujo de K^+ y la formación de especies reactivas de oxígeno (ROS) en el interior de las células (Kaiserer et al. 2003; Marx et al. 2005). Estas sustancias provocan daño celular desencadenando fenómenos apoptóticos y necrosis (Marx et al. 2008; Galgóczy et al. 2013). La reducción del metabolismo celular de las hifas de los mohos sensibles podría considerarse *a priori* como un efecto directo de la capacidad inhibitoria de AFP.

Por otra parte se ha apuntado la posibilidad de que la AFP ejerza algún tipo de señal apoptótica sobre las células tratadas, habiéndose descrito dos tipos de señales que podrían ejercer dicha acción: en el primero está involucrada la proteína heterotrimérica G junto a la transducción de señales y redes de regulación; el segundo se realizaría a través de la alteración de la homeostasis de Ca^{2+} de las células (Hegedus et al. 2011), donde volvería a jugar un papel determinante la membrana celular. También se ha postulado que la actividad de AFP y PAF están relacionadas con la señalización de la ruta metabólica de síntesis de quitina, estando involucrada la cascada de señalización de la proteína Rho1 (Binder et al. 2010; Ouedraogo et al. 2011) que es considerada la principal reguladora de la señalización de la pared celular (Levin 2005).

Algunas cepas presentan resistencia a este tipo de proteínas antifúngicas, relacionada con la capacidad de deponer quitina como protección frente a estas proteínas (Ouedraogo et al. 2011). Esta deposición de quitina colaboraría en el acceso de estas proteínas antifúngicas a receptores específicos relacionados con fosfolípidos de membrana. Además la presencia de cationes en el medio ejerce un efecto protector sobre los mohos sensibles, ya que se ven menos afectados por las proteínas antifúngicas (Thevissen et al. 1999; 1996; Theis et al. 2003; Kaiserer et al. 2003; Galgóczy et al. 2013). Se ha propuesto que los cationes pueden interferir con la AFP bien por inhibición directa de la unión a la membrana o por interacción específica con un posible

receptor en la membrana (Marx 2004). Este hecho limitaría la utilidad de proteínas antifúngicas sobre alimentos ricos en cationes divalentes, como quesos, que contienen altos niveles de calcio (Chekri et al. 2012). Por ello sería interesante conocer cómo actúan los cationes para reducir o anular la actividad de proteínas antifúngicas, para diseñar estrategias que contrarresten el efecto de los cationes divalentes y maximizar el efecto antifúngico de estas proteínas.

El efecto de estas proteínas antifúngicas sobre la señalización de las proteínas G podría influir en la producción de micotoxinas, ya que es requerida para producción de alguna de éstas (Hicks et al. 1997). Además, la inducción de ROS por estos antifúngicos ha sido descrita como desencadenante de estrés oxidativo, que, por otra parte, es un factor importante para la producción de micotoxinas (Reverberi et al. 2005; Kim et al. 2008). El estrés oxidativo provoca cambios en la fisiología de los mohos, induciendo la producción peroxisomas que regulan la β-oxidación de ácidos grasos, afectando ambos a la producción de alfatoxinas (Reverberi et al. 2012). Además, el metabolismo del glutatión es el encargado de contrarrestar la cantidad de ROS en la célula, existiendo una correlación entre la acción de la proteína glutatión S-transferasa y la producción de aflatoxinas (Saxena et al. 1988). Todos estos resultados indican que podría existir un estímulo de la producción de micotoxinas en respuesta a estrés oxidativo provocado por las ROS, que a su vez parecen ser inducidas por este tipo de proteínas antifúngicas. Sin embargo, el efecto inhibidor de las proteínas antifúngicas sobre mohos productores de micotoxinas evitaría el desarrollo de éstos y por consiguiente limitaría su producción, además no puede ser descartada una interacción de estas proteínas antifúngicas con rutas biosintéticas propias de aflatoxinas. Por lo tanto, dado que teóricamente existen fenómenos que pueden parecer contradictorios, es necesario establecer el efecto que las proteínas antifúngicas tienen sobre la producción de micotoxinas en mohos que puedan sobrevivir al tratamiento.

I.4. Proteómica

Para conocer cómo afectan estas proteínas sobre el metabolismo de los mohos frente a los que actúa, se podría emplear el análisis de la expresión génica total. Sin embargo la medición de la expresión de ARNm no suministra valores confiables de los cuales se pudiera deducir la abundancia y la presencia de las proteínas traducidas. Estas falta de precisión se debe principalmente a que el tiempo de vida media de proteínas en el interior de una célula o de un compartimiento celular es variable debido a la acción de proteasas y a la traslocación intra- y extracelular, junto con a la modificación de las proteínas durante su intervención en procesos biológicos. Por tanto, el estudio directo del perfil de proteínas, a través de la Proteómica, puede dar respuesta a estas cuestiones (Castellanos et al. 2004).

La proteómica se define como el estudio y caracterización del proteoma, entendiendo como tal a la totalidad de las proteínas expresadas a partir del genoma bajo unas condiciones y en una fase de desarrollo determinadas. El estudio del proteoma de un organismo puede ofrecer información útil relacionada con su estado fisiológico, relacionándolo con cambios producidos en el organismo por algún factor. El aumento o la disminución relativa de proteínas en un organismo sometido a una determinada variable con respecto a una situación control ofrecen una información valiosa relacionada con los cambios producidos por los factores en estudio sobre el organismo en cuestión. Este análisis basado en la comparación de proteomas se denomina proteómica comparativa, y ha sido empleado, entre otros fines, para conocer cómo afectan diversos compuestos antifúngicos a mohos sensibles (Gautam et al. 2008; Cagas et al. 2011). Para ello es necesario disponer de técnicas que permitan la separación de proteínas, la cuantificación del cambio de magnitud de provocado y finalmente su identificación. Existen varios métodos para llevar a cabo este tipo de análisis pudiendo diferenciarse dos metodologías distintas, dependiendo de si están basados o no en el empleo de electroforesis en geles de poliacrilamida (PAGE).

I.4.1. 2D-PAGE

Esta metodología es adecuada para estudiar el efecto de sustancias antifúngicas sobre mohos, por ello ha sido de elección para este fin en diversos trabajos (Cagas et al. 2011; Carberry et al. 2012). Se basa en conseguir una dispersión de las proteínas que forman el proteoma en un gel en dos dimensiones, en la horizontal las proteínas se distribuyen en base a su punto isoeléctrico (pI) y en la vertical se distribuyen en función de su tamaño. De este modo se consigue una separación óptima de las proteínas, que una vez teñidas, se deben analizar con ayuda de software para obtener las diferencias cuantitativas relativas entre muestras tratadas y muestras control. Para identificar las proteínas es necesario extraerlas del gel, digerirlas y analizarlas, habitualmente por nanocromatografía líquida (nano-LC), para obtener su espectro a través de espectrometría de masas. Finalmente son identificadas comparando el espectro a través de bases de datos disponibles en internet. Esta técnica es robusta y reproducible, siendo una de las mayores ventajas que la caracterizan la capacidad de separar proteínas completas con todas sus modificaciones (Kniemeyer et al. 2011). Sin embargo su sensibilidad reducida es un inconveniente para el estudio de las proteínas de membrana y de aquellas que se encuentran en una cantidad muy pequeña(Rabilloud et al. 2009; Görg et al. 2009). Además, una limitación intrínseca de este método es que trabaja en un rango de pH, generalmente 4-7 (Carberry et al. 2012) o 3-11 (Lessing et al. 2007), que no cubre el proteoma completo, dado que existen proteínas que quedan fuera de este rango.

I.4.2. Métodos no basados en PAGE

Las técnicas basadas en cromatografía líquida acoplada a espectrómetro de masas (LC-MS/MS) permite la cuantificación relativa de proteínas difícilmente separables mediante 2D-PAGE, como proteínas de membrana, proteínas hidrofóbicas o proteínas con pI o peso molecular extremo (Speers and Wu 2007). Los análisis de proteómica basados en MS se realizan tras digestión de los analitos y su posterior fragmentación y el procesado de los datos obtenidos mediante programas informáticos. Esta metodología es capaz de identificar de forma habitual entre 1000 y 2000 proteínas en una muestra biológica (Kniemeyer et al. 2011).

Dentro de esta metodología existen dos aproximaciones, los ensayos con marcaje (*labelled*) o sin él (*label-free*). La principal diferencia radica en que en el primero de los casos las proteínas son marcadas, siendo habitual que se analicen conjuntamente por el LC-MS/MS, mientras que las técnicas basadas en label-free, los analitos no se marcan, y son analizados siempre por separado. Esta última técnica ha sido recientemente usada para investigar sobre el proteoma de *Aspergillus fumigatus* (Dolan et al. 2014; Owens et al. 2014) presentando la ventaja de cubrir un mayor número de proteínas identificadas que los métodos que incluyen marcaje (Li et al. 2012). Sin embargo presenta la limitación de que no es capaz de diferenciar entre cambios habituales en las proteínas, tales como isoformas, observándose simplemente una cuantificación total de la proteína, con lo que puede resultar una interpretación errónea con motivo de la no diferenciación entre isoformas habitualmente envueltas en procesos fisiológicos.

Existen diferentes equipos que llevan a cabo este tipo de análisis, como ya se ha citado, suelen estar compuestos en primer lugar por un equipo de LC que permite separar los componentes del analito. A continuación, pueden ir conectados en serie diversos detectores de espectrometría de masas, que van desde baja resolución (trampa de iones) hasta alta alta resolución (q-TOF y Orbitrap) que permiten mejorar la resolución y la precisión del análisis. Los equipos de alta resolución son aquellos que permiten separar partículas con relación m/z muy próximas. Estos espectrómetros pueden ser combinados para formar un equipo híbrido, que junto con otros dispositivos permite una gran resolución y precisión. El conjunto de espectros obtenidos son normalizados previamente al análisis con software específicos, como por ejemplo MaxQuant, una plataforma ampliamente usada para el análisis de estos datos. Por tanto, debido al diferente rango pI analizado, a la presencia de proteínas de membrana e hidrofóbicas así como la diferente sensibilidad de ambos análisis (Rabilloud et al. 2009; Görg et al. 2009), no es esperable una total reproducibilidad de los resultados a través de ambas metodologías. Sin embargo, las limitaciones de un análisis se ven complementadas con el otro. Empleando este

tándem se incrementa considerablemente el número de proteínas analizadas y por tanto se revela un mayor número de aquellas afectadas dentro del proteoma. El análisis del proteoma empleando este tándem incluye además las modificaciones de estas proteínas a nivel estructural que se ven alteradas por la variable en estudio, por ejemplo isoformas.

I.5. Métodos para evaluar el efecto de proteínas antifúngicas sobre mohos

Para el estudio de los fenómenos provocados por proteínas antifúngicas que puedan ser deducidos por los estudios de proteómica, existen diversos métodos, los cuales pueden servir como ensayos confirmatorios. La mayoría se basan en técnicas de visualización utilizando colorantes vitales a través de microscopía fluorescencia. De este modo se ha estudiado la actividad metabólica a través de la tinción FUN®1 (Molecular Probes, Eugene, OR, USA) (Kaiserer et al. 2003), que difunde a través del citoplasma tiñéndolo de verde en todas las células, sin embargo solo en las que mantienen la capacidad metabólica y la membrana íntegra provoca una tinción intravacuolar roja.

La permeabilidad celular ha sido evaluada con SYTOX Green (Molecular Probes) (Kaiserer et al. 2003; Moreno et al. 2006) que tiñe los ácidos nucleicos cuando penetra a través de membranas comprometidas pero no en aquellas intactas. Para determinar la deposición de quitina se ha empleado el calcofluor White o fluorescent brightener 28 (Sigma, St. Louis, MO, USA) (Binder et al. 2010; Galgóczy et al. 2013) que muestra fluorescencia cuando está unido a la quitina, y para estudiar la distribución de los núcleos se ha empleado Hoechst 33258 (Molecular Probes)(Kaiserer et al. 2003) ya que se une al ADN y lo tiñe específicamente. También se ha evaluado la inducción de estas proteínas sobre la formación de ROS a través de 2', 7' dichlorofluorescein diacetate (Sigma-Aldrich, St. Louis, MO, USA)(Kaiserer et al. 2003; Leiter et al. 2005) que se vuelve fluorescente al ser oxidado.

Por último, dado que este tipo de proteínas ha inducido fenómenos apoptóticos en mohos sensibles, se ha evaluado la viabilidad de las hifas empleando el Apoptosis Detection Kit (Sigma-Aldrich) que tiene capacidad para diferenciar entre hifas viables, apoptóticas y necróticas (Leiter et al. 2005; Galgóczy et al. 2013). La anexina V-FITC se une a la fosfatidilserina y la tiñe de verde cuando está traslocada al exterior de la membrana celular, lo que es una señal inequívoca de apoptosis. Las hifas viables no son teñidas, mientras que en células necróticas, tanto la anexina V-FITC como el ioduro de propidio (que penetra en las células la membrana cuya membrana está comprometida), tiñen la célula de color verde y rojo respectivamente. También se ha empleado una tinción conjunta con bromuro de etidio y naranja de acridina para conocer la viabilidad de las células (Baskić et al. 2006; Byczkowska et al. 2012), de modo que el

naranja de acridina penetra todas las células, se une a los ácidos nucleicos y las tiñe de verde, mientras que el bromuro de etidio solo penetra en aquellas cuya integridad de membrana está comprometida, y tras unirse a los ácidos nucleicos produce fluorescencia naranja.

I.6. Métodos de detección de micotoxinas

Existen diversos tipos de métodos analíticos, incluyendo biológicos, inmuno-enzimáticos y cromatográficos, presentando cada uno de ellos diferentes ventajas e inconvenientes. Los métodos biológicos se basan en la exposición de células u organismos vivos frente a muestras que pueden contener micotoxinas. Evaluando la viabilidad de las células u organismos frente a la exposición de muestras problemas se puede asociar la presencia de micotoxinas en estas muestras. Uno de los métodos biológicos habitualmente empleado para la detección de tóxicos producidos por mohos se basa en el empleo de microcrustáceos de la especie *Artemia salina* (López-Díaz et al. 2001; Núñez et al. 1996a; Núñez et al. 2007). A pesar de ser un método sencillo, de aportar información sobre la toxicidad y cuyo coste es muy bajo, tiene el inconveniente de que los microcrustáceos no son únicamente sensibles a micotoxinas, por lo que se pueden dar falsos positivos (Harwig and Scott 1971). Además, no tiene la capacidad de identificar que tóxico o tóxicos son los causantes de la muerte. Por tanto, esta metodología es adecuada para trabajar con un gran número de extractos procedentes de mohos, para testar su capacidad de producir toxinas, a modo de cribado previo a otros estudios más sensibles y específicos.

A pesar de que las micotoxinas se caracterizan por carecer de inmunogenicidad, actualmente existe disponibilidad de técnicas inmuno-enzimáticas para prácticamente todas las micotoxinas de interés (Köppen et al. 2010).. Existen variantes de estos métodos, tanto cualitativos como cuantitativos, llegando su sensibilidad a 2,5 µg/kg para el ELISA y a 1 µg/kg para FIA (Zheng et al. 2006). Se caracteriza por ser una reacción rápida, 0,5-2h, en la que un gran número de muestras pueden tener lugar y ser medidas simultáneamente. Sin embargo, presenta la limitación de que se necesita un análisis para cada una de las micotoxinas a determinar, ya que cada anticuerpo es específico para una micotoxina.

Las técnicas cromatográficas son las más sensibles debido a su gran capacidad para separar compuestos y sobre todo a los detectores que se emplean para identificar o cuantificar las micotoxinas. Estas técnicas analíticas se aplican a alimentos y piensos pudiendo ofrecer resultados en horas (Zheng et al. 2006)

La más sencilla de estas técnicas es la thin-layer chromatography (TLC), que se realiza e una placa metálica en la que se asienta la fase estacionaria formado por un gel de sílice a través del cual se separan los componentes del analito arrastrados por una fase móvil, constante en

composición a lo largo del análisis y que asciende por capilaridad. Finalmente, la placa se visualiza con luz ultravioleta que excita a algunas micotoxinas lo que permite revelar su presencia. Este método es rápido, barato y ofrece estimaciones cualitativas o semicuantitativas por inspección visual (Cigić and Prosen 2009), por tanto es capaz de testar un gran número de muestras con un coste muy bajo (Köppen et al. 2010). Sin embargo presenta limitaciones relacionadas con la cuantificación, siendo generalmente empleadas como técnicas cualitativas, además solo algunas micotoxinas son excitables con luz ultravioleta, por lo que para el análisis para aquellas que no presentan esta característica las placas deben tratarse con reactivos que permitan la visualización de las micotoxinas, lo que incrementa el coste económico y operacional del análisis. Debido a estas limitaciones y a la sensibilidad de otros métodos, los métodos de detección basados en TLC no suelen ser empleados en otros análisis que no sean *screenings* (Cigić and Prosen 2009).

La cromatografía de gases (CG) es adecuada para el análisis de compuestos térmicamente estables, de compuestos semipolares y apolares, volátiles y semivolátiles. La mayoría de las micotoxinas son moléculas pequeñas, no volátiles y polares que tienen que ser derivatizadas antes de ser analizadas por este método (Köppen et al. 2010), limitaciones que hacen que no sea la más empleada para analizar estos compuestos.

La metodología más comúnmente empleada para el análisis de un amplio rango de micotoxinas es la cromatografía líquida de alta resolución (HPLC) (Rodríguez et al. 2011; Rodríguez et al. 2012d; Andrade et al. 2014), a la que se le pueden acoplar diversos detectores. El detector ultravioleta es adecuado siempre y cuando la resolución del método cromatográfico sea muy alta, ya que no distingue entre diferentes compuestos que puedan coeluir y pasar por el detector simultáneamente. El detector de fluorescencia ofrece grandes ventajas en cuanto a coste del equipo, sin embargo su principal desventaja es que la mayoría de las micotoxinas tienen que ser derivatizadas para su detección. En general, como se ha citado anteriormente, todos los detectores requieren una buena separación cromatográfica de los compuestos, sin embargo este requisito no es necesario para el detector de masas (MS) ya que éste admite el solapamiento de algunos picos (Cigić and Prosen 2009). Una de las razones principales que han establecido al MS como método de referencia de detección de micotoxinas ha sido el desarrollo de dos tipos de fuentes de ionización: electrospray e ionización química a presión atmosférica (Köppen et al. 2010) que son capaces de ionizar tanto en forma positiva como en negativa, así como alternarse en la misma carrera cromatográfica, lo que radica en la mejor detección posible para todos los analitos. El desarrollo de la espectrometría de masas multietapa (MS^n) acoplado a HPLC ha permitido el aumento de la sensibilidad usando el modo *single reaction monitoring*

(SRM) para la determinación e identificación de micotoxinas seleccionadas tanto por sus pérdidas secuenciales características en su espectro como por el escaneo mejorado de iones producto para confirmar el patrón de fraccionamiento (Köppen et al. 2010).

También la electroforesis capilar (CE) también ha sido empleada para la detección de diferentes micotoxinas. La electroforesis capilar en zona (CEZ) se realiza en un capilar que contiene un tampón encargado de transmitir la corriente así como de contener el analito, a este capilar se le aplica una diferencia de potencial que hará desplazarse a través del capilar a los distintos componentes de analito dependiendo de su relación *e/z*. La electroforesis capilar electromicelar (MECE) contiene en el capilar un compuesto tensoactivo (habitualmente dodecilsulfato de socio) que forma micelas, que es ideal para compuestos "neutros". Esta última es la más empleada para el análisis de micotoxinas(Martín et al. 2004; Rodríguez et al. 2011; Rodríguez et al. 2012a; Luque et al. 2013). A ambas se le pueden acoplar los mismos detectores que al GC o al HPLC.

I.7. Transcriptómica.

La transcriptómica se encarga de estudiar y comparar el transcriptoma, o conjunto de ARN mensajero o transcriptos presentes en una célula, tejido u organismo en un momento y unas circunstancias específicas. Los cambios provocados por las proteínas antifúngicas sobre los mohos pueden verse reflejados en la expresión génica, ya que es previsible que los antifúngicos influyan sobre ésta, bien por bloqueo de su síntesis en determinados genes como por la inducción en otros.

El estudio de la expresión génica permite conocer la respuesta que un organismo está ofreciendo en un momento determinado frente a cualquier agente. Conocer el valor de la expresión génica de un organismo tratado con respecto al no tratado para una serie de genes determinados ofrece información acerca de cómo el organismo se está viendo afectado por agente en cuestión y de cómo el organismo responde a dicho agente.

I.7.1. Métodos moleculares para la cuantificación de expresión génica

Entre las metodologías que se emplean de forma habitual para la cuantificación de expresión génica destacan los microarrays o chips y la PCR en tiempo real (qPCR). La primera es muy útil para la monitorización de múltiples genes simultáneamente, ofreciendo resultados globales en cuanto a cambios en la expresión abarcando todo el genoma. Sin embargo su principal desventaja es que el genoma a investigar debe haber sido secuenciado previamente. Cuando sólo se desea conocer la variación en la expresión de una serie de genes concretos o el

genoma completo no es conocido, pero sí los genes implicados en alguna ruta de interés, es habitual el uso de la RT-qPCR, en el que como paso previo se convierte el ARNm en ADN complementario (ADNc) mediante la enzima transcriptasa inversa. Este método no sólo permite conocer el desarrollo de la reacción en tiempo real, sino que además permite la cuantificación de la cantidad de ADN diana presente en la muestra. Además este tipo de técnicas presenta mayor sensibilidad y rapidez, y reduce la manipulación de las muestras (Heid et al. 1996)

I.7.2. Cuantificación de la expresión génica

Por lo tanto, mediante la RT-qPCR puede conocerse la cantidad de ARNm diana (tras convertirlo a ADNc) forma de presente en las muestras, y por lo tanto estudiarse la posible alteración de la expersión génica por la acción de proteínas antifúngicas. Para calcular su expresión existen principalmente dos métodos, cuantificación absoluta y cuantificación relativa.

La primera se basa en la cuantificación de las copias de genes diana presentes en el ADNc implicados en alguna ruta metabólica de interés. Mientras que el segundo se basa en la cuantificación de genes diana una vez realizada una normalización, ya sea con la expresión de otros genes que no se ven alterados por el tratamiento aplicado, denominados controles endógenos o con cantidad de ARN. Es muy recomendable que el gen elegido como control endógeno esté correctamente validado para cada experimento, de modo que la expresión génica no se vea afectada por el tratamiento empleado (Livak and Schmittgen 2001). Además son necesarios calibradores internos, que consisten en muestras similares pero que no son sometidas al tratamiento de estudio. De este modo se obtendrá la cuantificación relativa de la expresión génica en relación al calibrador interno.

Para ello existen dos alternativas, denominados método $2^{-\Delta\Delta Ct}$ y método $2^{-\Delta Ct}$, en función de los valores de eficiencia de las curvas estándar obtenidos previamente (Livak and Schmittgen 2001). En el primero las eficiencias de los genes diana y endógeno deben ser similares, no pudiendo ser las diferencias mayores del 10%, (Schmittgen and Livak 2008) y estar comprendidas entre 80 y 110%, lo que se corresponde con unos valores de pendiente de la recta de entre -3.1 y -3.6, además de que su valor de coeficiente de correlación (R^2) debe ser ≥ 0,98 según ha sido descrito (Suanthie et al. 2009). En este método, como se ha indicado anteriormente se emplea una normalización a través de un gen endógeno. Mientras que el método $2^{-\Delta Ct}$ se emplea cuando las eficiencias de las curvas estándar de ambos genes no son similares. En este caso la normalización se lleva a cabo a través de la cantidad de ARN añadida a la reacción de ADNc (Livak and Schmittgen 2001).

II. OBJETIVOS

II. OBJETIVOS

El presente trabajo se encuadra en la línea de investigación sobre la obtención y caracterización de proteínas antifúngicas producidas por mohos aislados de alimentos, desarrollada por el grupo de Higiene y Seguridad Alimentaria dentro del Instituto Universitario de Investigación de la Carne y Productos Cárnicos de la Universidad de Extremadura. Dado que en los alimentos madurados con humedad intermedia o baja, como quesos y derivados cárnicos se desarrollan mohos que pueden contribuir a las características del producto final, pero que también pueden alterarlo y producir micotoxinas, es necesario disponer de medidas para controlar la población fúngica superficial. Los métodos eficaces para lograr este objetivo resultan poco adecuados para este tipo de alimentos. Una de las estrategias más prometedoras es la utilización de proteínas con efecto antifúngico solas o conjuntamente con microorganismos inhibidores que puedan potenciar mutuamente su actividad antagonista frente a mohos toxigénicos. Además para diseñar adecuadamente su utilización resulta conveniente conocer tanto el mecanismo de acción de estas proteínas antifúngicas, como los posibles mecanismos de resistencia de los mohos toxigénicos.

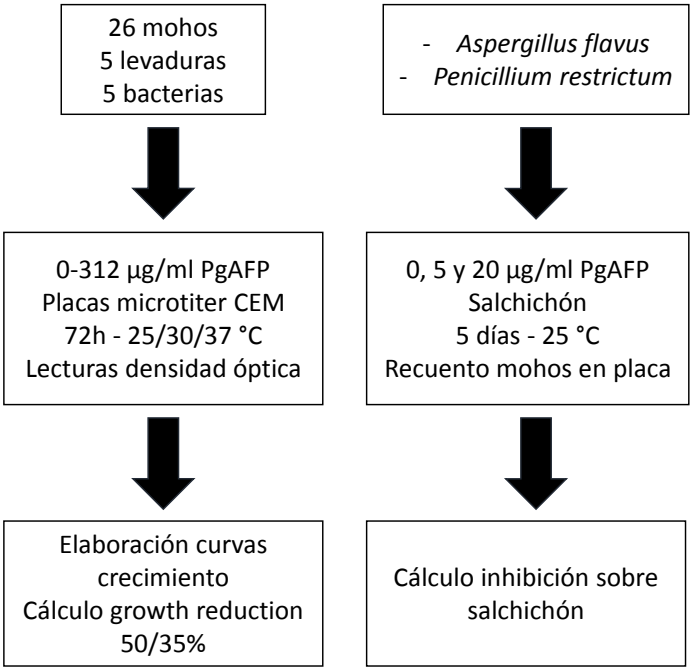
El objetivo fundamental del trabajo ha sido estudiar el efecto antifúngico y el mecanismo de acción de la proteína PgAFP producida por *Penicillium chrysogenum* asilado de jamón curado frente a mohos toxigénicos habituales en alimentos madurados. Para lograr este objetivo se plantearon los siguientes objetivos parciales:

- Establecer el espectro de inhibición de la proteína PgAFP frente a microorganismos habituales en alimentos madurados.
- Evaluar el efecto de PgAFP utilizada sola o en combinación con *Debaryomyces hansenii* o *Pedicoccocus acidilactici* sobre el crecimiento de mohos y la producción de micotoxinas.
- Estudiar el mecanismo de acción de PgAFP en mohos sensibles utilizando técnicas de proteómica comparativa y ensayos metabólicos y de viabilidad.
- Conocer la respuesta de mohos resistentes frente al tratamiento con PgAFP utilizando técnicas de proteómica comparativa y ensayos metabólicos y de viabilidad.
- Investigar el efecto de la presencia de calcio en el medio sobre la capacidad de inhibición de PgAFP en mohos sensibles utilizando técnicas de proteómica comparativa y ensayos metabólicos y de viabilidad.

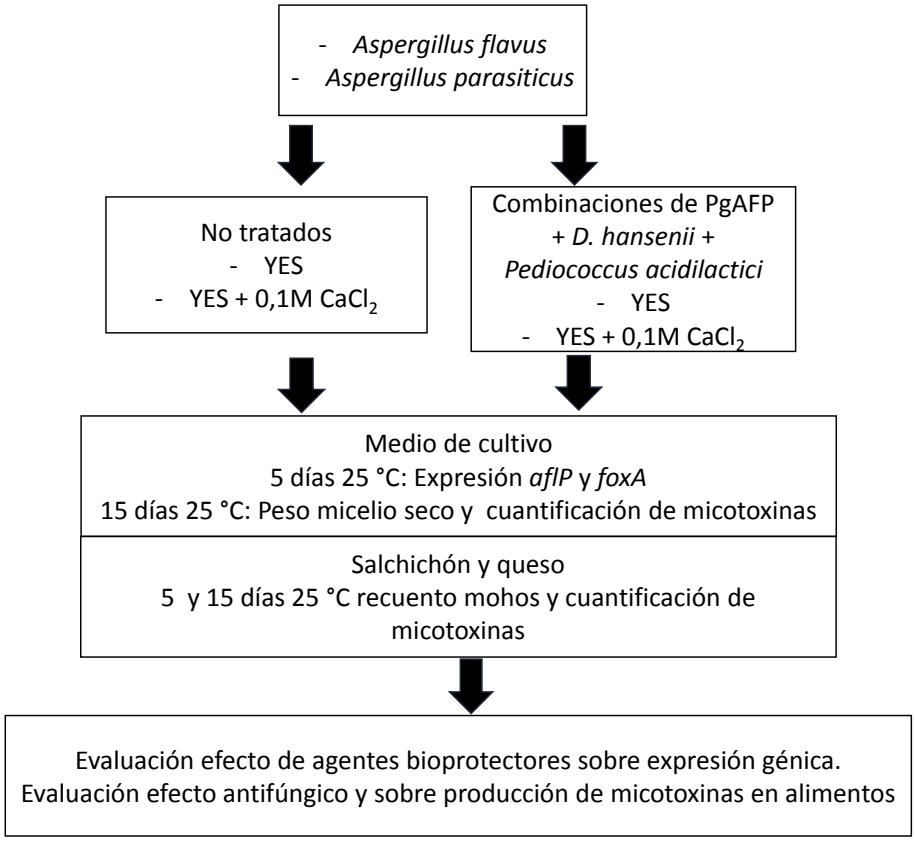
III. MATERIAL Y MÉTODOS

III.1. Diseño experimental

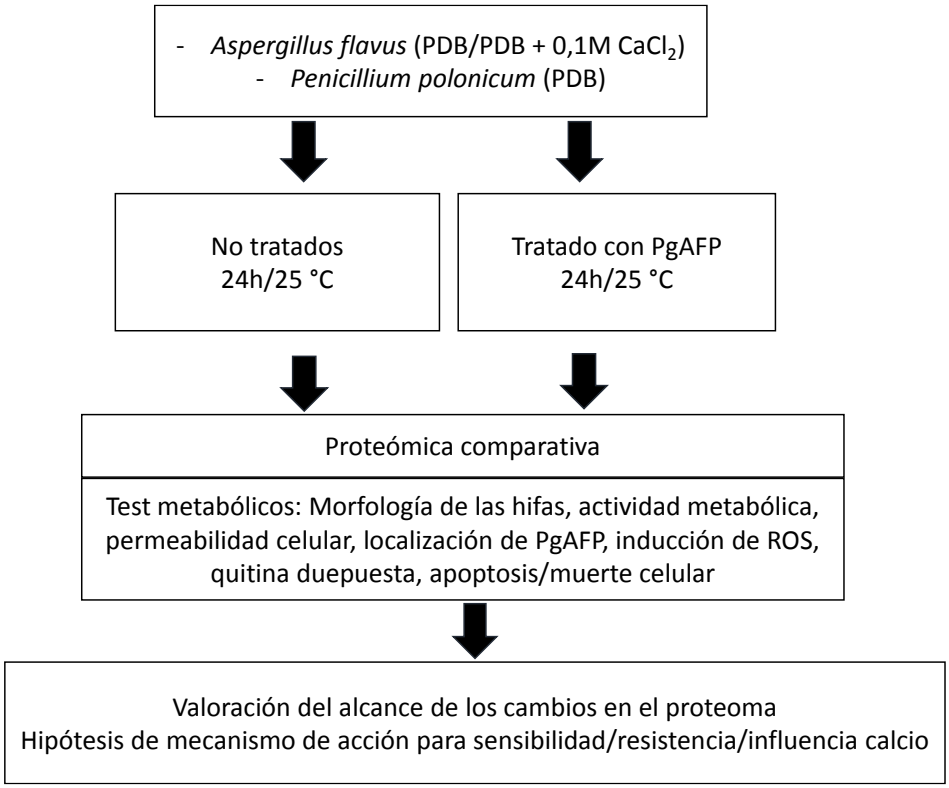
III.1.1. Estudio del espectro de inhibición de PgAFP



III.1.2. Estudio de la influencia de PgAFP sobre la síntesis de micotoxinas



III.1.3. Estudio del mecanismo de acción de PgAFP



III.2. Reactivos químicos

Los productos químicos empleados en el presente trabajo fueron calidad reactivo y suministrados por las firmas comerciales PANREAC (Castellar del Vallès, España), MERCK (Darmstadt, Alemania), Scharlau (Setmenat, España) y SIGMA (St. Louis, EEUU).

Los azúcares empleados fueron suministrados por la firma comercial SIGMA

Los colorantes fluorescentes FUN-1, SYTOX Green y Hoechst 33258 (Molecular Probes, Eugene, EEUU) fueron suministrados por Invitrogen y los colorantes fluorescentes 2', 7' dichlorofluorescein diacetate, apoptosis detection kit y fluorescent brightener 28 por SIGA. El marcaje de la proteína PgAFP con FITC fue realizado por la empresa DareBio S.L. (Elche, España).

Los reactivos SYBR green, ROX y el kit Prime Script™ RT reagent (Perfect Real Time) fueron provistos por Takara Bio Inc. El kit empleado para la extracción de ARN fue RNeasy® Plant Mini kit) (Quiagen, Hilden, Alemania) y el tratamiento con DNase I, RNase-free (Fermentas, St Leon, Alemania)

Los cebadores utilizados en las pruebas de PCR fueron suministrados por la empresa Biomol S.L. (Sevilla, España)

La quitinasa de *Streptomyces griseus* empleada fue adquirida de SIGMA (St. Louis, EEUU).

III.3. Medios de cultivo

Los medios de cultivo elaborados, así como los componentes utilizados procedieron de las casas comerciales OXOID (Unipath, Reino Unido), SCHARLAU (Setmenat, España), CULTIMED y MERCK (Darmstadt, Alemania).

En los diferentes ensayos realizados se utilizaron los siguientes medios:

Caldo extracto de malta (CEM)

Extracto de malta	20 g
Glucosa	20 g
Peptona	20 g
Agua destilada	1000 ml

Se esteriliza a 121°C durante 15 minutos y se ajusta al pH deseado

Caldo patata dextrosa (PDB)

Patata dextrosa	24 g
Agua destilada	1000 ml

Se esteriliza a 121°C durante 15 minutos y se ajusta al pH deseado

Agar patata dextrosa (PDA)

Patata dextrosa	24 g
Agar bacteriológico	20 g
Agua destilada	1000 ml

Se esteriliza a 121°C durante 15 minutos y se ajusta al pH deseado

Caldo yeast extract sucrose (YES)

Extracto de levadura	20 g
Sacarosa	125 g
Agua destilada	1000 ml

Se esteriliza a 121°C durante 15 minutos y se ajusta al pH deseado

III.4. Microorganismos

Se emplearon los siguientes mohos procedentes de la Colección Española de Cultivos Tipo (CECT, Valencia, España), del Centraalbureau voor Schimmelcultures (CBS, Utrecht, Holanda), o de la colección microbiana de Higiene y Seguridad Alimentaria, Universidad de

Extremadura (Cáceres, España): *Penicillium chrysogenum* (RP42C) CECT 20922, *Aspergillus awamori* CBS 101.702*, Aspergillus carbonarius* CECT 20384, *Aspergillus flavus* CECT 2687, *Aspergillus fumigatus* CBS 192.65, *Aspergillus ochraceoroseus* CBS 101.887*, Aspergillus ochraceus* CECT 2092, *Aspergillus oryzae* CECT 2095, *Aspergillus parasiticus* CECT 2682, *Aspergillus tamarii* CBS 109.63, *Aspergillus tubingensis* CECT 20545, *Aspergillus tubingensis* CECT 20932, *Aspergillus versicolor* CECT 2664, *Aspergillus westerdijkiae* CECT 2948, *Penicillium aurantiogriseum* CECT 2918, *P. chrysogenum* Pg222*, Penicillium commune* Pc131*, Penicillium commune* Pc332*, Penicillium echinulatum* Pe321, *Penicillium expansum* CECT 2280, *Penicillium griseofulvum* CECT 2919, *Penicillium nalgiovense* Pj261, *Penicilliumnordicum* CBS 110.769, *Penicillium polonicum* Pp51, *Penicillium restrictum* Pr341, *Penicillium solitum* Ps321, *Penicillium verrucosum* AB11C, *Rhizopus oryzae* CBS 607.68*Aspergillus tubingensis* CECT 20932. La cepa de levadura *Debayomyces hansenii* 253H procedió de la Colección Española de Cultivos Tipo (CECT, Valencia, España) y la cepa de *Pediococcus acidilactici* (Fargo-35) empleada fue suministrada por la empresa Laboratorios Amerex (Madrid, España)

III.5. Equipos

Los medios de cultivo y otras pesadas rutinarias se realizaron en una balanza KERN (Balingen, Alemania) mod. 440-33 con precisión de 0,01g y las de precisión en una balanza Sartorius (Goettingen, Alemania) mod. LA310S con precisión de 0,1mg.

Las medidas de pH se realizaron en un pH-metro CRISON (Barcelona, España) mod. Basic 20

La esterilización de medios de cultivo, soluciones y material de laboratorio se realizó en un autoclave SELECTA (Barcelona, España) mod. Pesoclave 75.

Para la preparación de medios de cultivo se utilizaron placas calefactoras con agitación SELECTA (Barcelona, España) mod Agimatic N y un baño termostático SELECTA (Barcelona, España) PRECISTERM mod S-140.

Los microorganismos se incubaron en estufas refrigeradas VELP SCIENTIFICA mod. FOC 225 E, en incubadora orbital CERTOMAT^{TM} IS Sartorius (Goettingen, Alemania), las esporas extraídas se conservaron en un congelador THERMO SCIENTIFIC mod. Forma 900 series, a -80 °C.

Las muestras de ADN, PgAFP, algunos reactivos que lo requerían y los extractos clorofórmicos o de acetonitrilo, previamente a su análisis, se almacenaron a -20 °C en un congelador vertical whirpool modelo 6th sense.

Para la homogeneización de muestra en tubos se utilizó un agita-tubos VELP SCIENTIFICA (Usmate, Italia) mod. Vortex mixer.

Para la agitación de las muestras en la extracción de micotoxinas se empleó un agitador Heidolph (Kelheim, Alemania) mod Unimax 2010.

Las centrifugaciones fueron realizadas en una microcentrífuga refrigerada mod. 5417 C/R de EPPENDORF (Hamburgo, Alemania)

El tratamiento por calor de las muestras se llevó a cabo en un bloque térmico mod. TEMBLOC de SELECTA (Barcelona, España)

Todas las manipulaciones que requerían condiciones de esterilidad, se realizaron en campanas de flujo laminar TELSTAR (Tarrasa, España) mod. AV-30/70.

La filtración de los extractos clorofórmicos se llevó a cabo en una campana de extracción de gases CRUMA (El Prat de Llobregat, España) mod. 1200.

Para la esterilización de la proteína se emplearon filtros con adaptador a jeringa, de acetato de celulosa estériles, tamaño de poro 0,22µm (Fisherbrand, Fisher scientific, Waltham, EEUU). Los extractos clorofórmicos se filtraron a través de filtros de 0,45 µm (Fisherbrand, Fisher scientific, Waltham, EEUU).

El agua destilada se obtuvo utilizando un destilador de USF mod. PURELAB pRO, (Fisher scientific, Waltham, EEUU).

Las placas estériles de 96 pocillos de fondo plano y sus correspondientes tapas empleadas en los diversos ensayos fueron de la marca Deltalab (Rubí, España).

Las cuantificación de fluorescencia en placas multipocillo se realizó en un lector de placas TECAN mod. Infinite M 2000 (Männedorf, Suiza).

Las lecturas de absorbancias de las placas multipocillo para la cuantificación del desarrollo fúngico se llevaron a cabo en un lector de MERCK (Darmstadt, Alemania) mod. MIOS MR 7000.

Las lecturas de absorbancia para la cuantificación proteica se realizaron en espectrofotómetro HitachiU-2000(Tokio, Japón).

El recuento de esporas se realizó en una cámara de Thoma de la marca Brand y un microscopio óptico Nikon SE. (Tokio, Japón)

Para la visualización de hifas con luz visible y sometidas a tinciones con colorantes fluorescentes se empleó un microscopio de fluorescencia Eclipse E200 equipado con una cámara digital DS-Fi2 (Nikon, Tokio, Japón)

La filtración de medios de cultivo y de tampones se realizó con ayuda de una bomba de succión LABOPORT (Trenton, USA) mod. KNF Lab, mediante un dispositivo de filtración de cristal y a través de filtros de membrana de acetato de celulosa de 47 mm de diámetro con poros de 8 µm, 1,2 µm, 0,45 µm y 0,22 µm (Sartorius, Goettingen, Alemania).

Para la evaporación de solventes orgánicos se empleó un rotavapor modelo VV2000 (Heidolph, Kelheim, Alemania)

La separación y purificación de los compuestos de naturaleza proteica con actividad antifúngica se llevó a cabo en un cromatógrafo líquido para la purificación rápida de proteínas (FPLC) mod. $ÄKTA_{FPLC}$ con un colector de fracciones mod. FRAC-950 (Amersham Biosciences, Uppsala, Suecia) . El análisis de los resultados obtenidos se realizó con el programa informático UNICORN versión 4.12. Se utilizaron columnas de sefarosa HiTrap™SP HP de intercambio catiónico, y columnas de filtración en gel HiLoad 26/60 Superdex™ 75, (Amersham Biosciences, Uppsala, Suecia).

Para la extracción proteica del micelio, se empleó una sonda de sonicación (Bandelin Sonopuls, Berlin, Alemania), el total de proteínas extraídas fue separado en base al punto isoeléctrico mediante tiras Immobiline Dry strips (IPG strip; Amersham Biosciences, Uppsala, Suecia) de 7 y 13 cm, mediante un sistema de isoelectroenfoque IPGphor™ ambos provistos por GE Healthcare Life sciences (Freiburg, Alemania).

Las electroforesis de proteínas se realizaron en un Mini-PROTEAN System (Bio Rad, Hercules, EEUU) las de una dimensión y en Protean Xi-II Cell (Bio Rad, Hercules, EEUU) las de dos dimensiones.

La evaporación del líquido que contenían las proteínas digeridas previamente a su análisis espectrométrico se realizó en un DNA Speed Vac Concentrator (Thermo Fischer Scientific, Austin, EEUU). Las muestras fueron filtradas a través de filtros de centrífuga de 0,22 µm (Agilent Technologies, Dublín, Irlanda). El análisis espectrométrico se llevó a cabo mediante un Ion Trap LC-Mass Spectrometer 6340 Model (Agilent Technologies, Dublín, Irlanda) usando ionización mediante electrospray. Las muestras fueron cargadas sobre un Zorbax 300 SB C-18 Nano-HPLC Chip (150 mm x 75 µm).

Para los ensayos de proteómica libre de marcaje se realizó un desalado previo al análisis mediante C18 ZipTips® (Millipore, Darmstadt, Alemania) para ser analizados mediante un

espectrómetro de masas Q-Exactive acoplado a Dionex RSLCnano (Thermo Scientific, Waltham, EEUU).

Las concentraciones de ADN y ARN fueron medidas con un biofotómetro NanoDrop 2000c (Thermo Scientific, Waltham, EEUU).

El ARN fue transcrito a ADNc en un termociclador Mastercycler epgradient (Eppendorf AG, Hamburgo, Germany).

Las reacciones de q-PCR se llevaron a cabo en un equipo ViiATM 7 Real-Time PCR System (Applied Biosystems, Foster City, EEUU).

El análisis de micotoxinas se realizó mediante cromatografía líquida de alta resolución y detección mediante espectrometría de masas utilizando un uHPLC dionex ultimate 3000 pnmp (Thermo Scientific, Waltham, EEUU), acoplado al espectrómetro de masas de tampa iónica Amazon (Bruker Daltonics, Bremen, Alemania). Para la cromatografía se empleó una columna C18 (10cm de longitud, 2,1mm diámetro interno y 2µm de tamaño de partícula) como fase estacionaria.

III.6. Software

Quant/Data analysisde Bruker se empleó para determinar la cantidad de micotoxinas que había en las muestras.

III.7. Páginas webs y herramientas empleadas

Para el estudio proteómico, las manchas seleccionadas de los geles 2D se identificaron utilizando MASCOT MS/MS ion search (http://www.matrixscience.com/cgi/search_form.pl?FORMVER=2&SEARCH=MIS). La búsqueda de proteínas homólogas y ortólogas se realizó en la base de datos del NCBI (National Centre for Biotechnology Information, www.ncbi.nlm.nih.gov/guide/proteins/). Para determinar la ruta metabólica en la que se encontraban involucradas las proteínas identificadas se utilizó el KEGG (Kyoto Encyclopedia of Genes and Genomes, www.genome.jp/kegg/). Para la búsqueda de secuencias genéticas y el diseño de cebadores se utiliz´la base de datos del NCBI (http://www.ncbi.nlm.nih.gov/gene/) y algunas de sus herramientas como “Pick primers”.

El tratamiento estadístico se llevó a cabo mediante el programa IBM SPSS v.22 (www-03.ibm.com/software/products/es/spss-stats-standard)

III.8. Métodos analíticos

III.8.1. Producción de PgAFP

La proteína PgAFP se obtuvo tras cultivar 10^7 esporas de *P. chrysogenum* RP42C en 500 ml de PDB a pH 4,5 durante 15 días a 25ºC. Tras a incubación se procedió a separar el micelio y filtrar el medio a través de una membrana con tamaño de poro de 0,22 µm. Un volumen de 450 ml del medio de cultivo filtrado se sometieron a cromatografía líquida rápida de proteínas (FPLC) mediante una columna de intercambio catiónico, y a continuación la fracción que contenía a PgAFP se volvió a someter a cromatografía utilizando una columna de filtración en gel como describe (Acosta et al. 2009). La proteína purificada se esterilizó por filtración utilizando una membrana de 0,22 µm, Fisher scientific, Waltham, EEUU) de diámetro, se determinó su concentración por el método de (Lowry et al. 1951) y se almacenó a -20 °C hasta su uso.

III.8.2. Ensayos de inhibición

Los ensayos de inhibición se realizaron en placas multipocillo, inoculando en cada pocillo 10^5 esporas en 200 µl de PDB. Las placas se incubaron a 25 °C durante 96 h en condiciones estáticas. Para probar la actividad antifúngica en diferentes ensayos se utilizaron concentraciones de la proteína PgAFP entre 1,17 y 312 µg/ml. En todos los ensayos se incluyeron controles no tratados con PgAFP de los mohos estudiados. Cada ensayo se realizó por sextuplicado y el desarrollo fúngico se estimó mediante la densidad óptica de lospocillos inoculados medida a 550 nm cada 24 horas.

III.8.3. Extracción de proteínas del micelio

La extracción del total de proteínas del micelio de los mohos se realizó por triplicado inoculando las cepas en 50 ml de PDB en presencia (10 µg/ml) o ausencia de PgAFP. Los cultivos se incubaron en agitación (200 rpm) durante 24 horas a 25 °C. El micelio fue recogido, filtrado a través de un dispositivo miracloth (Merck Millipore, Darmstadt, Alemania), lavado con PBS y lisado como se ha descrito previamente (Carberry et al. 2006). El lisado fue centrifugado (10.000 x g; 30 min) para eliminar los restos de micelio y el sobrenadante fue recogido. La concentración total de proteínas fue calculada mediante el método de Bradford, utilizando el Kit proporcionado por Bio-Rad y leyendo a 595 nm: La calidad fue chequeada mediante electroforesis en gel de poliacrilamida (SDS-PAGE) de una dimensión.

Los minigeles de poliacrilamida se elaboraron utilizando los reactivos que se recogen en las tablas II1 y II2.

Tabla II1. Proporción de reactivos utilizados para la elaboración de los geles de poliacrilamida de separación (12% acrilamida).

Número de mini geles	**5**
1,5 M Tris-HCl, pH 8,3	7 ml
10% Dodecilsulfato sódico (SDS)	280 µl
30% Acrilamida/0,8% Metilen bis acrilamida	11,3 ml
Agua destilada	9,3 ml
10% Amonio persulfato	100 µl
TEMED	23 µl

Tabla II2. Proporción de reactivos utilizados para la elaboración de los geles de poliacrilamida de concentración (4% acrilamida).

Número de mini geles	**5**
0,5 M Tris-HCl, pH 6,8	4 ml
10% Dodecilsulfato sódico (SDS)	160 µl
30% Acrilamida/0,8% Metilen bis acrilamida	1,5 ml
Agua destilada	9,6 ml
10% Amonio persulfato	150 µl
TEMED	15 µl

En cada pocillo del gel se depositaron 20 µg de proteínas, se le aplicó un voltaje de 80 V durante la primera hora, posteriormente se subió hasta 120 V y la electroforesis se dio por finalizada una vez que el frente llegó a la parte baja del gel. Una vez finalizada la carrera, el gel se tiñó durante 16 h con una solución compuesta por: 600 ml de agua destilada, 100 ml de ácido acético glacial, 300 ml de metanol y 1 g de comassie® brilliant blue R. Posteriormente, el gel se destiñó con una solución compuesta por 600ml de agua destilada, 100 ml de ácido acético glacial y 300 ml de metanol hasta que las bandas eran visibles sin ruido de fondo, y finalmente se lavó con agua destilada tres veces.

Una vez comprobada la calidad de las proteínas el lisado precipitado con ácido tricloroacético/acetona (Carpentier et al. 2005) para obtener el extracto con el que se llevaron a cabo dos ensayos proteómicos.

III.8.4. Análisis con 2D-PAGE

Un total de 250 µg de proteínas de cada extracto se resuspendieron en 200 µl de isoelectric focusing buffer (9,6 g de urea, 3,04 g de tiourea, 24 mg de Tris-base, 0,8 ml de chaps y 0,2 ml de Triton X-100, llevado a 20 ml de agua destilada) y se cargaron sobre las IPG strips. A continuación se realizó un electroisoenfoque y una electroforesis como se ha descrito previamente (Carberry et al. 2006). Los geles resultantes (3 réplicas biológicas y dos réplicas técnicas por tratamiento) fueron teñidas con Azul de Coomassie Coloidal, escaneadas y analizadas usando el software ProgenesisTM SameSpot (TotalLab, Newcastle, UK) (O'Keeffe et al. 2013; Collins et al. 2013; Owens et al. 2014). Previamente al análisis comparativo la intensidad de las manchas fue normalizada por el citado software para corregir cualquier variación en la cantidad de proteínas cargada, la tinción/destinción o la adquisición de imágenes. Las manchas que mostraron diferencias significativas en su intensidad ($p < 0,05$, con un cambio cualitativo ≥ 1,5) fueron recogidas y se realizó una digestión de las proteínas dentro del propio gel como se ha descrito previamente (Shevchenko et al. 2006). Los spots seleccionados fueron desteñidos por adición de 100 mM de amonio bicarbonato:acetonitrilo (1:1 v/v) durante 30 min. Se añadieron 500 µl de acetonitrilo a las muestras para deshidratar las piezas de gel recogidas, una vez deshidratadas el acetonitrilo se retiró y se añadieron 50 µl de tripsina (13 ng/µl). Las muestras fueron incubadas a 4 °C durante 2 h seguidos de una incubación overnight a 37 °C. Las muestras fueron sonicadas durante 10 minutos y el sobrenadante digerido fue transferido a tubos limpios para secarlo completamente con un DNA Speed Vac Concentrator, posteriormente se resuspendió cada muestra en 20 µl de ácido fórmico 0,1%. Las muestras se filtraron a través de filtros para centrífuga 0,22 µm. Las muestras se analizaron con un 6340 Model Ion Trap LC-Mass Spectrometer.. Para ello las muestras se cargaron sobre un Zorbax 300 SB C-18 Nano-HPLC Chip (150 mm x 75 µm) y se sometieron a un flujo de 4 µl/min con 0,1% (v/v) de ácido fórmico. Los péptidos eluídos fueron ionizados mediante electrospray y analizados por espectrometría de masas. El análisis de MSn fue llevado a cabo en los tres iones precursores de cada péptido, seleccionados automáticamente por el espectrómetro de masas. MASCOT MS/MS ion search, la base de datos NCBI (National Centre for Biotechnology Information, www.ncbi.nlm.nih.gov/guide/proteins/) y el KEGG (Kyoto Encyclopedia of Genes and Genomes, www.genome.jp/kegg/) se usaron para identificar las proteínas y su función.

III.8.5. Análisis con proteómica libre de marcaje

Para la cuantificación por proteómica libre de marcaje los lisados precipitados de tres replicas biológicas por tratamiento fueron resuspendidas en urea 8 M. Después de una reducción con dithiothreitol y alquilación mediada por ácido iodoacético (Owens et al. 2014), se añadió tripsina (grado secuenciación) combinada con ProteaseMax. Las muestras digeridas fueron desaladas previamente al análisis con C18 ZipTips® (Millipore, Darmstadt, Germany). de De cada muestra digerida se analizó 1 µg a través de un espectrómetro de masas Q-Exactive acoplado a un Dionex RSLCnano (Thermo Scientific, Waltham, MA, USA). La cromatografía líquida se llevó a cabo utilizando un gradiente desde 4 al 35 % B (A: 0,1 % AF, B: 80 % Acetonitrile, 0,1 % AF) durante más de 2 h, y los datos fueron recogidos usando un método Top15 para MS/MS scans (O'Keeffe et al. 2014; Dolan et al. 2014). La comparativa en la abundancia del proteoma así como el análisis de los datos se llevó a cabo con el software MaxQuant (Version 1.3.0.5; www.maxquant.org/downloads.htm; (Cox and Mann 2008), con Andromeda usado para la búsqueda en la base de datos y Perseus (Version 1.4.1.3) empleado para organizar los datos. Como modificación fija fue establecida la carbamidometilación de cisteínas, mientras que como modificaciones variables fueron fijadas la oxidación de metioninas y acetilación de N-terminales, para la identificación de proteínas mediante los citados softwares. . El máximo péptido/proteína false discovery rates (FDR) fue fijado en el 1 % basado en la comparación con una base de datos reversa. El algoritmo del análisis cuantitativo libre de marcaje fue usado para generar intensidades espectrales normalizadas e inferir la abundancia relativa de proteínas (Luber et al. 2010). Las proteínas fueron mantenidas en el análisis final si eran detectadas en al menos dos réplicas de al menos un tratamiento y las establecidas como contaminantes fueron eliminadas. El análisis cuantitativo fue llevado a cabo usando un t-test para comparar pares de muestras. Debido a la alta sensibilidad y un mayor rango dinámico que el análisis proteómico basado en geles, solo las proteínas con un cambio en cantidad ≥ 2 ($p < 0,05$) fueron incluidas en los resultados cuantitativos (O'Keeffe et al. 2014; Dolan et al. 2014). Los análisis cualitativos fueron llevados a cabo para detectar proteínas que fueron encontradas en al menos dos réplicas de una muestra en particular, pero no detectable en la comparación con el otro tratamiento.

III.8.6. Evaluación de la permeabilidad

Los mohos fueron cultivados a 25 °C durante 24 horas en presencia o ausencia de PgAFP de forma similar a la descrita en el epígrafe Ensayos de inhibición (III.8.2). Después de la incubación se añadió a los pocillos SYTOX Green para alcanzar una concentración final de 0,2 µM. La fluorescencia emitida fue medida en el minuto 10, 30 y 210 tras la adición de este

reactivo. Se empleó una longitud de onda de excitación de 480 nm (slit, 5 nm) y emisión de 530 nm (slit, 10 nm).

III.8.7. Morfología de las hifas

Las cepas fueron cultivadas en tubos que contenían 300 µl of PDB a 25 °C durante 24 h tanto en presencia y en ausencia de PgAFP. El micelio fue recuperado por centrifugación y observado por microscopía óptica.

III.8.8. Actividad metabólica

Para evaluar la actividad metabólica los mohos se cultivaron, tanto en presencia como en ausencia de PgAFP. Posteriormente el micelio fue lavado con 10 mM HEPES (pH 7,5) antes de teñir con 100µl del colorante vital FUN-1 durante 30 min a 25 °C (Kaiserer et al. 2003). Las hifas teñidas fueron examinadas y fotografiadas mediante microscopía de fluorescencia, utilizando una longitud de onda de excitación 482/35 y 562/40 nm.

III.8.9. Tinción de quitina

Las esporas fueron inoculadas en placas de petri que contenían 10 ml PDB e incubados en presencia y ausencia de PgAFP a 25 °C durante 24 h (Harris et al. 1994). El micelio se fijó y tiñó durante 5 minutos con *fluorescent brightener* 28 y fue lavado antes de ser visualizada la cantidad de quitina mediante microscopía de fluorescencia con una longitud de onda de excitación de of 387/11 nm.

III.8.10. Tinción del núcleo

Para visualizar la distribución de los núcleos en los mohos tratados y no tratados con PgAFP, los cultivos se tiñeron con 1.6 µM del colorante Hoechst 33258 durante 30 min a 25 °C (Kaiserer et al. 2003). Este compuesto fluorescente tiñe la doble cadena de ADN, y permite la visualización de los núcleos a través de microscopía de fluorescencia utilizando una longitud de onda de excitación de 387/11 nm.

III.8.11. Localización de PgAFP en los mohos tratados

PgAFP fue marcada con FITC por DareBio S.L. (Elche, Spain). Para ello, 100 µl de 20 mM FITC (Anaspec, Fremont, CA, USA) en dimethil sulfóxido fueron añadidos a 4 ml de PgAFP (369 µg/ml). La mezcla se dejó durante 8 h a temperatura ambiente en oscuridad. Posteriormente fueron añadidos 100 µl de 0,8 M Tris-HCl (pH 8,0) para llegar a una concentración final de 20 mM de Tris-HCl, y fue dializado frente a PBS. Para determinar el lugar de fijación de PgAFP las

cepas fueron cultivadas durante 24 h a 25 °C en presencia de 20 μg/ml de PgAFP marcado con FITC. A las 6 y a las 24 h las hifas fueron lavadas dos veces con PBS y visualizadas por microscopía de fluorescencia 482/35 nm. Como control, se llevó a cabo un ensayo adicional con FITC-PgAFP previamente tratado a 121 ºC durante 15 min fue. Además, para comprobar que el marcaje no inactivaba la proteína, se realizó un ensayo de inhibición con 20 μg/ml de PgAFP marcada con FITC.

III.8.12. Detección de especies reactivas de oxígeno (ROS)

La inducción de producción de ROS por parte de PgAFP sobre diferentes cepas fue evaluado usando el 2', 7' diacetato de diclorofluoresceina como describe (Kaiserer et al. 2003) con algunas modificaciones. Los mohos fueron cultivados con 20 μM del citado colorante en presencia y ausencia de PgAFP durante 2 h a 25 °C, para ser observadas posteriormente mediante microscopía de fluorescencia con una longitud de onda de excitación de 482/35 nm.

III.8.13. Naranja de acridina (NA)/bromuro de etidio (BE) doble tinción

Las cepas de mohos cultivadas a 25 °C durante 24 h tanto en presencia y ausencia de PgAFP fueron teñidas con 4 μg/ml de NA/BE, incubadas 30 min a temperatura ambiente y lavadas dos veces con PBS para ser observadas por microscopía de fluorescencia (longitud de onda de excitación: 482/35 y 562/40 nm).

III.8.14. Detección de apoptosis o necrosis

Para distinguir entre células necróticas, apoptóticas tardías, y viables los mohos se cultivaron a 25 °C durante 12 o 24 h tanto en presencia como en ausencia de PgAFP. El ensayo fue llevado a cabo utilizando el kit para la detección de células apoptóticas/necróticas de SIGMA, compuesto por anexina V marcada con isotiocianato de fluoresceína / ioduro de propidio (AnV-FITC/PI). Tras la tinción siguiendo a las instrucciones del fabricante los cultivos se observaron mediante microscopía de fluorescencia utilizando una longitud de onda de excitación de 482/35nm para el FITC y 562/40 nm para el PI.

III.8.15. Capacidad de unión de PgAFP a quitina regenerada

La quitina regenerada fue preparada siguiendo el protocolo descrito por (Souza et al. 2009). Se utilizaron 5 g de quitina pulverizada de conchas de cangrejos a la cual se le añadió 60 ml de HCl concentrado con agitación vigorosa durante una hora y fue filtrada, a continuación se le añadió etanol al 50%. El precipitado fue filtrado y lavado con agua sucesivas veces hasta alcanzar un pH de 7. La quitina coloidal fue almacenada a 4 °C en la oscuridad. El ensayo de

unión de PgAFP a la quitina se llevó a cabo como se ha descrito previamente (Liu et al. 2002). Para ello, 146, 292, y 635 µg de PgAFP se mezclaron con 4mg de quitina y completado hasta 1ml con el buffer de reacción (0,1M Tris/HCl pH 7,4, 150mM NaCl). La mezcla se incubó durante una hora en hielo con agitaciones periódicas cada 15 minutos. Tras la incubación las muestras se centrifugaron y la cantidad de PgAFP contenida en el sobrenadante fue medida por el procedimiento descrito anteriormente (Lowry et al. 1951).

III.8.16. Combinación Quitinasa y PgAFP

Para investigar el papel de la quitina en el mecanismo de defensa de *P. polonicum,* se realizó un ensayo en el que se trató con quitinasa al moho mientras se desarrollaba para debilitar su pared celular y ver como influía este hecho en la resistencia frente a PgAFP. *P. polonicum* se cultivó en placas en cuatro condiciones distintas:

- Control: Medio PDA
- Q: PDA con quitinasa a una concentración final de 0,4 ud/ml.
- P: PDA con PgAFP a una concentración final de 100 µg/ml.
- Q+P: PDA con quitinasa (0,4 ud/ml) y PgAFP (100 µg/ml)

Cada placa fue inoculada por triplicado con 10 µl de una suspensión que contenía 10^4 esporas y el diámetro de los triplicados fue medido cada 24 horas desde la hora 48 a la 144.

III.8.17. Extracción ADN

Para testar la sensibilidad de los cebadores diseñados para la qPCR se extrajo ADN de *A. flavus* y *A. parasiticus.*. Se realizó la extracción siguiendo el método previamente descrito por (Rodríguez et al. 2012b), para ello se cultivaron las cepas durante una semana en PDA a 25 °C, se recogió una muestra de 50 mg de micelio en condiciones de esterilidad, se congeló con nitrógeno líquido para facilitar la ruptura del micelio y fue machacado hasta pulverizarlo con ayuda de un mortero y una maza . Se incubaron en 500 µl de buffer CTAB que contenía 5 µl de β-mercaptoetanol y se le añadieron 10 µl de proteinasa K (10 mg/ml) y se incubó durante 1 h a 65 °C. Posteriormente se añadieron 10 µl de ARNasa (10 mg/ml). Entre cada uno de los anteriores tratamientos se aplicaron lavados con cloroformo que se eliminó tras ser separado a través de centrifugación. Se le añadió isopropanol (-20 °C) para precipitar el ADN, se lavó con etanol al 70% y se centrifugó para precipitar el ADN con el fin de retirar el etanol. Finalmente el ADN obtenido se resuspendió en 100 µl de Tris-EDTA buffer pH 8 y se congeló (-20 °C) hasta su posterior empleo.

III.8.18. Extracción ARN

Para evaluar la expresión de algunos genes de interés en presencia de diferentes microorganismos y de PgAFP, se inocularon 10^5 esporas/ml de *A. flavus* o *A. parasiticus* en dos lotes, por una parte 2 ml de YES y por otra 2 ml de YES suplementado con $CaCl_2$ para obtener una concentración final de 0,1M. Además se inocularon 10^6 células/ml de *D. hansenii* y *P. acidilactici* y 10 µl/ml de PgAFP tanto por separado como conjuntamente. Se incubó durante 5 días a 25 °C, realizándose cada ensayo por triplicado.

El micelio fue recuperado y lavado con PBS previamente a su congelación con nitrógeno líquido. Fue machacado mientras estaba sumergido en nitrógeno líquido con ayuda de un mortero y maza. El polvo resultante fue resuspendido en 750 µl de RLT buffer, proporcionado por el RNeasy® Plant Mini kit, suplementado con 15µl de β-mercaptoetanol y se siguió el protocolo de acuerdo con las instrucciones del fabricante. Para eliminar la contaminación del ADN genómico, las muestras fueron tratadas con ADNasa siguiendo las instrucciones del fabricante. La concentración y pureza del ARN se determinó a través de un espetrofotómetro nanodrop.

III.8.19. Desarrollo del micelio y extracción de micotoxinas en medio de cultivo

El efecto de *D. hansenii*, *P. acidilactici* y 10 µl/ml de PgAFP frente a *A. flavus* y *A. parasiticus* tanto de forma independiente, como de diferentes combinaciones se estudió en medio YES y en este medio enriquecido con 0,1 M de $CaCl_2$, utilizando los siguientes lotes:

- Lote control: inoculación con 10^5 esporas/ml de *A. flavus o A. parasiticus*.
- Lote Pg: inoculación con 10^5 esporas/ml de *A. flavus o A. parasiticus* y 10 µl/ml de PgAFP.
- Lote Dh: inoculación con 10^5 esporas/ml de *A. flavus o A. parasiticus* y 10^6 células/ml de *D. hansenii*.
- Lote Pa: inoculación con 10^5 esporas/ml de *A. flavus o A. parasiticus* y 10^6 células/ml de *P. acidilactici.*
- Lote Pg+Dh: inoculación con 10^5 esporas/ml de *A. flavus o A. parasiticus*, 10 µl/ml de PgAFP y 10^6 células/ml de *D. hansenii.*
- Lote Pg+Pa: inoculación con 10^5 esporas/ml de *A. flavus o A. parasiticus*, 10 µl/ml de PgAFP y 10^6 células/ml de *P. acidilactici.*
- Lote Dh+Pa: inoculación con 10^5 esporas/ml de *A. flavus o A. parasiticus*, 10^6 células/ml de *D. hansenii* y 10^6 células/ml de *P. acidilactici.*
- Lote Pg+Dh+Pg: inoculación con 10^5 esporas/ml de *A. flavus o A. parasiticus*, 10 µl/ml de PgAFP, 10^6 células/ml de *D. hansenii* y 10^6 células/ml de *P. acidilactici.*

Cada muestra contenía 5 ml del citado medio de cultivo y todos los lotes se incubaron durante 15 días a 25 °C. El crecimiento fúngico se evaluó mediante el peso seco del micelio. Para ello se recuperó el micelio con un filtro miracloth, se deshidrató a 100 °C durante 15 min y tras su enfriamiento en un desecador se pesó. La producción de micotoxinas se evaluó tras realizar una extracción clorofórmica. Una vez eliminado el micelio, a cada tubo que contenía el caldo de cultivo donde se habían desarrollado las cepas se añadieron 5 ml de cloroformo. Se incubó durante 1 h en agitación a 100 rpm a temperatura ambiente, posteriormente se separó el cloroformo y se dejó evaporar en una campana de gases durante 72 h en oscuridad. Todos los ensayos se realizaron por triplicado. Las micotoxinas se analizaron como se indica más adelante (apartado III.8.20.4).

III.8.20. Ensayos en alimentos

Para llevar a cabo los ensayos simulando el proceso de maduración de los alimentos (queso y salchichón) se emplearon recipientes de metacrilato que fueron esterilizados previamente a su empleo. Para ello se dejaron 24 horas conteniendo etanol y posteriormente se vaciaron y se dejaron secar 12h bajo luz ultravioleta. Para emular las condiciones ambientales de a maduración, se empleó una solución de KCl sobresaturada que proporciona una humedad relativa del 84% después del equilibrio de vapor. La carga microbiana de los alimentos se redujo mediante inmersión en etanol, que posteriormente se dejó evaporar en la cabina de flujo laminar. A continuación se inocularon los diferentes microorganismos y cantidades de PgAFP dependiendo del experimento a realizar.

III.8.20.1. Efecto antifúngico de PgAFP en alimentos madurados

Una solución de proteína PgAFP (200 µl) se añadió sobre la superficie de salchichón o queso para llegar a una concentración final de 5 y 20 µg/cm^2. La solución se distribuyó en la superficie y se esperó hasta que el líquido fue absorbido por el alimento. A continuación se procedió a la inoculación de 10^4 esporas de *A. flavus* o *P. restrictum*. Se preparó un lote control añadiendo un volumen de PBS equivalente al utilizado para incorporar la proteína. Todos los lotes se incubaron durante 5 días a 25 °C. Al final de la incubación se procedió a fotografiar los alimentos y se determinó el recuento de los mohos tras la siembra de diferentes diluciones decimales en placas de PDA, que se incubaron 72 h a 25 °C.

III.8.20.2. Efecto antifúngico de la aplicación conjunta de PgAFP, D. hansenii y P. acidilactici en alimentos madurados

En este ensayo, realizado en salchichón y queso siguiendo un procedimiento análogo al descrito en el apartado anterior se utilizaron los siguientes lotes:

- Lote control: alimentos inoculados con 10^5 esporas/cm^2 de *A. flavus o A. parasiticus*.
- Lote Pg+Dh: alimentos inoculados con 10^5 esporas/cm^2 de *A. flavus o A. parasiticus*, 10 µl/cm^2 de PgAFP y 10^6 células/cm^2 de *D. hansenii*.
- Lote Pg+Dh+Pa: alimentos inoculados con 10^5 esporas/cm^2 de *A. flavus o A. parasiticus*, 10 µl/cm^2 de PgAFP, 10^6 células/cm^2 de *D. hansenii* y 10^6 células/cm^2 de *P. acidilactici*

Los tres lotes se incubaron 15 días a 25 °C y se tomaron muestras a los 5 y 15 días para evaluar el desarrollo de los microorganismos así como la producción de micotoxinas. El desarrollo microbiano se evaluó mediante el recuento en placas de PDA (mohos y levaduras) y MRS (pediococos). Las colonias de mohos y levaduras se diferenciaron de acuerdo son su morfología. La determinación de micotoxinas se realizó como se describe en la siguiente sección. En todos los casos los ensayos se llevaron a cabo por triplicado.

III.8.20.3. Extracción de micotoxinas de alimento

Las micotoxinas producidas sobre el salchichón y queso se extrajeron de acuerdo al método descrito por (Rodríguez et al. 2012d). El alimento troceado se maceró en agitación durante una hora en un matraz opaco con 60 ml de acetonitrilo-agua (9:1, v/v) conteniendo 0,1% de ácido fórmico y además 50 ml de hexano. La fase constituida por acetonitrilo-agua se recuperó, fue filtrada a través de sodio sulfato anhidro. A continuación se le añadieron 50 ml de hexano adicionales y se maceró en agitación durante media hora. La fase compuesta por acetonitrilo-agua fue recuperada nuevamente, filtrada y evaporada por medio de un rotavapor a 40-45 °C. El residuo se resuspendió en 1 ml de cloroformo, filtrado a través de 0,45 µm (Fisher scientific, Waltham, EEUU) y evaporado. Se almacenaron a -20 °C hasta su análisis.

III.8.20.4. Detección y cuantificación de micotoxinas

El análisis y caracterización de las micotoxinas se realizó mediante uHPLC-MS, HPLC Thermo Scientific Dionex ultimate 3000 pnmp (Thermo Scientific, Waltham, MA, USA), a mass detector (MS) ion trap model Bruker Amazon S.L., an autosampler (Ultimate 3000), a degasser (3000 Ultimate) (Bruker Daltonics, Bremen, Alemania). La fase estacionaria empleada fue una columna de fase reversa C18 de 10 cm de longitud, 2,1 mm de diámetro y con tamaño de

partícula de 2 µm de diámetro. Mientras que la fase móvil empleada fue tampón 0,1% ácido fórmico-10 mM formiato amónico (solvente A) y acetonitrilo (solvente B), ambos fueron filtrados a vacío con una membrana de 0,22 µm de tamaño de poro previamente a su uso. La separación se realizó con flujo de 200 µl/min mediante un gradiente programado según se describe en la Tabla (II3)

Tabla II3. Gradiente utilizado para la separación mediante uHPLC.

Tiempo (min)	0,00	0,10	4,00	7,00	8,50	8,51	12,00	12,01	15,00
%B	2	40	60	80	80	98	98	2	2

La detección de las micotoxinas se llevó a cabo utilizando una fuente de ionización por electroespray (ESI) en las siguientes condiciones reflejadas en la Tabla II4:

Tabla II4. Condiciones de la fuente de ionización.

Gas de nebulización	N2, 7,3 psi
Gas de secado	N2, 4 l/min, 180ºC
Voltaje del capilar	4.500 v
End plate offset	500 v
Modo de trabajo	ESI-MS/MS
Velocidad de scan	32.500 u/s
Rango de m/z	70-2.200

La identificación de las micotoxinas se realizó en base a dos parámetros: tiempo de retención y relación masa/carga de los compuestos detectados. Los resultados de estos parámetros fueron comparados con los obtenidos mediante el análisis de patrones de las diferentes micotoxinas que figuran en la Tabla II5.

Tabla II5. Iones empleados para la detección y cuantificación de aflatoxinas.

Micotoxina	Ión precursor	Ión de cuantificación
Aflatoxina B1	313	285
Aflatoxina G1	329	311

IV. RESULTADOS

IV.1. Espectro de acción de PgAFP frente a mohos toxigénicos y capacidad antifúngica sobre producto crudo-curado madurado

Growth inhibition and stability of PgAFP from* Penicillium chrysogenum *against fungi common on dry-ripened meat products

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Growth inhibition and stability of PgAFP from *Penicillium chrysogenum* against fungi common on dry-ripened meat products

Josué Delgado, Raquel Acosta, Andrea Rodríguez-Martín, Elena Bermúdez, Félix Núñez, Miguel A. Asensio *

Food Hygiene and Safety, Institute of Meat Products, University of Extremadura, Avenida de la Universidad s/n, 10003 Cáceres, Spain

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ABSTRACT

Dry-ripened foods favor the development of a superficial fungal population that may include toxigenic molds. To combat unwanted molds, an antifungal protein from *Penicillium chrysogenum* (PgAFP) can be useful. The aim of the present work was to study the antimicrobial activity of PgAFP against microorganisms common in dry-ripened foods, and to evaluate its sensitivity to proteolytic enzymes and heat treatments that may be applied to foods, as well as to different pH values. The inhibitory effect of the purified protein on 38 microbial strains grown in culture medium was determined. PgAFP sensitivity to various proteases, heat treatments, and preincubation at different pH values was tested by means of the residual activity on selected reference strains. Inhibitory activity of PgAFP against unwanted molds was tested in a dry-fermented sausage. This protein exhibited potent inhibitory activity against unwanted molds, including the main mycotoxin-producing species of *Aspergillus* and *Penicillium* of concern for dry-ripened foods. PgAFP withstood most proteases, intense heat and a wide range of pH values. PgAFP efficiently reduced counts of *A. flavus* and *P. restrictum* inoculated on a dry-fermented sausage. This protein can be of interest to control hazardous molds in dry-ripened foods.

1. Introduction

Most dry-ripened foods favor the development of a superficial fungal population that may include toxigenic molds, mainly *Aspergillus* and *Penicillium* spp., and yeasts such as *Debaryomyces* and *Candida* spp. Surface treatments and packaging may help to control unwanted fungi, but they are not adequate to prevent fungal growth during ripening of mold-ripened cheese, ham, or sausage. Research on new antifungal agents has increased during the recent years due to the increase in human fungal infections, mainly involving immunocompromised patients (Fox, 1993). Many proteins and peptides with antifungal activity from plants, bacteria, arthropods, amphibians, or reptiles have been purified and characterized (Dimarcq et al., 1998; Selitrennikoff, 2001; Wang and Ng, 2003). The number of antifungal proteins described from molds so far is rather limited to AFP from *Aspergillus giganteus* (Nakaya et al., 1990; Lacadena et al., 1995), Anafp from *Aspergillus niger* (Lee et al., 1999), AcAFP from *Aspergillus clavatus* (Skouri-Gargouri and Gargouri, 2008), NFAP from *Neosartorya fischeri* (Kovács et al., 2011), PAF (Marx et al., 1995), PgAFP (Rodríguez-Martín et al., 2010), and Pc-Arctin (Chen et al., 2013) from *Penicillium chrysogenum*. Most of these proteins have some common characteristics, such as small size (5.8–6.6 kDa), high ratio of cysteine residues, and basic character due to the presence of a high content of arginine and lysine residues (Marx, 2004; Skouri-Gargouri et al., 2009; Rodríguez-Martín et al., 2010). The antifungal proteins from molds show potent activity against filamentous fungi, although differences in sensitivity have been reported (Marx, 2004). Only Anafp proved to be active against yeasts (Lee et al., 1999) but none has been shown to inhibit the bacteria tested so far (Marx, 2004).

The amino acid sequence of PgAFP showed only 34% identity with PAF, produced by a different strain of *P. chrysogenum* (Rodríguez-Martín et al., 2010). PgAFP is the only antifungal protein isolated from a foodborne mold, as the *P. chrysogenum* strain which produces it (CECT 20922; formerly *P. chrysogenum* RP42C) was isolated from dry-cured ham (Acosta et al., 2009). Given that PgAFP was active against some toxigenic species of both *Penicillium* and *Aspergillus* (Acosta et al., 2009), the potential inhibition of other unwanted organisms of significance for dry-ripened foods, deserves further investigation.

Microbial proteases are responsible for proteolysis on dry-ripened foods. The addition of enzymes of plant or microbial origin, such as papain or flavourzyme from *Aspergillus oryzae*, has been proposed to accelerate the ripening process of dry-fermented sausages (Fernández et al., 2000). Thus, the antifungal proteins intended for use in foods should be resistant to common proteolytic enzymes. Thus, evaluating the sensitivity of PgAFP to commercial proteases is of interest. The effectiveness of antifungal proteins from molds can also be limited by pH of the food and heat treatments applied.

The efficacy of PgAFP could be affected also by other characteristics of the food, such as water activity, temperature, chemical composition, and microbial population; thus the antifungal activity of PgAFP should be tested on dry-fermented meat products.

* Corresponding author. Tel.: +34 927 257124; fax: +34 927 257110.
E-mail address: masensio@unex.es (M.A. Asensio).

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The objective of this work was to study the antimicrobial activity of PgAFP against some of the main microorganisms of significance for dry-ripened foods, to evaluate the sensitivity of the protein to proteolytic enzymes and heat treatments that may be applied to foods, as well as to different pH values. Finally, the inhibitory activity of PgAFP was checked against unwanted molds on dry-fermented sausages.

2. Materials and methods

2.1. Reference organisms

Inhibition tests were carried out against 38 microbial strains from 26 fungal species, five yeasts, and five bacteria. The following strains were obtained from the Spanish Type Culture Collection (CECT, Valencia, Spain), the Centraalbureau voor Schimmelcultures (CBS, Utrecht, The Netherlands), or the microbial collection of Food Hygiene and Safety, University of Extremadura (Cáceres, Spain): *Aspergillus awamori* CBS 101.702, *Aspergillus carbonarius* CECT 20384, *Aspergillus flavus* CECT 2687, *Aspergillus fumigatus* CBS 192.65, *Aspergillus niger* An261, *Aspergillus ochraceoroseus* CBS 101.887, *Aspergillus ochraceus* CECT 2092, *Aspergillus oryzae* CECT 2095, *Aspergillus parasiticus* CECT 2682, *Aspergillus tamarii* CBS 109.63, *Aspergillus tubingensis* CECT 20545, *Aspergillus versicolor* CECT 2664, *Aspergillus westerdijkiae* CECT 2948, *Penicillium aurantiogriseum* CECT 2918, *P. chrysogenum* CECT 20922 (formerly *P. chrysogenum* RP42C), *P. chrysogenum* Pg222, *Penicillium commune* Pc131, *Penicillium commune* Pc332, *Penicillium echinulatum* Pe321, *Penicillium expansum* CECT 2280, *Penicillium griseofulvum* CECT 2919, *Penicillium nalgiovense* Pj261, *Penicillium nordicum* CBS 110.769, *Penicillium polonicum* Pp51, *Penicillium restrictum* Pr341, *Penicillium solitum* Ps321, *Penicillium verrucosum* AB11C, *Rhizopus oryzae* CBS 607.68; *Candida zeylanoides* CECT 10048, *Debaryomyces hansenii* CECT 10360, *Debaryomyces hansenii* Dh345, *Rhodotorula mucilaginosa* CECT 10359, *Yarrowia lipolytica* CECT 10358; *Brochothrix thermosphacta* PA7B2, *Escherichia coli* CECT 4267, *Listeria monocytogenes* CECT 4032, *Salmonella enterica* subsp. *enterica* CECT 4374, and *Serratia liquefaciens* PA7VRBG.

2.2. Protein purification

The PgAFP producing *P. chrysogenum* CECT 20922 was inoculated into malt extract broth (20 g/L malt extract, 20 g/L glucose, and 1 g/L peptone; MEB), pH 4.5, and incubated up to 21 days at 25 °C without shaking. PgAFP was obtained from the cell free medium by fast protein liquid chromatography with a cationic exchange column HiTrap SP HP (Amersham Biosciences, Uppsala, Sweden), further purified with a HiLoad 26/60 Superdex 75 gel filtration column for FPLC (Amersham Biosciences), and concentrated as previously described (Acosta et al., 2009; Rodríguez-Martín et al., 2010).

Protein concentration in the purified extract was estimated by protein nitrogen determination according to the Johnson method (Johnson, 1941). To calculate the concentration of protein, the nitrogen percentage of 19.17% deduced from the amino acid composition of PgAFP (Rodríguez-Martín et al., 2010) was used.

2.3. Growth inhibition of reference organisms

Quantitative assay for microbial growth inhibition was carried out by a microspectroscopic method (Acosta et al., 2009) adapted from Broekaert et al. (1990). The inhibition test was performed in 96-well microtiter plates, with 100 μL of the purified protein mixed with 100 μL of culture media containing ca. 10^6 CFU/mL of the reference organism per well. Molds and yeasts were grown in double-strength (82 g/L) MEB, whereas bacteria were cultivated in double-strength (74 g/L) brain heart infusion broth (BHI, Scharlab, Barcelona, Spain). The final concentration of PgAFP in the wells was set from 1.2 to 312.7 μg/mL (0.2 to 48.2 μM). The assay was run in sextuplicate wells, using separate plates for each reference strain. The corresponding fraction from uninoculated medium, also purified by gel filtration, was used as negative control. Fungal cultures were incubated for up to 120 h at 25 °C and bacterial cultures were incubated for 48 h at 20 °C. Growth was monitored by measuring the optical density variation at 595 nm every 24 h for fungi or 12 h for bacteria. Growth reduction (GR) was defined as the lowest PgAFP concentration that produced prominent growth reduction of 50% (GR50) or 35% (GR35) compared to control plates, according to Espinel-Ingroff et al. (1997).

2.4. Susceptibility to enzymes

The sensitivity of PgAFP to digestion by enzymes was tested using the following commercial enzymes dissolved individually as indicated: pepsin, in 0.3 M KCl, 0.15 M NaCl, pH 2; lysozyme and papain, in 0.3 M PO_4Na_2, 0.15 M NaCl, pH 6.2; ficin, in 0.3 M PO_4Na_2, 0.15 M NaCl, pH 7; flavourzyme, in 0.3 M PO_4Na_2, 0.15 M NaCl, pH 7.5; pronase E and trypsin, in 0.3 M PO_4Na_2, 0.15 M NaCl, pH 7.5. All enzymes were obtained from Sigma Chemical Co. (St. Louis, USA) and used at a final concentration of 500 μg/mL. PgAFP was added at different concentrations (8 to 130 μg/mL, 1.2 to 20 μM) to enzyme preparations, and the mixtures were incubated 12 h at the following optimal temperatures recommended for each enzyme by manufacturer: 25 °C for lysozyme, papain, and trypsin, and 37 °C for the remaining enzymes. Then, the residual antifungal activity against *A. flavus* CECT 2687, *A. niger* An261, *P. griseofulvum* CECT 2919, and *P. restrictum* Pr341 was tested by the microspectroscopic method. Aliquots of the prepared PgAFP concentrations without enzyme treatment were used as positive control. Additional tests with 500 μg/mL of each enzyme and no PgAFP were run to discount interferences with mold growth.

2.5. Stability to heat treatments

The study of the protein stability after heat treatment was carried out according to Okkers et al. (1999). Aliquots of PgAFP protein (300 μg/mL) were exposed to different combinations of temperatures (60, 80, and 100 °C) and times (10, 20, and 30 min) in a dry block heater Termobloc (JP Selecta, Barcelona, Spain), as well as to 121 °C for 15 min in an autoclave cycle. After heat treatment, the samples were cooled on ice and tested for antifungal activity in microtiter plates. The reference strains tested were *Aspergillus niger* An261 and *Penicillium restrictum* Pr341.

2.6. pH stability

PgAFP (300 μg/mL) was retained in microcon centrifugal filter units YM-3 (Millipore) and then dissolved in different buffers at the following values: pH 1, 2 (HCl/KCl); pH 3 (glycine/HCl); pH 4, 5, 6 (citric acid/sodium phosphate); pH 7 (sodium phosphate/NaCl); pH 8 (Tris/HCl); pH 9, 10 (Tris/NaOH); and pH 12 (KCl/NaOH). Samples were incubated at 25 °C for 2 h and the pH adjusted to 4.5 before testing the antifungal activity. Negative controls with no PgAFP added were prepared following the same procedure. The reference strains tested were *Aspergillus niger* An261 and *Penicillium restrictum* Pr341.

2.7. Antifungal activity of PgAFP on dry-fermented sausages

The effect of PgAFP on growth of toxigenic molds was tested using a commercial raw dry-fermented sausage "salchichón" (pH 5.4, 0.95 a_w) shortly after filling into natural casing from beef. The sausage was surface-sterilized by dipping in ethanol and longitudinally cut into ca. 10 cm^2 over 1 cm thick pieces in a laminar flow cabinet (Bio Flow II, Telstar, Tarrasa, Spain). To simulate the evolution of a_w during industrial sausage processing, the pieces were separately placed in pre-sterilized receptacles with humidity kept constant at 84% after vapor–liquid equilibrium by a saturated potassium chloride solution. A volume of 100 μL of *A. flavus* CECT 2687 or *P. restrictum* Pr341 spore suspensions was

spread onto the casing surface to reach a final concentration of 10^{-4} spores/cm^2 on each piece. In treated samples, PgAFP was added in 200 μL of phosphate buffer to treated samples at two concentrations (5 and 20 μg/cm^2) and was air-dried in the flow cabinet. Control batches received the same volume of phosphate buffer without PgAFP and were inoculated with *A. flavus* or *P. restrictum*. Each treatment was done in three replicates. After inoculation, the samples were incubated at 25 °C for 5 days. The mold load on the sausages was determined from a suspension of the whole piece in 90 mL of peptone water by plating decimal dilutions on Potato Dextrose Agar and incubating at 25 °C for 5 days.

2.8. Statistical analysis

Statistical analyses were performed with the IBM SPSS v.19.0. One way analysis of variance (ANOVA) was carried out to determine significant differences within and between groups. Tukey's test was applied to compare mean values.

3. Results

The concentrations of purified PgAFP obtained from *P. chrysogenum* CECT 20922 were 282 and 617 μg/mL at 7- and 14-day incubations in MEB, respectively. Only a limited increase in PgAFP (up to 678 μg/mL) was obtained by extending incubation for one additional week.

3.1. Growth inhibition of reference organisms

All reference organisms tested showed a fair growth in microtiter plates (OD over 1 absorbance unit). The highest concentration of PgAFP tested (312.7 μg/mL) displayed no inhibition against any bacteria (data not shown) or yeast tested, but efficiently retarded growth of most reference molds, including toxigenic, defect-causing, and desirable species. According to sensitivity, two inhibition levels were established (Table 1). In level H, 4.9 μg/mL of PgAFP significantly ($p < 0.001$) reduced over 50% growth of the reference molds, *A. carbonarius*, *A. flavus*, *A. niger*, *A. ochraceus*, *P. chrysogenum*, and *P. restrictum*, as well as the strain Pc332 of *P. commune*. Level L was characterized by a significant ($p < 0.01$) but moderate inhibition, where at least 4.9 μg/mL was necessary to reduce growth 35% for reference strains, such as *A. parasiticus*, *A. versicolor*, *P. expansum*, *P. griseofulvum*, and strain Pc131 of *P. commune*. Due to the slow growth of *P. nordicum* on MEB incubation was extended up to 120 h. At this incubation time a 40% growth reduction of *P. nordicum* was reached with 19.6 μg/mL. However, there was a group of non-sensitive fungi, including *P. polonicum* and *R. oryzae*, in which growth was not significantly ($p > 0.05$) retarded by any PgAFP concentration tested. Inhibition on sensitive molds showed a remarkable dose–effect relationship (Fig. 1). For the highly sensitive reference strains, a noticeable inhibition was observed even at the lowest PgAFP concentration tested (1.2 μg/mL).

3.2. Sensitivity of PgAFP activity to proteases

None of the enzymes tested lead to any statistically significant decrease ($p > 0.05$) on growth of the reference molds when used as a negative control with no antifungal protein. Preincubation of PgAFP with proteases decreased the antifungal activity on the reference molds, but the resulting effect depended not only on the enzyme, but also on both PgAFP concentration and sensitivity level of the reference mold (Fig. 2). Pronase E efficiently eliminated ($p < 0.001$) any inhibitory effect from PgAFP on every selected reference mold, even at the highest PgAFP concentration (130 μg/mL). Flavourzyme and trypsin lowered PgAFP activity, but the effect was less evident, particularly at the highest PgAFP concentration. These two enzymes efficiently eliminated the inhibition on *A. flavus* and *A. niger* by up to 65 μg/mL PgAFP ($p < 0.001$), but not so much at the highest PgAFP concentration ($p < 0.05$). The inhibition on the two penicillia strains was occasionally altered by flavourzyme and trypsin ($p < 0.05$). The effect of ficin, pepsin, and papain was less obvious with every reference strain, and decreased at higher PgAFP concentrations.

Table 1
In vitro minimal concentrations of PgAFP achieving over 50% (GR_{50}) or 35% growth reduction (GR_{35}) on fungal strains on malt extract broth at 72 h of incubation at 25 °C.

Inhibition level	Fungal strain	GR50 (μg/mL)	GR35 (μg/mL)
H	*A. carbonarius* CECT 20384	1.2	
	A. flavus CECT 2687	4.9	
	A. fumigatus CBS 192.65	2.4	
	A. niger An261	4.9	
	A. ochraceus CECT 2092	1.2	
	A. oryzae CECT 2095	2.4	
	A. tamarii CBS 109.63	2.4	
	A. westerdijkiae CECT 2948	2.4	
	P. chrysogenum Pg222	2.4	
	P. commune Pc332	4.9	
	P. nalgiovense Pj261	2.4	
	P. restrictum Pr341	2.4	
	P. solitum Ps321	4.9	
L	*A. awamori* CBS 101.702	19.6	9.8
	A. ochraceoroseus CBS 101.887	312.7	19.6
	A. parasiticus CECT 2682	312.7	39.1
	A. tubigensis CECT 20545	19.6	9.8
	A. versicolor CECT 2664	156.4	78.2
	P. aurantiogriseum CECT 2918	>	39.1
	P. commune Pc131	>	78.2
	P. echinulatum Pe321	>	19.6
	P. expansum CECT 2280	9.8	4.9
	P. griseofulvum CECT 2919	>	19.6
	P. nordicum CBS 110.769	312.7	19.6[a]
	P. verrucosum AB11C	>	9.8
Non-sensitive	*P. chrysogenum* CECT 20922	>	—
	P. polonicum Pp51	>	—
	R. oryzae CBS 607.68	>	—
	C. zeylanoides CECT 10048	>	—
	D. hansenii CECT 10360	>	—
	D. hansenii Dh345	>	—
	R. mucilaginosa CECT 10395	>	—
	Y. lipolytica CET 10358	>	—

>: 50% Growth reduction was not reached with 312.7 μg/mL PgAFP.
—: No significant growth reduction was obtained with 312.7 μg/mL PgAFP.
[a] Incubation time extended to 120 h.

3.3. Effect of heat-treatments and different pH values

PgAFP showed a remarkable stability at high temperatures, retaining the antifungal activity against *P. restrictum* and *A. niger* even after being heat-treated at 80 °C for 30 min or 100 °C for 15 min (Fig. 3). More intense heating decreased the antifungal activity, reaching an effective ($p < 0.001$) inactivation with the most severe treatments (100 °C for 30 min or autoclave cycle).

Preincubation in buffers at pH values from 1 to 12 had no deleterious effect ($p > 0.05$) on the activity of PgAFP against the reference molds (Fig. 4).

3.4. Antifungal activity of PgAFP on dry-fermented sausages

To test the potential use in foods, the efficiency of PgAFP against unwanted molds was assayed in dry-ripened sausages. The effect on growth of *A. flavus* and *P. restrictum* was evaluated by plating and CFU counting from both PgAFP treated and non-treated sausages. Lower counts were detected in the batches treated with PgAFP (Table 2, Fig. 5) compared to the non-treated control ($p < 0.05$).

4. Discussion

P. chrysogenum CECT 20922 had shown a strong inhibitory activity against *P. echinulatum*, *P. commune*, and *A. niger* due to production of

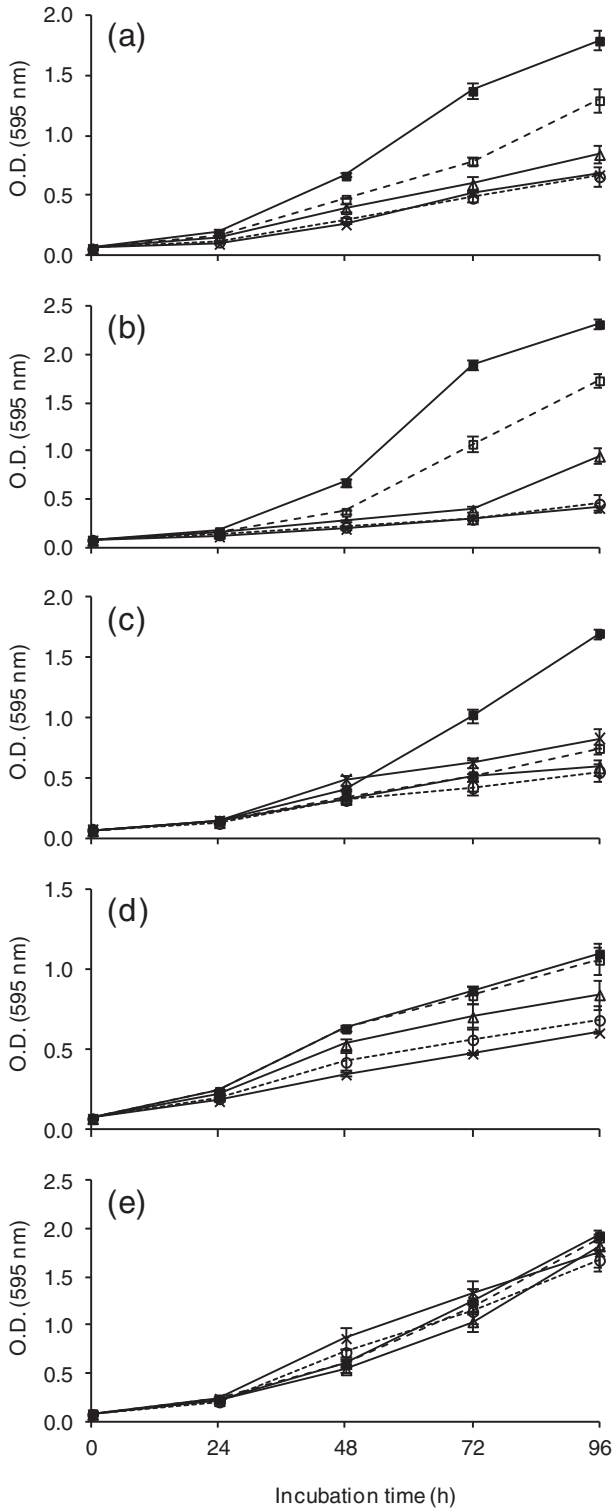

Fig. 1. Effect of PgAFP on growth of selected molds incubated with 0 (■), 1.2 (□), 2.4 (Δ), 18.8 (○), and 37.5 (×) μg/mL PgAFP. (a) *Aspergillus flavus* CECT 2687; (b) *Aspergillus niger* An261; (c) *Penicillium restrictum* Pr341; (d) *Penicillium griseofulvum* CECT2919; (e) *Penicillium polonicum* Pp51. Values are means with standard deviation of optical density of reference molds.

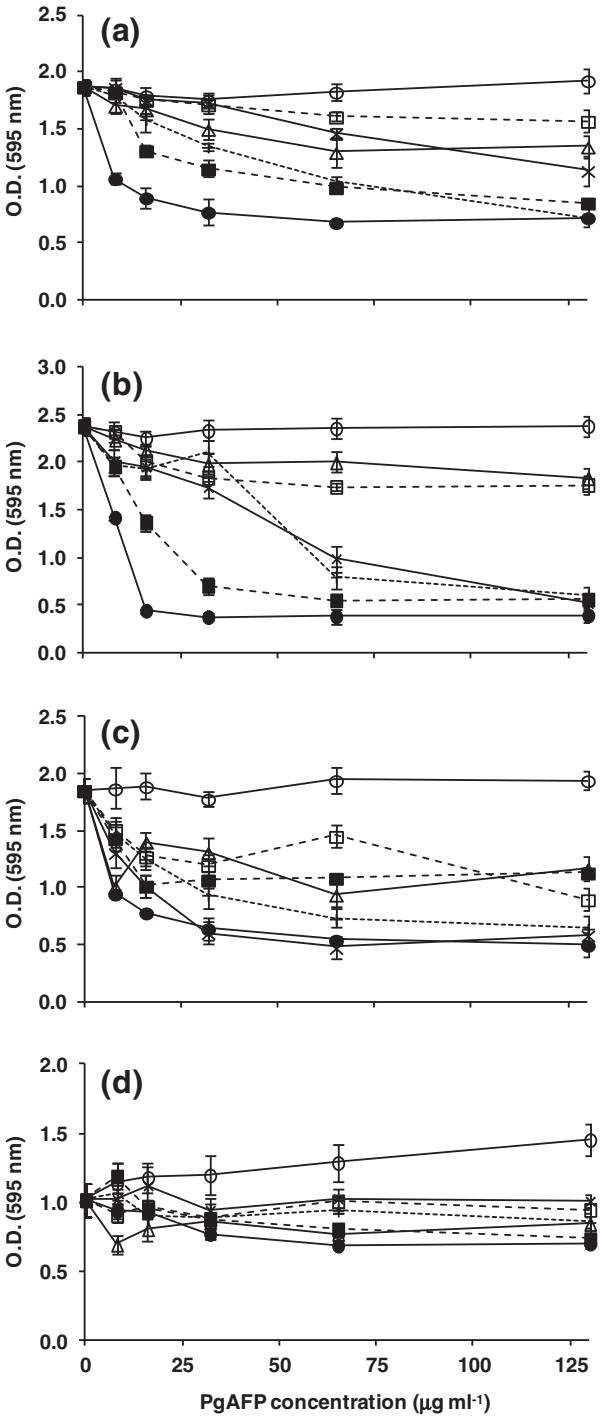

Fig. 2. Effect of proteases on the antifungal activity of different concentrations of PgAFP against selected reference molds. Treatments: (■) pepsin, (×) ficin, (+) papain, (Δ) flavourzyme, (○) pronase E, (□) trypsin, and (●) untreated. (a) *Aspergillus flavus* CECT 2687; (b) *Aspergillus niger* An261; (c) *Penicillium restrictum* Pr341; (d) *Penicillium griseofulvum* CECT2919. Values are means with standard deviation of optical density of reference molds grown for 96 h.

the cationic protein PgAFP (Acosta et al., 2009). The strain CECT 20922 of *P. chrysogenum* has been demonstrated to limit growth of the aflatoxin-producing *A. flavus* and ochratoxigenic molds on dry-cured ham (Bernáldez et al., 2014; Rodríguez et al., 2015). However, no mold growth, including that of protective cultures, is wanted in some types of dry-ripened sausage. Thus, the use of purified PgAFP could be of interest. To evaluate the activity of the purified protein, its effect on growth of penicillia, aspergilli, yeasts, and bacteria was assessed. No effect on growth of the tested yeasts and bacteria was observed, even at the highest concentration of PgAFP used (312.7 μg/mL). The lack of activity against yeasts and prokaryotes has also been reported for other small, basic antifungal proteins (Marx, 2004). In fact, the only activity reported is limited to Anafp on *Candida albicans*, *Saccharomyces*

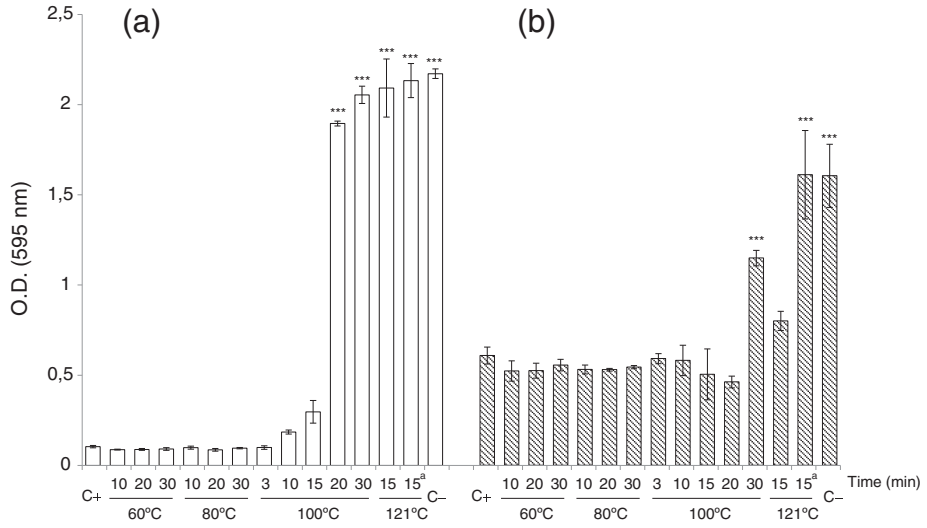

Fig. 3. Antifungal activity of 300 μg/mL heat-treated PgAFP expressed as mean and standard deviation of optical density of reference molds grown for 96 h. (a) *Aspergillus niger* An261; (b) *Penicillium restrictum* Pr341. Asterisks indicate statistically significant differences to growth of the positive control reference mold: *** ($p < 0.001$). C+: positive control with non-heated PgAFP; C−: negative control without PgAFP. [a]: Autoclave cycle.

cerevisiae, and *Trichosporon beigelii* (Lee et al., 1999). The lack of inhibitory activity on yeasts can be regarded as a positive property. First, because yeasts such as *D. hansenii* contribute to develop the desirable characteristics of dry-ripened meats with no detrimental effects. Second, a limited number of yeasts, including *D. hansenii*, also may combat toxigenic molds (Andrade et al., 2014; Simoncini et al, 2014; Núñez et al., 2015).

PgAFP retarded growth of most molds tested, including the selected aspergilli and most penicillia. Interestingly, the main toxigenic molds tested, such as those producing aflatoxin (*A. flavus* and *A. parasiticus*), ochratoxin A (*A. carbonarius, A. ochraceus*, and *P. nordicum*), sterigmatocistin (*A. versicolor*), and patulin (*P. expansum* and *P. griseofulvum*) were in the PgAFP-sensitive group of fungi. The observed effect is fungistatic, not achieving total inhibition of the sensitive mold at the highest concentration tested. Nonetheless, this effect would contribute to reduction of the hazard due to mycotoxins in dry-ripened foods because many secondary metabolites are produced mainly in the idiophase. Despite reports that mycotoxin production may increase in stressed toxigenic fungi, the strong growth inhibition shown in the sausage could be useful to control mycotoxin production, as discussed later. The fact that some molds, such as *P. polonicum* and *R. oryzae*, were not sensitive should not be regarded as a drawback, given that none of them is linked to foodborne mycotoxicosis (Richard, 2007). The minimal inhibitory concentration to reach over 50% growth reduction was in the range of 1.2–4.9 μg/mL (0.2–0.75 μM) PgAFP for the high sensitive strains (level H), whereas low sensitive strains (level L) required 4.9–78.2 μg/mL (0.75–12 μM) for a 35% growth reduction (Table 1). The inhibition rate for highly sensitive strains can be compared to that of 6 to 25 μM required for complete inhibition of sensitive molds by AFP (Lacadena et al., 1995). Growth inhibition differs greatly not only between species of the same genus, but also within the same species. Accordingly, *P. commune* Pc332 was highly sensitive to PgAFP, with 4.9 μg/mL GR_{50}, whereas *P. commune* Pc131 required 78.2 μg/mL for just a 35% growth reduction. GR_{50} for *P. chrysogenum* Pg222 was 2.4 μg/mL, but the PgAFP-producing strain *P. chrysogenum* CECT 20922 withstands 312.7 μg/mL, the maximum level tested. Similar differences in sensitivity to antifungal proteins have been reported for AFP, Anafp, PAF, and AcAFP, showing both sensitive and non-sensitive species in a limited number of strains from genera *Aspergillus*, *Penicillium*, or *Fusarium* (Lee et al., 1999; Kaiserer et al., 2003; Theis et al., 2003; Skouri-Gargouri and Gargouri, 2008).

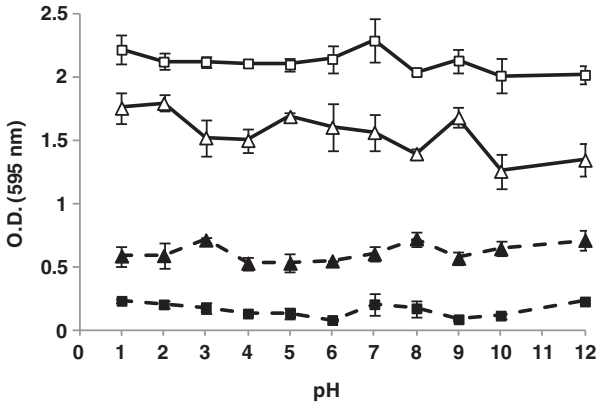

Fig. 4. Antifungal activity of PgAFP after incubation at different pH values, expressed as mean and standard deviation of optical density of reference molds grown for 96 h. *Aspergillus niger* An261 (■) and *Penicillium restrictum* Pr341 (▲) treated with 300 μg/mL PgAFP (closed symbols) or untreated negative controls (open symbols).

To study the effect of proteases on the antifungal activity of PgAFP the reference species selected included both sensitivity levels and fungal genera. The enzymes chosen are among the most active proteases that can be added to processed foods or, for flavourzyme and pronase E, have been proposed to enhance flavor development in dry fermented sausages (Fernández et al., 2000). No enzyme tested showed any effect on growth of reference strains (Fig. 2). The activity of the proteases against PgAFP was evidenced by the loss of activity at low PgAFP levels. At higher PgAFP concentrations, the more active proteases decreased the antifungal effect. The less active proteases were less efficient, and the residual amount of antifungal protein seems to be enough to limit growth of the reference molds. This effect was not observed with the low-sensitive *P. griseofulvum*, partially because the short extent

Table 2
Effect of PgAFP on growth of *Aspergillus flavus* and *Penicillium restrictum* on a dry-fermented sausage after 5 days at 25 °C. Mold growth is given as mean ± SD.

	Fungal species	
PgAFP (μg/cm^2)	*A. flavus* CECT 2687 (log CFU/cm^2)	*P. restrictum* Pr341 (log CFU/cm^2)
0	5.0 ± 0.21	4.7 ± 0.17
5	2.6 ± 0.24[a]	3.6 ± 0.19[a]
20	2.1 ± 0.15[a]	3.1 ± 0.25[a]

[a] Different ($p < 0.05$) from the non-treated control.

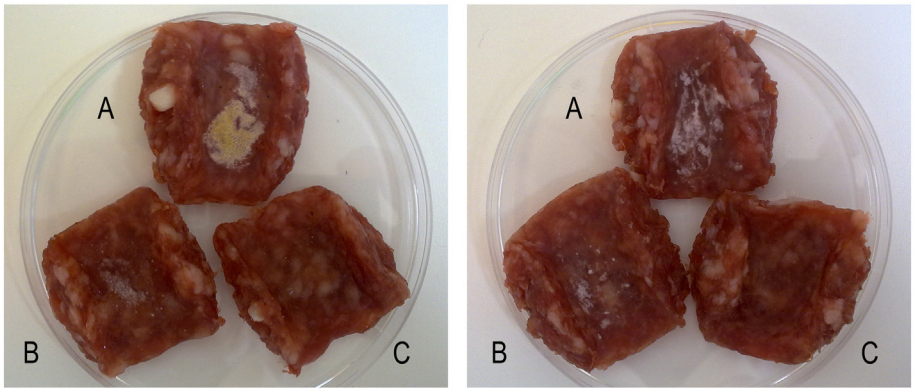

Fig. 5. Effect of 0 (A), 5 (B), and 20 (C) μg/cm^2 PgAFP on growth of *Aspergillus flavus* (left) and *Penicillium restrictum* (right) on dry-fermented sausage after 5 days at 25 °C.

between growth of PgAFP-treated and non-treated samples did not allow detecting the effect due to PgAFP degradation.

Given that PgAFP digestion was run under extreme conditions, for 12 h at favorable temperature and pH values for each enzyme, the observed residual activity reveals a remarkable ability to withstand proteases. Only the mixture of exopeptidases and endopeptidases from *S. griseus* contained in pronase E was able to efficiently inactivate 130 μg/mL PgAFP. With the latter result, the potential use of PgAFP might be argued, when proteolytic organisms were present. However, highly proteolytic molds from dry-ripened meats, such as *P. chrysogenum* Pg222 and *A. oryzae* CECT 2095 (ATCC 9362) (Trigueros et al., 1995; Benito et al., 2002), were among the highly sensitive molds. The observed protease resistance can be attributed to the compact structure of the small, basic, cysteine-rich antifungal proteins, as it has been proposed for AFP (Lacadena et al., 1995).

Among the main physicochemical factors affecting protein activity in foods are pH and heat treatments. To study the impact of these two factors on PgAFP activity, one sensitive strain from each genus was selected as reference. PgAFP was highly resistant to a wide range of temperature (Fig. 3). Intense heat treatments partially inactivated 300 μg/mL PgAFP, as can be inferred from the loss of inhibition on the less sensitive *A. niger* and the residual effect on the more sensitive *P. restrictum.* Similarly to its heat stability, PgAFP withstood a broad range of pH values (Fig. 4). These characteristics are similar to those of other antifungal proteins from molds. AFP from *A. giganteus* is stable to protease degradation, high temperature, and a broad pH range due to a specific folding pattern (Lacadena et al., 1995). Similarly, AcAFP from *A. clavatus* is also resistant to 100 °C and is effective in a 5–12 pH range (Skouri-Gargouri et al., 2010). AFP folds into a small and compact β-barrel, stabilized by four disulfide bridges formed by cysteine residues (Campos-Olivas et al., 1995). It has been assumed that AcAFP, Anafp, NAF, and PAF also have a similar tertiary structure, with three or four disulfide bridges formed by the cysteine residues present in these proteins (Marx, 2004; Skouri-Gargouri et al., 2009). PgAFP has characteristics common to these antifungal proteins, including six cysteine residues and a quite high similarity in the amino acid sequence, leading a tertiary structure based on a compact β-barrel (Rodríguez-Martín et al., 2010).

Treatment with the two PgAFP concentrations assayed was effective in reducing growth of *A. flavus* and *P. restrictum* in sausage samples (Table 2, Fig. 5). The counts of *A. flavus* in treated samples were always below 3.5 log CFU/g. This effect can serve to prevent development of hazardous levels at which aflatoxin B1 production has been described on dry-cured hams (Rodríguez et al., 2012). Given the observed fungistatic effect of PgAFP, it is not expected that sufficient inhibition would be maintained throughout the whole ripening time. Thus, the antifungal protein would be most efficient if applied at the time when the product is most susceptible to mold development. Direct application of PgAFP by spraying on the product in the key stages could be useful to delay mold growth to allow corrective actions to be taken before mycotoxins are produced. The low identity of PgAFP in relation to other antifungal proteins from molds, as well as the differences in site of action and possible targets (Marx, 2004) sustain the combined use of PgAFP with other antifungal proteins to take advantage of complementary effects.

Although the inhibitory activity of some antifungal proteins produced by molds has been reported (Lee et al., 1999; Kaiserer et al., 2003; Theis et al., 2003; Skouri-Gargouri and Gargouri, 2008), this is the first time that the inhibitory effect against toxigenic molds has been proved in foods. Given that *P. chrysogenum* is used to obtain generally recognized as safe (GRAS) compounds and has a long record of industrial use, the potential application of PgAFP in foods should be considered additionally with good manufacturing practice through HACCP procedures for reducing the health hazard due to mycotoxins in dry-fermented sausages. In addition, *P. chrysogenum* CECT 20922 is able to limit growth of aflatoxin and OTA-producing molds and OTA accumulation in dry-cured Iberian ham throughout the processing (Bernáldez et al., 2014; Rodríguez et al., 2015).

In conclusion, PgAFP showed an efficient inhibition of undesired molds, including some of the main toxigenic species for dry-ripened foods, when these fungi were grown in culture medium and in a dry-fermented sausage. Moreover, PgAFP withstands most proteases, intense heat and a wide range of pH values. This protein can be of interest to control unwanted fungi in dry-ripened foods.

Acknowledgments

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IV.2. Efecto de PgAFP y de su combinación con microorganismos bioprotectores para maximizar su efecto de inhibición sobre el crecimiento de mohos y producción de micotoxinas en alimentos madurados

IV.2.1. Evaluación en producto cárnico crudo-curado

Effect of PgAFP and protective cultures on* Aspergillus parasiticus *growth inhibition and aflatoxin production on dry-fermented sausage

Effect of PgAFP and protective cultures on *Aspergillus parasiticus* growth inhibition and aflatoxin production on dry-fermented sausage

Abstract

Toxigenic moulds can grow and produce mycotoxins on intermediate moisture foods. The antifungal protein PgAFP can control this population on dry-cured meat products, but the effect of this protein on mycotoxin production is unknown. Thus, the objective of this work was to study the effect of PgAFP on aflatoxin production through gene expression. In addition, given the limited inhibitory ability of PgAFP, to maximize the inhibitory ability, different combined treatments with PgAFP, *Debaryomyces hansenii* and/or *Pediococcus acidilactici* were studied in culture medium and on dry-fermented sausage against an aflatoxigenic strain of *Aspergillus parasiticus*. In culture medium, PgAFP increased aflatoxin production and *P. acidilactici* reduced it dramatically. Relative gene expression of *foxA* involved in peroxisomal β-oxidation and *aflP*, involved in aflatoxin biosynthesis, were studied to reveal the effect of a potential reactive oxygen species (ROS) induced by PgAFP in aflatoxin production. The aflatoxin overproduction by the effect of PgAFP cannot be linked to peroxisomal β-oxidation. The combination of PgAFP and *D. hansenii* provided a successful inhibitory effect on *A. parasiticus* growth as well as aflatoxin production for 15 days on dry-fermented sausage in a wide activity water range. *P. acidilactici* did not enhance the protective effect of the combination of these two agents. Therefore, the combined treatment of PgAFP and *D. hansenii* can provide a protective effect against toxigenic moulds in dry-cured foods.

Key words: Aflatoxin, antifungal protein, *Aspergillus parasiticus*, dry-fermented sausage.

1. Introduction

The environmental conditions during the ripening of dry-cured meat products favor growth of toxigenic molds (López-Díaz, Santos, García-López, & Otero, 2001; Núñez, Rodríguez, Bermúdez, Córdoba, & Asensio, 1996). These molds can produce mycotoxins, such as aflatoxins, ochratoxin A, and patulin on dry-cured meat products (Rodríguez, Rodríguez, Martín, Delgado, & Córdoba, 2012; Rodríguez, Rodríguez, Martín, Nuñez, & Córdoba, 2012). Aflatoxins, produced mainly by *Aspergillus flavus* and *Aspergillus parasiticus*, have oncogenic, immunosuppressive, and hepatotoxic properties (Bezerra da Rocha, Oliveira Freire, Feitosa Maia, Florindo Guedes, & Rondina, 2014), being classified as group 1 carcinogenic to humans by the International Agency for Research on Cancer. Therefore, it is necessary to carry out strategies to prevent aflatoxigenic molds from growing on dry-cured meat products.

Some molds produce proteins that inhibit other molds, whereas the activity against yeasts and prokaryotes is quite limited (Marx, 2004). These antimicrobial proteins may serve to combat unwanted molds in dry-cured meat products. PgAFP from *Penicillium chrysogenum* (Rodríguez-Martín et al., 2010) is one of these antifungal proteins showing multifactorial mechanism of action based on reactive oxygen species (ROS) production, membrane permeability increase, and apoptosis induction (Delgado, Owens, Doyle, Asensio, & Núñez, 2015). The antifungal protein PgAFP inhibits some toxigenic molds in culture medium and on dry-fermented sausage, requiring less than 4.9 μg/ml for the highly sensitive molds and from 9.8 μg/ml for low sensitive molds, including *A. parasiticus*. However, this effect is rather time-limited, displaying the main effect in the first 96 h of incubation (Delgado, Acosta, et al., 2015). PgAFP can also hamper aflatoxins biosynthesis. *A. flavus* treated with PgAFP for 24 h showed lower relative abundance of key enzymes in aflatoxin biosynthesis pathway, including O-methyltranferase, VERB synthase, and VER1 dehydrogenase (Delgado, Owens, et al., 2015), but the effect on aflatoxin production was not tested. On the other hand, ROS contribute to aflatoxin production (Jayashree & Subramanyan, 2000; Reverberi et al., 2005), which makes it necessary to study the influence of PgAFP on aflatoxin production.

The effect of ROS on aflatoxigenic molds is related to redox balance through β-oxidation, and expression of *foxA* gene has been used as a marker for β-oxidation (Reverberi et al., 2012). Thus, studying *foxA* expression could elucidate whether PgAFP treatment increase aflatoxin production by oxidative stress. Similarly, expression of *aflP* gene, coding for O-methyltransferase A, serves to assess the rate of aflatoxin biosynthesis (Lozano-Ojalvo, Rodríguez, Bernáldez, Córdoba, & Rodríguez, 2013).

On the other hand, the limited length of inhibition by PgAFP makes it necessary to develop strategies that extend growth inhibition to reduce mycotoxin levels. A plausible alternative can be based on the combined use of PgAFP and microbial strains endowed with antifungal activity. Among the microorganisms usually present on dry cured products, yeasts thrive on dry-cured hams for the whole ripening time, being most of them *Debaryomyces hansenii* in matured hams (Núñez, Rodríguez, Córdoba, Bermúdez, & Asensio, 1996). Some of these strains have shown antifungal capability against toxigenic penicillia cured meat products (Andrade, Thorsen, Rodríguez, Córdoba, & Jespersen, 2014; Núñez et al., 2015). Also lactic acid bacteria have been proved as potent mold inhibitors (Li et al., 2014). *Pediococcus acidilactici* are known producers of antifungal compounds (Effat, Ibrahim, Tawfik, & Sharaf, 2001), some of them being active against *A. parasiticus* (Mandal, Sen, & Mandal, 2013) and assumed to produce bacteriocins (Montiel, Bravo, & Medina, 2013).

The aim of this work was to investigate the antifungal capability of PgAFP, *D. hansenii* and *Pediococcus acidilactici* against *A. parasiticus* on culture medium and dry-fermented sausage. To understand how these agents affect mold growth and aflatoxin production, the effect on *foxA* and *aflP* genes expression were studied. This knowledge would allow to get the highest effect from potential biological agents to combat toxigenic molds in dry-cured meat products.

2. Material and methods

2.1. Strains

Two mold strains obtained from Spanish Type Culture Collection (CECT, Valencia, Spain) were used in this study: the PgAFP sensitive aflatoxin-producer *A. parasiticus* CECT 2682 and the PgAFP antifungal protein producer *P. chrysogenum* CECT 20922. In addition, two potential antifungal strains were used: the yeast *D. hansenii* Dh253 from the microbial collection of Food Hygiene and Safety of the University of Extremadura (Cáceres, Spain) and *P. acidilactici* fargo 35 supplied by Laboratorios Amerex (Colmenar Viejo, Spain).

2.2. PgAFP production and purification

P. chrysogenum CECT 20922 was grown in potato dextrose broth (PDB) pH 4.5 for 21 days at 25 °C. The mycelium was removed and the media was filtered to get cell free media. PgAFP was isolated from 450 ml of the cell-free media trough fast protein liquid chromatography (FPLC) with a cationic exchange column HiTrap SP HP (Amersham Biosciences, Uppsala, Sweden), further purified with a HiLoad 26/60 Superdex 75 gel filtration column for FPLC (Amersham Biosciences) as previously described (Acosta, Rodríguez-Martín, Martín, Núñez, & Asensio, 2009). The protein isolated and concentrated was sterilized through filtration (0.22 µm, Thermo Fisher Scientific, Waltham, MA, USA) and its concentration was assessed by the Lowry method (Lowry, Rosebrough, Farr, & Randall, 1951).

2.3. Growth inhibition in culture media and mycotoxin extraction

The effect of PgAFP, *D. hansenii*, and *P. acidilactici* on *A. parasiticus* was evaluated both separately and in all different combinations. For this, 5 ml of yeast extract sucrose broth (YES) were inoculated with 10^5 conidia/ml *A. parasiticus*. To provide a high level of the biological agents, 10^6 cells/ml *D. hansenii* (Dh), 10^6 cells/ml *P. acidilactici* (Pa), and 10 µg/ml PgAFP (Pg) the following 7 different batches were obtained: Pg, Dh, Pa, Pg+Dh, Pg+Pa, Dh+Pa, and Pg+Dh+Pa. Additionally, an untreated batch used as a control. Samples were incubated for 15 days at 25 °C to stimulate aflatoxin production (Lozano-Ojalvo et al., 2013). All the assays were carried out in triplicate. After incubation, 5 ml of chloroform were added to each test tube incubated for 1 h shaking at 100 rpm at room temperature in darkness. Then, the chloroform

was separated and evaporated to dryness under a gentle stream of N_2. The mycelium was recovered from the aqueous residue by filtering through a miracloth (Calbiochem, Darmstadt, Germany), dried at 100 °C up to constant weight, and weighed.

2.4. Growth inhibition on sausages and mycotoxin extraction

To test the potential of some combinations of protective cultures, the ripening stage on sausages was simulated using a commercial raw dry-fermented sausage (pH 5.8, aw 0.96) shortly after stuffing in natural casing from beef. The sausage was cut into 7-8 mm thick slices and dipped into ethanol to eliminate outer contamination. The ethanol was left to evaporate in a laminar flow cabinet (Bio Flow II, Telstar, Tarrasa, Spain) prior to placing the slices in pre-sterilized (ethanol and UV-light) receptacles containing a saturated KCl solution to keep relative humidity constant at 84% after vapour-liquid equilibrium. *A. parasiticus* was inoculated (10^5 conidia/cm^2) on both sides of each slice. No antifungal treatment was applied to the untreated batch. Two treated batches were made: Pg+Dh+Pa, with 10 µg/cm^2 PgAFP, 10^6 cells/cm^2 *D. hansenii*, and 10^6 cells/cm^2 *P. acidilactici*; and Pg+Dh, with 10 µg/cm^2 PgAFP and 10^6 cells/cm^2 *D. hansenii*, similarly to the culture medium. Every batch was carried out in triplicate. All samples received the same volume of liquid by adding sterile phosphate buffer as required, and the liquid excess was left to dry in the laminar flow cabinet. The samples were incubated for 5 and 15 days at 25 °C to stimulate aflatoxin production (Lozano-Ojalvo et al., 2013). A_w values were determined in a Novasina Lab Master from Novasina AG (Lachen, Switzerland). *A. parasiticus* and *D. hansenii* counts were assessed by plating in PDA and incubated for 72 h at 25 ºC, according to the characteristic colony morphology. Lactic acid bacteria counts were evaluated on MRS agar, incubated for 72 h at 30 °C.

Mycotoxins produced on sliced sausages were extracted as previously described (Rodríguez, Rodríguez, Martín, Delgado, et al., 2012). Briefly, each sausage slice was macerated under shaking in a dark flask with 60 ml acetonitrile-water (9:1, v/v) containing 0.1% formic acid together with 50 ml hexane. The acetonitrile-water phase was recovered and filtered through sodium sulphate anhydrous. Then, the filtrate was mixed with additional 50 ml of hexane and shaken. The acetonitrile-water phase was filtered again and evaporated in a rotatory evaporator at 40–45 °C. The residue was resuspended in 1 ml chloroform, filtered through a 0.45 µm nylon membrane (MSI, Westboro, MA, USA).

2.5. Mycotoxin quantification

Extracts from both culture medium and sausages were analysed by ultra high-performance liquid chromatography–mass spectrometry (uHPLC–MS) in an HPLC Thermo Scientific Dionex ultimate 3000 pnmp, a mass detector (MS) model Bruker Amazon S.L., an autosampler (Ultimate 3000), a degasser (3000 Ultimate) and an ion trap (Amazon SL.). A C18 reverse-

phase column of 10 cm length, 2.1 mm inside diameter and 2 µm particle size was used as stationary phase. As mobile phase a 0.1% formic acid-10 mM ammonium formiate (solvent A) and acetonitrile (solvent B) was used. The separation was performed with the flow rate set at 200 µl/min and the following gradient: [0 min] 2% B, [0-0.1 min], 40% B, [0.1-4 min] 60% B,[4-7 min] 80% B, [7-8.5 min] 80% B, [8.5-8.51 min] 98% B, [8.51-12 min] 98% B, [12-12.01 min] 2% B and [12.01-15 min] 2% B. Precursor ions 313 and 329, and quantitation ions 285 and 311 for aflatoxins B_1 and G_1 (AFB_1 and AFG_1), respectively.

These parameters were compared to those obtained from commercial mycotoxins (Sigma-Aldrich, Madrid, Spain). The calibration curves for AFB_1 and AFG_1 (1-500 ng) by uHPLC-MS revealed a linear relationship ($r^2 \geq 0.99$) between detector response and amount of AFB_1 and AFG_1 standards. The minimum detectable value or limit of detection (LOD) was estimated from the calibration curve, according to the equation: $LOD = 3\ (s_B^2 + s_i^2 + (i/m)^2\ s_m)^{1/2}/m$ (Long & Winefordner, 1983) being "m" the slope of the calibration curve, "I" the intercept term and "s_B", "s_i" and "s_m" the standard errors of the blank, the intercept term and the slope of the calibration curve, respectively. Assuming a normal distribution of the estimated quantities, α (error of the first type) = β (error of the second type) = 0.05, the quantification limit (LOQ) was 3.04 LOD (Currie, 1999). The LOD obtained in this study were 4 µg/kg and 1.5 µg/kg, and the LOQ were 12 µg/kg and 4.5 µg/kg respectively for AFB_1 and AFG_1.

2.6. RNA isolation and cDNA synthesis

To test the influence of PgAFP, *D. hansenii* and *P. acidilactici* on *A. parasiticus* gene expression, four batches were prepared in YES broth: *A. parasiticus* (10^5 conidia/ml) was co-cultivated in tubes separately with PgAFP (10 µg/ml), *D. hansenii* (10^6 cells/ml) or *P. acidilactici* (10^6 cells/ml), and with all of them together. The untreated batch was inoculated solely with *A. parasiticus*. The tubes were incubated at 25°C for 5 days. For RNA extraction, mycelium was -saline buffer (PBS), frozen in liquid nitrogen and ground with a mortar and pestle. Then the powder was resuspended in 750µl RLT buffer (RNeasy® Plant Mini kit, Qiagen, Hilden, Germany) containing 15µl β-mercaptoethanol. Samples were processed with the RNeasy® Plant Mini kit according to manufacturer's instructions. RNA quality and quantity was spectrophotometrically determined using in a NanoDrop 2000c spectrophotometer (Thermo Scientific, Waltham, MA, USA). Then, samples were treated with DNase I, RNase-free (Fermentas, St. Leon-Rot, Germany) following manufacturer's instructions, and checked for background double stranded DNA by qPCR for *β-tubulin* genes as described below. Finally, cDNA was synthesized using 500 ng RNA according to PrimeScript™ RT Reagent kit protocol (Takara, Otsu, Japan).

2.7. Real-time PCR analysis of gene expression

The expression of genes *aflP* (formerly *omt-1*) for aflatoxin biosynthesis (Yu et al., 2004), *foxA* for β-oxidation (Roze et al., 2010),and *β-tubulin* as housekeeping (Rodríguez, Medina, Córdoba, & Magan, 2014) were assessed to evaluate the effect of the treatments on *A. parasiticus*. Primers to evaluate the *foxA* expression were designed from the gene AFLA_041590 (GeneBank accession no. XM_002377580), as previously described (Roze et al., 2010). Similarly, to study *β-tubulin* expression a couple of primers were designed from *A. parasiticus* *β-tubulin* sequence (GeneBank accession no. FR775333.1)

To quantify the relative expression of the genes, *foxA* and *β-tubulin* genes expression were assessed by using the SYBR Green qPCR in an Applied Biosystems ViiATM 7 Real-Time PCR System (Applied Biosystems, Foster City, California, USA). To optimize the primer concentration, different concentrations from 800 to 200 nM were tested. The optimized SYBR Green protocol was carried out in a final volume of 25 µl containing 5 ml of template DNA, 12.5 µl of 2x SYBR® *Premix Ex Taq*™ (Takara, Otsu, Japan), 0.5 µl of 50x ROX™ Reference Dye (Takara) and 400 nM of each primer. The thermal cycling conditions were the following: a single step of 10 min at 95 °C, 40 cycles of 95 °C for 15 s and 60 °C for 1 min. After the final PCR cycle, a melting curve analysis of the PCR products was carried out by heating from 60 to 95 °C and continuous measurement of the fluorescence to verify the PCR product. The *aflP* gene expression was evaluated following the concentrations and conditions previously described (Rodríguez, Rodríguez, Luque, Martín, & Córdoba, 2012). Every qPCR assay described above was carried out by triplicate. Gene expression ratio was calculated using the $2^{-\Delta\Delta CT}$ method (Livak & Schmittgen, 2001). The endogenous control was set as the expression of *β-tubulin* gene and the untreated batch described above was used as calibrator sample. For every primer pair, a standard curve was generated to check the amplification efficiency from ten-fold serial dilution 100 to 0.01 ng/µl of DNA from *A. parasiticus*. In addition, the differences in amplification efficiencies between the housekeeping and the target gene were less than 10%, as required to apply the relative quantification method (Schmittgen & Livak, 2008).

2.8. Statistical analysis

Statistical analyses were performed with the IBM SPSS v.22. Data from mycelia weight, microbial counts, mycotoxin concentration and gene expression were tested for normality (Kolmogorov-Smirnov with Lilliefors correction) and homoscedasticity (Levene's test). Given that these data were non-normally distributed, mean values were compared using nonparametric Kruskal–Wallis test. To compare treatments in pairs, Mann-Withney U test was applied ($p \leq 0.05$). To study the relationship between expression of *aflP* and *foxA* genes, Spearman correlation was applied.

3. Results

3.1. Growth inhibition and mycotoxin production in YES broth

To study the antifungal capability of the three agents, both separately and in the different combinations, eight batches were tested against *A. parasiticus* at 15 days incubation in YES broth. *A. parasiticus* growth was substantial in all treatments tested, with average values ranging from 58 to 142 mg mycelium dry weight per 5 ml YES broth, though heterogeneous within batches. As a result, no statistically significant differences were found in *A. parasiticus* growth between the treatments. All expected mycotoxins were produced in the untreated batches by *A. parasiticus*. Aflatoxin production showed differences ($p \leq 0.05$) depending on the treatment applied. AFB_1 and AFG_1 production increased with PgAFP treatment, whereas all treatments containing *P. acidilactici* strongly lowered aflatoxins production. *D. hansenii* inoculation also led to lower AFB_1 production, and when combined with PgAFP seemed to counteract the stimulating effect of PgAFP. AFG_1 was also detected in higher quantity in PgAFP and *D. hansenii* co-inoculated than in the untreated batch (Fig. 1).

3.2. Growth inhibition and mycotoxin production on sausages

The effect of protective cultures on mould development was evaluated in fresh fermented sausages slices simulating the ripening environmental conditions. A_w values reached 0.93 and 0.86 at 5 and 15 incubation days, respectively. The microbial load in pre-sterilised slices just before inoculation was 2.3 log cfu/cm^2 for moulds, 1 log cfu/cm^2 for lactic acid bacteria, and lower than 1.7 log cfu/cm^2 for yeasts. Yeasts counts were always over 5 log cfu/cm^2 in *D. hansenii*-inoculated batches, but lower than 2 log cfu/cm^2 in the untreated batch. Similarly, MRS counts were over 6.8 log cfu/cm^2 in *P. acidilactici*-inoculated batches, but lower than 4.5 log cfu/cm^2 in all batches not inoculated with *P. acidilactici*. Mould counts from untreated batches both at 5 and 15 days were over 6.5 and 7.4 log cfu/cm^2 respectively. Pg+Dh or Pg+Dh+Pa treatments dramatically lowered mold counts about 3 log units in *A. parasiticus* batches.

On the other hand, mycotoxin production in the sausages was somehow parallel to fungal growth. *A. parasiticus* produced high AFB_1 and AFG_1 levels in untreated sausages, both at 5 and 15 incubation days (Table 1). Aflatoxin production by *A. parasiticus* in sausages subjected to any of the two treatments applied showed lower mycotoxin content (than the respective untreated batches both at days 5 and 15.

3.3. Gene expression

The amplification efficiencies from each primer pair used, calculated from the slopes of the standard curves, revealed that the maximum difference between the amplification efficiency

values of the housekeeping and the other two target genes was 5 % for *A. parasiticus* (Table 2), thus the $2^{-\Delta\Delta CT}$ method was applied. Noteworthy, CT values for a*flP* gene from all samples, including untreated batch, were very close to those obtained from the no template controls. On the other hand, the expression of *aflP* gene was repressed in *A. parasiticus* by the sole action of either PgAFP or *P. acidilactici* as well as the combined treatment of Pg+Dh+Pa, at 5 incubation day (Fig. 2).

To study the possible effect of ROS induction by PgAFP on *A. parasiticus* the *foxA* gene expression was evaluated at 5 incubation days to make sure that the activity of PgAFP on *A. parasiticus* was high. The expression of *foxA* from PgAFP-treated samples did not differ from untreated batch ($p > 0.05$). Only differed the combined treatment of Pg+Dh+Pa differed ($p \leq 0.05$) from the untreated batch, leading to a 4-fold over-expression. a*flP* gene expression values did not correlate with *foxA* values ($p > 0.05$).

4. Discussion

As expected, PgAFP did not show antifungal ability at 15 days on *A. parasiticus* grown on culture medium. The PgAFP concentration used was too low to reach a significant effect, as it was shown previously (Delgado, Acosta, et al., 2015). In addition, none of the two microbial strains, either alone or in any combination used, effectively inhibited mold growth in the culture medium. However, both Pg+Dh and Pg+Dh+Pa combinations showed a remarkable inhibition on *A. parasiticus* counts on the sausages (Table 1). Counts of *A. parasiticus* at day 5 in non-treated sausages were over 6.5 log cfu/cm^2, whereas in the two treated batches, i.e.: PgAFP+Db and PgAFP+Db+Pa, were below 3.5 log cfu/cm^2. Given that 3.5 log cfu/cm^2 has been suggested as the limit to keep minimal risk of AFB_1 accumulation in dry-cured hams (Rodríguez, Rodríguez, Martín, Nuñez, et al., 2012), the two combined treatments applied could be useful to control aflatoxigenic moulds in dry-cured meat products. At 15 days incubation time, period covering most of ripening stage of dry-fermented sausages, mold count in treated batches were still around 0.1% of the fungal load in the untreated sausages.

The lack of inhibitory effect of the tested antifungal agents in the culture medium as compared to the efficient inhibition in dry-fermented sausages can be attributed to the differences in substrate availability. The mode of action proposed for yeasts to control molds in culture media is competition for nitrogen compounds, sugars, and vitamins (Liu, Luo, & Long, 2013). However, production of some volatile compounds derived from branched amino acids by *D.* inhibition (Andrade, Córdoba, Casado, Córdoba, & Rodríguez, 2010; Núñez et al., 2015). The culture medium used contains 125 g/l sucrose and 20 g/l yeast extract, providing readily available sources of carbon and nitrogen compounds, as well as vitamins, especially those belonging to B complex. Conversely, sausages contain lower

amounts of sugars and vitamins, but higher levels of free amino acids throughout the ripening process (Demasi, Wardlaw, Dick, & Acton, 1990; Hierro, de la Hoz, & Ordóñez, 1999). Therefore, the lower amount of sugars and vitamins but higher amino acid content in the sausage can be the key factor for the efficient inhibition of *A. parasiticus* by *D. hansenii* and *P. acidilactici*.

Applying only PgAFP cannot be supported for dry-cured foods, given that this protein increased aflatoxins production on *A. parasiticus* in YES broth (Fig. 1) and its fungistatic effect was not enough to maintain sufficient inhibition throughout the whole ripening time (Delgado, Acosta, et al., 2015). On the other hand, the same strain of *D. hansenii* used here was barely active at lower (0.84) compared to high (0.94) a_w values when grown on dry-cured ham slices for 15 days (Andrade et al., 2014). Therefore, *D. hansenii* alone is not expected to efficiently inhibit *A. parasiticus* in sausages at a_w values around 0.85. Conversely, the combination of PgAFP and *D. hansenii* efficiently inhibited *A. parasiticus* growth in the sausage samples (Table 1). This has to be explained by the joint effect of the different mechanisms of action of these two antifungal agents. Thus, the limited effect of PgAFP can be decisive to help other biological agents reach an efficient inhibition of mycotoxigenic molds in dry-cured meats, particularly at low a_w values. Thus, the effect of the combinations Pg+Dh and Pg+Dh+Pa on aflatoxin production was tested on sausage. These two treatments efficiently lowered aflatoxin production for at least 15 days on sausage samples, with no additional effect attributable to *P. acidilactici*. Since yeast extract and glucose enhance production of antifungal metabolites in *P. acidilactici* (Effat, Ibrahim, Tawfik, & Sharaf, 2001), the lack of additional effect due to this bacteria can be explained by the shortage of glucose and readily available nitrogen compounds in sausage samples.

However, 10 μg/ml PgAFP increased aflatoxin production by *A. parasiticus* in YES broth (Fig. 1), whereas *P. acidilactici* led to lower aflatoxin levels. Therefore, mycotoxin production does not only depend on mould growth. The oxidative status in the fungal cell severely affects mycotoxin production (Schmidt-Heydt, Stoll, Schütz, & Geisen, 2014). Several antifungal proteins from moulds provoke ROS in sensitive strains (Galgóczy et al., 2013; Kaiserer et al., 2003), including PgAFP in *A. flavus* (Delgado, Owens, et al., 2015). ROS production is regarded as a prerequisite for the onset of aflatoxin production (Reverberi et al., 2005; Reverberi et al., 2012). Conversely, several antioxidant substances or enzymes inhibit aflatoxin production (Kim et al., 2008; Reverberi et al., 2005). For all this, the effect of PgAFP and *P. acidilactici* on the oxidative status and the rate of aflatoxin biosynthesis of *A. parasiticus* was studied.

The oxidative role of PgAFP could be related to the higher levels of aflatoxins found in *A. parasiticus*, as discussed later. Co-inoculation of *A. parasiticus* with *P. acidilactici* led to lower AFB_1 production in YES, irrespectively of the addition of PgAFP, whereas the separate

inoculation of *D. hansenii* had no significant effect. Therefore, *P. acidilactici* seems to prevent the increment of mycotoxin production provoked by PgAFP. The mechanism behind the lower aflatoxin biosynthesis is not known. The lower aflatoxin production with lactic acid bacteria has been related to inhibition of aflatoxin biosynthesis by low-molecular-weight inhibitory compounds as well as removing due to aflatoxin binding (Dalié, Deschamps, & Richard-Forget, 2010).

The PgAFP mechanism of action on sensitive molds seems to be multifactorial, where membrane permeabilization, ROS production or apoptosis induction play a key role (Delgado, Owens, et al., 2015). The effect of ROS on aflatoxin synthesis is related to redox balance through β-oxidation (Reverberi et al., 2012). The expression of genes *foxA* has been used as a marker for peroxisomal β-oxidation (Reverberi et al., 2012). Besides, *aflP* gene has been used to study the effect of environmental factors on aflatoxin production (Lozano-Ojalvo et al., 2013). Thus, *aflP* and *foxA* expression was studied to elucidate the effect of PgAFP on aflatoxin production and the potential role of oxidative stress on such production.

aflP expression in *A. parasiticus* grown in YES was very low, irrespectively of the treatment applied. PgAFP did not provoke *aflP* overexpression, but it rather repressed a*flP* expression (Fig. 2). Similarly, no statistically significant differences were found for *foxA* gene expression due to PgAFP treatment. These results are consistent with the lower relative abundance of O-methyltransferase, coded by *aflP* gene, and the unaffected level of peroxisomal muntifunctional β-oxidation protein, coded by *foxA* gene, found in PgAFP treated *A. flavus* (Delgado, Owens, et al., 2015). In addition, *D. hansenii* did not alter *foxA* and *aflP* expression, supporting that the effect of this yeast reducing antioxidant effect. Therefore, the aflatoxin overproduction observed in PgAFP-treated *A. parasiticus* at 15 days would not be initiated by an increased β-oxidation due to ROS. Given that ROS induction are among the early antifungal effects of PgAFP, no later effect on β-oxidation should be expected to be responsible for the observed aflatoxin production. In addition, the increased *foxA* expression in the combined treatmet of Pg+Dh+Pa does not correlate with a higher aflatoxin production at 15 days. These results suggest that the effect of ROS on aflatoxin biosynthesis cannot be explained solely through β-oxidation. In a recent paper (Roze et al., 2015) it is reported that upon exposure to exogenous ROS, secondary ROS are generated in endosomes during aflatoxins biosynthesis. It is suggested that this results in an adaptation of cellular metabolism to promote increased tolerance to H_2O_2 in the next generation of germinating spores. Studying the effect of PgAFP on the secondary ROS will require further studies.

On the other hand, *P. acidilactici*, either alone or combined with Pg and Dh, down-regulated *aflP* gene expression in *A. parasiticus* at day 5 (Fig. 2), which is parallel to a lower aflatoxin

346 levels at 15 incubation days. This results may be explained by the production low-molecular-
347 weight antimycotoxigenic compounds (Chang & Kim, 2007; Gourama & Bullerman, 1995)

348 *A. parasiticus* produced AFB_1 and AFG_1 when grown on the untreated sausages, reaching levels
349 well above the levels regarded as safe for various foods (European Commission, 2006) both at 5
350 and 15 days of incubation (Table 1). The amount of AFB_1 and AFG_1 produced on sausages was
351 higher than that obtained in YES. This can be explained by the limited availability of nutrients
352 (Miller, 2001) and the increased levels of free amino acids (Payne & Hagler Jr., 1983) that
353 would increase AFB_1 and AFG_1 biosynthesis in sausages by *A. parasiticus*. Aflatoxin
354 production was greatly reduced by the effect of the two protective combinations tested on
355 sausages, not being detected at day 5 of incubation and only at slightly higher levels than the
356 limits set in foods (European Commission, 2006) at 15 days. However, given that the conditions
357 set were favorable for the development and mycotoxin production, it is expected that any of the
358 two combinations tested be sufficient to control the usual fungal contamination in cellars.

359 The successful antifungal effect of both treatments with Pg+Dh on dry-fermented sausage
360 supports their use as a preventive measure against aflatoxigenic *A. parasiticus* or as a corrective
361 action when this mold has been detected on the meat product.

362 The inclusion of *P. acidilactici* to the protective culture did not substantially improve the
363 inhibition on *A. parasiticus* growth or mycotoxin production. Thus, the contribution of *P.*
364 *acidilactici* seems to be negligible. This fact has to be related to the above discussed lack of
365 growth on inoculated sausages.

366 In conclusion, the inhibition of *A. parasiticus* growth and mycotoxin production by the
367 combined treatment of PgAFP and *D. hansenii* has been proved in dry-fermented sausage at
368 similar conditions to The antifungal activity seems to be based on the
369 different mechanisms of action from every component of the protective mix, which enhances
370 this protective effect.

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6. Figures and tables

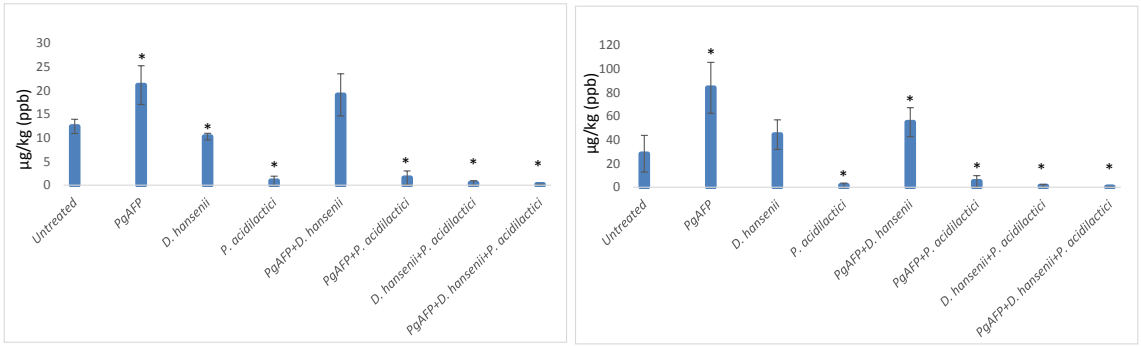

Figure 1. Effect of different combinations of protective agents in aflatoxin B_1 (left) and G_1 (right) production by *Aspergillus parasiticus* in yeast extract sucrose broth after 15 days. Bars represent standard deviation. * ($p \leq 0.05$)

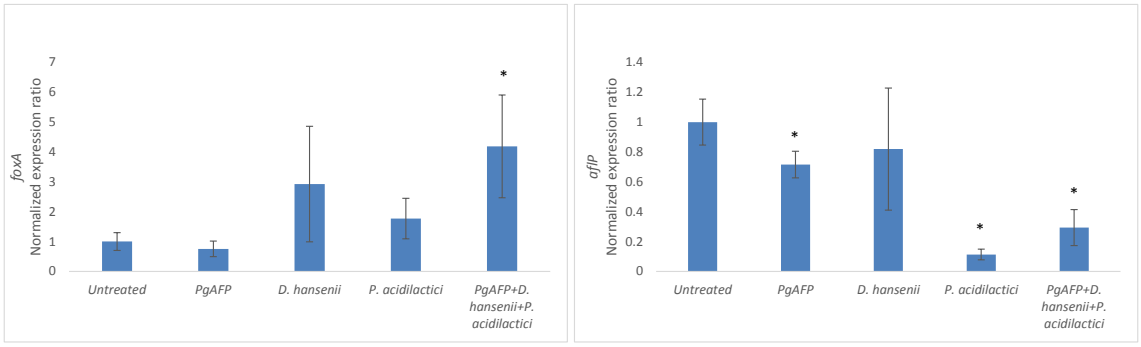

Figure 2. Effect of different antifungal agents on relative gene expression of *foxA* (left) and *aflP* (right) genes in yeast extract sucrose broth after 5 days. Bars represent standard deviation. * ($p \leq 0.05$)

Table1. Aflatoxin B_1 (AFB_1) and G_1 (AFG_1) concentrations (µg/kg) and mould counts (log cfu/cm^2) in dry-fermented sausage slices at 5 and 15 incubation days. Data are given as mean ± SD. * ($p \leq 0.05$)

	Day 5		
Mycotoxin	Control	Pg+Dh	Pg+Dh+Pa
AFB_1	86±8	<LOD	<LOD
AFG_1	152±9	<LOD	<LOD
Mould counts	6.54±0.22	<3[a]*	<3[a]*
	Day 15		
Mycotoxin	Control	Pg+Dh	Pg+Dh+Pa
AFB_1	115±0,43	<LOD*	<LOD*
AFG_1	170±31	8.3±4.5*	10±1.3*
Mould counts	7.42±0.09	4.26±0.28[a]	4.74±0.38[a]

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555 Table 2. Nucleotide sequence of primers used for qPCR assay

Primer name	Nucleotide sequences (5'-3')	Efficiencies	Product size	Position	Reference
F-Omt-1	GGCCGCCGCTTTGATCTAGG	104%	123	[a]1485	(Rodríguez, Rodríguez, Luque, Martín, & Córdoba, 2012)
R-Omt-1	ACCACGACCGCCGCC			1593	
F-β-tub	TCTTCATGGTTGGCTTCGCT	101%	98	[b]964	This study
R-β-tub	CTTGGGGTCGAACATCTGCT			1042	
F- foxA	ACCGCAACCCTCTTCACATT	106%	73	[c]1196	This study
R- foxA	AGACCGTGCAGGATAGGAGT			1268	

556 [a] Positions are in accordance with published sequence of the *aflP* (*omt-1*) gene of *A. flavus*
557 (GeneBank accession no. L25835.1).
558 [b] Positions are in accordance with the published sequences of the *β-tubulin* gene of *A.*
559 *parasiticus* (GeneBank accession no. FR775333.1).
560 [c] Positions are in accordance with published sequence of the *foxA* gene of *A. flavus* (GeneBank
561 accession no. XM_002377580).
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IV.2.2. Evaluación en queso

Effect of PgAFP and protective cultures on* Aspergillus flavus *and* Aspergillus parasiticus *growth inhibition and aflatoxin production in a calcium-enriched medium and on cheese

Effect of PgAFP and protective cultures on *Aspergillus flavus* and *Aspergillus parasiticus* growth inhibition and aflatoxin production in a calcium-enriched medium and on cheese

Intermediate-moisture foods are adequate substrates for various microorganisms, including lactic acid bacteria (LAB) (Casquete et al., 2012; Papadima and Bloukas, 1999), molds (Núñez et al., 1996) and yeasts (Asefa et al., 2009). These microorganisms play a key role in the development of sensory characteristics of intermediate moisture foods (Andrade et al., 2010; Martín et al., 2006; Urbach, 1995). However, some molds can have a negative impact by altering the sensory characteristics or producing toxic metabolites (Alapont et al., 2014; Filtenborg et al., 1996). Aflatoxins are among the most harmful mycotoxins, displaying oncogenic, immunosuppressive, hepatotoxic, and teratogenic effects (Bezerra da Rocha et al., 2014). Dairy products, including cheese and yoghurt, are susceptible to fungal attack (Crowley et al., 2013) and support the production of high levels of aflatoxins (Lie and Marth, 1967; Taniwaki et al., 2001). To control the mycotoxin risk, it is necessary to establish a Hazard Analysis Critical Control Point (HACCP) plan for intermediate-moisture products (Asefa et al., 2011).

Antifungals compounds can be used for this purpose, but chemical fungicides would leave residues, which is against consumers demand (Núñez et al., 2015). Protective cultures and their metabolic products could provide an effective means to control mycotoxins in intermediate moisture foods well accepted by consumers.

The antifungal protein PgAFP, produced by *P. chrysogenum* CECT 20922, is within the group of small, basic, and cysteine-rich antifungal proteins (Rodríguez-Martín et al., 2010). This protein inhibits various toxigenic molds and has proved to inhibit *A. flavus* on a dry-fermented sausage (Delgado et al., 2015a). However, the antifungal capability of this kind of proteins is dramatically reduced in presence of divalent cations, such as Ca^{+2} (Chen et al., 2013; Galgóczy et al., 2013; Kaiserer et al., 2003). Calcium provokes a strong inhibition on PgAFP antifungal ability, rendering this protein uneffective on cheese (Delgado et al., 2015c). To investigate further strategies to control the mycotoxigenic hazard in cheeses. LAB are commonly used as starter cultures on cheeses, some of them showing strong antifungal activity in dairy products (Cheong et al., 2014; Muhialdin et al., 2011). Yeasts are generally present in aged cheeses, being *Debaryomyces hansenii* the most abundant species isolated (Viljoen and Greyling, 1995; Welthagen and Viljoen, 1998). This yeast has been proposed for biocontrol of *Penicillium* spp. and *Aspergillus* spp. in cheese (Liu and Tsao, 2009). However, the effect of LAB and *D. hansenii* is also limited, not being able to efficiently inhibit aflatoxin production in cheese. Therefore, the combined action of the antifungal protein PgAFP with LAB and yeasts to prevent mold development and aflatoxin production deserves to be investigated.

PgAFP increased reactive oxygen species (ROS) levels on sensitive strains (Delgado et al., 2015b), but an enhanced response to oxidative stress was obtained when *A. flavus* was grown in 0.1 M $CaCl_2$, preventing the antifungal activity (Delgado et al., 2015c). ROS and is related with the regulation of β-oxidation and peroxisome proliferation that play a key role in aflatoxin biosynthesis. Thus, the expression of several genes involved in these processes have been used to relate them with aflatoxin production (Reverberi et al., 2012) The gene expression of some of these genes from aflatoxigenic strains treated with PgAFP and/or yeasts and LAB, and grown in cation-rich medium could offer information about the effect of these protective agents on the oxidative status of the mold as well as the aflatoxin biosynthesis.

On the other hand, the effect of the antifungal ability of the protective cultures should be evaluated on cheese. Thus, the aim of this work was to investigate the antifungal ability of PgAFP together with *D. hansenii* and/or *Pediococcus acidilactici* in a calcium enriched culture media to study the effect of these two microorganisms on β-oxidation and aflatoxin gene expression. A combined action with microorganisms endowed with other antifungal mechanism of action could alter the successful response of the aflatoxigenic molds to PgAFP. Additionally, the antifungal ability of the combinations and reduction of mycotoxin production on two aflatoxigenic strains were tested on cheese.

Material and methods

Strains

Three mold strains obtained from Spanish Type Culture Collection (CECT, Valencia, Spain) were used in this study: the PgAFP sensitives aflatoxin-producer *A. parasiticus* CECT 2682 and *Aspergillus flavus* CECT 2687, as well as the PgAFP antifungal protein producer *P. chrysogenum* CECT 20922. In addition, two potential antifungal strains were used: the yeast *D. hansenii* Dh253 from the microbial collection of Food Hygiene and Safety of the University of Extremadura (Cáceres, Spain) and *P. acidilactici* fargo 35 supplied by Laboratorios Amerex (Colmenar Viejo, Spain).

PgAFP production and purification

P. chrysogenum CECT 20922 was grown in potato dextrose broth (PDB) pH 4.5 for 21 days at 25 °C. The mycelium was removed and the media was filtered to get cell free media. PgAFP was isolated from 450 ml of the cell-free media trough fast protein liquid chromatography (FPLC) with a cationic exchange column HiTrap SP HP (Amersham Biosciences, Uppsala, Sweden), further purified with a HiLoad 26/60 Superdex 75 gel filtration column for FPLC (Amersham Biosciences) as previously described (Acosta et al., 2009). The protein isolated and concentrated was sterilized through filtration (0.22 µm, Thermo Fisher

Scientific, Waltham, MA, USA) and its concentration was assessed by the Lowry method (Lowry et al., 1951).

Growth inhibition in culture media and mycotoxin extraction

The effect of PgAFP, *D. hansenii*, and *P. acidilactici* on *A. flavus* and *A. parasiticus* was evaluated both separately and in all different combinations. For this, 5 ml of 0.1 M $CaCl_2$ Yeast Extract Supplemented broth (YES) were inoculated with 10^5 conidia/ml *A. flavus* or *A. parasiticus*. To provide a high level of the biological agents, 10^6 cells/ml *D. hansenii* (Dh), 10^6 cells/ml *P. acidilactici* (Pa), and 10 µg/ml PgAFP (Pg) the following 7 different batches were obtained: Pg, Dh, Pa, Pg+Dh, Pg+Pa, Dh+Pa, and Pg+Dh+Pa. Additionally, an untreated batch used as a control. Samples were incubated for 15 days at 25 °C to stimulate aflatoxin production (Lozano-Ojalvo et al., 2013). All the assays were carried out in triplicate. After incubation, 5 ml of chloroform were added to each test tube incubated for 1 h shaking at 100 rpm at room temperature in darkness. Then, the chloroform was separated and evaporated to dryness under a gentle stream of N_2. The mycelium was recovered from the aqueous residue by filtering through a miracloth (Calbiochem, Darmstadt, Germany), dried at 100 °C up to constant weight, and weighed.

Growth inhibition on cheese and mycotoxin extraction

To test the potential of selected combinations of protective cultures, the envionmental conditions for ripening were simulated using a Gouda cheese commercial type (a_w 0.96). The cheese was cut into 5 mm thick slices and dipped into ethanol to eliminate outer contamination. The ethanol was left to evaporate in a laminar flow cabinet (Bio Flow II, Telstar, Tarrasa, Spain) prior to placing the slices in pre-sterilized (ethanol and UV-light) receptacles containing a saturated KCl solution to keep relative humidity constant at 84% after vapour-liquid equilibrium. *A. flavus* or *A. parasiticus* was inoculated (10^5 conidia/cm^2) on both sides of each slice. No antifungal treatment was applied to the untreated batches. Two treated batches were made: Pg+Dh+Pa, with 10 µg/cm^2 PgAFP, 10^6 cells/cm^2 *D. hansenii*, and 10^6 cells/cm^2 *P. acidilactici*; and Pg+Dh, with 10 µg/cm^2 PgAFP and 10^6 cells/cm^2 *D. hansenii*, to test their ability against *A. flavus* and *A. parasiticus*, similarly to the culture medium. Every batch was carried out in triplicate. All samples received the same volume of liquid by adding sterile phosphate buffer as required, and the liquid excess was left to dry in the laminar flow cabinet. The samples were incubated for 5 and 15 days at 25 °C to stimulate aflatoxin production (Lozano-Ojalvo et al., 2013). A_w values were determined in a Novasina Lab Master from Novasina AG (Lachen, Switzerland). *A. parasiticus* and *D. hansenii* counts were assessed by plating in PDA and incubated for 72 h at 25 °C, according to the characteristic colony

morphology. Lactic acid bacteria counts were evaluated on MRS agar, incubated for 72 h at 30 °C.

Mycotoxins produced on cheese slices were extracted as previously described (Rodríguez et al., 2012b). Briefly, each cheese slice was macerated under shaking in a dark flask with 60 ml acetonitrile-water (9:1, v/v) containing 0.1% formic acid together with 50 ml hexane. The acetonitrile-water phase was recovered and filtered through sodium sulphate anhydrous. Then, the filtrate was mixed with additional 50 ml of hexane and shaken. The acetonitrile-water phase was filtered again and evaporated in a rotatory evaporator at 40–45 °C. The residue was resuspended in 1 ml chloroform, filtered through a 0.45 μm nylon membrane (MSI, Westboro, MA, USA).

Mycotoxin quantification

Extracts from both culture medium and cheese slices were analysed by ultra high-performance liquid chromatography–mass spectrometry (uHPLC–MS) in an HPLC Thermo Scientific Dionex ultimate 3000 pnmp, a mass detector (MS) model Bruker Amazon S.L., an autosampler (Ultimate 3000), a degasser (3000 Ultimate) and an ion trap (Amazon SL.). A C18 reverse-phase column of 10 cm length, 2.1 mm inside diameter and 2 μm particle size was used as stationary phase. As mobile phase a 0.1% formic acid-10 mM ammonium formiate (solvent A) and acetonitrile (solvent B) was used. The separation was performed with the flow rate set at 200 μl/min and the following gradient: [0 min] 2% B, [0-0.1 min], 40% B, [0.1-4 min] 60% B,[4-7 min] 80% B, [7-8.5 min] 80% B, [8.5-8.51 min] 98% B, [8.51-12 min] 98% B, [12-12.01 min] 2% B and [12.01-15 min] 2% B. Precursor ions 313 and 329, and quantitation ions 285 and 311 for aflatoxins B_1 and G_1 (AFB_1 and AFG_1), respectively.

These parameters were compared to those obtained from commercial mycotoxins (Sigma-Aldrich, Madrid, Spain). The calibration curves for AFB_1 and AFG_1 (1-500 ng) by uHPLC-MS revealed a linear relationship ($r^2 \geq 0.99$) between detector response and amount of AFB_1 and AFG_1 standards. The minimum detectable value or limit of detection (LOD) was estimated from the calibration curve, according to the equation: $LOD = 3\ (s_B^2 + s_i^2 + (i/m)^2\ s_m)^{1/2}/m$ (Long and Winefordner, 1983) being "m" the slope of the calibration curve, "I" the intercept term and "s_B", "s_i" and "s_m" the standard errors of the blank, the intercept term and the slope of the calibration curve, respectively. Assuming a normal distribution of the estimated quantities, α (error of the first type) = β (error of the second type) = 0.05, the quantification limit (LOQ) was 3.04 LOD (Currie, 1999). The LOD obtained in this study were 4 μg/kg and 1.5 μg/kg, and the LOQ were 12 μg/kg and 4.5 μg/kg respectively for AFB_1 and AFG_1.

RNA isolation and cDNA synthesis

To test the influence of PgAFP, *D. hansenii* and *P. acidilactici* on *A. flavus* and *A. parasiticus* gene expression, four batches were prepared in YES broth: *A. flavus* or *A. parasiticus* (10^5 conidia/ml) was co-cultivated in tubes separately with PgAFP (10 µg/ml), *D. hansenii* (10^6 cells/ml) or *P. acidilactici* (10^6 cells/ml), and with all of them together. The untreated batch was inoculated solely with *A. parasiticus*. The tubes were incubated at 25°C for 5 days. For RNA extraction, mycelium was harvested and washed twice with sterile phosphate-saline buffer (PBS), frozen in liquid nitrogen and ground with a mortar and pestle. Then the powder was resuspended in 750µl RLT buffer (RNeasy® Plant Mini kit, Qiagen, Hilden, Germany) containing 15µl β-mercaptoethanol. Samples were processed with the RNeasy® Plant Mini kit according to manufacturer's instructions. RNA quality and quantity was spectrophotometrically determined using in a NanoDrop 2000c spectrophotometer (Thermo Scientific, Waltham, MA, USA). Then, samples were treated with DNase I, RNase-free (Fermentas, St. Leon-Rot, Germany) following manufacturer's instructions, and checked for background double stranded DNA by qPCR for *β-tubulin* genes as described below. Finally, cDNA was synthesized using 500 ng RNA according to PrimeScript™ RT Reagent kit protocol (Takara, Otsu, Japan).

Real-time PCR analysis of gene expression

The expression of genes *aflP* (formerly *omt-1*) for aflatoxin biosynthesis (Yu et al., 2004), *foxA* for β-oxidation (Roze et al., 2010),and *β-tubulin* as housekeeping (Rodríguez et al., 2014) were assessed to evaluate the effect of the treatments on *A. parasiticus*. Primers to evaluate the *foxA* expression were designed from the gene AFLA_041590 (GeneBank accession no. XM_002377580), as previously described (Roze et al., 2010)(Reverberi et al., 2012). Similarly, to study *β-tubulin* expression a couple of primers were designed from *A. parasiticus β-tubulin* sequence (GeneBank accession no. FR775333.1)

To quantify the relative expression of the genes, *foxA* and *β-tubulin* genes expression were assessed by using the SYBR Green qPCR in an Applied Biosystems ViiATM 7 Real-Time PCR System (Applied Biosystems, Foster City, California, USA). To optimize the primer concentration, different concentrations from 800 to 200 nM were tested. The optimized SYBR Green protocol was carried out in a final volume of 25 µl containing 5 ml of template DNA, 12.5 µl of 2x SYBR® *Premix Ex Taq*™ (Takara, Otsu, Japan), 0.5 µl of 50x ROX™ Reference Dye (Takara) and 400 nM of each primer. The thermal cycling conditions were the following: a single step of 10 min at 95 °C, 40 cycles of 95 °C for 15 s and 60 °C for 1 min. After the final PCR cycle, a melting curve analysis of the PCR products was carried out by heating from 60 to 95 °C and continuous measurement of the fluorescence to verify the PCR product. The *aflP* gene expression was evaluated following the concentrations and conditions previously

described (Rodríguez et al., 2012a). Every qPCR assay described above was carried out by triplicate. Gene expression ratio was calculated using the $2^{-\Delta\Delta CT}$ method (Livak and Schmittgen, 2001). The endogenous control was set as the expression of *β-tubulin* gene and the untreated batch described above was used as calibrator sample. For every primer pair, a standard curve was generated to check the amplification efficiency from ten-fold serial dilution 100 to 0.01 ng/µl of DNA from *A. flavus* and *A. parasiticus*. In addition, the differences in amplification efficiencies between the housekeeping and the target gene were less than 10%, as required to apply the relative quantification method (Schmittgen and Livak, 2008).

Statistical analysis

Statistical analyses were performed with the IBM SPSS v.22. Data from mycelia weight, microbial counts, mycotoxin concentration and gene expression were tested for normality (Kolmogorov-Smirnov with Lilliefors correction) and homoscedasticity (Levene's test). Given that these data were non-normally distributed, mean values were compared using nonparametric Kruskal–Wallis test. To compare treatments in pairs, Mann-Withney U test was applied ($p \leq 0.05$).

Results

Growth inhibition and mycotoxin production in calcium-enriched YES

A. flavus grown for 15 days showed lower mycelium weight ($p \leq 0.05$) in the batches Pg+Dh, Dh+Pa and Pg+Dh+Pa than in non-treated batch (Fig 1). *A. parasiticus* was inhibited by all treatments except for those containing solely PgAFP or *P. acidilactici* (Fig 1). The combination Pg+Dh+Pa achieved the highest inhibition of both *A. flavus* and *A. parasiticus*.

A. flavus did not produce mycotoxins in Ca-enriched YES, neither in the untreated batch nor in any treatment tested. However, *A. parasiticus* produced AFB_1 and AFG_1 in the untreated batch (Fig 2) and small amounts of AFG_1 in the batch inoculated solely with *D. hansenii*. Therefore, none of the combinations of protective cultures tested increased aflatoxin production in Ca-enriched YES.

Growth inhibition and mycotoxin production on cheese slices

On cheese slices, the microbial load just before inoculation was about 3 log cfu/cm^2 for lactic acid bacteria and <2 log cfu/cm^2 for both molds and yeasts. LAB increased to 6-6.7 log cfu/cm^2 in Pg+Dh+Pa batch just after inoculation at day 0. At 5 and 15 incubation days, LAB counts were around 3.5 log cfu/cm^2 for batches not inoculated with *P. acidilactici* (untreated and Pg+Dh), but over 6 log cfu/cm^2 for Pg+Dh+Pa batches. Similarly, the yeast load was

always below 2 log cfu/cm^2 in the untreated control, but over 5 log cfu/cm^2 in Pg+Dh and Pg+Dh+Pa batches. A_w values of cheese slices incubated 5 and 15 days were 0.89 and 0.86, respectively. Mold loads at 5 incubation days in untreated Af and Ap batches were around 2 log units higher ($p \leq 0.05$) than in Pg+Dh and Pg+Dh+Pa batches (Table 1). At 15 incubation days, mold counts in untreated controls were over 7 log cfu/cm^2 for *A. flavus*-inoculated batch, but lower than 5 log cfu/cm^2 for *A. parasiticus* batch. Significant reductions ($p \leq 0.05$) close to 2-3 log cfu/cm^2 were obtained with Pg+Dh and Pg+Dh+Pa treatments for both molds. A similar level of inhibition was reached with Pg+Dh and Pg+Dh+Pa at both incubation times (Table 1).

The only mycotoxin produced at the conditions tested in cheese was AFG_1 in *A. parasiticus* untreated batch at 5 and 15 incubation days.

Gene expression

To study the effect of PgAFP, *D. hansenii*, and *P. acidilactici* on aflatoxin biosynthesis and β-oxidation in *A. parasiticus*, the expression of genes *aflP* for aflatoxin biosynthesis, *foxA* for β-oxidation, and *β-tubulin* as housekeeping were assessed.

The maximum differences in amplification efficiencie values showed between *aflP* and housekeeping were 6 % for *A. flavus* and 5 % for *A. parasiticus*, thus the $2^{-\Delta\Delta CT}$ method could was applied. The oxidative stress in *A. flavus* and *A. parasiticus*, according to *foxA* gene expression, did not differ ($p > 0.05$) between any of the treatments and the untreated control batches when grown in calcium-rich medium for 5 incubation days. However, *aflP* was overexpressed ($p \leq 0.05$) in Pa treated batches in both molds, whereas it was repressed ($p \leq 0.05$) in Pg batch in *A. parasiticus* (Fig 3).

Discussion

As it was expected, *A. flavus* or *A. parasiticus* grown in 0.1 M $CaCl_2$ YES were not inhibited by PgAFP. Thus, it was necessary to explore new alternatives to combat mycotoxigenic moulds in Ca^{2+}-rich foods. *A. parasiticus* was inhibited ($p \leq 0.05$) by most treatments tested, whilst *A. flavus* was inhibited only for three of the combinations (Fig. 1). The fact that the highest inhibition was reached by co-inoculation of PgAFP + *D. hansenii* + *P. acidilactici* seems to be a consequence of the combined effect of different mechanisms of action. The mechanism of action of PgAFP is based on permeability induction, loss of membrane integrity, and apoptosis induction as a consequence of ROS (Delgado et al., 2015b), whereas the inhibitory effect of *D. hansenii* is attributed to volatile compounds and competition for nutrient and space (Núñez et al., 2015). In addition, *P. acidilactici* produces bacteriocins and organic acids that inhibit mold growth (Cizeikiene et al., 2013; Montiel et al., 2013).

On the other hand, aflatoxin production was always inhibited in the batches containing any protective culture, except for AFG_1 in that inoculated only with *D. hansenii* (Fig 1).

The ROS induced by antifungal proteins trigger oxidative stress in sensitive molds (Delgado et al., 2015b; Galgóczy et al., 2013; Marx et al., 2008). This stress is a prerequisite for aflatoxin production in *A. parasiticus* (Jayashree and Subramanyan, 2000) and is also involved in peroxisomal β-oxidation of fatty acids, which is linked to aflatoxin biosynthesis (Reverberi et al., 2012). An anti-oxidant status in the fungal cell leads to a depressed aflatoxin production in *A. parasiticus* (Reverberi et al., 2005). *FoxA* gene expression has been used previously to monitor the fatty acids metabolism by β-oxidation in *A. flavus* (Maggio-Hall et al., 2005) and *A. parasiticus* (Roze et al., 2010). The expression of this gene was not altered at 5 incubation days in either *A. flavus* or *A. parasiticus* by the effect of PgAFP, *D. hansenii*, *P. acidilactici* or the three applied together (fig 3).. These results imply a mild oxidant effect of PgAFP on both molds grown in Ca-enriched YES, matching the lower aflatoxin production in PgAFP-treated samples (fig 2). These findings are consistent with the low levels of intracellular ROS detected in PgAFP-treated *A. flavus* grown with 0.1 M $CaCl_2$ PDB. The *aflP* gene was expressed at a higher level in both moulds treated only with *P. acidilactici*, but at a lower level in *A. parasiticus* treated only with PgAFP (Fig. 4). However, the mycotoxin levels obtained in these batches were all lower than those in the untreated control batch. Similar inconsistent results between gene expression and aflatoxins production have been obtained for the interaction of *Streptomyces sp.* and *A. flavus* (Verheecke et al., 2015), where reduced aflatoxin concentrations were not accompanied by significantly repressed aflP expression. According to these results, the effect of PgAFP promoting aflatoxin production can be ruled out in calcium enriched media.

Given that both mycelial weight and mycotoxin production were inhibited by some treatments in 0.1M $CaCl_2$ YES, the actual efficacy of the most effective treatments containing PgAFP was tested on cheese slices. Protective cultures require favorable environmental conditions to develop their antifungal properties. The low a_w levels reached during cheese ripening, as low as 0.80 at the outer-most layer of some cheeses, could restrict survival of *P. acidilactici* and *D. hansenii*. The a_w values in treated cheese slices decreased to 0.89 and 0.86 at days 5 and 15, respectively (Table 1), which are below the 0.90 minimum a_w level for *Pediococcus* growth in foods (Leistner et al. 1981), but not below the 0.83 minimum value for *D. hansenii* (Troller and Christian, 1978).

Both Pg+Dh and Pg+Dh+Pa treatments effectively inhibit *A. flavus* and *A. parasiticus* growth as well as AFG_1 production by *A. parasiticus* on cheese slices for 15 days, thus contributing to obtain a safer food. This effect was stronger than that reported by the sole action of *D. hansenii* on ochratoxigenic *P. nordicum* in dry-cured ham incubated at 0.84 a_w (Andrade

et al., 2014). No additional inhibition was observed by the combined use of *P.* acidilactici with PgAFP+Dh, which can be explained by the failure of *P. acidilactici* to correctly implantation or development of this strain can be hypothesized, but the counts of LAB showed the highest LAB load in the batches were *P. acidilactici* was inoculated. This lack of inhibitory activity has to be explained by the differences in the substrate between YES broth and cheese slices, but not to the fact of calcium concentration. In addition, a minor LAB load was noticed in the batch inoculated with *D. hansenii* and PgAFP, this fact can be due to a well substrate competition of *D. hansenii*, as reported previously (Núñez et al., 2015).

In non-treated slices, high levels of aflatoxin G1 were detected, being always over 10 ppb in both sampling days. The levels reached in this batch, in particular at 15 incubation days, were well over the limit established from the Spanish legislation that has been set in 10 ppb (Ministerio de Sanidad y Consumo, 1988)

In spite of the fact of a lower inhibition on cheese provided by the combination containing *P. acidilactici*, the mycotoxin content of the cheese slices was similar in both experimental batches where no mycotoxin was detected for 15 incubation days. Thus, the presence of *P. acidilactici* does not seem to hinder the antifungal activity of PgAFP and *D. hansenii*. However, given that *P. acidilactici* did not enhance the antifungal ability of PgAFP and *D. hansenii*, together with the fact of that *P. acidilactici* provoked overexpression of *aflP* gene in the first stages of the incubation in rich-calcium culture media, the inoculation of this strain should be avoid in cheese as protective culture.

The combination of PgAFP and *D. hansenii* could be proposed as the best combination for protective culture, given that no one provoked an overexpression of genes related to mycotoxin production and an enhanced antifungal ability has been proved on cheese.

This work studies the effect of a strain of *D. hansenii*, *P. acidilactici* and the antifungal protein PgAFP on aflatoxigenic strains grown in rich-calcium medium. In addition, it offers a complementary strategy to combat toxigenic molds in rich-calcium foods and their mycotoxin production, given the limited effect of PgAFP in these type of foods.

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Figure captions

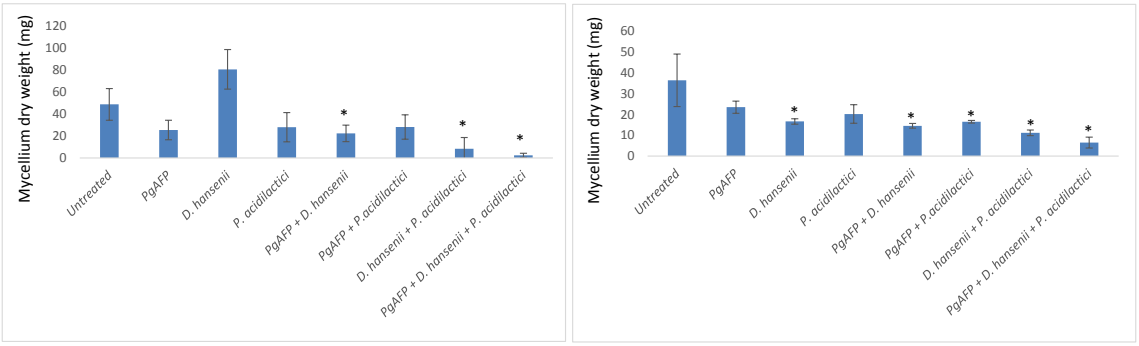

Figure 1. Mycelium dry weight of *A. flavus* (left) and *A. parasiticus* (right) cultured for 15 days in calcium-enriched Yeast Extract Sucrose broth with different combinations of antifungal agents. Bars represent standard deviation. * Means are significantly different from untreated batch ($p \leq 0.05$).

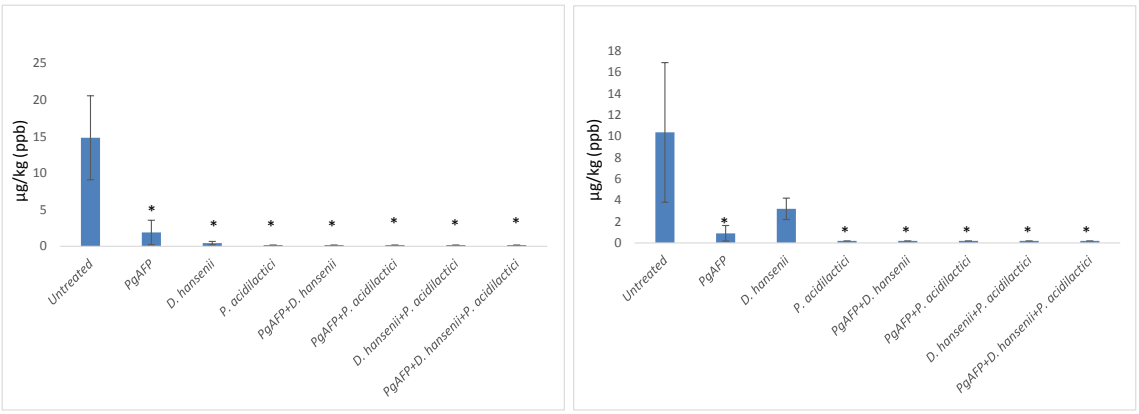

Figure 2. Effect of different combinations of protective agents on aflatoxin B_1 (left) and G_1 (right) production by *Aspergillus parasiticus* cultured in calcium-enriched Yeast Extract Sucrose broth for 15 days. Bars represent standard deviation. * Means are significantly different from untreated batch ($p \leq 0.05$).

Table 1. Water activity (a_w), mould counts (log cfu/cm^2) and aflatoxin G_1 concentration (µg/kg) in cheese slices inoculated with *A. flavus* or *A. parasiticus* at 5 and 15 days of incubation. Data are given as mean ± SD.

		Day 5		Day 15	
		A. flavus	*A. parasiticus*	*A. flavus*	*A. parasiticus*
Untreated	a_w	0.89	0.89	0.86	0.86
PgAFP+*D. hansenii*	a_w	0.89	0.89	0.86	0.86
PgAFP+*D. hansenii*+*P. acidilactici*	a_w	0.89	0.89	0.86	0.86
Untreated	Mould counts	3.93±0.54	4.12±0.57	7.42±0.09	4.87±0.21
PgAFP+*D. hansenii*	Mould counts	1.86±0.85*	2.31±0.64*	4.26±0.28*	<2*
PgAFP+*D. hansenii*+*P. acidilactici*	Mould counts	2.63±0.61*	2.39±0.75*	4.74±0.38*	2.99±0.67*
Untreated	Aflatoxin G_1	<LOD	11±7	<LOD	29±24
PgAFP+*D. hansenii*	Aflatoxin G_1	<LOD	<LOD*	<LOD	<LOD*
PgAFP+*D. hansenii*+*P. acidilactici*	Aflatoxin G_1	<LOD	<LOD*	<LOD	<LOD*

*Means are significantly different from untreated batch ($p \leq 0.05$)

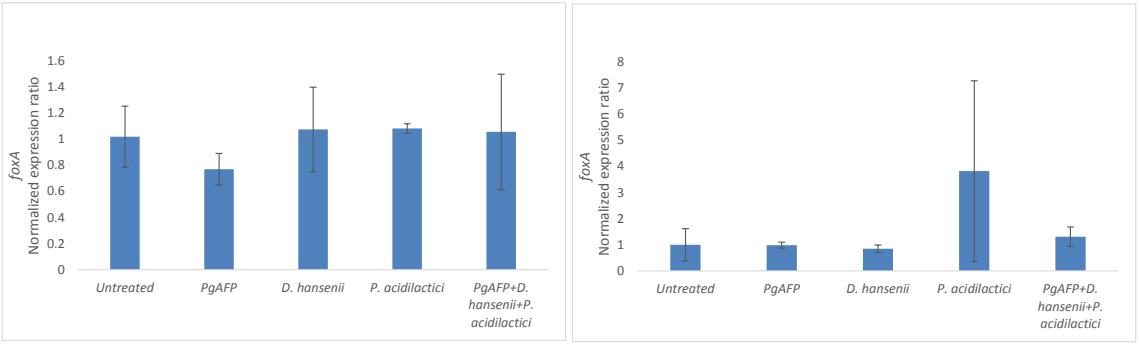

Figure 3. Effect of different antifungal agents on relative gene expression of *foxA* gene in *A. flavus* (left) and *A. parasiticus* (right) after 5 days in calcium-enriched Yeast Extract Sucrose broth. Bars represent standard deviation.

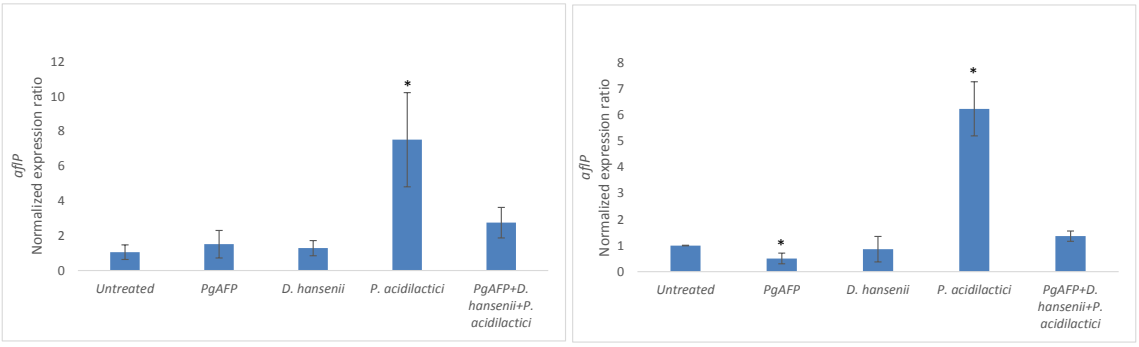

Figure 4. Effect of different antifungal agents on relative gene expression of *aflP* gene in *A. flavus* (left) and *A. parasiticus* (right) after 5 days in calcium-enriched Yeast Extract Sucrose broth. Bars represent standard deviation. * Means are significantly different from untreated batch ($p \leq 0.05$).

Table 2. Nucleotide sequence of primers used for qPCR assay.

Primer name	Nucleotide sequences (5'-3')	Efficiencies *A. flavus*/ *A. parasiticus*	Product size	Position	Reference
F-Omt-1	GGCCGCCGCTTTGATCTAGG	106/104%	123	[a]1485	(Rodríguez, Rodríguez, Luque, Martín, & Córdoba, 2012)
R-Omt-1	ACCACGACCGCCGCC			1593	
F-β-tub	TCTTCATGGTTGGCTTCGCT	101/101%	98	[b]964	This study
R-β-tub	CTTGGGGTCGAACATCTGCT			1042	
F- foxA	ACCGCAACCCTCTTCACATT	107/106%	73	[c]1196	This study
R- foxA	AGACCGTGCAGGATAGGAGT			1268	

[a] Positions are in accordance with published sequence of the *aflP* (*omt-1*) gene of *A. flavus* (GeneBank accession no. L25835.1).

[b] Positions are in accordance with the published sequences of the *β-tubulin* gene of *A. parasiticus* (GeneBank accession no. FR775333.1).

[c] Positions are in accordance with published sequence of the *foxA* gene of *A. flavus* (GeneBank accession no. XM_002377580).

IV.3. Estudio del mecanismo de acción de PgAFP en mohos

Impact of the antifungal protein PgAFP from Penicillium chrysogenum *on the protein profile in* Aspergillus flavus

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APPLIED MICROBIAL AND CELL PHYSIOLOGY

Impact of the antifungal protein PgAFP from *Penicillium chrysogenum* on the protein profile in *Aspergillus flavus*

Josué Delgado[1] · **Rebecca A. Owens**[2] · **Sean Doyle**[2] · **Miguel A. Asensio**[1] · **Félix Núñez**[1]

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Abstract Antifungal proteins produced by molds are generally small, highly basic, and cysteine-rich. The best known effects of these proteins include morphological changes, metabolic inactivation, and membrane perturbation on sensitive fungi. Reactive oxygen species (ROS) generation leads to apoptosis, with G -protein playing a key role in transduction of cell death signals. The antifungal protein PgAFP from *Penicillium chrysogenum* inhibits growth of some toxigenic molds. Here we analyzed the effect of the antifungal protein PgAFP on the growth of *Aspergillus flavus*. For this, comparative proteomic analysis was used to identify the whole protein profile and protein change in abundance after PgAFP treatment. PgAFP provoked metabolic changes related to reduced energy metabolism, cell wall integrity alteration, and increased stress response due to higher levels of ROS. The observed changes in protein abundance, favoring a higher glutathione concentration as well as the increased abundance in heat shock proteins, do not seem to be enough to avoid necrosis. The decreased chitin deposition observed in PgAFP-treated *A. flavus* is attributed to a lower relative quantity of Rho1. The reduced relative abundance of a β subunit of G -protein seems to be the underlying reason for modulation of apoptosis in PgAFP-treated *A. flavus* hyphae. We propose Rho1 and G -protein subunit β CpcB to be the main factors in the mode of action of PgAFP in *A. flavus*. Additionally, enzymes essential for the biosynthesis of aflatoxin were no longer detectable in *A. flavus* hyphae at 24 h, following treatment with PgAFP. This presents a promising effect of PgAFP, which may prevent *A. flavus* from producing mycotoxins. However, the impact of PgAFP on actual aflatoxin production requires further study.

Keywords Antifungal compounds · Toxigenic fungi · *Aspergillus flavus* · Apoptosis · Proteomics

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✉ Miguel A. Asensio
masensio@unex.es

[1] Food Hygiene and Safety, Institute of Meat Products, University of Extremadura, Cáceres, Spain

[2] Department of Biology, Maynooth University, Maynooth, Co. Kildare, Ireland

Introduction

Antimicrobial proteins are produced by different organisms throughout all kingdoms (Leiter et al. 2005). Some antifungal proteins produced by molds are small, highly basic, and cysteine-rich proteins, such as PAF from *Penicillium chrysogenum* Q176 (Marx et al. 1995), PgAFP from *P. chrysogenum* RP42C (Rodríguez-Martín et al. 2010), Pc-Arctin from *P. chrysogenum* A096 (Chen et al. 2013), AFP from *Aspergillus giganteus* (Nakaya et al. 1990), or NAFP from *Neosartorya fischeri* (Kovács et al. 2011). The expression of these proteins is induced in the presence of other fungi and contributes to an ecological advantage (Marx 2004). Antifungal proteins produced by molds may serve to combat unwanted molds. Toxigenic molds are among the main hazards in intermediate moisture foods, with the aflatoxin producer *Aspergillus flavus* being one of the main concerns. The mechanism of action of antifungal proteins seems to be multifactorial, leading to morphological changes, metabolic inactivation, or membrane perturbation in a dose-dependent manner (Kaiserer et al. 2003). The site of action on sensitive molds does not share the same pattern among antifungal proteins.

PAF penetrates into the cytoplasm (Oberparleiter et al. 2003; Batta et al. 2009); AFP showed co-localization with the nucleus in *Magnaporthe grisea* (Moreno et al. 2006), while it is bound mainly to cell wall in *Aspergillus niger* (Theis et al. 2003, 2005). Membrane permeabilization could be involved in the mechanism of action. Some non-fungal antimicrobial proteins destabilize membranes by pore formation, whereas PAF induces a selective permeability to potassium (Kaiserer et al. 2003; Marx et al. 2008). In addition, PAF and NAFP induce oxidative stress in sensitive fungi, with elevated levels of reactive oxygen species (ROS) being the main effect contributing to apoptosis (Leiter et al. 2005; Galgóczy et al. 2013). It has been proposed that G protein is responsible for the transduction of PAF-initiated apoptotic cell death signals (Leiter et al. 2005). This is achieved through modulation of the intracellular glutathione (GSH) and ROS levels in *Aspergillus nidulans* (Hegedus et al. 2011). Here we used PgAFP, one of these small, basic, and cysteine-rich proteins that inhibits growth of some toxigenic molds (Rodríguez-Martín et al. 2010), to study the effect on the growth of *A. flavus*. Among the possible effects derived from antifungal proteins on *A. flavus*, those related to aflatoxin biosynthesis would be of interest for practical applications. *P. chrysogenum* RP42C isolated from dry-cured ham produces PgAFP and was used here as a source of the antifungal protein.

The mechanism of action of PgAFP on sensitive molds is unknown, and elucidation of this mechanism would allow the evaluation of potential applications for PgAFP. Comparative proteomic analysis constitutes a valuable tool to explore the effect of PgAFP on sensitive molds, which may provide rewarding information to exploit the practical use against toxigenic molds. Comparative proteomic analyses have been used in previous studies to explore the effect of some substances, such as H_2O_2, on molds (Lessing et al. 2007), and to identify resistance to antifungal drugs (Gautam et al. 2008; Cagas et al. 2011). Comparative proteomic 2D-PAGE has the capability to separate proteins in high resolution, even those including post-translational modifications. We used this technique to identify 23 unique proteins, identified from protein spots that showed a significant change in abundance in *A. flavus* in response to PgAFP. However, this technique only reveals a small percentage of the whole proteome depending on the range of pH (Görg et al. 2009), and it is not optimal for the analysis of membrane and hydrophobic proteins (Rabilloud et al. 2009). These features lead to several proteins under-represented on 2D-PAGE. Label-free quantitative proteomics can be used to examine those proteins not analyzable by 2D-PAGE. Therefore, a second proteomic approach, involving label-free proteomics, was used to analyze the proteome quantitatively and qualitatively.

The results of comparative proteomics informed on the mechanisms and systems affected by the antifungal compound in a sensitive mold. Information generated was subsequently used to select adequate tests to confirm the changes attributed to proteins whose relative abundance is affected. The objective of the present work has been to study the effect of PgAFP on the proteomic profile and the structural and metabolic changes caused in *A. flavus*, a fungus that produces aflatoxins in foods.

Material and methods

Strains

In vitro tests were carried out with the PgAFP producer *P. chrysogenum* strain RP42C (CECT 20922) that resists at least 312.7 μg/ml PgAFP (Delgado et al. 2015), and *A. flavus* (CECT 2687), both from the Spanish Type Culture Collection (CECT). The latter strain produces aflatoxins in dry-cured ham (Bernáldez et al. 2014).

Purification of PgAFP

P. chrysogenum was grown in potato dextrose broth (PDB; Scharlab, Barcelona, Spain) pH 4.5, at 25 °C for 21 days. Mycelium was removed and the culture medium was filtered through a nitrocellulose 0.22-μm pore size (Sartorius, Goettingen, Germany) to obtain cell-free medium. The cell-free medium was applied to an ÄKTA FPLC with a cationic exchange column HiTrap SP HP (Amersham Biosciences, Uppsala, Sweden), equipped with a UV detector at 214 nm. The resulting fraction containing PgAFP was then chromatographed on a HiLoad 26/60 Superdex 75 column for FPLC (Amersham Biosciences, Uppsala, Sweden) as previously described (Acosta et al. 2009) to obtain an extract of the purified protein. The extract containing the purified PgAFP from several batches were pooled in a stock solution. The amount of protein in the stock solution was quantified by the Lowry method (Lowry et al. 1951). For the various assays, the PgAFP stock solution was diluted to the desired active concentration range according to the aim of the test.

Protein extraction

A. flavus CECT 2687 was cultured in triplicate in 50-ml PDB, at 25 °C with shaking at 200 rpm, in either presence (10 μg/ml) or absence of PgAFP for 24 h. Mycelia were harvested, filtered, washed, and lysed as described previously (Carberry et al. 2006). Mycelial lysates were centrifuged (10,000×*g*; 30 min) to remove cell debris and the subsequent supernatant precipitated with trichloroacetic acid/acetone (Carpentier et al. 2005). From these precipitated lysates, the two following proteomic analysis were carried out. Additionally, to confirm that cultures were in the exponential growth phase, growth in 24- to 48-h cultures was estimated by

mycelium dry weight determination at 100 °C to a constant weight.

Two-dimensional PAGE

For protein separation by 2D-PAGE, resuspended extracts containing 250 μg of protein were loaded onto Immobiline Dry strips (IPG strip; Amersham Biosciences) in the pH range 4–7, followed by electrofocusing, and electrophoresis using the Protean Xi-II Cell (Bio-Rad Laboratories) as described previously (Carberry et al. 2006). Resulting gels (three biological replicates and two technical replicates per treatment) were stained with colloidal Coomassie Blue (Sigma-Aldrich, St. Louis, MO, USA), scanned, and analyzed using Progenesis™ SameSpot software (TotalLab, Newcastle, UK) (O'Keeffe et al. 2013; Collins et al. 2013; Owens et al. 2014). Spot intensities were normalized in Progenesis SameSpot software using the total spot volume normalization method prior to comparative analysis, to correct for any variation in protein loading, staining/destaining, or image acquisition. Protein spots showing differences ($p < 0.05$, fold change ≥1.5) were excised and in-gel digested as described previously (Shevchenko et al. 2006). Briefly, selected spots were destained by addition of 100 μl of 100 mM ammonium bicarbonate:acetonitrile (1:1 *v*/*v*) for 30 min. Acetonitrile (500 μl) was added to samples to dehydrate the gel pieces, then discarded and replaced with 50 μl of trypsin (13 ng/μl). Samples were incubated at 4 °C for 2 h followed by overnight incubation at 37 °C. Then, samples were sonicated for 10 min, and the digested supernatant was transferred to clean tubes to be completely dried using a DNA Speed Vac Concentrator (Thermo Fischer Scientific, Austin, TX, USA) and resuspended in 0.1 % formic acid (FA; 20 μl). The samples were filtered through 0.22-μm cellulose spin filters (Agilent Technologies, Dublin, Ireland). The samples were analyzed by a 6340 Model Ion Trap LC-Mass Spectrometer (Agilent Technologies, Dublin, Ireland) using electrospray ionization. Samples (3 μl) were loaded onto a Zorbax 300 SB C-18 Nano-HPLC Chip (150 mm × 75 μm) with 0.1 % (*v*/*v*) FA at a flow rate of a 4 μl/min. The eluted peptides were ionized and analyzed by mass spectrometry. MS^n analysis was carried out on the three most abundant peptide precursor ions at each time point, as selected automatically by the mass spectrometer. MASCOT MS/MS ion search, National Centre for Biotechnology Information (NCBI; www.ncbi.nlm.nih.gov/guide/proteins/) database, and Kyoto Encyclopedia of Genes and Genomes (KEGG; www.genome.jp/kegg/) were used for protein identification and function.

Label-free comparative quantitative proteomic analysis

The protein precipitated lysates, from 3 biological replicates per treatment, were resuspended in 8 M urea. After dithiothreitol reduction and iodoacetic acid-mediated alkylation (Owens et al. 2014), sequencing-grade trypsin combined with ProteaseMax surfactant was added. Digested samples were desalted prior to analysis using C18 ZipTips® (Millipore, Darmstadt, Germany). A quantity (1 μg) was analyzed from each digest, a Q-Exactive mass spectrometer coupled to a Dionex RSLCnano (Thermo Scientific, Waltham, MA, USA). LC gradients ran from 4 to 35 % B (A: 0.1 % FA, B: 80 % acetonitrile, 0.1 % FA) over 2 h, and data was collected using a Top15 method for MS/MS scans (Dolan et al. 2014; O'Keeffe et al. 2014). Comparative proteome abundance and data analysis was performed using MaxQuant software (Version 1.3.0.5; www.maxquant.org/downloads.htm) (Cox and Mann 2008), with Andromeda used for database searching and Perseus (Version 1.4.1.3) used to organize the data. Carbamidomethylation of cysteines was set as a fixed modification, while oxidation of methionines and acetylation of N-terminals were set as variable modifications. The maximum peptide/protein false discovery rates (FDR) were set to 1 % based on comparison to a reverse database. The LFQ algorithm was used to generate normalized spectral intensities and infer relative protein abundance (Luber et al. 2010). Proteins that matched to a contaminant database or the reverse database were removed, and proteins were only retained in final analysis if detected in at least two replicates from at least one treatment. Quantitative analysis was performed using a *t* test to compare pairs of samples. Due to the high sensitivity and larger dynamic range of the gel-free proteomics analyses, only proteins with a fold change ≥2 ($p < 0.05$) were included in the quantitative results (Table S1 in the Supplementary Material) (Dolan et al. 2014; O'Keeffe et al. 2014). Qualitative analysis was also performed to detect proteins that were found in at least two replicates of a particular sample but undetectable in the comparison sample (Table S1 in the Supplementary Material).

Effect of PgAFP on *A. flavus* growth

The growth of PgAFP-treated *A. flavus* was evaluated on microtiter plates (DeltaLab, Rubí, Spain), with 200 μl of PDB and 10^5 conidia per well incubated at 25 °C during 96 h in static conditions. Seven serial 1:2 dilutions of PgAFP (i.e., 75, 37.5, 18.75, 9.38, 4.69, 2.34, and 1.17 μg/ml) and a non-treated control were assayed. Optical density was measured at 550 nm every 24 h in an Infinite M2000 microplate reader (TECAN, Männedorf, Switzerland).

SYTOX Green uptake

A. flavus was grown and treated with the seven PgAFP concentrations from 75 to 1.17 μg/ml described above. Additionally, *P. chrysogenum* was also used as a resistant control. After incubation of test samples for 24 h at 25 °C,

wells were supplemented with 0.2 μM SYTOX Green (Molecular Probes, Eugene, OR, USA). The fluorescence emitted was measured at 10, 30, and 210 min in an Infinite M2000 spectrophotometer (TECAN, Männedorf, Switzerland), with excitation wavelength of 480 nm (slit, 5 nm) and emission wavelength of 530 nm (slit, 10 nm).

Hyphal morphology

A. flavus was grown in tubes containing 300 μl of PDB at 25 °C for 24 h in either presence (20 and 75 μg/ml) or absence of PgAFP. Mycelium was collected by centrifugation and observed on a microscope Eclipse E200 equipped with a digital camera DS-Fi2 (Nikon, Tokyo, Japan).

FUN-1 staining

To evaluate the metabolic activity with a viability staining, the mycelium of *A. flavus* in either presence (20 μg/ml) or absence of PgAFP was washed with 10 mM HEPES (pH 7.5) before staining with 100 μl FUN-1 (Molecular Probes, Eugene, OR, USA) for 30 min at 25 °C as described previously (Kaiserer et al. 2003). The PgAFP producer strain *P. chrysogenum* was used as a resistant control. Stained hyphae were examined and photographed by fluorescence microscopy (Nikon, Tokyo, Japan).

Chitin staining

Conidia of *A. flavus* were inoculated on 10-ml PDB in a Petri dish containing a cover glass and incubated in presence (20 and 75 μg/ml) and absence of PgAFP at 25 °C for 24 h (Harris et al. 1994). Similarly, as a control, *P. chrysogenum* was treated with 75 μg/ml PgAFP. Mycelium was fixed and stained for 5 min with fluorescent brightener 28 (Sigma-Aldrich, St. Louis, MO, USA) and then washed to visualize chitin in a fluorescence microscopy with an excitation wavelength of 387/11 nm.

Nuclei staining

To visualize the distribution of nuclei in PgAFP-treated (20 and 75 μg/ml) and non-treated hyphae, double-stranded DNA was fluorescently labeled by incubating with 1.6 μM Hoechst 33258 dye (Molecular Probes, Eugene, OR, USA) for 30 min at 25 °C as described previously (Kaiserer et al. 2003) and visualized through fluorescence microscopy with excitation wavelength of 387/11 nm.

Localization of FITC-labeled PgAFP

PgAFP was labeled by DareBio S.L. (Elche, Spain). For this, 100 μl of 20 mM fluorescein isothiocyanate (FITC; Anaspec, Fremont, CA, USA) in dimethyl sulfoxide was added to 4 ml of PgAFP (369 μg/ml) and left for 8 h at room temperature in the dark. Then, 100 μl of 0.8 M Tris–HCl (pH 8.0) was added, to reach a final Tris–HCl concentration of 20 mM, and dialyzed against phosphate-buffered saline (PBS). The activity of 20 μg/ml of PgAFP labeled with FITC was checked in a growth inhibition assay as described above. Then, *A. flavus* was grown in PDB for 6 and 24 h at 25 °C in presence of 20 μg/ml of PgAFP labeled with FITC. Hyphae were washed twice with PBS and visualized by fluorescence microscopy with excitation wavelength of 482/35 nm. As controls, two additional tests were run: the PgAFP-resistant *P. chrysogenum* grown with PgAFP labeled with FITC and *A. flavus* grown with FITC-PgAFP previously treated at 121 °C for 15 min.

ROS detection

Induction of ROS production by PgAFP was evaluated using 2′,7′-dichlorofluorescein diacetate (Sigma-Aldrich, St. Louis, MO, USA) as described previously (Kaiserer et al. 2003) with some modifications. *A. flavus* was grown as described in FUN-1 assay section; hyphae were incubated for 2 h at 25 °C with 20 μM fluorescent dye and observed by fluorescence microscopy with excitation wavelength of 482/35 nm. Additionally, the resistant *P. chrysogenum* was used as negative control.

Acridine orange/ethidium bromide double staining

A. flavus incubated at 25 °C for 24 h in either presence (20 and 75 μg/ml) or absence of PgAFP was stained with 4 μg/ml of acridine orange/ethidium bromide (AO/EB; Sigma-Aldrich, St. Louis, MO, USA), incubated 30 min, and washed twice to be observed by fluorescence microscopy (excitation wavelengths, 482/35 and 562/40 nm). *P. chrysogenum* grown with 75 μg/ml PgAFP was also stained as negative control.

Apoptosis induction by PgAFP

Apoptosis Detection Kit (Sigma-Aldrich, St. Louis, MO, USA) composed by annexin V-fluorescein isothiocyanate/propidium iodide (AnV-FITC/PI) was carried out according to manufacturers' instruction to distinguish between necrotic, late apoptotic, and viable cells in cultures of *A. flavus* incubated at 25 °C for 12 and 24 h in either presence (20 μg/ml) or absence of PgAFP. Likewise, *P. chrysogenum* was assayed as negative control.

Statistical analysis

Statistical analyses were performed with IBM SPSS v.22 (www-03.ibm.com/software/products/es/spss-stats-standard). Growth inhibition and membrane permeability data were

tested for normality (Kolmogorov–Smirnov with Lilliefors correction) and homoscedasticity (Levene's test). Given that these data were non-normally distributed, mean values were compared using non-parametric Kruskal–Wallis test. To compare treatments in pairs, Mann–Whitney *U* test was applied ($p < 0.05$).

Results

Effect of PgAFP on *A. flavus* growth

The study of the inhibitory effect revealed that concentrations of PgAFP from 9.38 μg/ml reduced *A. flavus* growth at 48 h ($p < 0.05$) in static culture, with differences increasing up to the end of the incubation time (Fig. 1). According to optical density reductions, over 50 % growth inhibition was reached with 18.75 μg/ml PgAFP or above, at 96 h. However, no statistically significant difference was found among *A. flavus* inhibition with PgAFP concentrations over 9.38 μg/ml. No growth difference was observed at 24-h incubation among samples with the various concentrations assayed. All samples are in the exponential growth phase at 48 h (Fig. 1), revealing that the lag phase was very similar in all conditions tested, even the non-treated samples. Similarly, all cultures were at the exponential growth phase at 96-h incubation time.

Effect on protein profile

A comparative proteomic analysis of *A. flavus* in either presence or absence of PgAFP was carried out to study the metabolic pathways altered by this antifungal protein. A relatively low concentration of PgAFP was used in this assay (10 μg/ml) so as to reach a balance between fungistatic effect and sufficient growth in 24 h under continuous shaking. All samples showed a sufficient growth at harvesting time. Both untreated and PgAFP-treated cultures under continuous shaking were in the exponential growth phase from 24 to 48 h according to mycelium dry weight (data not shown). From gel-based proteomics, only 26 spots showed a fold change ≥1.5 between the relative abundance of PgAFP-treated and untreated samples and were identified ($p < 0.05$). However, it appeared that these 26 spots belong to 23 unique proteins. Three spots were isoforms of pyruvate carboxylase, and the putative Hsp70 chaperone HscA was identified from two spots (Table 1), each with different molecular masses and charges possibly due to breakdown and side-chain deamination. In PgAFP-treated samples, the relative abundance was 1.6–3.5-fold higher for 13 spots, whereas 13 were 1.6–3.6-fold lower (Table S2 in the Supplementary Material).

The label-free quantitative analysis led to the identification of 1733 unique proteins (identification by at least 2 peptides per protein), and with each validated protein detected in a minimum of 2/3 biological replicates from at least one treatment group. Of these proteins, 367 were identified whose relative abundance suffered some change, either quantitative ($n = 231$) or qualitative ($n = 136$) (Table S1 in the Supplementary Material), using methods described above. All 23 proteins showing significant changes in 2D gels were also identified by label-free quantitative analysis. From these, six proteins showed a similar fold change in both methods. The remaining 17 reached at least a 1.5-fold change in gel-based analysis but did not reach the twofold change threshold in label-free proteomic analysis. The presence of isoforms could explain these differences. PgAFP-treated samples contained 104 proteins with higher abundance, from 2- to 288-fold ($p < 0.05$), and 67 proteins were exclusively detected following PgAFP exposure. In addition, untreated samples showed 127 proteins in higher abundance, between 2- and 202-fold ($p < 0.05$), and 69 proteins were exclusively detected in these samples. Scatterplot analysis of data from the label-free study revealed strong correlation within the biological replicates from each respective treatment group (Pearson correlation values >0.95), confirming high

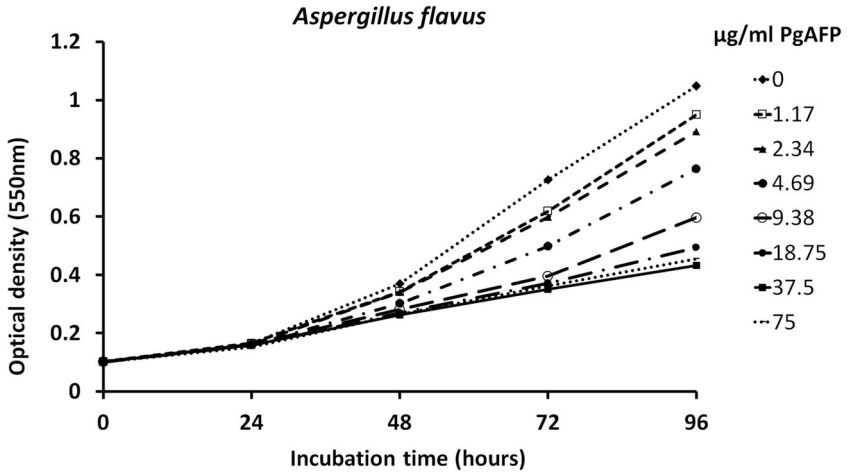

Fig. 1 Effect of different concentrations of PgAFP on *A. flavus* growth for 96 h

Table 1 Selected proteins whose relative abundance was affected by PgAFP in *A. flavus* reaching over 1.5-fold change in 2D-PAGE or 2.0-fold change in label-free proteomics (LFP) analysis. Data are given according to four groups of metabolic pathways

Proteins involved in pathways	Detection method	Fold change
Energy metabolism related to glycolysis and gluconeogenesis		
Pyruvate decarboxylase	2D-PAGE and LFP	+1.6 and <2
Phosphoglucomutase	2D-PAGE and LFP	+1.6 and <2
Pyruvate carboxylase (three isoforms)	2D-PAGE and LFP	−1.9/−1.7/−1.7, and −2.1
Acetate-CoA ligase	2D-PAGE and LFP	−1.7 and −2.7
Aldose 1-epimerase	LFP	NT[b]
Phosphoenolpyruvate carboxykinase	LFP	−2.67
Aldehyde dehydrogenase	LFP	−2.45
Phosphofructokinase	LFP	−3.34
Acetyl-CoA carboxylase[a]	LFP	−2.34
Malate synthase	LFP	−8.55
Stress response and glutathione metabolism		
Molecular chaperone and allergen Mod-E/Hsp90/Hsp1	2D-PAGE and LFP	+3.3 and <2
Hsp70 chaperone (two isoforms)	2D-PAGE and LFP	+1.7/+1.7 and <2
Chaperonin	LFP	+5.63
Cys-Gly metallodipeptidase Dug1	2D-PAGE and LFP	+1.7 and <2
Glutathione synthetase	2D-PAGE and LFP	+1.6 and <2
Elongation factor 1 gamma	LFP	NT
Gamma-glutamyltranspeptidase	LFP	−2.63
Glutathione S-transferase[a]	LFP	−2.42
G protein complex beta subunit CpcB	LFP	−2.85
Cell wall integrity, chitin biosynthesis, and permeability		
Actin Act1	2D-PAGE and LFP	−2.2 and −5.16
Septin AspA	2D-PAGE and LFP	−2 and −2.15
Probable beta-glucosidase btgE	LFP	+3.64
Cell wall glucanase	LFP	T[c]
Mannose-1-phosphate guanylyltransferase	LFP	−11.9
Glucosamine-fructose-6-phosphate aminotransferase	LFP	−5.64
Alpha, alpha-trehalose-phosphate synthase subunit putative	LFP	−4.21
Septin	LFP	−3.02
Rho GTPase Rho1	LFP	−2.68
GDP-mannose pyrophosphorylase A	LFP	−2.42
Septin AspB	LFP	−2.06
Aflatoxin biosynthesis		
Acetyl-CoA carboxylase[a]	LFP	−2.34
AflK/vbs/VERB synthase	LFP	NT
AflM/ver-1/dehydrogenase/ketoreductase	LFP	NT
Glutathione S-transferase[a]	LFP	−2.42
O-Methyltransferase, putative	LFP	−30.18

[a] Protein involved in more than one pathway

[b] NT: Protein only detected in non-treated samples

[c] T: Protein only detected in treated samples

reproducibility from the biological replicates (Fig. S1, Table S3 in the Supplementary Material). Among the characterized proteins, the highest increases in PgAFP-treated samples were detected for ribosomal 40S and 60S proteins, as well as other putative proteins such as translation initiation factors, small nuclear ribonucleoproteins, RNA binding, and splicing proteins, many being uniquely detected in PgAFP-treated samples.

According to KEGG, in addition to ribosomal, spliceosomal, RNA transport, and degradation proteins, hyphae biogenesis proteins also increased upon PgAFP exposure. Interestingly, PgAFP exposure attenuated abundance of proteins related to a number of cellular systems, such as glycolysis and gluconeogenesis, stress response, cell wall integrity, and aflatoxin biosynthesis (Table 1). Two of these proteins play crucial roles in signaling the cell response to external factors, including antifungal compounds in *A. nidulans* (Coca et al. 2000) and in *Saccharomyces cerevisiae* (Fuchs and Mylonakis 2009): the G protein complex β subunit CpcB and Rho-GTPase Rho1, respectively. The aflK/vbs/VERB synthase and AflM/ver-1/dehydrogenase/ketoreductase, both involved in the aflatoxin pathway (Yu et al. 2004) and identified in all control samples, were no longer detectable following PgAFP treatment. Additionally, acetyl-CoA carboxylase, *O*-methyltransferase, and glutathione S-transferase also related to aflatoxin production (Allameh et al. 2002) were found in lower relative amounts in PgAFP-treated samples.

Effect on metabolic activity

To obtain evidences of the metabolic alterations suggested by the comparative proteomics, the metabolic activity was checked with FUN-1 staining. The reduction of metabolic activity was assessed by the yellow-green fluorescence of treated sensitive hyphae, in contrast to the presence of intravacuolar red spots in unaffected controls, as described by Kaiserer et al. (2003). A dramatic difference between PgAFP-treated and untreated *A. flavus* was found. PgAFP-treated samples showed green fluorescence but almost no red intravacuolar fluorescence (Fig. 2), meaning metabolically inactive hyphae. In contrast, untreated *A. flavus* (Fig. 2) and PgAFP-treated *P. chrysogenum* (data not shown) exhibited a high content of red intravacuolar fluorescence due to unaltered metabolic activity.

Morphology

To study morphological changes, septa distribution, nuclei localization, and chitin deposition, in addition to the standard concentration of 20 μg/ml used in other assays, an additional test was run with 75 μg/ml PgAFP to obtain unambiguous results. Among the different tests used to visualize morphological changes induced by PgAFP, no changes in germination or branching were detected by bright light microscopy. Nuclei localization and distribution by fluorescence microscopy with Hoechst 33258 stain showed no abnormal distribution compared to control samples. Septa distribution, checked with fluorescent brightener 28, showed no differences between PgAFP-treated and untreated samples after 24-h incubation (data not shown). Figure 3 shows the fluorescence intensity of the stained PgAFP-treated and untreated hyphae at an early incubation time (12 h). Both micrographs were taken with the same exposure to compare the chitin present. The fluorescence of PgAFP-treated hyphae appeared to be lower than that of untreated samples (Fig. 3).

Effect on membrane permeability and PgAFP localization

Given that the activity of most studied small, highly basic, and cysteine-rich antifungal proteins from molds has been related to interactions with the outer layer of sensitive molds, the level of cell membrane compromise was tested with the SYTOX Green uptake test. Mean (±SD) fluorescence values at 210 min after SYTOX Green addition to *A. flavus* increased up to 23,342 (±2992) arbitrary units as PgAFP concentration increased from 0 to 4.69 μg/ml but progressively decreased down to 11,550 (±2155) arbitrary units from 9.38 to 75 μg/ml (Fig. 4). Nonetheless, the fluorescence in all PgAFP-treated *A. flavus* was at least 27 % ($p < 0.05$) higher than that in the untreated control, except for the lowest PgAFP concentration (1.2 μg/ml) at 10 min after SYTOX Green addition. In contrast, the fluorescence after SYTOX Green addition to the PgAFP producer *P. chrysogenum* did not exceed 25 % over that in non-treated samples at any PgAFP concentration assayed (data not shown). To determine the localization of PgAFP, *A. flavus* was treated with FITC-labeled PgAFP. To check whether FITC labeling decreased the antifungal activity of PgAFP, an antifungal assay was run. No differences ($p > 0.05$) were found between cultures treated with labeled

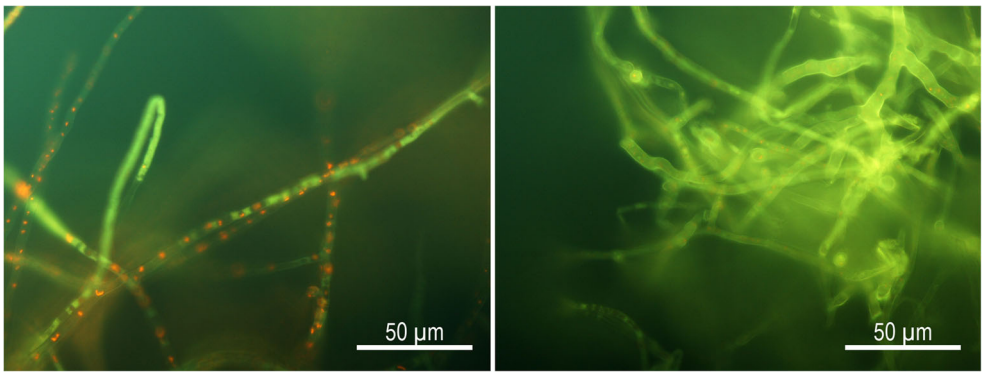

Fig. 2 Metabolic activity of *A. flavus* tested with FUN-1 staining. Non-treated hyphae (*left*) showed intravacuolar activity as red spots; hyphae treated with 20 μg/ml PgAFP for 24 h (*right*) showed scarcely red spots

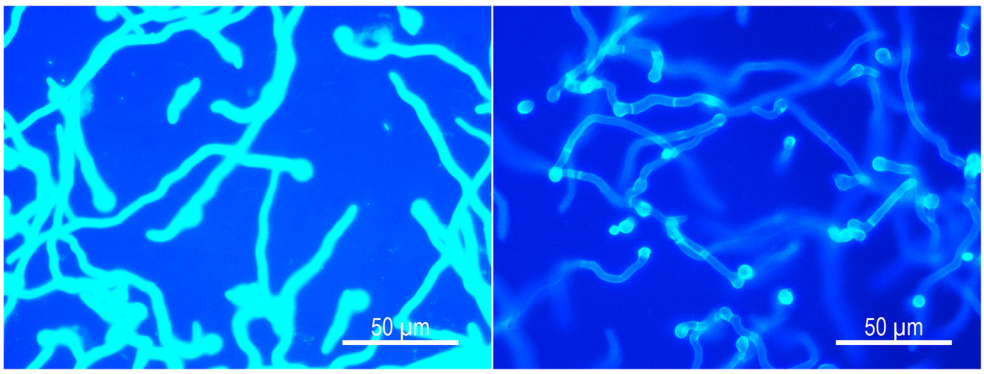

Fig. 3 Chitin distribution on *A. flavus* stained with fluorescent brightener 28. *Left*: non-treated hyphae; *right*: hyphae treated with 75 µg/ml PgAFP for 12 h

and those treated with non-labeled PgAFP (data not shown). Localization of PgAFP by fluorescence microscopy after treatment of *A. flavus* with FITC-labeled PgAFP revealed green fluorescence only at the outer layer at 6-h incubation time but both inside and bound to the outer layer on treated hyphae at 24 h (Fig. 5). In contrast, FITC-labeled PgAFP neither bound nor penetrated in the resistant *P. chrysogenum* (Fig. 5). Additionally, the heat-denatured FITC-PgAFP was not bound to or inside the hyphae (data not shown).

Effect on oxidative status and viability

To discern whether the changes in the proteins related to oxidative stress were provoked by a high ROS level, staining with 2′,7′-dichlorofluorescein diacetate was carried out, where a green fluorescence reveals the presence of intracellular ROS as described by Kaiserer et al. (2003). The most intense oxidative activity was observed in PgAFP-treated *A. flavus*, whereas non-treated hyphae only showed a very weak halo (Fig. 6). Given that ROS may induce severe cell damage, the viability of PgAFP-treated *A. flavus* was evaluated with the AO/EB double staining to check for necrosis and also with AnV-FITC/PI staining to detect apoptotic processes. With AO/EB double staining, an additional treatment with 75 µg/ml PgAFP was also tested to obtain unambiguous results. A massive loss in viability was observed at 24 h in hyphae treated with 75 µg/ml (Fig. 7). Untreated hyphae displayed a green color, meaning that they remained viable (Byczkowska et al. 2012). The intense orange staining revealed a high penetration of EB in the PgAFP-treated hyphae through a highly compromised cell membrane. Untreated samples were not stained by AnV-FITC/PI, indicating that they were viable. (Fig. 8a). The orange staining of DNA in PgAFP-treated samples by PI indicated cell membrane damage associated with a necrotic stage (Fig. 7b). The generalized necrosis observed can be due to the fact that an advanced stage of cell death was reached at 24 h in nearly all PgAFP-treated hyphae. AnV-FITC staining was used to detect phosphatidylserine translocation to the external side of the plasma membrane due to apoptosis. However, the green fluorescence observed in PgAFP-treated hyphae at 24 h cannot be attributed to apoptosis, because the compromised cell membrane would allow AnV-FITC to enter and bind phosphatidylserine at the inner layer of plasma membrane. To detect potential apoptotic signals previous to the necrotic stage, an additional AnV-FITC/PI staining was carried out at 12 h. The evaluation of phosphatidylserine translocation at this earlier stage revealed some hyphae showing solely green color due to apoptosis (Fig. 8c). All these ROS and viability assays for PgAFP-treated and untreated *P. chrysogenum* gave very similar results to those obtained for untreated *A. flavus* (data not shown).

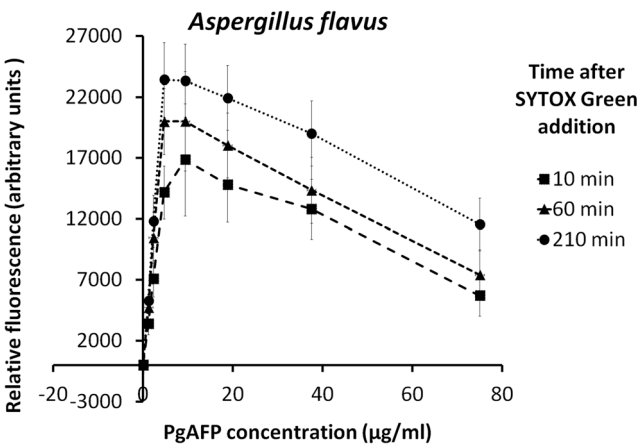

Fig. 4 SYTOX Green uptake with different concentrations of PgAFP on *A. flavus* at 24 h (*bars* represent standard deviation of the mean)

Discussion

PgAFP reduced *A. flavus* growth following a dose-dependent pattern (Fig. 1). The inhibition rate reached with PgAFP at 37.5 µg/ml was 59 %, calculated from the percent difference in OD_{550} compared to untreated controls. Similar results were obtained with PAF against *A. flavus*, reaching a 69 % growth reduction with 50 µg/ml (Kaiserer et al. 2003) and 50 % growth reduction with 3 µM (18.9 µg/ml) (Marx et al. 2008). The first 24 h of incubation did not show any statistical

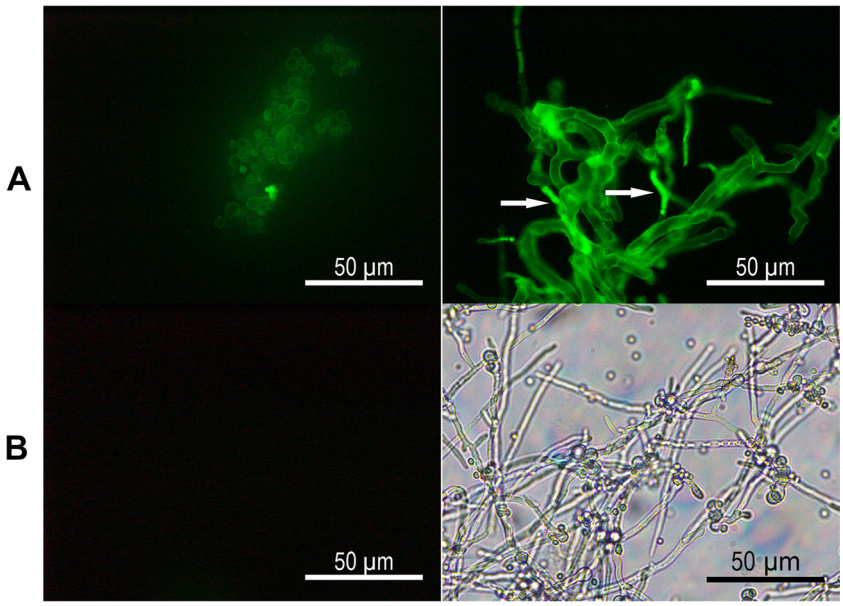

Fig. 5 PgAFP localization in *A. flavus* and *P. chrysogenum* treated with 20 μg/ml FITC-labeled PgAFP. (**a**) *A. flavus*. *Left*: At 6-h incubation, PgAFP was found solely bound to the outer layer. *Right*: At 24-h incubation, PgAFP was detected bound to the outer layer and occasionally inside the cell (*arrows*). (**b**) *P. chrysogenum*. *Left*: At 24-h incubation, PgAFP was neither bound nor inside the hyphae. *Right*: Bright field observation of the same preparation showing profuse growth

differences in growth, due to the limited fungal growth at this time point under the conditions assayed. Even the highest PgAFP concentrations tested (75 μg/ml) did not lead to total inhibition of *A. flavus*, which implies only a fungistatic effect.

Using gel-based proteomics, a total of 23 unique proteins, identified from 26 independent spots (Table S2 in the Supplementary Material), were observed to undergo a significant change in abundance in *A. flavus* in response to PgAFP. A concurrent analysis using label-free quantitative mass spectrometry-based proteomics revealed a more in-depth view of the response to PgAFP, with 231 quantitative changes in protein abundance and 136 qualitative differences following treatment. The dynamic range of gel-based proteomics, using colloidal Coomassie Blue stain as a visualization technique, is limited to approximately 1 order of magnitude (Gauci et al. 2011). As a result, the proportion of the proteome available for analysis using gel-based methods is constrained by relative protein abundance. In comparison, label-free proteomics is capable of measuring protein abundances across larger dynamic ranges, with proteins identified across 4 orders of magnitude in this study (Table S1 in the Supplementary Material). In order to reduce the possibility of inclusion of false positives in this larger data set, a fold change cutoff of 2 was employed. In addition, differing capacities for resolution of proteins with extremes in p*I*, molecular mass, and hydrophobicity (Owens et al. 2014) can contribute to the lower number of abundance changes detected using gel-based proteomics. Furthermore, the limitations of the label-free proteomic technique with regard to capability to analyze isoforms could explain the different quantification of proteins when isoforms were involved. For example, multiple Hsp70 isoforms have been described in the eukaryotic cytosol (Kabani and Martineau 2008). Although an increase of Hsp70 chaperone (HscA) was detected in gel-based proteomic analysis, no significant change in abundance was detected for Hsp70 chaperone (HscA) by label-free analysis. This may indicate that the abundance difference detected by 2D-PAGE for this protein may be the result of a post-translational event, which altered the ratio of the different isoforms instead of the total HscA protein abundance.

A substantial number of ribosomal proteins were detected with increased abundance in response to PgAFP, in addition to

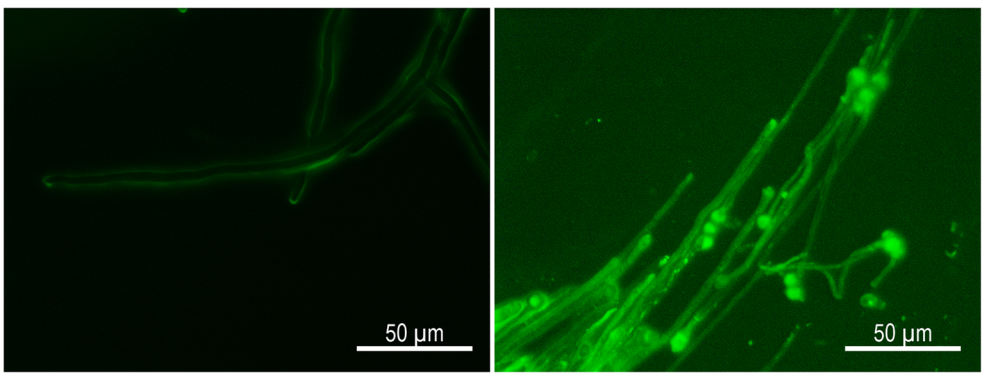

Fig. 6 ROS induction by PgAFP on *A. flavus* detected by 2′,7′-dichlorofluorescein diacetate staining. Non-treated *A. flavus* (*left*) did not show green fluorescence inside of the cells; hyphae treated with 20 μg/ml PgAFP for 24 h (*right*) showed strong green fluorescence due to intracellular ROS

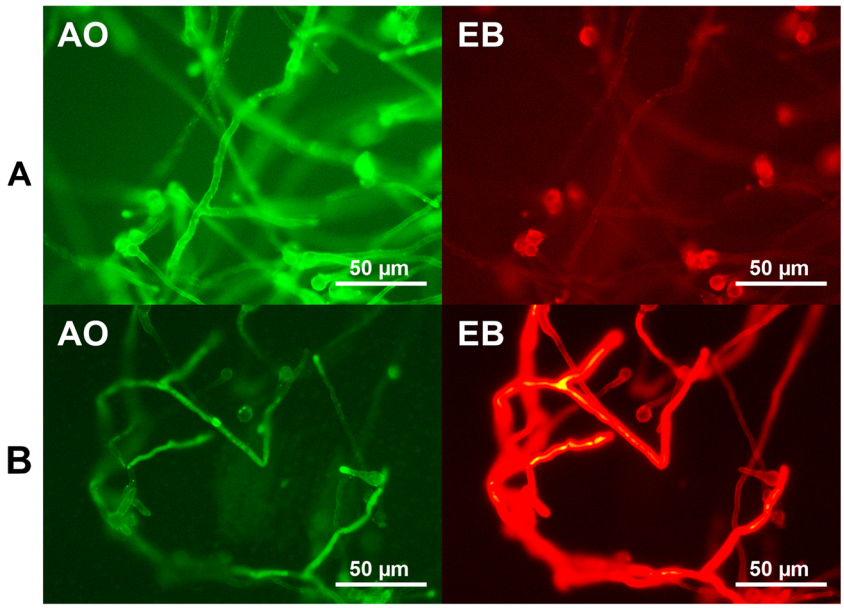

Fig. 7 Effect of PgAFP on hyphae viability evaluated with vital acridine orange (AO)/ethidium bromide (EB) staining. **a** Non-treated hyphae of *A. flavus* showing an intense green color (AO). **b** Seventy-five microgram per milliliter PgAFP-treated hyphae showing an intense red color (EB) due to compromised cell membrane

proteins involved in RNA transport and degradation, and the spliceosome. Ribogenesis and translation are energy-hungry processes, which are normally associated with germination or cell growth (Lamarre et al. 2008). This observed increase in the translational machinery, coupled with the decrease in metabolism-associated mechanisms, could lead to depletion of the cell energy reserves and result in the fungistatic effect of PgAFP on *A. flavus*. The main pathways identified with

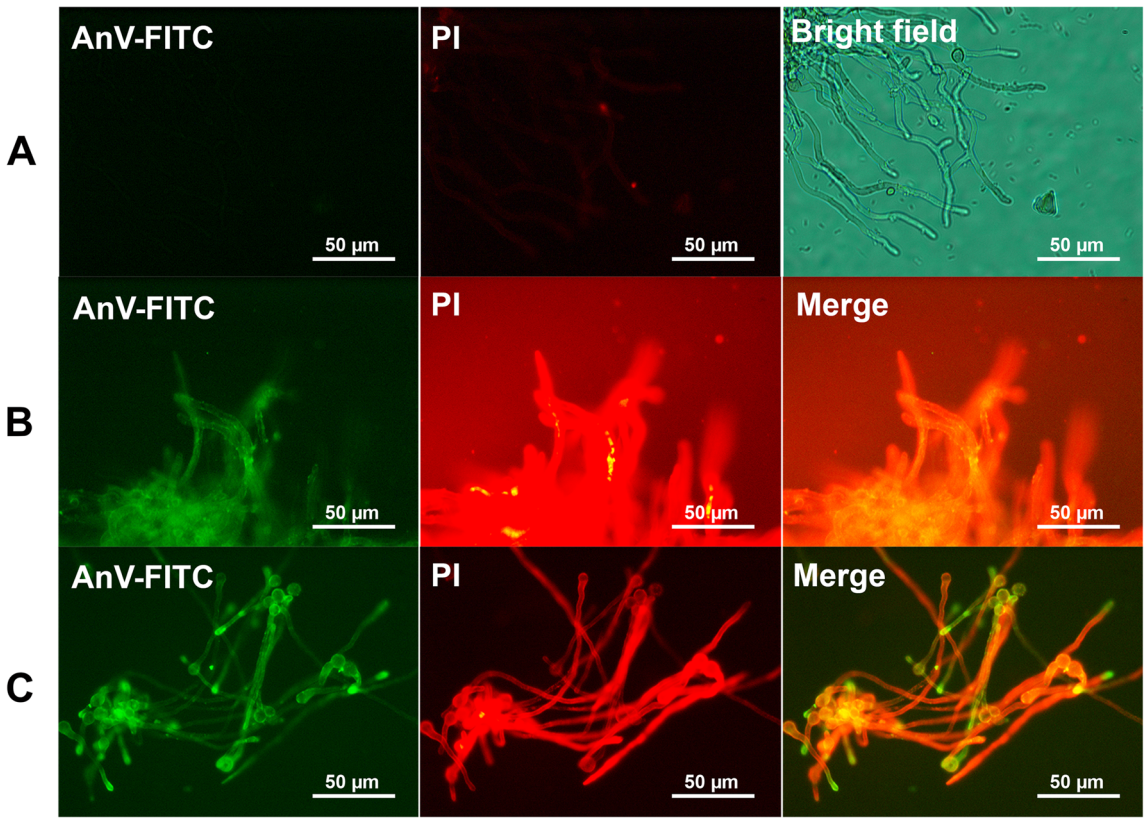

Fig. 8 Effect of PgAFP on *A. flavus* hyphae viability evaluated with apoptosis detection kit. **a** Non-treated hyphae showing no apoptosis or necrosis signal at 24 h. **b** Hyphae treated with 20 µg/ml PgAFP for 24 h showing an intense red color (PI) due to necrosis that leads to mainly orange color in the *merged picture*. **c** Hyphae treated with PgAFP for 12 h revealing apoptotic signals by the green fluorescence (AnV-FITC) that leads to green hyphae in the *merged picture*

proteins showing changes in relative abundance due to PgAFP are involved in energy metabolism, cell stress response, hyphae biogenesis, and aflatoxin biosynthesis (Table 1). The proteins related to energy metabolism showing a lower abundance in PgAFP-treated samples were pyruvate carboxylase, phosphofructokinase, aldose 1-epimerase, phosphoenolpyruvate carboxykinase, aldehyde dehydrogenase, malate synthase, acetate-CoA ligase, and acetyl-CoA carboxylase. These enzymes play essential roles in glycolysis and gluconeogenesis pathways, and the lower quantity would depress the metabolic activity. This effect is supported by the results obtained from the FUN-1 staining (Fig. 2) where PgAFP-treated samples showed reduced metabolic hyphae activity. A reduced metabolic activity has been also described with FUN-1 staining for PAF in *A. niger* (Kaiserer et al. 2003).

A. flavus is not completely killed, even at the highest PgAFP concentration assayed. This fact suggests that *A. flavus* invests in alternative ways to obtain the necessary energy to grow. This seems to be achieved through anaerobic pathways led by pyruvate decarboxylase, whose relative quantity was higher in PgAFP-treated samples. Pyruvate decarboxylase is involved in alcoholic fermentation under anaerobic stress (Lockington et al. 1997). Thus, the pyruvate presumptively accumulated due to the lower pyruvate carboxylase presence with PgAFP would be used as substrate by pyruvate decarboxylase. However, this pathway would not provide enough energy to keep a normal growth rate. The lower abundance of proteins involved in hyphae structure, such as septins and actin, may provoke morphological changes, such as those caused by AFP1 from *Streptomyces tendae* and PAF in sensitive molds (Bormann et al. 1999; Kaiserer et al. 2003). Septin AspA, AspB, and AspC are necessary for normal development and morphogenesis (Lindsey et al. 2010; Hernández-Rodríguez et al. 2012). Actin is necessary for cell wall and membrane extension (Fischer et al. 2008). The lower relative abundance of septins and actins detected in PgAFP-treated *A. flavus* suggests morphological changes, as it has been shown for *Aspergillus* spp. treated with PAF due to actin gene repression (Kaiserer et al. 2003; Binder et al. 2010). Despite the altered quantity of proteins, no morphological change was visualized in hyphae and nuclei distribution in PgAFP-treated *A. flavus*.

Similarly to PgAFP, AFP from *A. giganteus* did not cause morphological changes in sensitive molds (Theis et al. 2003) but binds to regenerated chitin (Liu et al. 2002) and specifically inhibits chitin synthesis, causing cell wall stress and disturbing cell integrity (Hagen et al. 2007). However, AFP1 also binds to chitin but causes severe alteration in cell morphogenesis (Bormann et al. 1999). In fact, proteins participating in chitin pathway were found in lower relative amount in PgAFP-treated *A. flavus*, such as the putative α-trehalose-phosphate synthase subunit α, glucosamine-fructose-6-phosphate aminotransferase, mannose-1-phosphate guanylyltransferase, and GDP-mannose pyrophosphorylase A. Furthermore, a cell wall glucanase, whose main function involves degrading chitin, was found exclusively in PgAFP-treated samples. These changes in the relative abundance of chitin-related proteins could explain a smaller deposition of chitin on cell wall of *A. flavus* at 12-h incubation time as suggested by the fluorescent brightener 28 staining (Fig. 3). A lower quantity of chitin may be related to the mode and the site of action of PgAFP, as it has been reported for AFP (Hagen et al. 2007). Regarding cell wall glucanase, its detection only in PgAFP-treated samples can be a consequence to counteract PgAFP binding to chitin. PAF exposure resulted in a deregulation of the chitin deposition at hyphal tips (Binder et al. 2010). Therefore, the smaller amount of septins, actin, and chitin, seems not to be enough to provoke morphological changes in hyphae but could affect normal growth and cell wall integrity. In addition, eleven proteins related to cell wall integrity showed lower relative abundance in PgAFP-treated samples (Table 1). Rho1 GTPase is considered the master regulator of cell wall integrity signaling and it is involved in actin organization in *S. cerevisiae* (Levin 2005). *A. nidulans* cells treated with PAF fail to activate MpkA, a target of GTPase RhoA signaling, disrupting basal resistance towards antifungal activity (Binder et al. 2010). In addition, *A. nidulans* lacking RhoA display pronounced hypersensitivity to cell wall-interfering drugs (Guest et al. 2004). GDP-mannose pyrophosphorylase has been described as essential for cell wall integrity, morphogenesis, and viability of *Aspergillus fumigatus* (Jiang et al. 2008), and it also seems to be related to regulation of the selective permeability (Agaphonov et al. 2001).

AFP specifically inhibits in situ activity of chitin synthases classes III and V in sensitive fungi, which would disturb cell integrity, but it strongly induced cell wall integrity pathway in *A. niger* as a compensatory response (Hagen et al. 2007). Similarly, reinforcement of chitin synthesis has been described as a distinctive feature of AFP-moderate sensitive and AFP-resistant fungi, whereas it is not realized in AFP-sensitive fungi (Ouedraogo et al. 2011). This elevation of chitin levels has been interpreted as the necessary response to survive an AFP attack. Therefore, it seems that the mode of action of AFP is based on cell wall alterations. However, as it has been mentioned above, PgAFP repressed the cell wall integrity pathway and chitin biosynthesis in treated *A. flavus*. This would increase membrane exposure to PgAFP. Actually, PgAFP increased permeability at all concentrations tested (Fig. 4). Notwithstanding this, the highest SYTOX Green uptake was observed at low PgAFP concentrations (4.69 μg/ml). A similar fact has been described for plant defensin DmAMP1, whose dose–response curves for SYTOX Green uptake declined at doses above those providing maximum effect (Thevissen et al. 1999). In contrast, the inhibition assay exhibited a dose–response effect of PgAFP in the whole range of

concentrations tested. The lower SYTOX Green uptake at the highest PgAFP concentrations could be related to the apparent dependency of membrane polarization, as it has been shown for various antifungal proteins that depolarize the membrane (Thevissen et al. 1996).

Treatment of *A. flavus* with PgAFP-FITC revealed that PgAFP is bound to outer layer and also is present in the cytoplasm. Other antifungal proteins, such as AFP, bind the outer layer of sensitive fungi and also can be found intracellularly in collapsed and dead cells (Theis 2003, 2005). The antifungal activity of AFP is related to its ability to interact with anionic phospholipids (Lacadena et al. 1998). Such interaction would promote the insertion of the antifungal protein into the plasma membrane of the sensitive fungi (Marx et al. 2008). In contrast, PAF is actively internalized only in sensitive fungi (Oberparleiter et al. 2003; Batta et al. 2009). Thus, it seems that PgAFP induces the aforementioned changes in membrane permeability after binding to the outer layer. Given that the results obtained at 24 h did not allow the confirmation that PgAFP is inside non-compromised cells, PgAFP internalization cannot be ruled out.

Additionally, the above changes in energy metabolism and cell wall integrity are aggravated by cell damage due to ROS generation. Among other negative effects on lipids and nucleic acids, ROS also cause protein aggregation and amyloid formation (Squier 2001), compromising cell viability (Cabiscol et al. 2000). Heat shock proteins were found in higher relative abundance in PgAFP-treated samples. These proteins are involved in stress, preventing aggregation and assisting refolding of misfolded proteins (Bukau and Horwich 1998). The observed higher abundance of heat shock proteins could represent a defense mechanism to neutralize ROS effects on proteins.

Increased abundance of two proteins involved in the glutathione pathway was also found: glutathione synthetase (GS) and Cys-Gly metallodipeptidase Dug1. Glutathione (GSH) has pivotal roles in protection against oxidative stress provoked by exposure of cells to ROS (Penninckx 2002). Therefore, GSH overproduction due to the increased GS could counteract ROS present in the cell, as it has been described for PAF (Leiter et al. 2005). A higher amount of ROS was confirmed by fluorescence staining in PgAFP-treated samples (Fig. 6). In addition, γ-glutamyltranspeptidase (γGT) was found in lower amount in PgAFP-treated *A. flavus*. This enzyme is involved in glutathione catabolism, releasing the Cys-Gly dipeptide (Kaur et al. 2009). Furthermore, the Cys-Gly metallodipeptidase Dug1 degrades the Cys-Gly dipeptide, recovering glycine and cysteine for GSH synthesis by GS. The higher relative abundance of Cys-Gly metallodipeptidase Dug1 observed in PgAFP-treated *A. flavus* would help counteract high ROS levels. Thus, it seems that *A. flavus* also uses GSH metabolism to counteract PgAFP action due to ROS production. However, as discussed later, G protein subunit β CpcB may also play an essential role modulating the intracellular levels of glutathione and ROS.

Despite the production of heat shock proteins and GSH to combat ROS, the defense mechanism of *A. flavus* does not seem to be effective against PgAFP. The observed increase of ROS in PgAFP-treated samples could explain *A. flavus* inhibition. These substances can act as primary triggers of apoptosis (Slater et al. 1995). The loss of cell membrane integrity revealed by AO/EB double staining and the annexin V-FITC and PI staining (Figs. 7 and 8) is a necrotic signal derived from the observed apoptotic process, likely triggered by ROS (Hamann et al. 2008). Thus, the *A. flavus* response to counteract ROS seems insufficient to prevent the necrotic process. PAF needs active G protein signaling to inhibit the growth of the sensitive organism (Leiter et al. 2005). A lower relative amount of G protein complex β subunit CpcB was found in PgAFP-treated *A. flavus*, but changes in neither G protein complex α subunit GpaA/FadA nor G protein complex β subunit SfaD were detected. Thus, the relative abundance of the G protein complex β subunit CpcB seems to be the key factor involved in the modulation of apoptotic cell death signals, and the lower amount of this protein could be responsible for the modulating PgAFP toxicity in *A. flavus*.

Until now, the effect of antifungal proteins from molds has been explained by signaling processes via G protein and RhoA (Binder et al. 2010; Ouedraogo et al. 2011). We propose the lower relative abundance of Rho1 and G protein subunit β CpcB to be the main factors in the mode of action of PgAFP. The precise mechanisms responsible for the decrease of these proteins, either by a higher degradation or a decreased biosynthesis, cannot be established at present.

In addition, several proteins involved in the biosynthesis of secondary metabolites were found at lower relative abundance in PgAFP-treated samples. This fact seems to be related to the reduced metabolic hyphae activity revealed with FUN-1 staining (Fig. 2). The suppression of non-essential functions, such as biosynthesis of secondary metabolites, could be explained by the lack of energy due to the described shortage of proteins related to energy metabolism. Among the secondary metabolites produced by *A. flavus*, the hepatocarcinogenic aflatoxins are of utmost interest (Kim et al. 2008). The proteomic analysis did not detect aflK/vbs/VERB synthase and AflM/ver-1/dehydrogenase/ketoreductase following PgAFP treatment, which are essential enzymes in key steps for aflatoxin synthesis in *A. flavus* and *Aspergillus parasiticus* (Yu et al. 2004). Additionally, glutathione S-transferase was found in lower quantities in PgAFP-treated samples. A higher activity of this protein was always associated with increased aflatoxin production in *A. flavus* (Saxena et al. 1988) and *A. parasiticus* (Allameh et al. 2002). These results suggest that aflatoxin production is likely to be delayed in PgAFP-treated *A. flavus*. Despite these results having been obtained in an incubation time of only 24 h, the lack of enzymes essential for aflatoxin

biosynthesis together with the slower hyphae development could delay aflatoxin production in a longer incubation time. On the other hand, oxidative stress has been shown to stimulate aflatoxin biosynthesis in *A. parasiticus* (Jayashree and Subramanyan 2000; Reverberi et al. 2005). Due to the induction of ROS by PgAFP, the impact of this antifungal protein on aflatoxin biosynthesis enzymes and also on aflatoxin production will require additional studies.

In conclusion, the mode of action of PgAFP seems to be multifactorial implying membrane changes, reduced metabolic activity, and intracellular ROS production. The changes in the proteins that favor a higher GSH concentration and the increase in heat shock proteins by *A. flavus* do not seem to be enough to avoid apoptosis. There is also a depression of proteins involved in the biosynthesis of secondary metabolites, including aflatoxin. However, further investigations are required to discern the effect of PgAFP on aflatoxin production prior to the use of this protein to control toxigenic molds.

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Conflict of interest The authors declare that they have no competing interests.

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Supplementary Information

Impact of the antifungal protein PgAFP from *Pencillium chrysogenum* on the protein profile in *Aspergillus flavus*

Josué Delgado,[a] Rebecca A. Owens,[b] Sean Doyle,[b] Miguel A. Asensio[a] and Félix Núñez.[a]

[a] Food Hygiene and Safety, Institute of Meat Products, University of Extremadura, Cáceres, Spain.
[b] Department of Biology, Maynooth University, Maynooth, Co. Kildare, Ireland.

Corresponding author:
Miguel A. Asensio
masensio@unex.es, Tel.: +34 927 257124; Fax: +34 927 257110.

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
27.7208	28.5406	27.6937	28.3946	28.635	28.2656	1.11E-42	3480300000	6	6	1	51.5	11.356	28.2084	27.985	28.4317	6	3	3	B8N4Q3	B8N4Q3	1	AFLA_017620	Histone H4
ND	23.6015	24.7384	ND	ND	ND	1.73E-06	58775000	2	2	2	8.5	36.25	24.17	24.17	ND	2	2	0	B8MVP1	B8MVP1	1	AFLA_072380	Putative uncharacterized protein
24.0383	23.8563	ND	24.221	24.1957	23.8998	3.14E-06	179460000	2	2	2	10.4	45.208	24.0422	23.9473	24.1055	5	2	3	B8MWB8	B8MWB8	1	AFLA_088080	Aspartate aminotransferase, putative
26.0859	26.9276	27.0822	26.4146	ND	25.9395	1.39E-86	717750000	2	2	2	59	11.188	26.49	26.6986	26.1771	5	3	2	B8MWE1	B8MWE1	1	AFLA_088310	Putative uncharacterized protein
25.7827	25.7235	25.7778	25.9624	25.7135	25.6868	1.35E-14	657860000	2	2	2	40.5	8.3184	25.7744	25.7613	25.7876	6	3	3	B8MWS2	B8MWS2	1	AFLA_088720	Iron/copper transporter Atx1, putative
ND	24.5816	ND	ND	25.6623	25.0586	3.16E-06	254650000	2	2	2	20.8	21.662	25.1008	24.5816	25.3604	3	1	2	B8MWS9	B8MWS9	1	AFLA_088790	DUF814 domain protein, putative
25.4538	24.6882	23.9493	27.0254	26.5576	25.5933	3.36E-17	516450000	2	2	2	20.9	20.307	25.5446	24.6971	26.3921	6	3	3	B8MX51	B8MX51	1	AFLA_076380	Mitochondrial intermembrane space protein Mia40
25.1271	25.0883	24.1211	25.3537	25.075	25.0564	1.48E-06	323900000	2	2	2	20.5	16.838	24.9703	24.7788	25.1617	6	3	3	B8MX88	B8MX88	1	AFLA_076750	Putative uncharacterized protein
23.7298	23.5731	23.3884	ND	ND	ND	1.08E-06	103080000	2	2	2	4	68.226	23.5638	23.5638	ND	3	3	0	B8MXU4	B8MXU4	1	AFLA_078810	Oxidoreductin
27.5137	27.9422	27.4859	27.5886	27.7421	27.9303	4.16E-102	1867400000	2	2	2	17.6	17.669	27.7005	27.6473	27.7537	6	3	3	B8MY87	B8MY87	1	AFLA_080240	ATP synthase delta chain, mitochondrial, putative
23.4953	23.2562	ND	ND	23.8543	23.6805	1.56E-05	145780000	2	2	2	7.4	40.508	23.5716	23.3758	23.7674	4	2	2	B8MYI8	B8MYI8	1	AFLA_081260	60S ribosome biogenesis protein Brx1, putative
23.6767	23.4087	ND	ND	ND	ND	7.02E-05	89201000	2	2	2	9.5	34.601	23.5427	23.5427	ND	2	2	0	B8MYK0	B8MYK0	1	AFLA_081380	Cytochrome C1/Cyt1, putative
24.541	24.517	24.7689	24.9986	ND	24.8976	2.58E-06	259590000	2	2	2	13.7	20	24.7446	24.6089	24.9481	5	3	2	B8MYK9	B8MYK9	1	AFLA_081480	IgE-binding protein
25.3355	25.3589	25.4424	25.0083	25.1893	ND	9.24E-06	387140000	2	2	2	5.1	46.698	25.2669	25.379	25.0988	5	3	2	B8MZE9;B8	B8MZE9;B8	2	AFLA_084390	Putative uncharacterized protein
22.6475	23.2012	22.811	ND	23.2144	ND	3.35E-05	76860000	2	2	2	6.2	49.373	22.9685	22.8866	23.2144	4	3	1	B8MZK1	B8MZK1	1	AFLA_084910	Exosome complex exonuclease Rrp6, putative
ND	ND	ND	24.2478	24.2413	ND	4.17E-06	93864000	2	2	2	5.8	40.69	24.2446	ND	24.2446	2	0	2	B8MZQ8	B8MZQ8	1	AFLA_085480	Cell wall glucanase, putative
25.9084	25.4734	26.3552	25.0423	24.5201	24.8919	1.39E-12	317140000	2	2	2	7.5	33.809	25.3652	25.9123	24.8181	6	3	3	B8N008	B8N008	1	AFLA_086480	Translational initiation factor 2 beta
24.4779	24.4769	24.5591	25.7121	24.9512	24.7102	0.0001314	292040000	2	2	2	19.9	28.306	24.8146	24.5046	25.1245	6	3	3	B8N036	B8N036	1	AFLA_086760	ATP-dependent Clp protease proteolytic subunit
23.3744	23.2002	23.2843	23.2847	23.2448	23.8306	1.21E-14	134540000	2	2	2	2.8	76.372	23.3698	23.2863	23.4534	6	3	3	B8N0C4	B8N0C4	1	AFLA_087650	Chromatin assembly factor 1 subunit B, putative
25.4422	23.3621	23.7985	23.2926	24.1124	23.04	1.79E-05	119690000	2	2	2	5	65.278	23.8413	24.2009	23.4817	6	3	3	B8N0E4	B8N0E4	1	AFLA_022880	Oligopeptide transporter, putative
24.6535	25.8395	25.034	25.0759	25.4807	25.4428	7.23E-26	567190000	2	2	2	29.5	12.164	25.2544	25.1757	25.3331	6	3	3	B8N1G1	B8N1G1	1	AFLA_030260	Putative uncharacterized protein
24.5011	24.3422	24.6287	ND	ND	ND	4.02E-07	84066000	2	2	2	17.1	18.542	24.4907	24.4907	ND	3	3	0	B8N1R8	B8N1R8	1	AFLA_032220	DNA damage response protein (Dap1), putative
24.2487	ND	ND	24.0658	ND	23.5279	2.55E-08	171770000	2	2	2	4.3	71.329	23.9475	24.2487	23.7968	3	1	2	B8N1S4	B8N1S4	1	AFLA_032280	Putative uncharacterized protein
24.5787	ND	24.665	ND	ND	ND	6.18E-10	159850000	2	2	2	18.7	23.738	24.6218	24.6218	ND	2	2	0	B8N2G6	B8N2G6	1	AFLA_036510	Methionine-R-sulfoxide reductase SelR, putative
24.2991	23.3292	24.3142	24.7523	26.0779	ND	5.57E-09	244760000	2	2	2	26.1	14.955	24.5546	23.9809	25.4151	5	3	2	B8N345	B8N345	1	AFLA_025690	Putative uncharacterized protein
22.6955	22.7751	ND	22.6662	22.7392	22.6466	6.56E-06	60868000	2	2	2	4.2	80.268	22.7045	22.7353	22.684	5	2	3	B8N389	B8N389	1	AFLA_027020	Putative uncharacterized protein
22.3087	23.2391	ND	26.0933	25.3263	25.481	6.01E-09	220660000	2	2	2	14.2	18.42	24.4897	22.7739	25.6335	5	2	3	B8N3C6	B8N3C6	1	AFLA_027390	Ubiquinol-cytochrome c reductase complex 17 kd protein
ND	ND	ND	23.5114	ND	23.3465	1.28E-05	111500000	2	2	2	23.6	23.229	23.4289	ND	23.4289	2	0	2	B8N3G2	B8N3G2	1	AFLA_028650	Rhodanese domain protein
23.6435	23.8158	23.9186	24.2057	23.7756	24.1181	1.51E-05	105060000	2	2	2	3.7	95.002	23.9129	23.7926	24.0331	6	3	3	B8N3N3	B8N3N3	1	AFLA_031170	Putative uncharacterized protein
25.5494	25.7611	25.6007	25.3192	25.5269	25.7022	0.0001539	508780000	2	2	2	1.3	188.25	25.5766	25.6371	25.5161	6	3	3	B8N4K1	B8N4K1	1	AFLA_037050	HEAT repeat protein (DRIM), putative
23.2931	23.0886	23.4219	23.5007	23.6955	23.5162	5.45E-05	118310000	2	2	2	3.3	61.235	23.4193	23.2679	23.5708	6	3	3	B8N4K2	B8N4K2	1	AFLA_037060	CwfJ domain protein
ND	ND	ND	26.4722	23.4352	24.7111	2.38E-19	275430000	2	2	2	14.3	24.904	24.8728	ND	24.8728	3	0	3	B8N4S4	B8N4S4	1	AFLA_017830	Small nuclear ribonucleoprotein complex protein Nhp2, putative
22.9544	23.4826	23.2408	23.4174	23.7894	23.1371	7.68E-06	94934000	2	2	2	4	56.521	23.3369	23.2259	23.4479	6	3	3	B8N4T0	B8N4T0	1	AFLA_017890	SET domain protein
ND	ND	ND	24.5665	23.7097	23.9068	9.79E-10	146190000	2	2	2	6.1	63.38	24.061	ND	24.061	3	0	3	B8N507	B8N507	1	AFLA_020450	Nucleolar protein nop5
24.098	23.2303	24.0718	ND	ND	ND	0.0001783	175160000	2	2	2	6.4	44.19	23.8	23.8	ND	3	3	0	B8N521	B8N521	1	AFLA_020590	Aldose 1-epimerase, putative
23.98	23.8764	24.5421	23.5062	23.924	23.5973	2.64E-05	131040000	2	2	2	2.7	84.822	23.9043	24.1328	23.6758	6	3	3	B8N5D6	B8N5D6	1	AFLA_022640	Protein O-mannosyl transferase
25.9836	25.5913	25.7085	23.5698	24.3497	24.2394	1.34E-43	692850000	2	2	2	19.3	14.322	24.9071	25.7612	24.053	6	3	3	B8N5T3	B8N5T3	1	AFLA_014260	Conidial hydrophobin RodB/HypB
23.4907	23.3795	23.3715	ND	23.2607	23.0419	2.38E-07	112770000	2	2	2	18.4	19.631	23.3089	23.4139	23.1513	5	3	2	B8N5W1	B8N5W1	1	AFLA_014540	Acetyltransferase, GNAT family, putative
24.5239	24.0482	23.8534	22.6655	23.5094	ND	3.18E-08	84142000	2	2	2	16.2	18.613	23.7201	24.1418	23.0875	5	3	2	B8N5W4	B8N5W4	1	AFLA_014570	Putative uncharacterized protein
25.2882	23.65	24.0222	23.5669	24.1725	23.6308	2.93E-10	149440000	2	2	2	4.2	87.437	24.0551	24.3201	23.79	6	3	3	B8N5Z4	B8N5Z4	1	AFLA_015780	Small oligopeptide transporter, OPT family
22.7481	22.7815	22.7128	23.6528	22.7092	22.7606	0.0002227	76747000	2	2	2	7	32.54	22.8942	22.7475	23.0409	6	3	3	B8N6J2	B8N6J2	1	AFLA_015050	Methyltransferase family protein
ND	ND	ND	23.4807	23.3685	23.4433	0.0001907	84988000	2	2	2	2.3	114.51	23.4309	ND	23.4309	3	0	3	B8N789	B8N789	1	AFLA_021110	Histone transcription regulator Hir1, putative
24.9114	24.9521	24.6509	27.5016	24.6773	25.2479	6.75E-18	391670000	2	2	2	18.6	20.09	25.3235	24.8381	25.809	6	3	3	B8N877	B8N877	1	AFLA_106710	Putative uncharacterized protein
ND	ND	25.5582	26.0245	ND	25.5248	3.06E-09	262080000	2	2	2	40.9	12.619	25.7025	25.5582	25.7747	3	1	2	B8NA79	B8NA79	1	AFLA_113750	Putative uncharacterized protein
ND	ND	ND	25.5376	25.5403	25.4022	1.02E-05	403510000	2	2	2	26	20.449	25.4934	ND	25.4934	3	0	3	B8NBS0	B8NBS0	1	AFLA_046450	Small subunit of nuclear cap-binding protein complex
24.7297	24.3242	24.6867	24.454	24.2786	24.1622	1.37E-50	331790000	2	2	2	29.8	9.3906	24.4392	24.5802	24.2983	6	3	3	B8NBZ1	B8NBZ1	1	AFLA_047160	Cytochrome b5, putative
ND	ND	ND	28.5085	28.2485	28.1437	8.31E-75	1780200000	2	2	2	10.8	25.563	28.3002	ND	28.3002	3	0	3	B8NC17	B8NC17	1	AFLA_047420	Putative uncharacterized protein
ND	25.2238	25.6194	ND	ND	ND	6.39E-08	285330000	2	2	2	5.9	50.604	25.4216	25.4216	ND	2	2	0	B8NCN0	B8NCN0	1	AFLA_039370	Acid phosphatase, putative
27.2294	25.8868	26.1972	ND	ND	ND	4.18E-06	489360000	2	2	2	48.5	13.96	26.4378	26.4378	ND	3	3	0	B8NCN3	B8NCN3	1	AFLA_039400	Extracellular guanyl-specific ribonuclease RntA
24.3751	24.7244	24.5717	26.497	26.17	25.869	5.73E-14	540750000	2	2	2	16.5	14.216	25.3679	24.5571	26.1787	6	3	3	B8NCX5	B8NCX5	1	AFLA_042100	Small nuclear ribonucleoprotein (LSM7), putative
22.841	23.3475	23.3564	23.4134	22.4693	22.6561	0.0002311	61293000	2	2	2	7.2	41.896	23.0139	23.1816	22.8462	6	3	3	B8NDZ2	B8NDZ2	1	AFLA_057230	Zinc finger protein gcs1
24.9418	25.452	25.449	ND	24.5296	ND	1.99E-07	220070000	2	2	2	5.7	64.67	25.0931	25.2809	24.5296	4	3	1	B8NE34	B8NE34	1	AFLA_057650	Phenylacetyl-CoA ligase, putative
25.1809	ND	24.6983	ND	ND	24.9468	6.80E-09	264930000	2	2	2	17.4	21.01	24.942	24.9396	24.9468	3	2	1	B8NEE9	B8NEE9	1	AFLA_060580	NEDD8 conjugating enzyme (UbcL), putative
ND	ND	ND	24.9814	ND	24.9224	1.56E-08	267070000	2	2	2	20.7	16.051	24.9519	ND	24.9519	2	0	2	B8NEW9	B8NEW9	1	AFLA_058330	Mitochondrial intermembrane space translocase subunit Tim9, putative
24.2711	ND	23.5608	24.8079	25.4287	24.3612	1.67E-08	124230000	2	2	2	4.6	51.532	24.486	23.916	24.866	5	2	3	B8NF61	B8NF61	1	AFLA_061050	Putative uncharacterized protein
26.4756	24.1725	26.4819	ND	ND	25.3009	1.14E-11	407580000	2	2	2	12	26.52	25.6077	25.71	25.3009	4	3	1	B8NFD0	B8NFD0	1	AFLA_062640	Putative uncharacterized protein
23.423	23.6985	24.384	23.033	23.1973	23.0771	0.0001299	88960000	2	2	2	5.5	47.754	23.4688	23.8352	23.1025	6	3	3	B8NFL5	B8NFL5	1	AFLA_131060	14-alpha sterol demethylase Cyp51B
24.4738	24.432	24.9637	ND	23.8826	23.949	1.39E-05	110090000	2	2	2	4.7	65.925	24.3402	24.6231	23.9158	5	3	2	B8NFR6	B8NFR6	1	AFLA_133450	CTP synthase
ND	ND	ND	23.7677	23.3192	23.4335	0.0001001	79670000	2	2	2	3.5	83.606	23.5068	ND	23.5068	3	0	3	B8NFR7	B8NFR7	1	AFLA_133460	Ku family DNA helicase, putative
23.8692	ND	24.1657	ND	23.8898	ND	0.0001955	173500000	2	2	2	8	37.374	23.9749	24.0174	23.8898	3	2	1	B8NGM2	B8NGM2	1	AFLA_136490	NAD dependent epimerase/dehydratase, putative
25.4321	ND	26.1263	25.1802	24.6265	ND	0.0001314	460860000	2	2	2	2.9	94.875	25.3413	25.7792	24.9034	4	2	2	B8NH48	B8NH48	1	AFLA_132720	MYB DNA binding protein (Tbf1), putative
25.7019	25.5029	25.7986	ND	ND	ND	1.44E-16	461570000	2	2	2	15.8	23.454	25.6678	25.6678	ND	3	3	0	B8NH69	B8NH69	1	AFLA_132930	Secretory pathway protein Ssp120, putative
26.3668	26.8876	26.1664	27.7672	26.5282	26.9375	4.88E-58	946700000	2	2	2	17	20.117	26.7756	26.4736	27.0776	6	3	3	B8NH79	B8NH79	1	AFLA_133030	Cytochrome c subunit Vb, putative
ND	23.5636	23.3881	24.8503	23.7795	23.829	0.0002317	123120000	2	2	2	19.9	20.107	23.8821	23.4759	24.1529	5	2	3	B8NHQ5	B8NHQ5	1	AFLA_137490	Putative uncharacterized protein
ND	ND	ND	24.7525	23.3429	ND	3.69E-05	121460000	2	2	2	4.5	71.725	24.0477	ND	24.0477	2	0	2	B8NID3	B8NID3	1	AFLA_066290	RNA binding protein Ligatin/Tma64, putative
24.0454	24.2051	24.0184	26.4983	24.6204	25.639	1.01E-08	285650000	2	2	2	6.6	40.824	24.8378	24.0896	25.5859	6	3	3	B8NIF9	B8NIF9	1	AFLA_066550	Alcohol dehydrogenase, putative
ND	ND	ND	24.9201	24.78	ND	4.12E-06	212900000	2	2	2	6	56.002	24.85	ND	24.85	2	0	2	B8NIS7	B8NIS7	1	AFLA_069550	Pre-mRNA splicing factor (Prp31), putative
23.7381	23.9022	24.2912	24.4692	24.2203	ND	3.10E-05	188600000	2	2	2	9.8	33.689	24.1242	23.9772	24.3448	5	3	2	B8NIV0	B8NIV0	1	AFLA_069780	Kynurenine formamidase

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
26.5478	26.6741	26.5436	24.6836	24.1216	24.2545	1.19E-34	895060000	2	2	2	38.5	8.7148	25.4709	26.5885	24.3532	6	3	3	B8NIX3	B8NIX3	1	AFLA_070010	Putative uncharacterized protein
24.6902	25.3638	25.281	25.5992	ND	25.0535	4.04E-08	471800000	2	2	2	8	28.278	25.1976	25.1117	25.3264	5	3	2	B8NIY1	B8NIY1	1	AFLA_070090	Putative uncharacterized protein
ND	ND	ND	24.6922	ND	24.162	4.80E-07	55628000	2	2	2	6.1	36.444	24.4271	ND	24.4271	2	0	2	B8NJP3	B8NJP3	1	AFLA_068530	Ribosomal RNA processing protein, putative
ND	ND	ND	ND	23.3996	23.0914	8.66E-05	24332000	2	2	2	0.5	578.43	23.2455	ND	23.2455	2	0	2	B8NJX3	B8NJX3	1	AFLA_069330	Nonribosomal peptide synthase Pes1
26.8905	25.4141	26.3417	24.0966	24.3649	24.3178	2.12E-10	329970000	2	2	2	10.7	28.721	25.2376	26.2155	24.2598	6	3	3	B8NKD1	B8NKD1	1	AFLA_090060	Aspergillopepsin, putative
ND	21.4292	ND	24.7355	23.14	23.275	6.24E-09	92011000	2	2	2	9.5	36.615	23.1449	21.4292	23.7168	4	1	3	B8NKP2	B8NKP2	1	AFLA_092960	Small nuclear ribonucleoprotein, putative
24.0555	ND	24.027	ND	24.0612	23.8174	0.0001875	111520000	2	2	2	6.2	39.037	23.9903	24.0412	23.9393	4	2	2	B8NKS0	B8NKS0	1	AFLA_093240	G-protein complex beta subunit SfaD
25.3496	25.4355	25.9496	ND	24.8867	24.9645	3.48E-05	433230000	2	2	2	7.2	37.126	25.3172	25.5782	24.9256	5	3	2	B8NKZ7	B8NKZ7	1	AFLA_095800	Short-chain dehydrogenases/reductase, putative
23.3126	23.6143	ND	ND	24.1332	24.2192	8.61E-07	155230000	2	2	2	12.6	32.787	23.8198	23.4634	24.1762	4	2	2	B8NL76	B8NL76	1	AFLA_089120	Inositol monophosphatase, putative
22.9768	ND	23.5591	23.102	23.0015	22.727	5.15E-05	101350000	2	2	2	3.1	97.176	23.0733	23.2679	22.9435	5	2	3	B8NLR9	B8NLR9	1	AFLA_092850	WD repeat protein
23.9068	23.9515	ND	23.7526	ND	23.2826	0.0002764	149000000	2	2	2	7.2	28.588	23.7234	23.9292	23.5176	4	2	2	B8NLW3	B8NLW3	1	AFLA_094190	Putative uncharacterized protein
24.4214	24.8337	24.9857	24.2831	25.0073	ND	2.70E-11	186660000	2	2	2	8.7	44.744	24.7062	24.7469	24.6452	5	3	2	B8NM89	B8NM89	1	AFLA_095210	Methionine aminopeptidase
23.2209	22.7037	22.7167	23.0162	23.1826	22.7584	2.68E-05	154800000	2	2	2	3.9	65.705	22.9331	22.8804	22.9857	6	3	3	B8NMX2	B8NMX2	1	AFLA_123160	Laccase, putative
ND	ND	ND	22.6757	ND	22.489	0.0001006	101530000	2	2	2	3.8	49.076	22.5823	ND	22.5823	2	0	2	B8NNC0	B8NNC0	1	AFLA_127310	CAIB/BAIF family enzyme
ND	22.7278	22.9617	ND	ND	ND	9.36E-06	37583000	2	2	2	3.4	62.629	22.8447	22.8447	ND	2	2	0	B8NND4	B8NND4	1	AFLA_127450	Nuclear localization protein NPL6, putative
ND	ND	ND	24.88	24.7236	ND	3.80E-05	307430000	2	2	2	3.5	80.926	24.8018	ND	24.8018	2	0	2	B8NP31	B8NP31	1	AFLA_128140	Sister chromatid separation protein (Src1), putative
25.3855	ND	25.5874	ND	25.0686	ND	1.29E-08	455880000	2	2	2	3.1	167.13	25.3472	25.4865	25.0686	3	2	1	B8NP76	B8NP76	1	AFLA_128590	CCR4-NOT core complex subunit Not4, putative
24.7349	24.4527	24.7497	24.9089	24.5803	24.8257	2.90E-05	289460000	2	2	2	3.6	100.95	24.7087	24.6457	24.7717	6	3	3	B8NPA0	B8NPA0	1	AFLA_128830	PHD finger domain protein, putative
ND	24.6593	ND	23.7929	25.5412	25.0134	1.33E-17	347650000	2	2	2	19.7	16.916	24.7517	24.6593	24.7825	4	1	3	B8NPB6	B8NPB6	1	AFLA_128990	Ubiquitin conjugating enzyme Ubc8, putative
24.4243	25.0286	25.0861	ND	ND	ND	1.49E-07	121630000	2	2	2	15.1	21.403	24.8463	24.8463	ND	3	3	0	B8NPB9	B8NPB9	1	AFLA_129910	Rho GTPase ModA, putative
24.5579	25.7406	ND	25.0331	27.0477	27.1815	6.86E-64	780230000	2	2	2	28.6	13.678	25.9122	25.1493	26.4208	5	2	3	B8NPD8	B8NPD8	1	AFLA_130100	SnRNP and snoRNP protein (Snu13), putative
ND	24.1064	23.9833	ND	ND	ND	3.10E-05	180980000	2	2	2	3.5	66.297	24.0448	24.0448	ND	2	2	0	B8NPG9	B8NPG9	1	AFLA_130410	Autophagy ubiquitin-activating enzyme ApgG, putative
24.0339	26.0127	24.8074	23.9757	ND	24.1136	1.26E-12	157520000	2	2	2	55.2	9.8752	24.5887	24.9514	24.0447	5	3	2	B8NPM3	B8NPM3	1	AFLA_000870	Putative uncharacterized protein
ND	ND	25.3886	26.0532	26.1075	ND	8.78E-13	275270000	2	2	2	5.8	81.361	25.8498	25.3886	26.0803	3	1	2	B8NQH7	B8NQH7	1	AFLA_006590	Class III chitinase ChiA1
23.7617	24.1553	24.0473	ND	ND	ND	3.08E-05	159330000	2	2	2	3.1	81.025	23.9881	23.9881	ND	3	3	0	B8NQT8	B8NQT8	1	AFLA_002320	Sorting nexin Mvp1
24.4354	ND	25.1908	25.1933	ND	ND	0.000148	383780000	2	2	2	0.6	328.26	24.9398	24.8131	25.1933	3	2	1	B8NQV9	B8NQV9	1	AFLA_003430	Putative uncharacterized protein
24.8195	ND	25.2616	ND	ND	ND	3.11E-07	246270000	2	2	2	40.9	12.007	25.0405	25.0405	ND	2	2	0	B8NS13	B8NS13	1	AFLA_052440	Putative uncharacterized protein
ND	ND	ND	27.282	27.1296	26.954	4.28E-09	941750000	2	2	2	17.6	19.894	27.1219	ND	27.1219	3	0	3	B8NS36	B8NS36	1	AFLA_052670	RNA recognition motif (Rrm) domain containing protein, putative
22.4843	23.1186	23.2185	25.0988	ND	22.6685	9.60E-27	171980000	2	2	2	25.8	9.5302	23.3177	22.9405	23.8836	5	3	2	B8NS55	B8NS55	1	AFLA_052860	Chaperone/heat shock protein Hsp12, putative
24.6909	25.5988	24.8092	24.6521	24.2678	24.2432	1.92E-06	204910000	2	2	2	6.2	59.127	24.7103	25.0329	24.3877	6	3	3	B8NSK2	B8NSK2	1	AFLA_049530	Carboxylesterase, putative
25.7159	25.5733	26.972	26.3848	26.1766	26.1135	1.57E-06	884160000	2	2	2	16.3	15.924	26.156	26.0871	26.225	6	3	3	B8NT42	B8NT42	1	AFLA_053250	Putative uncharacterized protein
ND	24.462	24.6598	ND	ND	22.6084	6.01E-07	140140000	2	2	2	4.7	50.484	23.91	24.5609	22.6084	3	2	1	B8NTI6	B8NTI6	1	AFLA_098260	AP-1 adaptor complex subunit mu, putative
ND	21.446	ND	25.9402	25.2324	25.2834	4.12E-11	205410000	2	2	2	9.8	28.186	24.4755	21.446	25.4853	4	1	3	B8NTI7	B8NTI7	1	AFLA_098270	RNase III domain protein
24.8655	ND	22.5485	21.0545	ND	20.8104	8.17E-30	314870000	2	2	2	8.8	23.433	22.3197	23.707	20.9325	4	2	2	B8NTJ8	B8NTJ8	1	AFLA_098380	Conidial hydrophobin RodA/RolA
25.1928	25.125	25.3992	25.1515	24.1246	24.7179	3.05E-05	357960000	2	2	2	7.9	23.479	24.9518	25.239	24.6646	6	3	3	B8NTL6	B8NTL6	1	AFLA_099460	Transcription factor RfeG, putative
ND	ND	ND	25.2676	24.8993	ND	2.71E-07	158580000	2	2	2	9.9	29.157	25.0835	ND	25.0835	2	0	2	B8NTQ5	B8NTQ5	1	AFLA_099860	Pre-mRNA splicing factor, putative
24.1162	24.3101	24.2651	25.259	24.6342	24.791	0.0003105	255030000	2	2	2	10	38.17	24.5626	24.2305	24.8947	6	3	3	B8NTT6	B8NTT6	1	AFLA_100170	Complex I intermediate associated protein (Cia30), putative
26.6302	25.2718	26.7498	24.9452	26.2588	24.6372	1.77E-06	522190000	2	2	2	6.1	38.612	25.7488	26.2173	25.2804	6	3	3	B8NUC3	B8NUC3	1	AFLA_098850	Putative uncharacterized protein
28.2744	27.2087	ND	27.1425	27.7414	26.947	4.50E-122	2238900000	2	2	2	25.2	12.024	27.4628	27.7416	27.277	5	2	3	B8NUF3	B8NUF3	1	AFLA_099150	Thioredoxin
29.821	29.338	29.5099	28.2027	28.9789	28.9235	6.98E-102	5961100000	2	2	2	34.9	7.1109	29.129	29.5563	28.7017	6	3	3	B8NUL0	B8NUL0	1	AFLA_100630	Putative uncharacterized protein
25.6478	25.5753	25.5356	25.1416	25.1686	25.5723	3.05E-16	428130000	2	2	2	8	41.753	25.4402	25.5862	25.2942	6	3	3	B8NVJ1	B8NVJ1	1	AFLA_116780	Homocysteine S-methyltransferase, putative
28.0365	26.4064	28.305	24.346	24.8803	24.8003	2.27E-12	902250000	2	2	2	29.9	11.998	26.1291	27.5826	24.6755	6	3	3	B8NVS7	B8NVS7	1	AFLA_117640	CipC-like antibiotic stress responsive protein
23.4799	24.8247	ND	ND	23.7807	23.4767	0.0003092	97288000	2	2	2	7.7	44.068	23.8905	24.1523	23.6287	4	2	2	B8NVU1	B8NVU1	1	AFLA_117780	Farnesyl-diphosphate farnesyltransferase, putative
25.5832	ND	25.2405	ND	ND	ND	3.39E-07	206980000	2	2	2	4.4	58.265	25.4119	25.4119	ND	2	2	0	B8NWK2	B8NWK2	1	AFLA_120390	Putative uncharacterized protein
23.5185	23.2014	23.6159	23.4837	ND	ND	5.25E-06	76535000	2	2	2	5.4	51.017	23.4549	23.4453	23.4837	4	3	1	B8NX26;B8	B8NX26;B8	2	AFLA_122130	Mannan endo-1,6-alpha-mannosidase DCW1, putative
25.3237	ND	25.0587	ND	ND	ND	5.03E-05	154330000	2	2	2	14.3	26.709	25.1912	25.1912	ND	2	2	0	B8NYA9	B8NYA9	1	AFLA_010790	Elongation factor 1 gamma, putative
ND	22.8717	22.8319	22.8903	22.2784	ND	4.59E-05	39208000	2	2	2	2.2	118.15	22.7181	22.8518	22.5844	4	2	2	B8NYK7	B8NYK7	1	AFLA_011770	Putative uncharacterized protein
24.568	24.0394	ND	ND	ND	24.1717	2.86E-05	136360000	2	2	2	2.4	148.14	24.2597	24.3037	24.1717	3	2	1	B8NYR3	B8NYR3	1	AFLA_114250	Reverse transcriptase, putative
24.2676	24.1991	22.9883	ND	25.5253	25.4429	1.28E-32	214510000	5	2	2	9.4	68.358	24.4846	23.8183	25.4841	5	3	2	B8MZR1	B8MZR1	1	AFLA_085510	Trytophan synthase alpha subunit, putative
23.9958	23.0399	ND	ND	ND	ND	1.42E-13	147820000	3	3	3	18.1	31.57	23.5178	23.5178	ND	2	2	0	B8MVS8	B8MVS8	1	AFLA_072750	Pyrroline-5-carboxylate reductase, putative
22.7811	ND	23.9363	ND	ND	ND	1.57E-09	108320000	3	3	3	10	32.46	23.3587	23.3587	ND	2	2	0	B8MWF3	B8MWF3	1	AFLA_088430	Protein kinase activator (Mob2), putative
26.7158	26.5905	26.9016	28.1817	27.0577	27.2489	2.53E-81	1290300000	3	3	3	27.3	21.81	27.116	26.736	27.4961	6	3	3	B8MWX6	B8MWX6	1	AFLA_075630	Putative uncharacterized protein
24.663	24.7407	24.6137	26.619	25.1455	25.1753	6.09E-06	382760000	3	3	3	25.7	25.879	25.1595	24.6725	25.6466	6	3	3	B8MXD7	B8MXD7	1	AFLA_077240	Putative uncharacterized protein
ND	23.754	23.6204	26.0716	25.4269	25.1568	1.76E-24	238810000	3	3	3	8	61.824	24.8059	23.6872	25.5518	5	2	3	B8MXP5	B8MXP5	1	AFLA_078320	Probable beta-glucosidase btgE
ND	24.6137	ND	ND	25.3315	25.0745	1.31E-12	320680000	3	3	3	23.6	21.459	25.0066	24.6137	25.203	3	1	2	B8MXT0	B8MXT0	1	AFLA_078670	RNA polymerase II subunit 7
24.609	ND	24.6728	25.2346	24.8723	24.6278	8.89E-13	367640000	3	3	3	9.4	39.141	24.8033	24.6409	24.9116	5	2	3	B8MYL0	B8MYL0	1	AFLA_081490	Nucleoside diphosphatase Gda1
ND	ND	ND	24.4461	23.8885	23.8563	1.00E-06	147130000	3	3	3	4.9	96.417	24.0636	ND	24.0636	3	0	3	B8MYW6	B8MYW6	1	AFLA_082550	Cleavage and polyadenylation specifity factor, 73 kDa subunit
28.5542	28.7296	27.6592	25.6828	25.027	27.1667	6.29E-48	2592300000	3	3	3	36.8	7.6649	27.1366	28.3143	25.9589	6	3	3	B8MZ58	B8MZ58	1	AFLA_083470	Ribosomal protein S28e
ND	ND	ND	23.5683	23.3992	ND	1.81E-10	256550000	3	3	3	9.2	52.445	23.4837	ND	23.4837	2	0	2	B8MZJ4	B8MZJ4	1	AFLA_084840	Putative uncharacterized protein
25.1986	25.5673	25.4408	26.2035	25.8177	25.7709	7.06E-23	595020000	3	3	3	27	13.408	25.6665	25.4022	25.9307	6	3	3	B8MZL4	B8MZL4	1	AFLA_085040	Putative uncharacterized protein
25.1504	26.2197	26.2552	24.4404	24.3679	24.6698	6.07E-27	290610000	3	3	3	7.6	58.844	25.1839	25.8751	24.4927	6	3	3	B8MZN7	B8MZN7	1	AFLA_085270	T-complex protein 1, zeta subunit, putative
23.9707	23.2133	23.685	26.1592	25.8527	26.1392	2.20E-30	546390000	3	3	3	40	14.692	24.8367	23.623	26.0504	6	3	3	B8MZR4	B8MZR4	1	AFLA_085540	Putative uncharacterized protein
26.1673	25.6264	26.0912	25.0732	25.2066	24.9632	3.95E-13	438230000	3	3	3	15.7	26.982	25.5213	25.9617	25.081	6	3	3	B8N004	B8N004	1	AFLA_086440	SH3 domain protein
25.3291	24.6886	25.4192	ND	ND	ND	1.67E-09	171120000	3	3	3	23.5	25.272	25.1456	25.1456	ND	3	3	0	B8N097	B8N097	1	AFLA_087380	Isochorismatase family hydrolase, putative
22.9732	23.7292	ND	ND	ND	ND	1.21E-05	100660000	3	3	3	7.4	56.208	23.3512	23.3512	ND	2	2	0	B8N0B4	B8N0B4	1	AFLA_087550	Serine/threonine-protein phosphatase
ND	ND	22.7142	23.5879	23.4598	23.3677	5.11E-06	64735000	3	3	3	7.3	47.051	23.2824	22.7142	23.4718	4	1	3	B8N0I0	B8N0I0	1	AFLA_024230	Putative uncharacterized protein
24.9194	24.6262	24.4684	ND	ND	ND	5.68E-06	211750000	3	3	3	9.6	47.944	24.6713	24.6713	ND	3	3	0	B8N0U8	B8N0U8	1	AFLA_026330	CaaX farnesyltransferase beta subunit Ram1
20.5531	22.8877	22.5334	23.9487	23.3502	23.4276	5.78E-17	236010000	3	3	3	18.6	17.754	22.7834	21.9914	23.5755	6	3	3	B8N123	B8N123	1	AFLA_027980	NUDIX domain, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
24.983	24.7402	25.083	24.3867	24.1424	24.2539	1.35E-09	254830000	3	3	3	11.8	40.182	24.5982	24.9354	24.261	6	3	3	B8N139	B8N139	1	AFLA_028140	Vacuolar protein sorting-associated protein 26, putative
25.2992	25.4952	24.9837	25.662	25.8166	25.5499	2.37E-15	539400000	3	3	3	19.7	26.568	25.4678	25.2593	25.6762	6	3	3	B8N143	B8N143	1	AFLA_028180	RWD domain protein (Gir2), putative
ND	ND	ND	24.6159	25.5624	24.5391	3.58E-08	420290000	3	3	3	42.6	11.061	24.9058	ND	24.9058	3	0	3	B8N199	B8N199	1	AFLA_029640	Dynein light chain type 1, putative
23.6311	23.8822	23.9939	25.0363	23.7739	23.7789	3.90E-05	145240000	3	3	3	5.5	66.225	24.0161	23.8358	24.1964	6	3	3	B8N1B7	B8N1B7	1	AFLA_029820	SAM domain protein
26.0378	25.7444	26.1526	26.4236	26.4888	25.9365	6.99E-48	805680000	3	3	3	25.7	16.107	26.1306	25.9782	26.283	6	3	3	B8N1F2	B8N1F2	1	AFLA_030170	Cytosine deaminase, putative
ND	ND	ND	ND	24.8735	23.5532	6.37E-06	213970000	3	3	3	20.4	21.449	24.2133	ND	24.2133	2	0	2	B8N1K7	B8N1K7	1	AFLA_030720	RNA exonuclease Rex2, putative
27.3592	27.4025	27.7005	27.8348	27.4212	27.6705	9.88E-131	2238600000	3	3	3	25.6	14.068	27.5648	27.4874	27.6422	6	3	3	B8N1S1	B8N1S1	1	AFLA_032250	Nuclear transport factor NTF-2, putative
24.0278	24.1256	24.3033	24.8575	ND	24.5009	5.99E-13	266690000	3	3	3	4.5	97.559	24.363	24.1522	24.6792	5	3	2	B8N205	B8N205	1	AFLA_033990	Spindle pole body component, putative
ND	ND	ND	23.8836	ND	22.9423	5.24E-05	35752000	3	3	3	8.4	43.459	23.413	ND	23.413	2	0	2	B8N225	B8N225	1	AFLA_034190	NADH-ubiquinone oxidoreductase 39 kDa subunit, putative
26.7037	26.8614	27.7863	26.1875	26.2763	27.2397	5.08E-23	1005100000	3	3	3	24.8	23.314	26.8425	27.1171	26.5679	6	3	3	B8N240	B8N240	1	AFLA_034340	40S ribosomal protein S10b
23.0241	ND	ND	23.9664	24.795	23.5851	6.45E-05	99927000	3	3	3	5.3	60.431	23.8426	23.0241	24.1155	4	1	3	B8N2R4	B8N2R4	1	AFLA_023480	Alpha-amylase, putative
ND	25.3019	ND	ND	24.7984	26.2352	4.96E-16	757790000	3	3	3	30.4	19.541	25.4452	25.3019	25.5168	3	1	2	B8N351	B8N351	1	AFLA_025760	50S ribosomal protein L12
25.8006	25.4271	25.526	25.6885	25.8878	25.4278	4.67E-70	630030000	3	3	3	22.8	25.508	25.6263	25.5846	25.668	6	3	3	B8N360	B8N360	1	AFLA_026730	Vesicle transport v-snare protein, putative
ND	22.911	22.954	23.8899	23.4079	23.5997	5.68E-10	96185000	3	3	3	3.3	123.88	23.3525	22.9325	23.6325	5	2	3	B8N368	B8N368	1	AFLA_026810	Ubiquitin-protein ligase (Tom1), putative
25.3938	24.3462	25.4144	25.0489	24.5534	24.566	3.89E-15	354190000	3	3	3	11.2	39.489	24.8871	25.0514	24.7228	6	3	3	B8N3D2	B8N3D2	1	AFLA_027450	Sucrase/ferredoxin-like family protein, putative
23.0601	23.0142	23.2199	23.5614	23.3574	23.0334	8.30E-08	115120000	3	3	3	10.1	45.99	23.2077	23.0981	23.3174	6	3	3	B8N3E5	B8N3E5	1	AFLA_028480	C2H2 finger domain protein, putative
23.3659	24.5545	22.8454	23.1573	23.1342	24.553	4.28E-08	243240000	3	3	3	18.9	25.75	23.6017	23.5886	23.6148	6	3	3	B8N3F2	B8N3F2	1	AFLA_028550	CCAAT-binding factor complex subunit HapC
ND	ND	24.2871	25.5843	24.6854	24.5438	6.90E-07	263010000	3	3	3	7.6	40.709	24.7752	24.2871	24.9378	4	1	3	B8N3T8	B8N3T8	1	AFLA_031720	Peroxisomal membrane protein receptor Pex19, putative
26.6417	26.2687	26.7883	25.5704	25.0942	25.2423	1.01E-21	457930000	3	3	3	26.3	15.049	25.9343	26.5662	25.3023	6	3	3	B8N418	B8N418	1	AFLA_033410	Putative uncharacterized protein
24.0425	ND	22.8078	23.6822	23.81	23.9609	4.08E-25	328760000	3	3	3	9	48.41	23.6607	23.4252	23.8177	5	2	3	B8N429	B8N429	1	AFLA_033520	Ubiquitin-like protein DskB, putative
24.6155	24.7504	24.8029	24.9948	24.6109	24.5048	1.25E-40	393540000	3	3	3	35.7	13.675	24.7132	24.7229	24.7035	6	3	3	B8N444	B8N444	1	AFLA_033670	Lipid transfer protein, putative
24.6455	25.3102	24.4675	28.2423	27.6382	27.5605	6.53E-94	1412000000	3	3	3	45.5	13.43	26.3107	24.8077	27.8136	6	3	3	B8N488	B8N488	1	AFLA_035010	Small nuclear ribonucleoprotein SmD1, putative
ND	ND	ND	24.7219	24.1242	24.2864	3.07E-09	183070000	3	3	3	9.6	55.155	24.3775	ND	24.3775	3	0	3	B8N4A4	B8N4A4	1	AFLA_035170	Kelch repeats protein, putative
24.9032	23.9219	24.7713	ND	ND	ND	7.72E-08	83524000	3	3	3	9	62.227	24.5321	24.5321	ND	3	3	0	B8N4H4	B8N4H4	1	AFLA_036780	General amidase GmdA, putative
25.4855	25.4713	25.661	25.9901	26.0149	25.6523	4.11E-22	624180000	3	3	3	18.2	26.494	25.7125	25.5393	25.8858	6	3	3	B8N4I1	B8N4I1	1	AFLA_036850	Putative uncharacterized protein
24.1818	ND	23.7592	25.1861	ND	ND	6.38E-08	194360000	3	3	3	9.8	43.943	24.3757	23.9705	25.1861	3	2	1	B8N4M5	B8N4M5	1	AFLA_037300	Methionyl-tRNA formyltransferase family protein, putative
24.2107	26.1956	22.8719	ND	26.2413	25.6037	2.72E-12	536890000	3	3	3	16.9	15.333	25.0246	24.4261	25.9225	5	3	2	B8N4Q2	B8N4Q2	1	AFLA_017610	Histone H3
ND	25.7771	25.1284	ND	ND	24.8608	2.25E-10	239140000	3	3	3	12.7	34.926	25.2555	25.4528	24.8608	3	2	1	B8N4X5	B8N4X5	1	AFLA_018340	G-protein complex alpha subunit GpaA/FadA
ND	24.7991	23.712	ND	ND	ND	1.08E-05	130890000	3	3	3	10.2	29.815	24.2556	24.2556	ND	2	2	0	B8N535	B8N535	1	AFLA_020730	Putative uncharacterized protein
ND	23.5466	ND	ND	23.7671	23.7739	1.06E-06	83990000	3	3	3	4.4	95.857	23.6959	23.5466	23.7705	3	1	2	B8N5A2	B8N5A2	1	AFLA_022300	Chromosome segregation protein (SepB), putative
22.9716	23.1324	ND	25.0549	24.5601	23.3492	5.34E-07	99990000	3	3	3	25.8	20.598	23.8136	23.052	24.3214	5	2	3	B8N5D0	B8N5D0	1	AFLA_022580	Zinc knuckle domain protein (Byr3), putative
24.7482	23.9083	ND	ND	ND	ND	2.32E-07	58024000	3	3	3	7.3	59.897	24.3283	24.3283	ND	2	2	0	B8N5D1	B8N5D1	1	AFLA_022590	YdiU domain protein
24.9322	24.8109	24.9725	25.5913	25.3328	24.8256	1.21E-16	370470000	3	3	3	8	57.516	25.0775	24.9052	25.2499	6	3	3	B8N5T8	B8N5T8	1	AFLA_014310	Acyl-CoA dehydrogenase family protein
24.7974	25.6393	25.6742	ND	24.4517	23.5471	1.29E-28	189580000	3	3	3	19.5	28.466	24.8219	25.3703	23.9994	5	3	2	B8N5X6	B8N5X6	1	AFLA_014690	Translocon-associated protein, alpha subunit, putative
24.0357	23.7704	23.8196	26.1905	25.7139	25.5371	3.05E-10	404610000	3	3	3	34.7	11.23	24.8445	23.8752	25.8138	6	3	3	B8N5Y8	B8N5Y8	1	AFLA_015720	Small nuclear ribonucleoprotein (LSM2), putative
24.2799	24.5286	ND	24.2439	24.8683	24.4748	1.11E-05	161530000	3	3	3	3.8	118.04	24.4791	24.4042	24.529	5	2	3	B8N676	B8N676	1	AFLA_018400	Regulator of nonsense transcripts, putative
24.6475	ND	23.5511	ND	ND	ND	1.32E-07	98556000	3	3	3	5.3	98.644	24.0993	24.0993	ND	2	2	0	B8N6B6	B8N6B6	1	AFLA_018800	Nitrite reductase NiiA
24.1481	22.2248	23.2465	ND	22.456	ND	1.20E-06	57701000	3	3	3	5	97.516	23.0188	23.2065	22.456	4	3	1	B8N6B7	B8N6B7	1	AFLA_018810	Nitrate reductase
24.5028	23.8533	25.3767	ND	ND	ND	1.55E-06	199970000	3	3	3	3.1	109.68	24.5776	24.5776	ND	3	3	0	B8N6H2	B8N6H2	1	AFLA_014850	Phosphatidylethanolamine N-methyltransferase
26.0666	25.6168	25.9071	26.2766	26.1975	25.9284	2.09E-08	827900000	3	3	3	17.1	29.458	25.9988	25.8635	26.1342	6	3	3	B8N6K4	B8N6K4	1	AFLA_015170	SNARE complex subunit (Syn8), putative
24.6091	25.0708	25.4509	25.4605	ND	ND	2.56E-31	514470000	3	3	3	13.3	37.568	25.1478	25.0436	25.4605	4	3	1	B8N6Q6	B8N6Q6	1	AFLA_015690	Putative uncharacterized protein
25.7536	25.8189	25.8327	ND	25.7407	25.613	3.79E-46	591490000	3	3	3	19.6	30.146	25.7518	25.8018	25.6768	5	3	2	B8N6T8	B8N6T8	1	AFLA_016910	26S proteasome regulatory subunit S5A
ND	25.8376	ND	26.0688	26.0925	26.0423	1.26E-14	366730000	3	3	3	31	19.414	26.0103	25.8376	26.0679	4	1	3	B8N6W2	B8N6W2	1	AFLA_017150	RNA polymerase subunit
23.8868	24.5104	24.5074	24.0277	24.146	24.1752	7.23E-10	145370000	3	3	3	10	49.046	24.2089	24.3015	24.1163	6	3	3	B8N710	B8N710	1	AFLA_019430	Monoxygenase, putative
25.5437	25.5817	25.5485	ND	ND	ND	1.41E-06	157270000	3	3	3	25.8	24.386	25.558	25.558	ND	3	3	0	B8N718	B8N718	1	AFLA_019510	Putative uncharacterized protein
25.7842	26.0742	26.2795	26.9909	26.2391	26.3603	2.72E-39	791520000	3	3	3	23.3	24.227	26.288	26.046	26.5301	6	3	3	B8N799	B8N799	1	AFLA_021210	Ankyrin repeat protein
24.8741	24.8646	24.7872	25.1149	24.6157	24.5209	1.88E-13	318010000	3	3	3	23.1	21.767	24.7963	24.842	24.7505	6	3	3	B8N7E7	B8N7E7	1	AFLA_021690	Vacuolar protein sorting 29, putative
25.8288	25.9462	26.0024	24.6161	24.3117	24.2985	2.04E-11	329370000	3	3	3	29.2	21.547	25.1673	25.9258	24.4087	6	3	3	B8N8D6	B8N8D6	1	AFLA_107300	3-hydroxyanthranilate 3,4-dioxygenase Bna1, putative
24.3978	24.4292	24.1588	25.3578	24.8246	24.7592	7.22E-12	268820000	3	3	3	16.2	24.284	24.6546	24.3286	24.9805	6	3	3	B8N8P7	B8N8P7	1	AFLA_108420	NUDIX domain protein
24.0696	ND	23.9988	24.3162	ND	23.8832	2.91E-07	219320000	3	3	3	10.4	51.484	24.0669	24.0342	24.0997	4	2	2	B8N8U1	B8N8U1	1	AFLA_108860	1,3-beta-glucanosyltransferase Gel2
ND	23.2814	ND	ND	23.081	23.1147	4.96E-05	94719000	3	3	3	2.7	134.52	23.159	23.2814	23.0978	3	1	2	B8N9J0	B8N9J0	1	AFLA_111360	DNA mismatch repair protein Msh6, putative
ND	23.4891	23.8834	ND	ND	ND	4.05E-10	124790000	3	3	3	8.1	56.561	23.6863	23.6863	ND	2	2	0	B8N9T7	B8N9T7	1	AFLA_112330	SnRNP assembly factor, putative
28.2257	27.872	28.1029	27.3367	27.8147	27.6063	2.06E-16	2943600000	3	3	3	20.5	17.792	27.8264	28.0669	27.5859	6	3	3	B8NA13	B8NA13	1	AFLA_113090	Putative uncharacterized protein
23.5285	ND	23.1439	23.8591	ND	ND	9.65E-07	129850000	3	3	3	12.3	41.483	23.5105	23.3362	23.8591	3	2	1	B8NAP7	B8NAP7	1	AFLA_042720	Putative uncharacterized protein
24.2869	24.1834	24.5347	24.4699	24.4776	24.096	3.76E-07	223790000	3	3	3	8.6	54.862	24.3414	24.335	24.3478	6	3	3	B8NB51	B8NB51	1	AFLA_044260	Kynureninase
ND	ND	24.0032	25.3908	24.133	24.1828	1.02E-09	181720000	3	3	3	12.2	30.065	24.4275	24.0032	24.5689	4	1	3	B8NBL1	B8NBL1	1	AFLA_045860	NADH-ubiquinone dehydrogenase 24 kDa subunit, putative
ND	ND	ND	24.3069	ND	23.8656	6.59E-05	184620000	3	3	3	3.9	105.37	24.0863	ND	24.0863	2	0	2	B8NBM4	B8NBM4	1	AFLA_045990	DNA ligase
25.2662	24.567	24.6134	25.7923	25.5869	24.6042	1.73E-10	385810000	3	3	3	24.9	27.241	25.0717	24.8155	25.3278	6	3	3	B8NC02	B8NC02	1	AFLA_047270	Beta-1,6-glucan boisynthesis protein (Knh1), putative
24.3397	ND	24.5075	ND	ND	ND	7.19E-07	139840000	3	3	3	8.3	56.279	24.4236	24.4236	ND	2	2	0	B8NCH7	B8NCH7	1	AFLA_038840	Putative uncharacterized protein
26.6659	27.4293	26.4363	27.6211	27.5171	27.015	6.41E-139	1603200000	3	3	3	22.9	37.182	27.1141	26.8438	27.3844	6	3	3	B8NCP9	B8NCP9	1	AFLA_039560	WW domain protein
ND	24.4944	ND	25.2394	ND	24.5603	7.89E-06	148550000	3	3	3	4.6	99.577	24.7647	24.4944	24.8999	3	1	2	B8NCV8	B8NCV8	1	AFLA_041930	Putative uncharacterized protein
25.4561	25.4021	25.4864	ND	ND	ND	9.03E-11	169700000	3	3	3	9.5	63.659	25.4482	25.4482	ND	3	3	0	B8ND72	B8ND72	1	AFLA_056330	Amidophosphoribosyltransferase
ND	23.5053	23.6073	23.9263	ND	23.883	1.95E-09	140460000	3	3	3	7.6	52.328	23.7305	23.5563	23.9046	4	2	2	B8NE31	B8NE31	1	AFLA_057620	CCR4-NOT core complex subunit Caf1, putative
23.6764	23.7204	24.1058	ND	23.1911	ND	3.76E-05	78068000	3	3	3	3.2	103.1	23.6734	23.8342	23.1911	4	3	1	B8NEF0;B8	B8NEF0	2	AFLA_060590	Chitin synthase ChsG
25.4522	25.2009	25.6975	25.1351	24.343	24.9954	1.64E-11	329440000	3	3	3	14.3	39.939	25.1374	25.4502	24.8245	6	3	3	B8NEJ7	B8NEJ7	1	AFLA_061950	Autophagy-related protein 3
23.7851	24.4613	23.3581	ND	23.3442	24.2471	3.96E-10	173020000	3	3	3	24	28.61	23.8391	23.8681	23.7956	5	3	2	B8NEL9	B8NEL9	1	AFLA_062170	AI-BP family protein
23.9102	ND	24.7944	24.4757	24.332	24.246	1.21E-07	249810000	3	3	3	4.6	64.422	24.3517	24.3523	24.3512	5	2	3	B8NEM1	B8NEM1	1	AFLA_062190	RNA binding protein
24.6483	ND	24.3231	ND	ND	ND	8.25E-26	223620000	3	3	3	19	35.133	24.4857	24.4857	ND	2	2	0	B8NES9	B8NES9	1	AFLA_063660	Polysaccharide deacetylase family protein

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
ND	ND	ND	24.8791	23.822	23.9469	1.45E-10	128050000	3	3	3	5.8	73.65	24.216	ND	24.216	3	0	3	B8NFA3	B8NFA3	1	AFLA_061470	DSB repair complex subunit Ku70, putative
23.9961	24.1342	23.982	26.8974	25.2004	26.2606	1.16E-10	327750000	3	3	3	11.2	47.213	25.0785	24.0374	26.1195	6	3	3	B8NG30	B8NG30	1	AFLA_131910	Putative uncharacterized protein
25.0678	25.9498	ND	26.1207	26.0117	23.9522	2.98E-12	503510000	3	3	3	17.6	22.928	25.4205	25.5088	25.3615	5	2	3	B8NG77	B8NG77	1	AFLA_134160	V-type ATPase F subunit, putative
23.2724	23.9284	ND	26.0393	25.806	25.7442	1.12E-19	374700000	3	3	3	31.4	13.537	24.9581	23.6004	25.8632	5	2	3	B8NGE7	B8NGE7	1	AFLA_134870	U6 snRNA-associated Sm-like protein LSM4, putative
21.2692	24.2495	24.0275	27.1139	ND	26.6558	3.09E-08	512790000	3	3	3	29.3	10.958	24.6632	23.1821	26.8848	5	3	2	B8NGG5	B8NGG5	1	AFLA_135920	Cytochrome c oxidase polypeptide vib
24.2275	24.5894	ND	24.7057	24.4591	24.6334	1.91E-10	277270000	3	3	3	24.5	17.865	24.523	24.4084	24.5994	5	2	3	B8NGG8	B8NGG8	1	AFLA_135950	Nudix/MutT family protein
24.6503	24.0151	24.6808	ND	ND	ND	3.80E-13	220260000	3	3	3	6.4	57.774	24.4487	24.4487	ND	3	3	0	B8NGK6	B8NGK6	1	AFLA_136330	Exoenzymes regulatory protein aepA, putative
25.77	25.7368	26.1975	ND	25.6389	ND	1.22E-06	298700000	3	3	3	16	33.003	25.8358	25.9014	25.6389	4	3	1	B8NH91	B8NH91	1	AFLA_133150	Catechol dioxygenase, putative
24.3231	24.877	25.0444	23.9965	23.8068	23.9382	3.59E-08	213670000	3	3	3	20.8	27.961	24.331	24.7481	23.9138	6	3	3	B8NHD1	B8NHD1	1	AFLA_135360	Hydroxymethylglutaryl-CoA lyase
ND	24.5856	25.0872	ND	24.056	24.2955	2.06E-06	184920000	3	3	3	9.1	45.821	24.5061	24.8364	24.1757	4	2	2	B8NHK5	B8NHK5	1	AFLA_136990	Calcium/calmodulin-dependent protein kinase, putative
25.0913	24.2916	24.8085	ND	ND	ND	4.57E-06	89030000	3	3	3	6.4	70.264	24.7305	24.7305	ND	3	3	0	B8NHY3	B8NHY3	1	AFLA_139190	AflK/ vbs/ VERB synthase
24.6884	24.3438	24.7058	ND	22.53	23.012	5.31E-08	92711000	3	3	3	8.7	76.204	23.856	24.5793	22.771	5	3	2	B8NIJ2	B8NIJ2	1	AFLA_067790	Acetoacetyl-CoA synthase
25.8068	25.904	25.2851	26.029	25.9007	24.9228	3.32E-09	678930000	3	3	3	40	12.545	25.6414	25.6653	25.6175	6	3	3	B8NIN3	B8NIN3	1	AFLA_068200	Putative uncharacterized protein
27.6387	27.3613	27.6649	27.3617	28.5308	28.0658	6.92E-114	2679000000	3	3	3	38.6	13.55	27.7705	27.5549	27.9861	6	3	3	B8NIT4	B8NIT4	1	AFLA_069620	Putative uncharacterized protein
25.6951	25.4392	25.1647	25.9803	25.3927	25.3922	9.33E-25	621440000	3	3	3	18.4	21.535	25.5107	25.433	25.5884	6	3	3	B8NJ02	B8NJ02	1	AFLA_071190	Vacuolar ATP synthase subunit G, putative
ND	25.656	25.7899	ND	24.532	ND	8.82E-05	184730000	3	3	3	5.1	86.709	25.326	25.723	24.532	3	2	1	B8NJ45	B8NJ45	1	AFLA_071620	ATP12 protein, putative
26.8733	ND	ND	25.9113	ND	25.6576	4.30E-07	746660000	3	3	3	12	29.518	26.1474	26.8733	25.7844	3	1	2	B8NJ49;B8	B8NJ49	2	AFLA_071660	Xylitol dehydrogenase
24.5101	23.6986	24.6799	23.8578	23.8852	23.3712	2.33E-22	326220000	3	3	3	8.5	45.369	24.0005	24.2962	23.7047	6	3	3	B8NJE1	B8NJE1	1	AFLA_065740	7-dehydrocholesterol reductase, putative
29.1564	29.6506	29.1188	28.9491	29.3527	29.4437	2.77E-94	6670500000	3	3	3	25.4	18.467	29.2785	29.3086	29.2485	6	3	3	B8NJM4	B8NJM4	1	AFLA_067450	Glycine cleavage system H protein
25.0626	25.3189	25.2517	26.1009	25.8381	25.6493	1.77E-13	594870000	3	3	3	22.4	18.183	25.5369	25.2111	25.8627	6	3	3	B8NJP6	B8NJP6	1	AFLA_068560	Mago nashi domain protein
ND	24.4704	ND	ND	24.9875	24.7162	1.99E-06	523630000	3	3	3	17.7	25.724	24.7247	24.4704	24.8518	3	1	2	B8NJV1	B8NJV1	1	AFLA_069110	Glycerol-3-phosphate phosphatase (GppA), putative
28.9865	28.0448	28.4047	28.3692	28.329	27.7462	3.71E-256	2000600000	3	3	3	12.2	23.382	28.3134	28.4787	28.1481	6	3	3	B8NKJ9	B8NKJ9	1	AFLA_091650	GPI anchored protein, putative
24.4857	25.3333	24.7927	25.2983	24.8544	24.4939	1.54E-26	348110000	3	3	3	8.6	57.01	24.8764	24.8705	24.8822	6	3	3	B8NKM7	B8NKM7	1	AFLA_091930	Homoserine O-acetyltransferase
ND	22.9611	22.9827	ND	ND	ND	3.81E-05	65771000	3	3	3	8.5	47.582	22.9719	22.9719	ND	2	2	0	B8NKP9	B8NKP9	1	AFLA_093030	Serine/threonine-protein phosphatase
24.211	24.2254	24.2811	25.4923	24.5835	24.3074	4.56E-10	248530000	3	3	3	12.5	49.653	24.5168	24.2392	24.7944	6	3	3	B8NKU4	B8NKU4	1	AFLA_093480	Aminomethyl transferase, putative
24.957	25.2156	25.2829	27.1739	26.8009	26.6866	1.05E-65	847040000	3	3	3	39.6	10.908	26.0195	25.1519	26.8871	6	3	3	B8NKW0	B8NKW0	1	AFLA_093640	U6 small nuclear ribonucleoprotein (Lsm3), putative
ND	ND	ND	26.9555	26.5675	25.8458	3.80E-25	520080000	3	3	3	42.6	13.05	26.4563	ND	26.4563	3	0	3	B8NKX6	B8NKX6	1	AFLA_093800	Small nuclear ribonucleoprotein SmD2, putative
24.307	24.5751	24.4546	24.9821	24.9944	25.0649	1.62E-14	317220000	3	3	3	31.7	13.373	24.7297	24.4456	25.0138	6	3	3	B8NKX8	B8NKX8	1	AFLA_093820	SsDNA binding protein Ssb3, putative
24.5233	24.4092	24.6658	25.122	24.7469	24.3806	8.33E-09	308960000	3	3	3	6.3	60.549	24.6413	24.5328	24.7498	6	3	3	B8NLL1	B8NLL1	1	AFLA_092270	Penicillin-binding protein, putative
23.9747	24.0156	24.1308	24.1	23.3051	23.4514	2.98E-10	142140000	3	3	3	11	40.817	23.8296	24.0404	23.6188	6	3	3	B8NLR1	B8NLR1	1	AFLA_092770	TOR signaling pathway regulator (TapA), putative
27.9045	25.9435	27.9422	ND	25.5535	ND	2.03E-47	728030000	3	3	3	12.1	35.87	26.8359	27.2634	25.5535	4	3	1	B8NMB4	B8NMB4	1	AFLA_095460	Putative uncharacterized protein
27.6263	27.8453	27.9665	27.5101	27.6695	27.4021	6.32E-24	2211500000	3	3	3	35.2	11.497	27.67	27.8127	27.5272	6	3	3	B8NMS5	B8NMS5	1	AFLA_126880	Peptidyl-prolyl cis-trans isomerase
22.3203	23.7891	ND	23.585	25.7044	23.5822	1.05E-09	466850000	3	3	3	24.5	16.505	23.7962	23.0547	24.2905	5	2	3	B8NNG9	B8NNG9	1	AFLA_127800	40S ribosomal protein S26
ND	ND	ND	25.5993	24.1112	ND	3.52E-06	129370000	3	3	3	23.3	24.593	24.8553	ND	24.8553	2	0	2	B8NNR4	B8NNR4	1	AFLA_129650	NADH-ubiquinone oxidoreductase 18 kDa subunit, putative
23.8674	23.0727	23.1278	ND	ND	ND	8.57E-07	112110000	3	3	3	8.8	52.116	23.356	23.356	ND	3	3	0	B8NP48	B8NP48	1	AFLA_128310	Phosphotyrosyl phosphatase activator
24.3603	24.3898	24.603	ND	24.1448	ND	2.00E-08	101350000	3	3	3	8.8	55.817	24.3745	24.4511	24.1448	4	3	1	B8NPC4	B8NPC4	1	AFLA_129960	Oligosaccharyl transferase subunit (Alpha), putative
24.8131	25.0189	25.0037	25.9899	26.0096	25.1645	9.48E-12	528630000	3	3	3	37.2	13.168	25.3333	24.9452	25.7213	6	3	3	B8NPD9	B8NPD9	1	AFLA_130110	Putative uncharacterized protein
ND	25.8734	26.0226	25.6743	26.4393	25.4151	9.95E-11	670450000	3	3	3	9.9	42.125	25.8849	25.948	25.8429	5	2	3	B8NPH6	B8NPH6	1	AFLA_130480	Replication protein A 70 kDa DNA-binding subunit
ND	25.1565	24.5391	26.8323	26.1376	26.9394	1.88E-28	622120000	3	3	3	29.3	10.128	25.921	24.8478	26.6364	5	2	3	B8NPV3	B8NPV3	1	AFLA_002560	60S ribosomal protein L37a
24.3081	23.8873	ND	26.7158	26.7285	25.8303	1.44E-34	541510000	3	3	3	33.8	18.242	25.494	24.0977	26.4248	5	2	3	B8NPY8	B8NPY8	1	AFLA_002910	Putative uncharacterized protein
23.8384	24.1838	25.1715	ND	ND	22.5893	7.09E-08	108680000	3	3	3	7.6	53.72	23.9458	24.3979	22.5893	4	3	1	B8NQ44	B8NQ44	1	AFLA_004350	Phosphatidylserine decarboxylase family protein
ND	ND	24.5524	24.0753	ND	23.9683	5.71E-07	122220000	3	3	3	3.3	139.61	24.1987	24.5524	24.0218	3	1	2	B8NQ70	B8NQ70	1	AFLA_004610	ATP dependent DNA ligase domain protein
25.2224	25.5682	25.5303	26.1746	26.0059	25.6739	1.33E-43	618150000	3	3	3	45.2	14.756	25.6959	25.4403	25.9515	6	3	3	B8NQV0	B8NQV0	1	AFLA_002440	Putative uncharacterized protein
26.3042	26.6608	26.7535	27.3975	26.9247	26.7135	2.71E-26	1398800000	3	3	3	5.3	74.929	26.7924	26.5729	27.0119	6	3	3	B8NR18	B8NR18	1	AFLA_004020	Putative uncharacterized protein
23.7835	23.4651	24.4011	ND	23.2781	22.6868	3.65E-09	116190000	3	3	3	9.7	45.489	23.5229	23.8832	22.9824	5	3	2	B8NR26	B8NR26	1	AFLA_004100	Transesterase (LovD), putative
23.8428	24.5074	24.3502	24.1404	24.168	24.659	3.38E-16	177240000	3	3	3	7.6	36.687	24.278	24.2335	24.3225	6	3	3	B8NRB2	B8NRB2	1	AFLA_005870	GTP cyclohydrolase I, putative
27.4172	27.2818	27.7038	26.1113	26.7321	26.8696	2.18E-55	880320000	3	3	3	18.3	19.015	27.0193	27.4676	26.571	6	3	3	B8NRH1	B8NRH1	1	AFLA_048760	Membrane biogenesis protein (Yop1), putative
24.4017	24.6081	24.3027	24.4414	24.1868	24.0552	1.39E-08	213840000	3	3	3	11.4	46.226	24.3327	24.4375	24.2278	6	3	3	B8NS01	B8NS01	1	AFLA_052320	Aspartic endopeptidase (AP1), putative
ND	ND	ND	28.115	27.873	27.5837	6.47E-11	1523000000	3	3	3	16.3	11.278	27.8572	ND	27.8572	3	0	3	B8NS34	B8NS34	1	AFLA_052650	Putative uncharacterized protein
23.9922	24.6022	23.877	ND	23.9776	24.5104	1.45E-06	135450000	3	3	3	7.4	56.465	24.1919	24.1571	24.244	5	3	2	B8NSG2	B8NSG2	1	AFLA_048250	1,3-beta-glucan biosynthesis protein, putative
25.4923	24.7189	25.3326	26.1462	26.1175	25.6913	5.78E-25	704070000	3	3	3	12	34.662	25.5831	25.1813	25.985	6	3	3	B8NT56	B8NT56	1	AFLA_053390	GPI-anchored cell wall beta-1,3-endoglucanase EglC
23.7924	ND	ND	24.2338	24.1304	24.0271	2.75E-08	126470000	3	3	3	7.2	62.91	24.0459	23.7924	24.1304	4	1	3	B8NTI4	B8NTI4	1	AFLA_098240	Probable D-xylulose kinase A
27.191	ND	ND	27.219	27.1613	26.9361	4.76E-05	824870000	3	3	3	1.2	276.97	27.1269	27.191	27.1055	4	1	3	B8NTQ4	B8NTQ4	1	AFLA_099850	Myosin type II heavy chain, putative
ND	23.7649	ND	23.3799	ND	23.6923	2.55E-06	148800000	3	3	3	14.8	37.59	23.6124	23.7649	23.5361	3	1	2	B8NTT3	B8NTT3	1	AFLA_100140	Metallo-beta-lactamase superfamily protein
25.6029	24.7627	25.151	24.7986	24.9921	24.6486	9.01E-09	349990000	3	3	3	17.8	32.364	24.9927	25.1722	24.8131	6	3	3	B8NTU8	B8NTU8	1	AFLA_101190	Putative uncharacterized protein
25.3604	ND	25.8738	ND	ND	ND	3.79E-09	235390000	3	3	3	21.7	28.058	25.6171	25.6171	ND	2	2	0	B8NU84	B8NU84	1	AFLA_098460	Putative uncharacterized protein
24.9549	24.5646	ND	ND	ND	ND	8.71E-16	167460000	3	3	3	12.8	40.381	24.7598	24.7598	ND	2	2	0	B8NUG2	B8NUG2	1	AFLA_099240	D-arabinitol dehydrogenase ArbD, putative
26.1061	26.2782	26.3073	ND	24.348	25.2223	1.04E-20	442050000	3	3	3	27	26.851	25.6524	26.2305	24.7851	5	3	2	B8NUN1	B8NUN1	1	AFLA_100840	Pyridoxamine phosphate oxidase, putative
25.353	25.458	25.7131	25.4847	25.1307	24.9377	5.76E-10	646890000	3	3	3	25.4	16.755	25.3462	25.508	25.1843	6	3	3	B8NUQ4	B8NUQ4	1	AFLA_101070	Sorting nexin Snx3, putative
25.0469	24.8959	24.9924	25.5534	24.6006	24.3898	4.48E-10	411330000	3	3	3	15.2	42.101	24.9132	24.9784	24.8479	6	3	3	B8NUQ7	B8NUQ7	1	AFLA_101100	RRM domain protein
24.7493	24.7008	24.4039	ND	ND	ND	4.21E-12	121480000	3	3	3	13.3	45.392	24.618	24.618	ND	3	3	0	B8NUR6	B8NUR6	1	AFLA_102090	Phosphopantothenate-cysteine ligase, putative
ND	ND	24.2913	24.2523	ND	24.2654	4.39E-07	217180000	3	3	3	7.2	59.719	24.2696	24.2913	24.2588	3	1	2	B8NV09	B8NV09	1	AFLA_103030	Pre-mRNA splicing factor, putative
ND	26.818	25.7482	27.521	27.4622	26.7832	1.46E-18	1687700000	3	3	3	15.1	18.155	26.8665	26.2831	27.2555	5	2	3	B8NV35	B8NV35	1	AFLA_103290	Histone H1
27.8191	28.3095	28.3115	28.5844	28.1741	27.7303	9.84E-65	3992000000	3	3	3	10.5	58.197	28.1548	28.1467	28.1629	6	3	3	B8NV39	B8NV39	1	AFLA_103330	Glutaryl-CoA dehydrogenase, putative
24.4972	27.4083	25.6051	ND	25.7412	ND	1.57E-16	2261700000	3	3	3	29.3	14.092	25.813	25.8369	25.7412	4	3	1	B8NVA8;B8	B8NVA8	2	AFLA_104030	Histone H2A
23.7702	23.9432	23.4699	24.5789	23.3098	23.6735	4.61E-07	136320000	3	3	3	4.1	92.574	23.7909	23.7278	23.8541	6	3	3	B8NW19	B8NW19	1	AFLA_119470	Topoisomerase II associated protein (Pat1), putative
26.7323	26.8089	26.9237	26.7489	28.1188	26.8841	5.12E-69	892390000	3	3	3	22.5	30.301	27.0361	26.8216	27.2506	6	3	3	B8NWE1	B8NWE1	1	AFLA_119780	Neutral protease 2 homolog AFLA_119780
25.6771	25.8896	25.9286	ND	ND	ND	5.94E-35	215770000	3	3	3	10.8	42.861	25.8318	25.8318	ND	3	3	0	B8NWU6	B8NWU6	1	AFLA_121330	Methyltransferase LaeA-like, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
24.49	ND	24.252	24.196	24.1836	24.1791	1.85E-06	259690000	3	3	3	10.2	31.025	24.2601	24.371	24.1862	5	2	3	B8NWV7	B8NWV7	1	AFLA_121440	Fumarylacetoacetate hydrolase, putative
23.3069	23.6153	ND	25.281	24.8996	23.4328	1.99E-09	162480000	3	3	3	4.9	83.122	24.1071	23.4611	24.5378	5	2	3	B8NX31	B8NX31	1	AFLA_122180	Putative uncharacterized protein
26.4545	26.6568	26.855	26.7236	26.921	26.5337	9.88E-21	1162600000	3	3	3	53	17.169	26.6908	26.6554	26.7261	6	3	3	B8NXL1	B8NXL1	1	AFLA_008300	Ubiquitin conjugating enzyme (UbcB), putative
25.0663	24.5698	ND	ND	24.3097	ND	2.55E-10	232980000	3	3	3	15.9	39.503	24.6486	24.818	24.3097	3	2	1	B8NYN8	B8NYN8	1	AFLA_012080	Glucosamine-6-phosphate deaminase, putative
26.7943	26.6041	26.4806	26.7347	26.8703	26.7128	2.71E-34	1443700000	3	3	3	32.1	15.135	26.6995	26.6263	26.7726	6	3	3	B8NYT2	B8NYT2	1	AFLA_114440	L-PSP endoribonuclease family protein Brt1, putative
24.3631	24.4487	24.736	23.8429	24.0551	24.0405	6.95E-09	161450000	3	3	3	9.9	37.175	24.2477	24.5159	23.9795	6	3	3	B8NYX8	B8NYX8	1	AFLA_114900	Thymidylate synthase
25.2788	22.9302	23.8493	ND	ND	ND	2.15E-16	104090000	4	3	3	11	46.976	24.0194	24.0194	ND	3	3	0	B8N3I4	B8N3I4	1	AFLA_028870	Aspartate aminotransferase
26.4242	26.0389	26.6337	25.3326	25.4382	26.2329	8.66E-17	876360000	4	3	3	22.7	29.604	26.0167	26.3656	25.6679	6	3	3	B8NCF9	B8NCF9	1	AFLA_041340	Oxidoreductase, short-chain dehydrogenase/reductase family
30.6407	30.5176	30.6736	31.2377	30.7967	30.7646	3.61E-249	20159000000	7	7	3	50	17.628	30.7718	30.6106	30.933	6	3	3	B8N3Q5;B8	B8N3Q5;B8	2	AFLA_031390	Ubiquitin (UbiC), putative
24.2386	24.7495	ND	ND	23.6689	ND	3.11E-10	167550000	4	4	4	23.1	23.68	24.219	24.494	23.6689	3	2	1	B8MWH6	B8MWH6	1	AFLA_088660	DUF431 domain protein
26.0847	26.0235	26.2028	26.9496	26.1187	25.875	3.16E-52	766700000	4	4	4	56.9	13.302	26.2091	26.1037	26.3144	6	3	3	B8MX15	B8MX15	1	AFLA_076020	Tropomyosin-1, putative
25.4197	26.2736	25.9741	24.5942	24.8852	25.0204	3.64E-10	559540000	4	4	4	23.4	25.648	25.3612	25.8891	24.8333	6	3	3	B8MX61	B8MX61	1	AFLA_076480	Glutathione S-transferase, putative
25.0678	25.697	25.5867	25.7568	25.9751	25.2201	2.82E-19	596740000	4	4	4	31.5	25.589	25.5506	25.4505	25.6507	6	3	3	B8MX75	B8MX75	1	AFLA_076620	Siroheme synthase Met8, putative
ND	ND	24.2589	26.4583	26.4625	26.3381	5.46E-11	486610000	4	4	4	50.5	10.64	25.8794	24.2589	26.4196	4	1	3	B8MXA7	B8MXA7	1	AFLA_076940	Small nuclear ribonucleoprotein SmE, putative
25.4471	24.9986	25.2789	ND	23.2206	23.1716	1.09E-13	145750000	4	4	4	16.3	42.727	24.4234	25.2415	23.1961	5	3	2	B8MXB2	B8MXB2	1	AFLA_076990	Alpha-ketoglutarate-dependent taurine dioxygenase
ND	ND	ND	25.3344	24.8987	25.0469	2.05E-09	153740000	4	4	4	10.9	37.363	25.0933	ND	25.0933	3	0	3	B8MXX9	B8MXX9	1	AFLA_079160	Ribosome biogenesis protein, putative
ND	ND	ND	23.6404	ND	23.4405	6.99E-09	114850000	4	4	4	5.2	100.79	23.5405	ND	23.5405	2	0	2	B8MY66	B8MY66	1	AFLA_080030	Topoisomerase I
25.2837	ND	24.8836	23.5432	ND	ND	5.63E-08	196990000	4	4	4	17.6	43.085	24.5702	25.0836	23.5432	3	2	1	B8MY91	B8MY91	1	AFLA_080280	Phosphotransferase enzyme family domain protein
25.4418	25.1079	24.6784	ND	24.1542	24.6794	1.04E-07	236470000	4	4	4	21.8	37.787	24.8124	25.076	24.4168	5	3	2	B8MY93	B8MY93	1	AFLA_080300	Pyridoxal kinase, putative
25.163	25.3734	25.5537	25.1468	ND	24.3911	9.12E-12	290530000	4	4	4	12.6	54.068	25.1256	25.3634	24.769	5	3	2	B8MYJ5	B8MYJ5	1	AFLA_081330	Glycerol 3-phosphate dehydrogenase (GfdA), putative
24.6368	23.8357	24.335	ND	23.5518	23.441	5.40E-10	96899000	4	4	4	12.3	49.239	23.9601	24.2692	23.4964	5	3	2	B8MYW5	B8MYW5	1	AFLA_082540	Aminotransferase, class III
ND	ND	ND	21.8022	22.2551	22.729	3.76E-24	985710000	4	4	4	31.5	9.9816	22.2621	ND	22.2621	3	0	3	B8MZ16	B8MZ16	1	AFLA_083050	40S ribosomal protein S25, putative
23.2063	25.0178	23.3236	24.8407	24.9346	24.7449	5.01E-15	331560000	4	4	4	7.7	82.41	24.3447	23.8492	24.8401	6	3	3	B8MZ59	B8MZ59	1	AFLA_083480	Importin beta-2 subunit, putative
26.1019	24.7824	25.3303	24.7206	ND	24.2411	8.10E-30	407040000	4	4	4	19.3	38.204	25.0353	25.4049	24.4809	5	3	2	B8MZP5	B8MZP5	1	AFLA_085350	AMMECR1 family protein
25.9277	27.01	26.4818	26.9685	26.1923	26.4562	2.65E-24	1058500000	4	4	4	38.3	13.319	26.5061	26.4732	26.539	6	3	3	B8MZP9	B8MZP9	1	AFLA_085390	Prefoldin subunit 6, putative
ND	ND	ND	26.3398	ND	26.338	5.36E-28	943250000	4	4	4	20.6	16.934	26.3389	ND	26.3389	2	0	2	B8N003	B8N003	1	AFLA_086430	Coactivator bridging factor 1 (Mbf1), putative
28.358	29.3064	28.5144	31.1727	31.0251	30.6844	7.69E-293	16010000000	4	4	4	40.2	13.622	29.8435	28.7262	30.9607	6	3	3	B8N014	B8N014	1	AFLA_086540	Glycine-rich RNA-binding protein, putative
ND	25.0294	25.1067	25.6426	25.8805	25.6748	1.42E-10	496800000	4	4	4	35.8	16.872	25.4668	25.0681	25.7326	5	2	3	B8N071	B8N071	1	AFLA_087110	Polymerase (RNA) II (DNA directed) polypeptide D
ND	24.3911	ND	ND	24.9906	25.612	2.24E-08	310640000	4	4	4	15.8	54.176	24.9979	24.3911	25.3013	3	1	2	B8N072	B8N072	1	AFLA_087120	tRNA (guanine(37)-N1)-methyltransferase
25.393	25.7688	25.8551	25.721	25.1888	25.3184	2.78E-36	668080000	4	4	4	12.7	47.261	25.5408	25.6723	25.4094	6	3	3	B8N090	B8N090	1	AFLA_087310	Putative uncharacterized protein
24.6493	24.6259	ND	24.6867	ND	25.3234	1.58E-12	229830000	4	4	4	19.8	40.882	24.8213	24.6376	25.005	4	2	2	B8N0P2	B8N0P2	1	AFLA_024850	Deoxyhypusine synthase, putative
25.7193	25.8071	26.1489	24.7812	24.419	25.8561	1.17E-157	419980000	4	4	4	27.9	26.199	25.4553	25.8918	25.0188	6	3	3	B8N0R4	B8N0R4	1	AFLA_025990	Clathrin light chain
24.7785	24.858	24.6909	25.7352	24.4041	24.8124	3.60E-16	583220000	4	4	4	16.2	35.085	24.8798	24.7758	24.9839	6	3	3	B8N0R5	B8N0R5	1	AFLA_026000	DUF618 domain protein
ND	ND	ND	25.5238	23.7559	24.6062	3.55E-11	160510000	4	4	4	10.3	71.219	24.6287	ND	24.6287	3	0	3	B8N0T4	B8N0T4	1	AFLA_026190	Signal recognition particle subunit SRP72
24.5312	25.089	24.6235	28.0923	27.6383	27.6195	3.73E-15	1531100000	4	4	4	36.2	12.867	26.2657	24.7479	27.7834	6	3	3	B8N0U1	B8N0U1	1	AFLA_026260	Small nuclear ribonucleoprotein SmD3, putative
26.5185	26.495	26.6027	26.959	26.5163	26.5686	3.19E-40	1198100000	4	4	4	31.4	23.29	26.61	26.5388	26.6813	6	3	3	B8N0X3	B8N0X3	1	AFLA_026580	Mitochondrial chaperone Frataxin, putative
ND	24.5796	24.9588	24.6208	24.6802	ND	8.13E-12	277050000	4	4	4	6.2	91.283	24.7099	24.7692	24.6505	4	2	2	B8N173	B8N173	1	AFLA_029380	Urease
24.7909	25.4065	24.6282	25.7482	25.8222	25.4953	7.19E-24	601850000	4	4	4	9.6	64.417	25.3152	24.9419	25.6886	6	3	3	B8N1K8	B8N1K8	1	AFLA_030730	Putative uncharacterized protein
ND	ND	ND	26.3981	24.8133	25.5339	1.23E-16	449890000	4	4	4	13.3	35.184	25.5818	ND	25.5818	3	0	3	B8N1X2	B8N1X2	1	AFLA_032760	Pre-RNA splicing factor Srp2, putative
ND	ND	ND	23.1051	21.7938	23.197	3.13E-12	107610000	4	4	4	15.8	20.056	22.6986	ND	22.6986	3	0	3	B8N234	B8N234	1	AFLA_034280	40S ribosomal protein S29, putative
25.0413	25.5642	25.5311	24.6696	24.9104	24.7888	5.56E-10	233140000	4	4	4	9.7	58.222	25.0842	25.3788	24.7896	6	3	3	B8N2C8;B8	B8N2C8	2	AFLA_036130	14-alpha sterol demethylase Cyp51A
25.5542	25.0437	26.3738	25.6685	25.1862	24.7214	6.41E-34	371930000	4	4	4	11.4	63.462	25.4246	25.6572	25.192	6	3	3	B8N2D2	B8N2D2	1	AFLA_036170	T-complex protein 1, epsilon subunit, putative
24.6916	25.1611	25.0668	ND	24.706	24.3787	3.76E-10	172640000	4	4	4	47.4	17.057	24.8008	24.9732	24.5424	5	3	2	B8N2Y5	B8N2Y5	1	AFLA_025090	Phosphate transporter (Pho88), putative
24.3063	24.993	24.9255	25.92	ND	ND	1.78E-09	199820000	4	4	4	16.6	35.015	25.0362	24.7416	25.92	4	3	1	B8N369	B8N369	1	AFLA_026820	Phosphoribosyl diphosphate synthase isoform 4
ND	23.9022	23.7702	23.4246	23.7666	24.3272	3.07E-11	187630000	4	4	4	17.9	36.657	23.8382	23.8362	23.8395	5	2	3	B8N375	B8N375	1	AFLA_026880	Nicotinamide riboside kinase, putative
25.7903	25.4651	25.5018	25.9184	25.513	25.524	1.43E-64	547100000	4	4	4	34.9	14.631	25.6188	25.5857	25.6518	6	3	3	B8N3F0	B8N3F0	1	AFLA_028530	Prefoldin subunit 2, putative
24.4583	ND	23.9482	26.2005	26.3324	25.9285	4.68E-24	658240000	4	4	4	7.2	98.636	25.3736	24.2033	26.1538	5	2	3	B8N3F7	B8N3F7	1	AFLA_028600	DNA replication licensing factor Mcm3, putative
27.4428	24.749	27.2741	24.254	25.3023	23.8478	4.75E-231	526650000	4	4	4	19.2	33.983	25.4783	26.4886	24.468	6	3	3	B8N3I0	B8N3I0	1	AFLA_028830	FG-GAP repeat protein, putative
ND	23.898	ND	25.5555	25.8687	26.9548	4.42E-20	432630000	4	4	4	13.4	40.373	25.5693	23.898	26.1263	4	1	3	B8N3J4	B8N3J4	1	AFLA_028970	30S ribosomal protein S7, putative
ND	ND	ND	24.2677	23.9925	23.6545	9.65E-08	114570000	4	4	4	19.8	46.735	23.9716	ND	23.9716	3	0	3	B8N3Q7	B8N3Q7	1	AFLA_031410	Ribonuclease T2 family, putative
26.1672	25.3221	26.2864	24.26	24.525	24.3925	8.16E-26	296690000	4	4	4	22.4	24.037	25.1589	25.9252	24.3925	6	3	3	B8N3Y9	B8N3Y9	1	AFLA_033120	BAP31 domain protein, putative
ND	ND	23.8104	24.9727	24.1716	25.5188	3.71E-12	221270000	4	4	4	7	73.913	24.6184	23.8104	24.8877	4	1	3	B8N511	B8N511	1	AFLA_020490	Pseudouridylate synthase 3
25.6257	24.9487	25.2405	25.9062	26.0059	25.6028	4.45E-45	321510000	4	4	4	7.3	78.442	25.555	25.2716	25.8383	6	3	3	B8N531	B8N531	1	AFLA_020690	Extracellular serine-threonine rich protein
ND	ND	ND	23.726	22.6377	ND	2.12E-12	152240000	4	4	4	5.3	90.123	23.1819	ND	23.1819	2	0	2	B8N5B4	B8N5B4	1	AFLA_022420	Microtubule binding protein HOOK3, putative
24.268	24.5173	24.421	ND	ND	ND	9.22E-08	160040000	4	4	4	6	86.491	24.4021	24.4021	ND	3	3	0	B8N5W5	B8N5W5	1	AFLA_014580	Chromatin remodeling complex subunit (Arp5), putative
25.6473	25.9481	25.9864	26.8061	25.5154	25.8243	1.84E-31	714610000	4	4	4	23.9	31.263	25.9546	25.8606	26.0486	6	3	3	B8N649	B8N649	1	AFLA_016330	Alpha/beta fold family hydrolase, putative
25.3058	24.5432	25.2243	ND	24.327	23.1563	7.79E-12	456710000	4	4	4	26.9	25.425	24.5113	25.0244	23.7416	5	3	2	B8N656	B8N656	1	AFLA_016400	Glutathione S-transferase, putative
ND	ND	ND	25.2458	24.8686	26.0363	1.95E-20	178430000	4	4	4	11.9	44.244	25.3836	ND	25.3836	3	0	3	B8N6D2	B8N6D2	1	AFLA_018960	60S ribosomal protein L3
27.1012	28.832	28.2572	29.0924	25.9166	27.9634	2.96E-56	2848300000	4	4	4	33.7	18.052	27.8605	28.0635	27.6575	6	3	3	B8N6F9	B8N6F9	1	AFLA_019230	Mismatched base pair and cruciform DNA recognition protein, putative
28.8158	28.5765	28.9762	28.475	28.3484	28.1092	3.70E-70	5132800000	4	4	4	58.1	17.225	28.5502	28.7895	28.3109	6	3	3	B8N6G4	B8N6G4	1	AFLA_019280	Peroxiredoxin, putative
26.7646	26.7175	27.0914	26.7056	26.4516	26.1726	1.04E-124	1192200000	4	4	4	22.3	34.522	26.6506	26.8578	26.4433	6	3	3	B8N6J3	B8N6J3	1	AFLA_015060	Phytanoyl-CoA dioxygenase family protein
ND	ND	23.825	24.0159	23.9268	23.5212	7.21E-10	226020000	4	4	4	5.9	93.405	23.8222	23.825	23.8213	4	1	3	B8N6J6;B8	B8N6J6	2	AFLA_015090	HET-C domain protein
24.4549	24.243	24.4866	25.8581	25.4225	25.2344	1.84E-31	408560000	4	4	4	43.8	12.738	24.9499	24.3948	25.505	6	3	3	B8N6L9	B8N6L9	1	AFLA_015320	Transcription initiation factor IIA subunit 2
ND	25.4238	ND	28.125	27.8243	27.5846	2.67E-30	1251000000	4	4	4	39.8	10.067	27.2394	25.4238	27.8446	4	1	3	B8N6N8	B8N6N8	1	AFLA_015510	Small nuclear ribonucleoprotein SmF, putative
ND	ND	ND	24.8615	25.3914	24.3905	3.40E-12	302480000	4	4	4	39.6	16.977	24.8811	ND	24.8811	3	0	3	B8N729	B8N729	1	AFLA_019620	Putative uncharacterized protein
24.9927	25.7726	25.2628	24.365	ND	ND	5.13E-11	204490000	4	4	4	15.6	53.084	25.0983	25.3427	24.365	4	3	1	B8N7Q0	B8N7Q0	1	AFLA_104930	6-hydroxy-D-nicotine oxidase, putative
24.9088	24.8045	25.0458	25.3073	25.1763	25.1521	9.70E-15	335430000	4	4	4	22.1	22.845	25.0658	24.9197	25.2119	6	3	3	B8N861	B8N861	1	AFLA_106550	Peptidyl-prolyl cis-trans isomerase
29.783	30.1972	29.8885	31.8998	31.7801	31.4349	3.46E-217	21966000000	4	4	4	48.8	13.13	30.8306	29.9562	31.7049	6	3	3	B8N8I7	B8N8I7	1	AFLA_107810	Heterogeneous nuclear ribonucleoprotein G, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
24.4784	24.241	24.4149	24.6664	24.7169	24.2626	1.33E-10	313620000	4	4	4	11.9	60.716	24.4634	24.3781	24.5486	6	3	3	B8N8P1	B8N8P1	1	AFLA_108350	Alpha/beta hydrolase, putative
28.1167	27.2719	28.2162	26.0075	26.5409	26.0745	4.77E-44	3533700000	4	4	4	59.8	11.573	27.0379	27.8683	26.2076	6	3	3	B8N8S9	B8N8S9	1	AFLA_108740	Putative uncharacterized protein
25.6125	25.6099	26.2353	25.51	25.4915	25.2675	4.26E-09	859320000	4	4	4	25.3	27.489	25.6211	25.8192	25.423	6	3	3	B8N953	B8N953	1	AFLA_109990	SNARE protein Ykt6, putative
ND	24.661	ND	25.8562	25.4982	26.7117	4.82E-24	442930000	4	4	4	19.2	33.102	25.6818	24.661	26.0221	4	1	3	B8N9A8	B8N9A8	1	AFLA_110540	Putative uncharacterized protein
24.1541	23.9442	24.2177	24.3352	23.9652	23.5216	1.96E-09	174880000	4	4	4	6.1	69.165	24.023	24.1053	23.9406	6	3	3	B8N9F0	B8N9F0	1	AFLA_110960	Lysophospholipase Plb1
ND	ND	ND	24.4364	23.3329	23.5753	1.31E-09	166410000	4	4	4	10.4	62.23	23.7815	ND	23.7815	3	0	3	B8N9I7	B8N9I7	1	AFLA_111330	Aspartyl-tRNA synthetase, putative
25.2666	25.1804	25.5558	25.6876	25.3816	25.4572	5.28E-12	469440000	4	4	4	17.7	37.584	25.4215	25.3343	25.5088	6	3	3	B8N9K7	B8N9K7	1	AFLA_111530	Zinc-containing alcohol dehydrogenase, putative
23.1819	22.8198	23.1591	24.4144	23.6426	23.2924	1.79E-06	118220000	4	4	4	18	27.414	23.4184	23.0536	23.7831	6	3	3	B8N9P9	B8N9P9	1	AFLA_111950	Putative uncharacterized protein
25.4019	25.6473	25.6266	24.8216	25.163	25.0816	6.78E-46	448980000	4	4	4	17.5	40.552	25.2903	25.5586	25.0221	6	3	3	B8N9Q6	B8N9Q6	1	AFLA_112020	CaaX farnesyltransferase alpha subunit Ram2
24.1469	24.0788	24.0559	24.6021	24.5754	24.3703	5.91E-08	257840000	4	4	4	9.6	55.154	24.3049	24.0938	24.5159	6	3	3	B8N9U4	B8N9U4	1	AFLA_112400	UBX domain protein, putative
24.9373	24.4717	ND	24.3194	23.525	24.7419	1.05E-09	232740000	4	4	4	12.8	51.872	24.3991	24.7045	24.1954	5	2	3	B8N9Y3	B8N9Y3	1	AFLA_112790	Acyl-CoA thioester hydrolase, putative
27.0468	26.6787	25.1248	24.8203	26.2886	24.5814	6.55E-25	500410000	4	4	4	14.5	37.064	25.7568	26.2834	25.2301	6	3	3	B8NA08	B8NA08	1	AFLA_113040	Outer mitochondrial membrane protein porin
24.6378	24.1401	24.8011	22.5672	23.9778	23.0192	2.68E-16	133610000	4	4	4	11.2	46.831	23.8572	24.5263	23.1881	6	3	3	B8NA14	B8NA14	1	AFLA_113100	N-glycosyl-transferase
ND	24.359	ND	26.0697	25.958	25.4133	1.43E-35	376820000	4	4	4	17.5	39.67	25.45	24.359	25.8136	4	1	3	B8NA82	B8NA82	1	AFLA_113780	Casein kinase II beta subunit CKB1
23.6023	23.5752	24.5228	ND	23.1271	23.9449	1.39E-08	113130000	4	4	4	9.2	83.008	23.7544	23.9001	23.536	5	3	2	B8NA96	B8NA96	1	AFLA_113920	Translation initiation regulator (Gcn20), putative
27.7273	27.9605	28.3379	28.3907	27.4088	27.8449	4.97E-14	2395800000	4	4	4	30.2	13.075	27.945	28.0086	27.8815	6	3	3	B8NAU0	B8NAU0	1	AFLA_043150	40S ribosomal protein S10a
25.5822	25.4833	ND	ND	24.081	ND	6.84E-16	178310000	4	4	4	8.8	75.098	25.0488	25.5327	24.081	3	2	1	B8NB18	B8NB18	1	AFLA_043930	MFS phosphate transporter, putative
25.2033	25.3355	25.5345	24.6918	25.1331	25.1319	5.24E-16	254280000	4	4	4	18.5	34.312	25.1717	25.3578	24.9856	6	3	3	B8NBF6	B8NBF6	1	AFLA_045310	HVA22 domain membrane protein
26.0001	25.6513	25.7544	25.4301	25.4414	25.1012	1.62E-17	844230000	4	4	4	42.2	12.542	25.5631	25.8019	25.3242	6	3	3	B8NBL0	B8NBL0	1	AFLA_045850	Putative uncharacterized protein
23.341	22.7728	23.3438	25.4263	24.7211	23.9863	4.80E-09	143490000	4	4	4	6.5	78.912	23.9319	23.1525	24.7112	6	3	3	B8NBL5	B8NBL5	1	AFLA_045900	Phenylalanine ammonia-lyase
25.8393	ND	25.5678	ND	24.5627	ND	1.10E-15	153340000	4	4	4	12.2	56.94	25.3233	25.7035	24.5627	3	2	1	B8NBZ4	B8NBZ4	1	AFLA_047190	L-ornithine N5-oxygenase SidA
26.4499	26.3847	25.5353	24.8637	25.2776	26.1018	6.45E-13	515260000	4	4	4	12.3	43.656	25.7688	26.1233	25.4144	6	3	3	B8NC20	B8NC20	1	AFLA_047450	Gamma-glutamyl phosphate reductase
24.7269	24.3508	24.5361	24.7774	24.8376	24.1053	4.70E-10	289590000	4	4	4	19.8	27.783	24.5557	24.5379	24.5734	6	3	3	B8NCQ7	B8NCQ7	1	AFLA_041420	GMP synthase
ND	23.8976	ND	24.2963	24.1877	26.427	7.97E-19	287550000	4	4	4	13	55.58	24.7021	23.8976	24.9703	4	1	3	B8NCZ6	B8NCZ6	1	AFLA_054670	Tryptophanyl-tRNA synthetase, putative
25.5475	23.929	25.4198	23.4287	22.934	23.7272	1.08E-06	206900000	4	4	4	8.8	61.463	24.1644	24.9655	23.3633	6	3	3	B8ND16	B8ND16	1	AFLA_054870	6-phosphofructo-2-kinase, putative
ND	24.3686	24.4873	ND	24.641	23.619	1.43E-10	175670000	4	4	4	15.2	40.105	24.2789	24.4279	24.13	4	2	2	B8NDB3	B8NDB3	1	AFLA_056740	GTP binding protein (Gtp1), putative
ND	ND	ND	27.5426	ND	27.1176	2.65E-06	444510000	4	4	4	1.5	266.76	27.3301	ND	27.3301	2	0	2	B8NDF2	B8NDF2	1	AFLA_057130	THO complex component (Rlr1), putative
28.2214	27.9935	28.4101	ND	24.0701	ND	1.06E-42	1572400000	4	4	4	32.2	19.57	27.1738	28.2083	24.0701	4	3	1	B8NDN7	B8NDN7	1	AFLA_059760	Putative uncharacterized protein
24.2162	24.2748	25.5068	ND	24.3141	ND	1.52E-07	132290000	4	4	4	10.5	58.595	24.578	24.6659	24.3141	4	3	1	B8NE15	B8NE15	1	AFLA_057460	Chaperone binding protein, putative
25.6401	25.7277	26.2243	23.9146	24.87	24.3063	1.15E-26	281310000	4	4	4	10.5	52.195	25.1138	25.864	24.3637	6	3	3	B8NEJ4	B8NEJ4	1	AFLA_061920	Protein transport protein Sec61 alpha subunit, putative
ND	24.3031	23.3253	24.9193	24.439	24.5442	2.99E-10	250660000	4	4	4	8.4	74.268	24.3062	23.8142	24.6342	5	2	3	B8NEL5	B8NEL5	1	AFLA_062130	Alpha-actinin, sarcomeric (F-actin cross linking protein)
ND	ND	ND	27.0827	26.7843	27.2357	1.65E-58	632400000	4	4	4	64.1	11.564	27.0343	ND	27.0343	3	0	3	B8NEM0	B8NEM0	1	AFLA_062180	37S ribosomal protein S16
24.1432	25.8777	24.6197	23.7445	ND	ND	4.54E-08	206520000	4	4	4	9.9	70.661	24.5963	24.8802	23.7445	4	3	1	B8NEN9	B8NEN9	1	AFLA_062370	Mitochondrial outer membrane translocase receptor (TOM70), putative
24.2013	24.9576	24.3512	25.0693	24.8287	ND	8.50E-11	244000000	4	4	4	22.9	28.045	24.6816	24.5034	24.949	5	3	2	B8NFS4	B8NFS4	1	AFLA_133530	Phosducin family protein
25.5279	24.5641	25.5085	24.5787	24.6752	24.2205	5.28E-34	550170000	4	4	4	21.1	30.397	24.8458	25.2002	24.4915	6	3	3	B8NFW6	B8NFW6	1	AFLA_133950	Triosephosphate isomerase
25.9374	25.9193	25.6353	26.3062	25.9773	26.2376	1.01E-18	727540000	4	4	4	15.5	36.36	26.0022	25.8307	26.1737	6	3	3	B8NG67	B8NG67	1	AFLA_132280	Thiamin pyrophosphokinase-related protein
25.2915	ND	ND	26.9503	26.4537	26.152	2.71E-197	685970000	4	4	4	24.7	19.411	26.2119	25.2915	26.5186	4	1	3	B8NGD0	B8NGD0	1	AFLA_134700	Small nuclear ribonucleoprotein (LSM1), putative
25.0333	ND	25.2148	ND	ND	ND	9.35E-17	248090000	4	4	4	28.2	27.56	25.1241	25.1241	ND	2	2	0	B8NGD5	B8NGD5	1	AFLA_134750	Putative uncharacterized protein
24.2632	25.0102	24.632	25.8983	25.4986	24.9612	3.25E-07	449030000	4	4	4	13.7	58.589	25.0439	24.6351	25.4527	6	3	3	B8NGE8	B8NGE8	1	AFLA_134880	Histone acetyltransferase type b catalytic subunit, putative
24.7058	25.2983	24.4026	ND	25.2622	25.2044	2.33E-28	443410000	4	4	4	19.4	32.89	24.9747	24.8023	25.2333	5	3	2	B8NGH4	B8NGH4	1	AFLA_136010	Pyrimidine 5-nucleotidase, putative
24.5054	ND	24.5812	ND	ND	ND	5.54E-21	277180000	4	4	4	11.2	49.272	24.5433	24.5433	ND	2	2	0	B8NGI3	B8NGI3	1	AFLA_136100	GATA transcription factor (AreB), putative
27.9167	27.6316	27.9521	27.9863	28.7343	27.9106	9.76E-30	2327400000	4	4	4	14.1	70.487	28.0219	27.8335	28.2104	6	3	3	B8NGY8	B8NGY8	1	AFLA_138570	Protease S8 tripeptidyl peptidase I, putative
25.686	25.3111	25.4042	25.693	25.5767	25.2186	4.16E-27	557630000	4	4	4	11.3	58.551	25.4816	25.4671	25.4961	6	3	3	B8NH40	B8NH40	1	AFLA_132640	mRNA cleavage and polyadenylation factor CLP1
25.862	25.6061	25.9985	24.5418	25.5465	25.1413	7.18E-14	375640000	4	4	4	8.2	44.239	25.4494	25.8222	25.0765	6	3	3	B8NHG2	B8NHG2	1	AFLA_135670	Translocation protein Sec62, putative
24.6057	24.2589	24.6243	24.9877	24.5871	24.5265	4.78E-08	269110000	4	4	4	6.9	59.379	24.5984	24.4963	24.7004	6	3	3	B8NHG6	B8NHG6	1	AFLA_135710	NADPH:adrenodoxin oxidoreductase, mitochondrial
23.6499	22.7229	23.8793	22.6947	ND	ND	5.71E-07	86327000	4	4	4	13.5	45.802	23.2367	23.4174	22.6947	4	3	1	B8NIK6	B8NIK6	1	AFLA_067930	Nucleoside hydrolase, putative
26.1831	ND	25.7123	27.1726	ND	26.2945	2.70E-13	668020000	4	4	4	17.1	33.454	26.3406	25.9477	26.7335	4	2	2	B8NIP3	B8NIP3	1	AFLA_068300	1,3-beta-glucanosyltransferase Bgt1
ND	ND	ND	25.1738	25.0094	24.8386	5.86E-09	232030000	4	4	4	11.3	53.513	25.0072	ND	25.0072	3	0	3	B8NJ17	B8NJ17	1	AFLA_071340	Cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative
23.3134	24.8807	24.3306	26.603	25.4331	25.852	2.24E-34	302350000	4	4	4	26.1	24.268	25.0688	24.1749	25.9627	6	3	3	B8NJ19	B8NJ19	1	AFLA_071360	Zinc knuckle nucleic acid binding protein, putative
24.7346	24.4744	24.4931	ND	24.5135	24.341	7.08E-10	315870000	4	4	4	19.3	37.635	24.5113	24.5674	24.4273	5	3	2	B8NJF2	B8NJF2	1	AFLA_066730	Alcohol dehydrogenase, putative
24.3384	23.8554	24.2449	ND	23.675	ND	1.59E-08	225000000	4	4	4	16.5	36.622	24.0284	24.1462	23.675	4	3	1	B8NJL3	B8NJL3	1	AFLA_067340	Putative uncharacterized protein
24.6148	24.6797	24.6545	ND	ND	ND	3.89E-09	117000000	4	4	4	10.3	55.533	24.6497	24.6497	ND	3	3	0	B8NJL7	B8NJL7	1	AFLA_067380	Nucleoside diphosphatase Gda1
25.1196	25.0869	25.691	26.2833	25.7545	25.4554	1.09E-25	539820000	4	4	4	14.1	44.344	25.5651	25.2992	25.8311	6	3	3	B8NJQ3	B8NJQ3	1	AFLA_068630	Nuclear mRNA splicing factor-associated protein, putative
23.4514	24.4625	ND	ND	ND	24.0484	2.85E-09	215430000	4	4	4	19.1	25.299	23.9874	23.9569	24.0484	3	2	1	B8NJT4	B8NJT4	1	AFLA_068940	Proteasome regulatory particle subunit (Nas6), putative
25.3936	25.4718	25.3212	24.9532	ND	ND	1.97E-13	287790000	4	4	4	26.5	27.893	25.285	25.3955	24.9532	4	3	1	B8NJX6	B8NJX6	1	AFLA_070250	Putative uncharacterized protein
26.168	25.8475	26.1168	25.9719	26.0007	25.7313	5.90E-39	729900000	4	4	4	12.7	51.384	25.9727	26.0441	25.9013	6	3	3	B8NK20	B8NK20	1	AFLA_070690	Cystathionine gamma-synthase
23.8826	23.9328	ND	24.1648	23.751	24.0547	2.35E-10	121170000	4	4	4	12.3	45.501	23.9572	23.9077	23.9902	5	2	3	B8NKS8	B8NKS8	1	AFLA_093320	Pseudouridine synthase
25.4935	24.8174	26.1493	25.1088	25.2803	24.9658	1.65E-15	477180000	4	4	4	21.7	33.761	25.3025	25.4867	25.1183	6	3	3	B8NL00	B8NL00	1	AFLA_095840	Fe-S cluster assembly protein dre2
25.1683	24.688	25.3538	24.7223	24.7786	24.2969	7.65E-19	401940000	4	4	4	32.5	18.57	24.8346	25.07	24.5993	6	3	3	B8NLI0	B8NLI0	1	AFLA_091070	Putative uncharacterized protein
25.3634	25.8262	25.7589	24.7271	24.3396	25.2973	2.44E-17	383620000	4	4	4	10.7	69.82	25.2188	25.6495	24.788	6	3	3	B8NLK8	B8NLK8	1	AFLA_092240	Calcium/calmodulin-dependent protein kinase, putative
26.5481	26.8731	26.984	27.6966	27.5455	27.187	3.80E-64	1643400000	4	4	4	46.2	17.393	27.139	26.8017	27.4763	6	3	3	B8NLN2	B8NLN2	1	AFLA_092480	RNA binding protein (Rbm8A), putative
25.6448	25.5054	25.4089	26.5684	26.0397	25.8686	2.76E-32	472480000	4	4	4	25.8	23.215	25.8393	25.5197	26.1589	6	3	3	B8NMM0	B8NMM0	1	AFLA_124560	Putative uncharacterized protein
ND	ND	ND	22.8028	24.0298	24.7857	3.86E-08	63141000	4	4	4	11.5	45.78	23.8728	ND	23.8728	3	0	3	B8NN65	B8NN65	1	AFLA_124990	Putative uncharacterized protein
ND	24.0004	25.6211	23.115	ND	23.7316	1.98E-12	118260000	4	4	4	11.5	53.733	24.117	24.8108	23.4233	4	2	2	B8NNC7	B8NNC7	1	AFLA_127380	Trimethyllysine dioxygenase TmlH, putative
26.3663	25.9418	25.9086	25.7224	26.305	26.2646	2.41E-28	990900000	4	4	4	14.5	44.199	26.0848	26.0722	26.0973	6	3	3	B8NNG3	B8NNG3	1	AFLA_127740	Metacaspase CasA
ND	ND	ND	ND	24.6262	24.45	1.17E-08	177560000	4	4	4	7.6	71.548	24.5381	ND	24.5381	2	0	2	B8NNH8	B8NNH8	1	AFLA_127890	Protein phophatase 2C family protein
24.1644	ND	25.0632	25.5785	ND	24.6512	4.76E-13	305330000	4	4	4	15.5	60.648	24.8643	24.6138	25.1148	4	2	2	B8NNK3	B8NNK3	1	AFLA_129040	Metallopeptidase family M24, putative
25.0232	25.4294	25.5085	26.5714	25.6257	26.013	9.18E-17	608390000	4	4	4	17.9	31.527	25.6952	25.3204	26.07	6	3	3	B8NNN4	B8NNN4	1	AFLA_129350	Putative uncharacterized protein

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
ND	ND	ND	26.0785	ND	25.601	9.87E-39	255770000	4	4	4	8.1	89.01	25.8397	ND	25.8397	2	0	2	B8NNR8	B8NNR8	1	AFLA_129690	Cell division control protein (Cdc5), putative
ND	23.6546	24.0367	24.4026	23.8559	23.6361	8.79E-06	158180000	4	4	4	15.6	37.519	23.9172	23.8457	23.9649	5	2	3	B8NNS2	B8NNS2	1	AFLA_129730	mRNA decapping hydrolase, putative
23.8958	24.4893	23.1051	26.5757	25.2608	25.933	1.19E-52	525130000	4	4	4	11.9	51.306	24.8766	23.8301	25.9231	6	3	3	B8NP37	B8NP37	1	AFLA_128200	FK506-binding protein
ND	23.7209	23.6006	25.2691	25.4516	24.62	4.99E-13	226490000	4	4	4	9.4	60.765	24.5324	23.6607	25.1135	5	2	3	B8NPT7	B8NPT7	1	AFLA_001510	Glutamyl-tRNA(Gln) amidotransferase subunit A, putative
23.1143	23.0302	22.8771	24.5874	24.4753	24.0446	6.42E-14	176390000	4	4	4	5.8	78.653	23.6881	23.0072	24.3691	6	3	3	B8NPX8	B8NPX8	1	AFLA_002810	tRNA nucleotidyltransferase
25.6325	24.5355	25.4563	26.3862	26.0449	25.796	1.19E-26	418010000	4	4	4	30.4	17.901	25.6419	25.2081	26.0757	6	3	3	B8NQA4	B8NQA4	1	AFLA_004950	Cytochrome c oxidase subunit Va, putative
23.7726	ND	ND	23.7283	ND	23.6709	3.04E-10	172430000	4	4	4	9.3	50.661	23.7239	23.7726	23.6996	3	1	2	B8NQK5	B8NQK5	1	AFLA_006870	SGT1 and CS domain protein
25.1161	26.2974	26.7108	ND	ND	ND	3.31E-26	266270000	4	4	4	17.4	47.811	26.0414	26.0414	ND	3	3	0	B8NQZ7	B8NQZ7	1	AFLA_003810	Endonuclease/exonuclease/phosphatase family protein
26.169	26.8926	26.1562	27.1232	26.6306	26.4661	4.03E-24	1089200000	4	4	4	66.2	7.7117	26.573	26.4059	26.74	6	3	3	B8NR19	B8NR19	1	AFLA_004030	Putative uncharacterized protein
26.9496	27.8729	26.268	25.0582	26.9729	27.0851	1.37E-101	2065200000	4	4	4	48.6	11.543	26.7011	27.0301	26.372	6	3	3	B8NR25	B8NR25	1	AFLA_004090	Putative uncharacterized protein
23.6587	23.5543	24.2945	23.709	ND	ND	1.10E-07	165350000	4	4	4	27.4	21.518	23.8041	23.8358	23.709	4	3	1	B8NRQ7	B8NRQ7	1	AFLA_050480	ESCRT-II complex component (Vps25), putative
24.5355	24.9142	24.7899	26.1303	25.6009	25.3269	3.54E-12	404890000	4	4	4	13.6	36.963	25.2163	24.7465	25.686	6	3	3	B8NRQ8	B8NRQ8	1	AFLA_050490	tRNA (guanine-N(7)-)-methyltransferase
25.6924	25.868	25.5736	24.9107	25.544	ND	5.66E-17	483280000	4	4	4	26.5	24.352	25.5177	25.7113	25.2273	5	3	2	B8NS53	B8NS53	1	AFLA_052840	Ran-interacting protein Mog1, putative
28.3036	28.3419	28.4648	29.4613	28.8135	28.7835	1.53E-201	4686900000	4	4	4	60.2	10.01	28.6948	28.3701	29.0194	6	3	3	B8NSF0	B8NSF0	1	AFLA_048130	Mitochondrial intermembrane space translocase subunit Tim10, putative
23.8896	23.8969	ND	ND	24.2136	24.1966	5.62E-08	157760000	4	4	4	9.4	65.081	24.0492	23.8932	24.2051	4	2	2	B8NSJ9	B8NSJ9	1	AFLA_048620	Histone acetyltransferase, putative
26.4709	26.356	26.4472	26.4234	26.3468	25.9988	2.65E-14	1020900000	4	4	4	8.9	82.71	26.3405	26.4247	26.2563	6	3	3	B8NSQ4	B8NSQ4	1	AFLA_050050	AP-1 adaptor complex subunit gamma, putative
24.446	24.219	25.1448	25.2889	25.4153	24.791	1.14E-10	275640000	4	4	4	7.8	85.794	24.8842	24.6032	25.1651	6	3	3	B8NSQ9	B8NSQ9	1	AFLA_050100	LMBR1 domain protein
26.3739	26.0249	26.0089	27.3119	25.8569	26.9608	4.58E-53	948260000	4	4	4	40.5	13.392	26.4229	26.1359	26.7099	6	3	3	B8NST6	B8NST6	1	AFLA_050370	Prefoldin subunit 1, putative
24.8565	24.837	25.2144	25.3555	25.2733	ND	4.36E-19	334830000	4	4	4	8.2	58.248	25.1073	24.9693	25.3144	5	3	2	B8NT12	B8NT12	1	AFLA_052050	Calponin domain-containing protein, putative
25.2855	25.3658	25.3614	25.4403	25.1267	25.1187	2.88E-11	491460000	4	4	4	27.5	26.051	25.2831	25.3375	25.2286	6	3	3	B8NTG4	B8NTG4	1	AFLA_098040	Aldo-keto reductase (AKR), putative
25.2452	25.1199	25.7443	ND	24.9045	23.7948	5.29E-17	200220000	4	4	4	11.6	50.947	24.9618	25.3698	24.3497	5	3	2	B8NTL9	B8NTL9	1	AFLA_099490	Oligosaccharyl transferase subunit (Beta), putative
23.9426	24.6231	24.4815	25.0362	24.2132	25.267	4.41E-11	293260000	4	4	4	13.8	33.554	24.5939	24.3491	24.8388	6	3	3	B8NTS7	B8NTS7	1	AFLA_100080	Transcription elongation factor S-II
27.6792	26.8447	27.3568	27.193	27.1317	26.3889	8.35E-19	1462200000	4	4	4	20.5	35.409	27.0991	27.2936	26.9045	6	3	3	B8NU93	B8NU93	1	AFLA_098550	Nitrilase, putative
26.0415	25.6339	26.6244	24.7234	25.1363	24.8848	1.19E-19	514250000	4	4	4	39.2	17.83	25.5074	26.0999	24.9148	6	3	3	B8NUF7	B8NUF7	1	AFLA_099190	Putative uncharacterized protein
24.8557	25.4268	25.2504	ND	ND	ND	4.43E-09	129760000	4	4	4	11.1	51.434	25.1776	25.1776	ND	3	3	0	B8NUL7	B8NUL7	1	AFLA_100700	Phosphoserine phosphatase
26.498	27.4151	27.0006	27.3468	24.7895	25.8299	2.34E-56	903910000	4	4	4	30.7	13.011	26.48	26.9712	25.9887	6	3	3	B8NUZ4	B8NUZ4	1	AFLA_102880	Translation initiation factor SUI1, putative
24.3499	24.5857	24.0748	ND	ND	ND	1.68E-08	265490000	4	4	4	6.2	106.32	24.3368	24.3368	ND	3	3	0	B8NV56	B8NV56	1	AFLA_103500	Oxysterol binding protein (Osh3), putative
23.746	24.1488	ND	ND	ND	ND	2.17E-13	158430000	4	4	4	6.4	106.31	23.9474	23.9474	ND	2	2	0	B8NVZ7	B8NVZ7	1	AFLA_119250	DNA replication licensing factor Mcm6, putative
24.7428	25.6356	24.8955	25.4141	25.9635	25.7184	3.31E-37	414190000	4	4	4	24	36.013	25.395	25.0913	25.6987	6	3	3	B8NW03	B8NW03	1	AFLA_119310	Putative uncharacterized protein
ND	25.2439	25.5897	25.3809	25.1873	24.5758	7.14E-09	355000000	4	4	4	7.7	78.476	25.1955	25.4168	25.048	5	2	3	B8NW15	B8NW15	1	AFLA_119430	Sec1 family superfamily
24.974	24.9003	24.6751	25.7251	25.5084	25.2867	1.51E-97	869580000	4	4	4	20.4	32.476	25.1783	24.8498	25.5067	6	3	3	B8NW67	B8NW67	1	AFLA_118140	SNARE domain protein
24.9389	25.0198	25.2586	26.0375	25.3676	25.2367	1.80E-13	489500000	4	4	4	9.3	66.744	25.3098	25.0724	25.5473	6	3	3	B8NW69	B8NW69	1	AFLA_118160	AMP-binding enzyme, putative
ND	24.2983	24.5993	ND	23.6927	24.1859	6.38E-09	212160000	4	4	4	18.8	35.987	24.1941	24.4488	23.9393	4	2	2	B8NWB0	B8NWB0	1	AFLA_118570	Short-chain dehydrogenases/reductase, putative
24.2385	24.6617	26.4202	23.03	22.9392	23.3998	6.60E-17	231910000	4	4	4	9.8	64.728	24.1149	25.1068	23.123	6	3	3	B8NWT6	B8NWT6	1	AFLA_121230	L-amino acid oxidase LaoA
ND	ND	ND	25.4241	25.0097	25.2198	8.32E-38	471300000	4	4	4	39.7	21.287	25.2178	ND	25.2178	3	0	3	B8NX71	B8NX71	1	AFLA_122590	RNA binding protein Tma22, putative
25.1511	ND	24.9424	ND	ND	ND	3.16E-18	278230000	4	4	4	38.9	21.849	25.0468	25.0468	ND	2	2	0	B8NX75	B8NX75	1	AFLA_122630	Cytidine deaminase, putative
29.7622	29.8067	30.0603	29.7016	29.1025	29.4524	4.15E-24	9238800000	4	4	4	34.2	8.5718	29.6476	29.8764	29.4188	6	3	3	B8NY04	B8NY04	1	AFLA_009740	Putative uncharacterized protein
24.8943	25.5113	25.5052	24.4096	24.0242	24.6831	2.31E-33	240430000	4	4	4	10	60.179	24.838	25.3036	24.3723	6	3	3	B8NYN6	B8NYN6	1	AFLA_012060	Choline oxidase (CodA), putative
24.6688	ND	24.3466	24.3798	24.8507	24.4569	3.90E-07	310620000	4	4	4	11.9	54.189	24.5406	24.5077	24.5625	5	2	3	B8NYN7	B8NYN7	1	AFLA_012070	Betaine aldehyde dehydrogenase (BadH), putative
26.039	26.0439	26.3399	25.5079	25.5202	25.6167	4.56E-16	738030000	4	4	4	28.7	20.109	25.8446	26.141	25.5483	6	3	3	B8NYQ7	B8NYQ7	1	AFLA_012270	Peptidyl-prolyl cis-trans isomerase
ND	ND	ND	24.2902	24.5375	26.1045	5.56E-13	199330000	4	4	4	10.5	48.761	24.9774	ND	24.9774	3	0	3	H9CNZ7	H9CNZ7	1	AFLA_m0250	Ribosomal protein S5
24.838	24.4315	24.9449	24.4755	24.6803	25.3737	4.48E-22	447010000	5	4	4	31.8	27.628	24.7907	24.7381	24.8432	6	3	3	B8N3W1	B8N3W1	1	AFLA_031950	RAB GTPase Vps21/Ypt51, putative
ND	24.0936	24.4484	24.0101	24.6185	24.3404	1.44E-17	237720000	5	4	4	28.7	23.323	24.3022	24.271	24.323	5	2	3	B8N6N1	B8N6N1	1	AFLA_015440	RAS small monomeric GTPase Rab6, putative
26.6429	25.9136	26.6531	24.4014	25.3806	25.0228	1.88E-57	910060000	6	6	4	17.3	51.944	25.6691	26.4032	24.9349	6	3	3	B8MXA1	B8MXA1	1	AFLA_076880	Stearic acid desaturase (SdeA), putative
26.7613	26.8894	27.1717	26.2263	25.5858	26.5713	2.36E-93	775410000	5	5	5	37.7	19.685	26.5343	26.9408	26.1278	6	3	3	B8MWS6	B8MWS6	1	AFLA_088760	Septin
ND	ND	ND	25.1286	25.4973	ND	5.00E-18	224200000	5	5	5	12.1	60.752	25.3129	ND	25.3129	2	0	2	B8MWW4	B8MWW4	1	AFLA_075510	General amidase, putative
ND	25.2714	25.2836	25.386	25.672	26.5068	1.33E-22	413910000	5	5	5	17.9	36.068	25.624	25.2775	25.8549	5	2	3	B8MX91	B8MX91	1	AFLA_076780	Ribonucleoprotein, putative
24.5225	24.5034	24.226	25.5742	25.1842	24.7918	3.44E-15	436870000	5	5	5	4.7	178.78	24.8003	24.4173	25.1834	6	3	3	B8MXQ2	B8MXQ2	1	AFLA_078390	Transcription factor (Sin3), putative
26.3336	26.3267	ND	ND	26.4983	26.3013	2.12E-21	848580000	5	5	5	13.9	56.668	26.365	26.3301	26.3998	4	2	2	B8MXT1	B8MXT1	1	AFLA_078680	Putative uncharacterized protein
25.3748	25.9619	24.8813	29.2348	29.7716	30.8372	1.23E-47	8014500000	5	5	5	35.8	17.937	27.6769	25.406	29.9478	6	3	3	B8MY77	B8MY77	1	AFLA_080140	60S ribosomal protein L12
26.2477	26.4461	26.6458	26.0271	25.8801	26.3421	1.75E-70	812080000	5	5	5	13.1	66.988	26.2648	26.4466	26.0831	6	3	3	B8MYC5	B8MYC5	1	AFLA_080620	Endoplasmic reticulum and nuclear membrane proteinc Npl4, putative
29.6592	28.963	29.4656	28.9918	29.28	28.7077	1.44E-123	7037000000	5	5	5	59.6	11.926	29.1779	29.3626	28.9931	6	3	3	B8MZ23	B8MZ23	1	AFLA_083120	Thioredoxin
24.4519	24.7774	24.4817	26.2713	25.6092	25.4945	5.21E-13	370680000	5	5	5	10.9	64.216	25.181	24.5703	25.7917	6	3	3	B8MZ71	B8MZ71	1	AFLA_083600	RNA splicing factor (Pad-1), putative
24.5578	24.7281	24.7669	24.9436	24.2861	24.6616	3.03E-19	297380000	5	5	5	12	68.153	24.6573	24.6843	24.6304	6	3	3	B8MZD5	B8MZD5	1	AFLA_084240	Poly(A) polymerase Pap
26.8423	26.7827	26.0221	25.7341	26.7777	26.131	1.05E-26	668530000	5	5	5	18.9	32.749	26.3817	26.549	26.2143	6	3	3	B8MZE3;B8	B8MZE3	2	AFLA_084330	Mitochondrial phosphate carrier protein (Mir1), putative
25.2891	24.8598	25.3465	23.1746	23.3628	23.2114	2.21E-11	247460000	5	5	5	19.9	36.327	24.2073	25.1651	23.2496	6	3	3	B8MZF4	B8MZF4	1	AFLA_084440	Autophagy protein Atg27, putative
25.9168	25.2018	26.3455	24.2391	24.5226	24.2063	9.65E-25	459000000	5	5	5	33.8	29.098	25.072	25.8214	24.3227	6	3	3	B8MZS0	B8MZS0	1	AFLA_085600	Putative uncharacterized protein
23.6512	25.6966	23.8679	24.7611	26	28.0284	4.18E-76	983010000	5	5	5	49.5	12.429	25.3342	24.4052	26.2632	6	3	3	B8N023	B8N023	1	AFLA_086630	60S ribosomal protein L35Ae
25.9342	25.8641	26.2091	26.2146	26.0205	25.9113	1.75E-54	869170000	5	5	5	27.5	38.458	26.0256	26.0025	26.0488	6	3	3	B8N0B7	B8N0B7	1	AFLA_087580	DUF52 domain protein
24.4237	26.092	24.5674	25.8773	26.2103	26.8421	1.47E-39	1334000000	5	5	5	29.4	18.491	25.6688	25.0277	26.3099	6	3	3	B8N0D5	B8N0D5	1	AFLA_087760	40S ribosomal protein S11
ND	24.171	ND	24.9802	25.1684	25.4206	1.49E-34	246150000	5	5	5	8.4	91.64	24.9351	24.171	25.1898	4	1	3	B8N0X7	B8N0X7	1	AFLA_026620	Small nucleolar ribonucleoprotein complex component (Utp5), putative
24.9761	25.2037	25.0033	26.1574	24.9195	25.6429	3.10E-14	467330000	5	5	5	33	22.026	25.3172	25.061	25.5733	6	3	3	B8N119	B8N119	1	AFLA_027940	Caffeine-induced death protein Cid2, putative
26.5605	26.8912	26.4886	27.6818	26.9381	26.9973	4.11E-39	1409200000	5	5	5	50	10.285	26.9263	26.6468	27.2057	6	3	3	B8N184	B8N184	1	AFLA_029490	Mitochondrial intermembrane space translocase subunit Tim10, putative
ND	24.2054	ND	27.2122	26.6539	27.3985	3.36E-73	658380000	5	5	5	27.6	24.22	26.3675	24.2054	27.0882	4	1	3	B8N208	B8N208	1	AFLA_034020	Putative uncharacterized protein
26.6436	26.8353	26.5585	27.0308	26.8905	26.7537	2.09E-130	1065100000	5	5	5	45.9	23.369	26.7854	26.6791	26.8916	6	3	3	B8N2D7	B8N2D7	1	AFLA_036220	Putative uncharacterized protein
ND	26.3512	ND	27.3219	26.4043	26.0389	8.96E-120	1079100000	5	5	5	30.6	29.688	26.5291	26.3512	26.5884	4	1	3	B8N2H4	B8N2H4	1	AFLA_037490	Eukaryotic translation initiation factor 3 subunit J
28.0091	27.757	28.1422	28.3656	27.6425	27.835	7.37E-209	1781500000	5	5	5	55.5	14.434	27.9586	27.9695	27.9477	6	3	3	B8N2S7	B8N2S7	1	AFLA_023610	Putative uncharacterized protein
25.6815	25.4584	25.6869	25.0245	25.1143	24.8984	5.02E-16	436580000	5	5	5	12.7	90.77	25.3107	25.6089	25.0124	6	3	3	B8N2W5	B8N2W5	1	AFLA_024890	Cell differentiation and development protein Fsr1/Pro11

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
25.1864	26.6005	25.942	24.895	24.8212	25.3849	1.60E-12	371500000	5	5	5	10.4	61.045	25.4717	25.9096	25.0337	6	3	3	B8N350	B8N350	1	AFLA_025750	T-complex protein 1, theta subunit, putative
24.5036	25.4728	24.9027	ND	ND	ND	6.66E-10	202540000	5	5	5	17.3	49.641	24.9597	24.9597	ND	3	3	0	B8N362	B8N362	1	AFLA_026750	AAA family ATPase Pontin, putative
ND	ND	ND	25.8987	24.7135	25.2262	2.24E-15	257100000	5	5	5	13.1	67.022	25.2795	ND	25.2795	3	0	3	B8N3F9	B8N3F9	1	AFLA_028620	Signal recognition particle subunit SRP68
ND	25.8321	26.1104	26.1575	ND	25.522	1.59E-15	470190000	5	5	5	17.6	58.287	25.9055	25.9713	25.8397	4	2	2	B8N3L1	B8N3L1	1	AFLA_029140	Siderophore biosynthesis protein, putative
26.0273	26.1944	26.3948	27.0728	26.5555	26.5204	3.88E-77	1097400000	5	5	5	30.4	36.058	26.4608	26.2055	26.7162	6	3	3	B8N3M1	B8N3M1	1	AFLA_029240	NifU-related protein
26.9213	26.4711	27.0144	26.9487	26.4874	26.0938	2.88E-21	918310000	5	5	5	24.5	48.256	26.6561	26.8023	26.51	6	3	3	B8N3Q4	B8N3Q4	1	AFLA_031380	Class V chitinase, putative
24.6057	24.589	25.2385	25.1524	24.8386	24.4869	1.56E-16	242030000	5	5	5	7.1	108.52	24.8185	24.8111	24.826	6	3	3	B8N3S6	B8N3S6	1	AFLA_031600	SNARE-dependent exocytosis protein (Sro7), putative
25.8756	24.8715	25.4305	ND	ND	ND	4.94E-16	410590000	5	5	5	10.1	92.445	25.3925	25.3925	ND	3	3	0	B8N3U2	B8N3U2	1	AFLA_031760	Glutaminase, putative
29.292	29.912	29.8183	30.1155	29.5436	29.4545	3.25E-273	8673600000	5	5	5	47.8	12.756	29.6893	29.6741	29.7045	6	3	3	B8N439	B8N439	1	AFLA_033620	RNA binding protein, putative
ND	24.3724	ND	25.1261	24.9816	24.7013	2.30E-10	260810000	5	5	5	17.3	49.719	24.7954	24.3724	24.9364	4	1	3	B8N471;B8	B8N471	2	AFLA_034840	Putative uncharacterized protein
24.7938	25.3331	24.8516	25.9708	25.5284	25.28	4.39E-28	514620000	5	5	5	5.6	153.92	25.2929	24.9929	25.593	6	3	3	B8N4B0	B8N4B0	1	AFLA_035230	Nuclear pore complex subunit Nup159, putative
25.9915	26.0388	26.2812	26.3703	25.4457	25.8967	5.59E-25	819070000	5	5	5	14	69.532	26.004	26.1038	25.9042	6	3	3	B8N4E1	B8N4E1	1	AFLA_035540	Signal transducing adapter molecule, putative
23.6812	25.6994	24.5103	24.6089	24.1305	24.2271	1.96E-22	337990000	5	5	5	10.2	73.648	24.4762	24.6303	24.3222	6	3	3	B8N4L5	B8N4L5	1	AFLA_037200	Putative uncharacterized protein
ND	24.237	ND	26.3828	26.5115	27.1568	1.09E-14	496450000	5	5	5	27	34.242	26.072	24.237	26.6837	4	1	3	B8N514	B8N514	1	AFLA_020520	30S ribosomal protein S15
26.3359	26.0286	26.4492	25.891	26.0184	25.4423	1.55E-43	754030000	5	5	5	33.1	29.961	26.0275	26.2712	25.7839	6	3	3	B8N580	B8N580	1	AFLA_022080	Putative uncharacterized protein
23.0174	ND	23.3687	ND	22.8626	22.8593	2.11E-16	194270000	5	5	5	30.1	27.431	23.027	23.193	22.861	4	2	2	B8N595	B8N595	1	AFLA_022230	DSBA-like thioredoxin domain protein
26.628	25.4141	27.3624	ND	ND	ND	2.45E-29	374460000	5	5	5	31	23.258	26.4681	26.4681	ND	3	3	0	B8N5H5	B8N5H5	1	AFLA_013180	Williams-beuren syndrome chromosome region, putative
25.7116	25.0427	26.4415	24.781	25.8766	24.2543	8.87E-17	288090000	5	5	5	23.3	29.986	25.3513	25.7319	24.9706	6	3	3	B8N628	B8N628	1	AFLA_016120	O-methyltransferase family protein
27.4369	26.6834	25.6087	ND	24.4541	ND	1.84E-66	385120000	5	5	5	61.4	16.866	26.0458	26.5763	24.4541	4	3	1	B8N630	B8N630	1	AFLA_016140	Conidial pigment biosynthesis scytalone dehydratase Arp1
25.0448	25.6612	26.3517	25.6709	26.281	26.1571	1.56E-14	462130000	5	5	5	8.5	61.681	25.8611	25.6859	26.0364	6	3	3	B8N6G7	B8N6G7	1	AFLA_014800	T-complex protein 1 subunit alpha
24.7322	24.9388	24.637	24.1825	24.6557	24.0781	1.13E-13	346680000	5	5	5	17.3	44.079	24.5374	24.7693	24.3055	6	3	3	B8N736	B8N736	1	AFLA_019690	3-ketoacyl-CoA ketothiolase (Kat1), putative
24.6472	24.774	25.0231	24.8944	24.9977	ND	1.54E-09	214810000	5	5	5	6.8	119.12	24.8673	24.8148	24.946	5	3	2	B8N754	B8N754	1	AFLA_019870	Phosphatidylserine decarboxylase Psd2, putative
25.521	25.5402	25.6285	26.4141	26	26.0802	1.29E-94	646450000	5	5	5	9.6	79.17	25.864	25.5632	26.1648	6	3	3	B8N791	B8N791	1	AFLA_021130	Lupus la ribonucleoprotein, putative
27.8888	27.5511	28.1777	28.1186	27.6955	27.464	2.24E-136	1816100000	5	5	5	69.6	10.59	27.816	27.8725	27.7594	6	3	3	B8N7E6	B8N7E6	1	AFLA_021680	Putative uncharacterized protein
24.295	24.643	24.9455	ND	ND	ND	2.61E-12	264510000	5	5	5	9.6	70.731	24.6278	24.6278	ND	3	3	0	B8N802	B8N802	1	AFLA_105960	Autophagy protein Atg20, putative
24.6982	26.138	26.0523	27.2356	28.0557	29.0843	4.10E-59	4761700000	5	5	5	61.5	11.246	26.8774	25.6295	28.1252	6	3	3	B8N837	B8N837	1	AFLA_106310	Chaperonin, putative
26.2147	25.6665	26.1422	26.2239	26.1934	26.0449	8.28E-14	780540000	5	5	5	15.8	56.376	26.0809	26.0078	26.1541	6	3	3	B8N8E2	B8N8E2	1	AFLA_107360	Pre-mRNA splicing factor, putative
25.0328	24.8827	25.1888	24.9681	24.071	23.987	1.70E-11	291720000	5	5	5	15.8	43.37	24.6884	25.0348	24.342	6	3	3	B8N8Q0	B8N8Q0	1	AFLA_108450	Serine/threonine-protein phosphatase
24.4002	25.0476	23.8767	25.8055	26.5921	25.1057	1.22E-10	323090000	5	5	5	39.4	18.668	25.138	24.4415	25.8344	6	3	3	B8N8U3	B8N8U3	1	AFLA_108880	Mitochondrial import receptor subunit (Tom20), putative
25.6745	25.6815	25.4926	26.056	26.5813	25.9704	3.92E-13	841570000	5	5	5	23.2	28.801	25.9094	25.6162	26.2026	6	3	3	B8N8X3	B8N8X3	1	AFLA_109190	Possible replication factor-a protein
29.798	29.4461	29.6534	ND	25.4929	ND	3.03E-266	4424100000	5	5	5	17.5	54.729	28.5976	29.6325	25.4929	4	3	1	B8N9F8	B8N9F8	1	AFLA_111040	Phytase
24.1789	24.4578	24.2882	28.132	27.5781	27.482	1.56E-64	1323700000	5	5	5	35.5	19.836	26.0195	24.3083	27.7307	6	3	3	B8N9R2	B8N9R2	1	AFLA_112080	Small nuclear ribonucleoprotein SmB, putative
ND	24.6132	24.6972	ND	24.8615	ND	2.35E-10	263500000	5	5	5	6.8	105.89	24.724	24.6552	24.8615	3	2	1	B8N9T5	B8N9T5	1	AFLA_112310	Small nucleolar ribonucleoprotein complex subunit, putative
ND	24.5343	23.4033	27.6266	27.4386	30.9352	4.91E-22	4391000000	5	5	5	39	11.978	26.7876	23.9688	28.6668	5	2	3	B8N9U3	B8N9U3	1	AFLA_112390	60S ribosomal protein L36
28.1258	27.9028	28.1899	28.5212	28.4839	28.1166	2.58E-211	3827700000	5	5	5	44.7	22.466	28.2233	28.0728	28.3739	6	3	3	B8N9U5	B8N9U5	1	AFLA_112410	Proteasome subunit beta type
26.4518	26.5654	26.4758	26.7085	27.1267	26.7701	1.78E-28	1442600000	5	5	5	22.5	30.771	26.683	26.4977	26.8684	6	3	3	B8NA04	B8NA04	1	AFLA_113000	Integral ER membrane protein Scs2, putative
ND	ND	ND	25.5252	25.2387	24.8165	7.79E-15	194780000	5	5	5	7.7	81.936	25.1934	ND	25.1934	3	0	3	B8NA76	B8NA76	1	AFLA_113720	Ribosome biogenesis (Nop4), putative
22.8023	ND	22.631	ND	ND	ND	2.19E-35	270930000	5	5	5	15	52.932	22.7167	22.7167	ND	2	2	0	B8NAC3	B8NAC3	1	AFLA_039680	Putative uncharacterized protein
25.9258	26.251	26.0189	26.0266	25.8477	25.5827	3.05E-33	815660000	5	5	5	31.2	26.601	25.9421	26.0652	25.819	6	3	3	B8NAC4	B8NAC4	1	AFLA_039690	Phosphoglycerate mutase, putative
26.7187	26.4841	27.0973	26.3664	26.0743	25.757	8.15E-18	682870000	5	5	5	24.6	36.352	26.4163	26.7667	26.0659	6	3	3	B8NAC6	B8NAC6	1	AFLA_039710	Quinone oxidoreductase, putative
26.1186	25.9556	25.2867	24.9507	26.141	25.8628	5.17E-27	625750000	5	5	5	14	61.574	25.7192	25.787	25.6515	6	3	3	B8NAT7	B8NAT7	1	AFLA_043120	Phosphoglucomutase, putative
25.7228	26.1142	26.1202	26.4499	26.3911	26.0503	4.39E-20	1014100000	5	5	5	13.1	51.848	26.1414	25.9857	26.2971	6	3	3	B8NAZ8	B8NAZ8	1	AFLA_043730	Nuclear protein export protein Yrb2, putative
25.1187	25.2925	24.9864	26.1741	25.6589	25.2074	2.09E-25	343500000	5	5	5	31.1	26.9	25.4063	25.1325	25.6802	6	3	3	B8NB26	B8NB26	1	AFLA_044010	NADH-ubiquinone oxidoreductase 299 kDa subunit, putative
26.3203	26.9773	26.3512	25.116	26.6033	27.7042	7.71E-44	1250700000	5	5	5	39.9	15.923	26.512	26.5496	26.4745	6	3	3	B8NB36	B8NB36	1	AFLA_044110	40S ribosomal protein Rps16, putative
28.8816	28.9177	28.8594	29.2374	28.8769	29.4409	0	7225400000	5	5	5	58.2	17.502	29.0357	28.8862	29.1851	6	3	3	B8NB78	B8NB78	1	AFLA_044530	40S ribosomal protein S15, putative
24.1179	24.1092	24.4909	25.7868	23.8842	24.1661	3.24E-13	245660000	5	5	5	8.7	95.284	24.4258	24.2393	24.6124	6	3	3	B8NBA3	B8NBA3	1	AFLA_044780	Rbm25 protein, putative
ND	ND	ND	24.4254	24.867	24.7292	5.14E-10	408540000	5	5	5	11	74.691	24.6739	ND	24.6739	3	0	3	B8NBF0	B8NBF0	1	AFLA_045250	Biotin apo-protein ligase, putative
26.0145	25.8521	25.9646	26.2073	25.9008	25.7388	9.46E-26	747170000	5	5	5	29.8	26.915	25.9463	25.9437	25.949	6	3	3	B8NBN5	B8NBN5	1	AFLA_046100	Dihydrofolate reductase, putative
25.6414	25.2496	25.9798	25.4049	24.9634	24.8937	9.82E-18	442720000	5	5	5	38.8	24.123	25.3555	25.6236	25.0873	6	3	3	B8NBT1	B8NBT1	1	AFLA_046560	Acetyltransferase, CysE/LacA/LpxA/NodL family
26.0031	24.6934	26.5741	25.593	26.3043	25.4602	9.47E-16	390170000	5	5	5	17.8	44.463	25.7713	25.7569	25.7858	6	3	3	B8NC70	B8NC70	1	AFLA_038650	Aspartic-type endopeptidase, putative
24.9962	24.7882	27.0786	ND	24.8989	ND	1.72E-26	250070000	5	5	5	21.4	57.779	25.4405	25.621	24.8989	4	3	1	B8NCT4	B8NCT4	1	AFLA_041690	Cysteine synthase B, putative
26.4944	26.1395	25.7757	ND	ND	25.8039	4.27E-38	798000000	5	5	5	25.1	30.817	26.0534	26.1366	25.8039	4	3	1	B8ND19	B8ND19	1	AFLA_054900	ABC transporter, putative
25.03	25.8286	25.4515	25.7786	25.5088	25.3042	5.67E-81	807240000	5	5	5	38.5	23.231	25.4836	25.4367	25.5305	6	3	3	B8NDQ7	B8NDQ7	1	AFLA_055480	Calcineurin Ca2+-binding regulatory subunit CnaB
27.0895	26.9634	27.0261	27.0877	27.0713	26.6539	4.12E-49	1565800000	5	5	5	16.4	45.792	26.982	27.0264	26.9376	6	3	3	B8NE44	B8NE44	1	AFLA_057750	FAD binding domain protein
28.1623	28.6854	28.5419	28.2313	27.7156	27.8178	1.53E-91	3278800000	5	5	5	61.7	14.42	28.1924	28.4632	27.9215	6	3	3	B8NE67	B8NE67	1	AFLA_057980	Putative uncharacterized protein
25.2009	24.8048	25.919	ND	25.2668	ND	8.20E-09	585840000	5	5	5	24.2	30.447	25.2979	25.3082	25.2668	4	3	1	B8NEB8	B8NEB8	1	AFLA_060270	Enoyl-CoA hydratase/isomerase family protein
23.7124	24.5235	22.949	ND	ND	23.8435	1.13E-11	224340000	5	5	5	16.1	48.922	23.7571	23.7283	23.8435	4	3	1	B8NEJ3	B8NEJ3	1	AFLA_061910	Arginine biosynthesis bifunctional protein ArgJ, mitochondrial
26.4212	25.8923	26.2028	26.3138	26.8811	26.341	8.91E-22	1173200000	5	5	5	44.9	23.102	26.342	26.1721	26.512	6	3	3	B8NEL1	B8NEL1	1	AFLA_062090	MutT/nudix family protein
24.2945	25.0195	24.672	27.7502	27.4408	26.7852	2.77E-48	974930000	5	5	5	21.7	36.186	25.9937	24.662	27.3254	6	3	3	B8NEL6	B8NEL6	1	AFLA_062140	RNA binding protein, putative
26.7312	25.1897	26.54	24.3202	24.9068	24.2464	7.60E-34	722550000	5	5	5	36.5	21.537	25.3224	26.1536	24.4911	6	3	3	B8NEU7	B8NEU7	1	AFLA_058110	Cupin domain protein
24.6484	26.2164	25.9388	24.3031	24.8679	24.9309	8.49E-21	293390000	5	5	5	15.6	53.058	25.1509	25.6012	24.7006	6	3	3	B8NFA6	B8NFA6	1	AFLA_061500	Squalene monooxygenase Erg1
ND	25.4269	ND	25.9596	25.5332	25.6546	2.05E-14	490900000	5	5	5	16.9	59.92	25.6436	25.4269	25.7158	4	1	3	B8NFV7	B8NFV7	1	AFLA_133860	Putative uncharacterized protein
23.9454	24.1381	24.5747	24.2356	23.8817	23.8498	5.34E-11	270020000	5	5	5	6.6	104.9	24.1042	24.2194	23.989	6	3	3	B8NGC3	B8NGC3	1	AFLA_134630	Signal transduction protein BroA, putative
24.4559	24.2561	24.7613	ND	ND	ND	9.66E-15	79467000	5	5	5	5.6	94.76	24.4911	24.4911	ND	3	3	0	B8NGD3	B8NGD3	1	AFLA_134730	Transcriptional corepressor Cyc8, putative
23.3001	23.2266	23.3616	25.2218	23.8393	24.1	3.67E-20	186600000	5	5	5	13	52.197	23.8416	23.2961	24.387	6	3	3	B8NGK7	B8NGK7	1	AFLA_136340	Aminotransferase family protein (LolT), putative
25.6087	25.5159	25.6772	25.3184	25.7448	25.7116	8.48E-12	480800000	5	5	5	14.1	58.327	25.5961	25.6006	25.5916	6	3	3	B8NGN2	B8NGN2	1	AFLA_136590	Phenylalanyl-tRNA synthetase alpha subunit (PodG), putative
27.2094	26.4443	26.7532	26.195	26.1657	26.1797	8.75E-36	785320000	5	5	5	25.3	31.925	26.4912	26.8023	26.1801	6	3	3	B8NGT0	B8NGT0	1	AFLA_137980	NADH-cytochrome b5 reductase
25.0108	25.2083	25.076	24.8549	24.3143	24.8065	3.28E-13	377490000	5	5	5	15.7	52.026	24.8785	25.0984	24.6586	6	3	3	B8NH39	B8NH39	1	AFLA_132630	APSES transcription factor, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
24.5539	ND	ND	25.9362	25.6552	25.5319	9.23E-17	333510000	5	5	5	14.3	58.708	25.4193	24.5539	25.7078	4	1	3	B8NH56	B8NH56	1	AFLA_132800	tRNA(M5U54)methyltransferase
23.4882	24.0452	ND	24.5042	25.2211	24.8671	1.38E-12	194250000	5	5	5	8	87.029	24.4252	23.7667	24.8641	5	2	3	B8NH67	B8NH67	1	AFLA_132910	Pre-mRNA splicing factor RNA helicase (Prp43), putative
27.9605	27.9696	27.9674	28.4779	28.0548	28.0783	1.23E-89	3253900000	5	5	5	63.4	12.036	28.0847	27.9658	28.2037	6	3	3	B8NH98	B8NH98	1	AFLA_135030	Mitochondrial intermembrane space translocase subunit Tim13, putative
25.0431	25.657	25.7734	25.1499	25.1339	26.0904	3.04E-18	504740000	5	5	5	14.7	67.705	25.4746	25.4912	25.4581	6	3	3	B8NHH5	B8NHH5	1	AFLA_135800	Pre-rRNA processing protein Tsr1, putative
25.964	25.1094	25.7621	25.1717	25.3882	25.1349	1.26E-14	676550000	5	5	5	31.4	30.934	25.4217	25.6118	25.2316	6	3	3	B8NHW6	B8NHW6	1	AFLA_139020	Putative uncharacterized protein
23.8302	22.8528	22.9213	26.4737	26.8975	25.53	1.65E-12	480400000	5	5	5	28	28.345	24.7509	23.2014	26.3004	6	3	3	B8NI48	B8NI48	1	AFLA_064530	Glutathione S-transferase GliG-like, putative
26.5833	26.8735	26.9127	25.7615	26.1605	26.189	6.23E-90	629690000	5	5	5	17.2	51.498	26.4134	26.7899	26.037	6	3	3	B8NIK7	B8NIK7	1	AFLA_067940	Putative uncharacterized protein
23.9554	23.784	23.8923	24.3972	23.9214	24.0449	3.48E-11	281740000	5	5	5	7	94.493	23.9992	23.8772	24.1211	6	3	3	B8NIR2	B8NIR2	1	AFLA_069400	Formin binding protein (FNB3), putative
ND	24.4057	ND	26.5764	26.5241	26.0417	1.38E-39	549450000	5	5	5	30.5	34.445	25.887	24.4057	26.3808	4	1	3	B8NIV1	B8NIV1	1	AFLA_069790	Casein kinase 2 beta regulatory subunit Ckb2, putative
24.1286	ND	24.0884	24.9915	24.9016	25.0491	7.40E-11	213490000	5	5	5	20	33.095	24.6318	24.1085	24.9808	5	2	3	B8NJ26	B8NJ26	1	AFLA_071430	U5 snRNP complex subunit, putative
26.0544	26.8453	26.5512	26.1028	25.7486	26.9886	6.55E-93	1873100000	5	5	5	79.3	10.245	26.3818	26.4836	26.28	6	3	3	B8NJR3	B8NJR3	1	AFLA_068730	Ubiquitin-like modifier SUMO, putative
25.6642	26.3821	26.0033	26.0595	25.5277	26.1683	2.06E-35	702780000	5	5	5	34.9	18.559	25.9675	26.0165	25.9185	6	3	3	B8NJT0	B8NJT0	1	AFLA_068900	Prefoldin subunit 5, putative
ND	25.9515	ND	26.1226	ND	25.2363	2.92E-07	424440000	5	5	5	7	96.007	25.7701	25.9515	25.6795	3	1	2	B8NJT5	B8NJT5	1	AFLA_068950	M protein repeat protein
27.891	27.916	28.1707	24.1296	24.3819	ND	4.15E-67	1190300000	5	5	5	22.3	39.792	26.4979	27.9926	24.2558	5	3	2	B8NJU9	B8NJU9	1	AFLA_069090	GPI anchored protein, putative
24.3422	25.0622	24.6616	24.7649	24.2167	24.5748	3.75E-10	172130000	5	5	5	4.9	141.86	24.6038	24.6887	24.5188	6	3	3	B8NK59	B8NK59	1	AFLA_071080	DNA-directed RNA polymerase
27.3445	27.779	26.9085	26.0172	27.1361	27.8097	1.67E-115	1918300000	5	5	5	62.4	16.988	27.1658	27.344	26.9877	6	3	3	B8NKF7	B8NKF7	1	AFLA_091230	Ubiquitin conjugating enzyme (UbcM), putative
25.6986	25.2382	25.6877	25.6804	25.8334	25.463	1.08E-15	654780000	5	5	5	25.1	23.162	25.6002	25.5415	25.6589	6	3	3	B8NKJ6	B8NKJ6	1	AFLA_091620	Putative uncharacterized protein
25.0109	25.5307	ND	26.0305	25.4399	24.8717	1.74E-14	290920000	5	5	5	9.5	80.72	25.3767	25.2708	25.4474	5	2	3	B8NKL5	B8NKL5	1	AFLA_091810	Putative uncharacterized protein
25.3017	24.5406	25.2933	25.5146	25.2351	24.9505	9.43E-32	488620000	5	5	5	30.5	20.676	25.1393	25.0452	25.2334	6	3	3	B8NKT0	B8NKT0	1	AFLA_093340	Putative uncharacterized protein
24.9108	24.9252	25.6457	24.6937	24.431	24.9655	2.91E-19	348820000	5	5	5	13.8	73.101	24.9287	25.1606	24.6968	6	3	3	B8NLB1	B8NLB1	1	AFLA_090380	Chromatin remodeling complex subunit (Arp9), putative
26.5442	25.446	26.2959	ND	25.5587	ND	3.16E-09	331320000	5	5	5	14.3	59.895	25.9612	26.0954	25.5587	4	3	1	B8NLH3	B8NLH3	1	AFLA_091000	Cytochrome P450 monooxygenase, putative
28.1851	27.9318	28.1108	26.4536	27.831	27.6451	0	2328700000	5	5	5	42.6	19.583	27.6929	28.0759	27.3099	6	3	3	B8NLJ1	B8NLJ1	1	AFLA_091180	ARP2/3 complex 20 kDa subunit (P20-ARC), putative
28.7505	29.8247	29.4526	29.9753	29.0167	29.9453	4.67E-159	8098600000	5	5	5	56.8	10.007	29.4942	29.3426	29.6458	6	3	3	B8NLJ6	B8NLJ6	1	AFLA_092120	40S ribosomal protein S21
ND	25.0699	25.551	25.7323	25.3253	25.1337	1.85E-12	707660000	5	5	5	43.9	14.677	25.3624	25.3105	25.3971	5	2	3	B8NLM1	B8NLM1	1	AFLA_092370	Alkaline serine protease
25.487	25.8304	25.0242	ND	25.2906	25.7535	1.05E-11	533680000	5	5	5	44.4	21.258	25.4771	25.4472	25.522	5	3	2	B8NLN5	B8NLN5	1	AFLA_092510	Putative uncharacterized protein
25.1856	25.2336	25.4358	25.3899	25.272	24.502	9.82E-20	302180000	5	5	5	6.4	105.72	25.1698	25.285	25.0546	6	3	3	B8NLS8	B8NLS8	1	AFLA_092940	DNA repair and transcription protein (Xab2), putative
26.9912	26.8588	ND	26.0796	27.0026	26.4781	2.46E-07	788270000	5	5	5	3.6	195.22	26.682	26.925	26.5201	5	2	3	B8NLX8	B8NLX8	1	AFLA_094340	Kinesin family protein
26.4021	26.4938	26.4741	27.4062	27.0065	26.9095	1.11E-57	1287300000	5	5	5	20.7	49.642	26.782	26.4567	27.1074	6	3	3	B8NM13	B8NM13	1	AFLA_094690	Cell cycle control protein (Cwf8), putative
ND	ND	ND	23.9788	25.069	23.579	2.82E-08	191600000	5	5	5	22.6	27.235	24.209	ND	24.209	3	0	3	B8NM17	B8NM17	1	AFLA_094730	Exosome complex subunit Csl4, putative
26.747	26.7415	26.9285	28.0175	27.0476	27.4246	7.58E-55	1208900000	5	5	5	23.5	33.303	27.1511	26.8057	27.4966	6	3	3	B8NMQ6	B8NMQ6	1	AFLA_126690	Putative uncharacterized protein
27.2664	26.5575	26.5364	ND	24.1803	24.2028	2.15E-58	539240000	5	5	5	32.5	21.151	25.7487	26.7868	24.1916	5	3	2	B8NMV8	B8NMV8	1	AFLA_127210	Pathogenesis associated protein Cap20, putative
26.7987	25.4721	26.7275	ND	ND	ND	5.20E-32	436160000	5	5	5	31.5	34.269	26.3328	26.3328	ND	3	3	0	B8NN48;RE	B8NN48	2	AFLA_124820	Putative uncharacterized protein
27.1761	27.3162	27.107	26.4749	26.1102	26.9037	5.63E-19	1295200000	5	5	5	14.7	42.33	26.848	27.1998	26.4963	6	3	3	B8NNB5	B8NNB5	1	AFLA_127260	Cop9 signalosome complex subunit, putative
27.4425	27.3201	27.5944	27.4536	27.3487	27.3267	4.96E-60	1882600000	5	5	5	35.2	25.024	27.4143	27.4523	27.3763	6	3	3	B8NNC1	B8NNC1	1	AFLA_127320	Riboflavin synthase, alpha subunit
ND	23.64	ND	24.6999	24.9573	26.8888	3.27E-28	385580000	5	5	5	17.8	52.303	25.0465	23.64	25.5153	4	1	3	B8NNE9	B8NNE9	1	AFLA_127600	40S ribosomal protein S2, putative
25.8909	26.1582	26.1787	24.5745	25.3492	25.3838	7.82E-30	558090000	5	5	5	14.7	55.437	25.5892	26.0759	25.1025	6	3	3	B8NNG1	B8NNG1	1	AFLA_127720	CBS domain protein
28.2846	29.8689	28.099	31.4298	31.1463	31.5532	3.90E-184	15004000000	5	5	5	27.8	24.904	30.0636	28.7508	31.3764	6	3	3	B8NNH5	B8NNH5	1	AFLA_127860	60S acidic ribosomal protein P1
24.859	24.3518	24.9409	25.652	24.7618	25.0863	6.25E-20	315660000	5	5	5	9.3	88.502	24.942	24.7173	25.1667	6	3	3	B8NNT1	B8NNT1	1	AFLA_129820	Differentiation regulator (Nrd1), putative
27.0963	27.2701	27.4466	27.3391	27.031	27.0396	4.75E-87	1695700000	5	5	5	36.1	25.396	27.2038	27.271	27.1365	6	3	3	B8NNT5	B8NNT5	1	AFLA_129860	Putative uncharacterized protein
25.3846	26.1028	25.957	24.6349	25.1648	25.3367	4.82E-17	398290000	5	5	5	21.8	35.37	25.4301	25.8148	25.0455	6	3	3	B8NP80	B8NP80	1	AFLA_128630	Ubiquinone biosynthesis methlytransferase Coq5, putative
25.3897	25.2474	25.1497	26.4078	25.7468	26.6976	6.46E-14	726770000	5	5	5	23	24.979	25.7732	25.2623	26.2841	6	3	3	B8NP93	B8NP93	1	AFLA_128760	Putative uncharacterized protein
26.1353	26.3156	26.477	26.5353	25.5209	25.5659	3.29E-34	861870000	5	5	5	41.9	21.753	26.0917	26.3093	25.874	6	3	3	B8NPC7	B8NPC7	1	AFLA_129990	Riboflavin kinase, putative
26.0741	26.5716	25.8165	ND	26.685	26.7421	9.95E-33	900790000	5	5	5	26.3	26.124	26.3779	26.154	26.7136	5	3	2	B8NPG7	B8NPG7	1	AFLA_130390	Glutamine amidotransferase:cyclase
24.8012	25.8279	25.6708	25.7028	24.8556	25.4655	2.51E-28	334870000	5	5	5	14.5	45.487	25.3873	25.4333	25.3413	6	3	3	B8NPN7	B8NPN7	1	AFLA_001010	Benzoate 4-monooxygenase cytochrome P450, putative
ND	ND	ND	26.332	ND	26.2352	1.47E-72	999740000	5	5	5	34.4	14.925	26.2836	ND	26.2836	2	0	2	B8NQW4	B8NQW4	1	AFLA_003480	60S ribosomal protein L32
25.0661	25.8104	25.2924	27.4119	26.5955	26.5292	1.35E-16	624670000	5	5	5	11.4	80.83	26.1176	25.3897	26.8455	6	3	3	B8NRF2	B8NRF2	1	AFLA_007190	NADH-ubiquinone oxidoreductase, subunit G, putative
30.6399	30.4815	30.99	24.6733	27.6946	24.5637	5.34E-125	10468000000	5	5	5	15.1	49.097	28.1738	30.7038	25.6439	6	3	3	B8NRS0	B8NRS0	1	AFLA_050610	Acid phosphatase PHOa
24.5963	26.4401	26.9328	26.7743	26.7421	26.3889	1.80E-15	1160500000	5	5	5	23.8	25.085	26.3124	25.9898	26.6351	6	3	3	B8NSV9	B8NSV9	1	AFLA_051520	Putative uncharacterized protein
24.344	25.6892	24.8043	26.936	26.6547	25.8786	5.80E-25	435860000	5	5	5	16.1	51.057	25.7178	24.9458	26.4898	6	3	3	B8NTD8	B8NTD8	1	AFLA_097780	Isoamyl alcohol oxidase, putative
24.1828	25.4318	ND	25.6771	25.8543	25.7595	3.52E-20	554800000	5	5	5	25.8	33.125	25.3811	24.8073	25.7636	5	2	3	B8NTG5	B8NTG5	1	AFLA_098050	Gamma-cysteine synthetase regulatory subunit, putative
24.1029	24.229	24.0444	23.5561	22.9993	23.057	1.27E-13	211690000	5	5	5	13.3	66.502	23.6648	24.1254	23.2041	6	3	3	B8NTU3	B8NTU3	1	AFLA_100240	Glucose dehydrogenase, putative
ND	24.4205	ND	25.0696	25.0704	24.6379	1.90E-16	258650000	5	5	5	12.6	58.533	24.7996	24.4205	24.926	4	1	3	B8NTV0	B8NTV0	1	AFLA_101210	Septin
26.895	24.7742	26.3183	ND	ND	23.2633	4.25E-56	319060000	5	5	5	11.6	80.695	25.3127	25.9959	23.2633	4	3	1	B8NU54	B8NU54	1	AFLA_097260	Dynamin family GTPase, putative
26.4378	25.828	26.5436	24.1394	25.6115	24.9921	6.08E-24	666920000	5	5	5	24.3	39.966	25.5921	26.2698	24.9143	6	3	3	B8NU58	B8NU58	1	AFLA_097300	Putative uncharacterized protein
ND	ND	ND	25.5396	ND	25.7866	1.06E-14	282030000	5	5	5	17.6	41.092	25.6631	ND	25.6631	2	0	2	B8NU88	B8NU88	1	AFLA_098500	Putative uncharacterized protein
29.1609	28.3438	29.1752	25.9654	26.8606	26.0383	8.12E-79	4279100000	5	5	5	28	31.386	27.5907	28.8933	26.2881	6	3	3	B8NUA8	B8NUA8	1	AFLA_098700	Carbonyl reductase, putative
25.563	26.0505	25.5707	26.0849	26.3297	26.2107	8.28E-27	726510000	5	5	5	29.3	32.471	25.9682	25.7281	26.2084	6	3	3	B8NUB0	B8NUB0	1	AFLA_098720	Putative uncharacterized protein
26.3656	27.163	27.1678	27.9963	26.2109	27.3116	2.02E-95	2223000000	5	5	5	44.1	15.474	27.0358	26.8988	27.1729	6	3	3	B8NV07	B8NV07	1	AFLA_103010	DsDNA-binding protein PDCD5, putative
25.3036	25.0615	25.4882	24.7837	25.2539	24.8295	2.38E-13	373530000	5	5	5	15.3	66.553	25.12	25.2844	24.9557	6	3	3	B8NV95	B8NV95	1	AFLA_103900	Cystathionine gamma-synthase, putative
27.1254	28.1072	27.3029	27.0417	27.684	27.5408	1.24E-134	4139200000	5	5	5	31.9	14.972	27.467	27.5118	27.4222	6	3	3	B8NVA9	B8NVA9	1	AFLA_104040	Histone H2B
24.8116	25.2249	25.4006	25.4538	25.2199	25.6354	5.15E-10	473760000	5	5	5	29.1	23.51	25.291	25.1457	25.4363	6	3	3	B8NVN9	B8NVN9	1	AFLA_117260	N-acetyltransferase, GNAT family, putative
26.8723	26.2296	27.0476	26.698	26.9466	26.1969	3.78E-64	945630000	5	5	5	39.1	20.206	26.6652	26.7165	26.6138	6	3	3	B8NVQ0	B8NVQ0	1	AFLA_117370	Putative uncharacterized protein
25.2581	25.3168	26.0968	ND	25.256	ND	5.23E-10	438550000	5	5	5	17.8	45.494	25.4819	25.5572	25.256	4	3	1	B8NVY4	B8NVY4	1	AFLA_119120	Beta-lactamase family protein
ND	ND	ND	24.2854	24.4757	24.3477	2.24E-10	170990000	5	5	5	5.8	102.45	24.3696	ND	24.3696	3	0	3	B8NXL0	B8NXL0	1	AFLA_008290	Kinesin family protein (KinA), putative
26.1171	26.004	25.6566	26.1858	26.32	26.2512	9.37E-30	807040000	5	5	5	29.1	34.334	26.0891	25.9259	26.2523	6	3	3	B8NY47	B8NY47	1	AFLA_010170	Tropinone reductase, putative
24.7422	ND	24.3633	ND	ND	ND	2.41E-16	164650000	5	5	5	12.6	54.048	24.5528	24.5528	ND	2	2	0	B8NY90	B8NY90	1	AFLA_010600	Siderophore biosynthesis acetylase AceI, putative
26.7414	26.9115	25.9667	26.1696	25.5121	26.1415	2.61E-49	728710000	5	5	5	31.8	26.331	26.2404	26.5398	25.941	6	3	3	B8NYG8	B8NYG8	1	AFLA_011380	Putative uncharacterized protein
25.7962	26.0402	26.5884	23.381	22.909	23.4103	2.12E-14	329760000	5	5	5	13.2	64.473	24.6875	26.1416	23.2334	6	3	3	B8NYH6	B8NYH6	1	AFLA_011460	GMC oxidoreductase, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
25.0606	25.0464	25.0949	25.8008	25.6031	25.3376	4.44E-12	429130000	5	5	5	18.2	50.034	25.3239	25.0673	25.5805	6	3	3	B8NYX7	B8NYX7	1	AFLA_114890	Queuine tRNA-ribosyltransferase
ND	ND	ND	25.4157	24.5721	ND	2.33E-07	211650000	5	5	5	5.1	158.06	24.9939	ND	24.9939	2	0	2	B8NYY7	B8NYY7	1	AFLA_114990	DEAD helicases superfamily protein (Aquarius), putative
25.7927	25.3337	25.7884	25.6062	25.7519	ND	2.60E-26	588540000	6	5	5	15.3	34.294	25.6546	25.6383	25.679	5	3	2	B8NH86	B8NH86	1	AFLA_133100	Aldehyde reductase, putative
27.3529	27.1326	27.3336	26.8706	26.4157	27.0607	3.21E-69	1912600000	6	6	5	30.8	29.823	27.0277	27.273	26.7823	6	3	3	B8NRN2	B8NRN2	1	AFLA_049370	Short-chain dehydrogenase/reductase family protein, putative
27.4608	27.0168	27.579	25.171	25.137	25.5272	2.10E-38	785190000	8	8	5	22.8	53.831	26.3153	27.3522	25.2784	6	3	3	B8N0C2	B8N0C2	1	AFLA_087630	Alpha,alpha-trehalose-phosphate synthase subunit, putative
24.8413	24.7971	25.1464	25.6102	25.499	25.1884	5.40E-24	284540000	6	6	6	16.1	51.22	25.1804	24.9283	25.4325	6	3	3	B8MVZ4	B8MVZ4	1	AFLA_073410	L-galactose dehydrogenase (L-GalDH), putative
24.5505	24.6332	24.8597	24.8564	24.9498	24.745	2.18E-19	340360000	6	6	6	20.6	58.784	24.7658	24.6811	24.8504	6	3	3	B8MW12	B8MW12	1	AFLA_073590	UBX domain protein (Ubx5), putative
25.9498	26.6464	26.5516	27.4155	26.1976	26.144	5.77E-19	870030000	6	6	6	23.7	38.82	26.4841	26.3826	26.5857	6	3	3	B8MW33	B8MW33	1	AFLA_073800	Short chain dehydrogenase/reductase family
24.9843	24.4893	25.1879	24.727	25.3856	24.6511	1.10E-13	306040000	6	6	6	18.5	51.882	24.9042	24.8872	24.9213	6	3	3	B8MWA2	B8MWA2	1	AFLA_087920	F-box domain protein
ND	23.651	ND	26.119	26.28	26.4053	1.84E-16	433240000	6	6	6	54.7	18.499	25.6138	23.651	26.2681	4	1	3	B8MWA9	B8MWA9	1	AFLA_087990	40S ribosomal protein S8
25.0862	26.3599	26.0631	24.95	24.4859	24.5296	3.09E-13	346470000	6	6	6	24.9	44.186	25.2458	25.8364	24.6552	6	3	3	B8MWG2	B8MWG2	1	AFLA_088520	CUE domain protein, putative
26.1516	25.8136	25.7623	27.04	27.213	26.4669	4.51E-34	1434400000	6	6	6	18.5	62.782	26.4079	25.9092	26.9066	6	3	3	B8MWP0	B8MWP0	1	AFLA_074980	Splicing factor u2af large subunit
23.9849	25.0531	23.6882	24.911	24.6286	25.4446	8.36E-50	1045300000	6	6	6	39.7	16.816	24.6184	24.242	24.9948	6	3	3	B8MWP5	B8MWP5	1	AFLA_075030	40S ribosomal protein S13
27.1438	26.9562	26.9045	27.4972	26.7192	26.9299	5.34E-48	1675300000	6	6	6	44.5	20.11	27.0251	27.0015	27.0488	6	3	3	B8MXB0	B8MXB0	1	AFLA_076970	Putative uncharacterized protein
24.438	ND	24.5463	ND	24.4222	ND	2.43E-13	117570000	6	6	6	5.3	150.72	24.4688	24.4922	24.4222	3	2	1	B8MXB1	B8MXB1	1	AFLA_076980	Non-repetitive nucleoporin, putative
24.8551	23.1888	23.7902	ND	22.6696	ND	4.64E-25	251700000	6	6	6	17.8	59.924	23.6259	23.9447	22.6696	4	3	1	B8MXJ8	B8MXJ8	1	AFLA_077850	Phenylalanine ammonia-lyase
27.5485	27.3141	27.5094	27.548	27.3789	26.9691	1.70E-32	1708700000	6	6	6	13.5	73.106	27.378	27.4573	27.2987	6	3	3	B8MXT5	B8MXT5	1	AFLA_078720	Peroxisomal targeting receptor pex5, putative
26.8009	26.7964	26.8667	26.6495	26.4635	26.4991	1.35E-38	1431100000	6	6	6	53.1	26.272	26.6794	26.8213	26.5374	6	3	3	B8MY08	B8MY08	1	AFLA_079450	Ureidoglycolate hydrolase, putative
25.6427	26.4659	26.6216	25.3674	25.546	25.3802	9.55E-22	632990000	6	6	6	8.7	93.504	25.8373	26.2434	25.4312	6	3	3	B8MY31	B8MY31	1	AFLA_079680	Vesicular fusion ATPase, putative
25.2702	26.7664	25.5753	30.6179	28.2592	30.0702	2.21E-42	8558100000	6	6	6	46	14.147	27.7599	25.8706	29.6491	6	3	3	B8MY51	B8MY51	1	AFLA_079880	60S ribosomal protein L22, putative
25.7837	25.7987	25.9745	26.0382	25.2422	25.541	5.41E-18	547480000	6	6	6	25.8	33.516	25.7297	25.8523	25.6071	6	3	3	B8MY53	B8MY53	1	AFLA_079900	Recombination hotspot-binding protein (Translin), putative
25.722	25.4868	25.8801	25.8324	25.6572	25.5642	9.07E-57	618970000	6	6	6	18.7	40.183	25.6905	25.6963	25.6846	6	3	3	B8MYG4	B8MYG4	1	AFLA_081020	Ubiquitin fusion degradation protein Ufd1, putative
26.4548	26.5474	26.7455	27.2841	26.6636	26.4427	9.41E-32	1606500000	6	6	6	25	44.689	26.6897	26.5826	26.7968	6	3	3	B8MZ47	B8MZ47	1	AFLA_083360	Extracellular cell wall glucanase Crf1/allergen Asp F9
26.1439	26.2328	26.475	26.7542	26.6648	26.1162	0	2151000000	6	6	6	24.3	46.201	26.3978	26.2839	26.5117	6	3	3	B8MZ70	B8MZ70	1	AFLA_083590	Fatty acid hydroxylase, putative
26.0558	26.2309	26.7575	ND	ND	ND	1.79E-89	650170000	6	6	6	23.4	38.608	26.348	26.348	ND	3	3	0	B8MZ75	B8MZ75	1	AFLA_083640	3-isopropylmalate dehydrogenase
26.2695	25.0851	25.6125	27.4554	27.4601	28.0962	3.57E-58	1577200000	6	6	6	56.9	14.737	26.6632	25.6557	27.6706	6	3	3	B8MZ85	B8MZ85	1	AFLA_083740	40S ribosomal protein S22
25.7573	25.4846	25.7949	25.7301	25.6131	25.5329	1.00E-16	627310000	6	6	6	16.7	55.816	25.6522	25.6789	25.6254	6	3	3	B8MZI5	B8MZI5	1	AFLA_084750	Probable Xaa-Pro aminopeptidase AFLA_084750
27.0884	27.7768	27.5202	28.1509	27.8505	27.988	3.55E-115	1975900000	6	6	6	33.1	28.051	27.7291	27.4618	27.9965	6	3	3	B8MZQ5	B8MZQ5	1	AFLA_085450	Eukaryotic translation initiation factor 3 subunit K
27.132	26.8571	26.9685	ND	ND	ND	1.35E-58	857140000	6	6	6	21.6	50.64	26.9859	26.9859	ND	3	3	0	B8MZU5	B8MZU5	1	AFLA_085850	Putative uncharacterized protein
25.8128	26.2191	25.634	25.9689	26.6092	26.2764	2.58E-48	950880000	6	6	6	22.2	33.592	26.0867	25.8886	26.2848	6	3	3	B8N034	B8N034	1	AFLA_086740	4-nitrophenylphosphatase
28.6583	28.619	28.538	29.1906	28.915	28.6711	5.71E-154	5082300000	6	6	6	59.7	14.523	28.7653	28.6051	28.9256	6	3	3	B8N0A7	B8N0A7	1	AFLA_087480	Peptidyl-prolyl cis-trans isomerase
25.8335	26.187	26.113	ND	23.9269	ND	2.39E-16	370900000	6	6	6	11.4	72.168	25.5151	26.0445	23.9269	4	3	1	B8N116	B8N116	1	AFLA_027910	Serine/threonine protein kinase, putative
26.341	26.5617	26.629	26.0529	25.9281	26.3185	2.46E-50	776940000	6	6	6	27.4	46.545	26.3052	26.5106	26.0998	6	3	3	B8N131	B8N131	1	AFLA_028060	Anthranilate phosphoribosyltransferase, putative
25.0758	24.5867	24.813	25.5697	25.088	24.7178	2.10E-16	448710000	6	6	6	13	50.892	24.9752	24.8252	25.1252	6	3	3	B8N1C6	B8N1C6	1	AFLA_029910	Disulfide isomerase, putative
27.4754	28.1074	27.4345	27.0514	27.0355	26.8904	5.09E-58	1700500000	6	6	6	26.9	45.393	27.3324	27.6724	26.9924	6	3	3	B8N1F3	B8N1F3	1	AFLA_030180	Protein mitochondrial targeting protein (Mas1), putative
25.5211	25.4722	25.684	25.9352	25.9008	25.6606	5.22E-19	579890000	6	6	6	28.4	28.156	25.6957	25.5591	25.8322	6	3	3	B8N1J6	B8N1J6	1	AFLA_030610	Transcription regulator PAB1642, putative
30.2185	29.8408	29.7312	30.6086	30.2332	29.9596	9.56E-178	13152000000	6	6	6	54.8	11.945	30.0986	29.9301	30.2671	6	3	3	B8N1N5	B8N1N5	1	AFLA_031000	Nucleosome binding protein (Nhp6a), putative
23.615	25.2967	24.8913	24.5602	ND	23.6458	2.70E-18	200430000	6	6	6	11.8	103.95	24.4018	24.601	24.103	5	3	2	B8N1Q5	B8N1Q5	1	AFLA_032090	Putative uncharacterized protein
27.4966	27.0991	27.6193	27.2317	27.1167	26.7903	9.33E-84	1925700000	6	6	6	27.7	50.762	27.2256	27.405	27.0462	6	3	3	B8N1Y5	B8N1Y5	1	AFLA_032890	Putative uncharacterized protein
29.5138	29.2736	29.7627	28.8089	28.9078	28.5003	3.27E-149	6964500000	6	6	6	38.9	26.953	29.1279	29.5167	28.739	6	3	3	B8N230	B8N230	1	AFLA_034240	Dienelactone hydrolase family protein
25.4664	25.4299	25.73	25.4913	25.9126	25.4585	2.37E-12	482220000	6	6	6	21.9	37.621	25.5815	25.5421	25.6208	6	3	3	B8N237	B8N237	1	AFLA_034310	Putative uncharacterized protein
27.7516	26.9228	27.8888	26.8588	27.1267	26.5942	3.85E-43	1440800000	6	6	6	19.1	48.326	27.1905	27.5211	26.8599	6	3	3	B8N247	B8N247	1	AFLA_034410	Aspartate aminotransferase, putative
24.8815	ND	24.882	ND	ND	ND	3.07E-24	461500000	6	6	6	37.8	25.614	24.8818	24.8818	ND	2	2	0	B8N2C2	B8N2C2	1	AFLA_036070	Maleylacetoacetate isomerase MaiA
25.1178	24.8263	25.6372	ND	24.5447	23.6862	4.32E-23	241280000	6	6	6	8.3	109.14	24.7625	25.1938	24.1155	5	3	2	B8N2H6	B8N2H6	1	AFLA_037510	Endoplasmic reticulum calcium ATPase, putative
27.8916	27.8685	27.9272	28.269	28.1911	27.9183	1.68E-71	3181800000	6	6	6	35.4	28.945	28.0109	27.8957	28.1261	6	3	3	B8N2K9	B8N2K9	1	AFLA_037840	Proteasome subunit beta type
ND	24.585	24.6272	24.3332	ND	24.858	9.68E-31	458330000	6	6	6	3.7	213.75	24.6009	24.6061	24.5956	4	2	2	B8N391	B8N391	1	AFLA_027040	Nucleoporin SONB, putative
26.9429	26.8823	27.0511	27.3071	27.0557	26.7652	3.83E-34	1428300000	6	6	6	27.6	23.805	27.0007	26.9588	27.0427	6	3	3	B8N3A9	B8N3A9	1	AFLA_027220	Putative uncharacterized protein
26.4593	26.8383	26.5856	25.9681	26.7195	26.4131	1.10E-56	846910000	6	6	6	32.2	31.172	26.4973	26.6278	26.3669	6	3	3	B8N3B1	B8N3B1	1	AFLA_027240	Carbonic anhydrase
26.2421	25.972	25.9627	25.6473	25.9777	25.3812	1.34E-50	751190000	6	6	6	17.9	62.301	25.8638	26.0589	25.6687	6	3	3	B8N3E0	B8N3E0	1	AFLA_027530	Glycerol kinase, putative
ND	26.9883	ND	27.8671	27.5973	27.5316	0	1921100000	6	6	6	38.6	31.923	27.4961	26.9883	27.6653	4	1	3	B8N3S8	B8N3S8	1	AFLA_031620	Histone chaperone ASF1, putative
ND	ND	ND	25.8494	25.2845	27.498	6.81E-24	1347700000	6	6	6	37.4	14.069	26.2106	ND	26.2106	3	0	3	B8N446	B8N446	1	AFLA_033690	60S ribosomal protein L31e
26.6799	26.6691	26.0534	25.2878	26.4354	26.3998	1.03E-35	1077600000	6	6	6	32.4	24.935	26.2542	26.4675	26.041	6	3	3	B8N4A9	B8N4A9	1	AFLA_035220	Putative uncharacterized protein
25.7705	25.9356	26.0103	25.499	25.0653	25.404	1.74E-24	416230000	6	6	6	10.2	78.088	25.6141	25.9055	25.3227	6	3	3	B8N4C0	B8N4C0	1	AFLA_035330	Translation release factor eRF3, putative
26.6823	26.48	26.5437	24.9716	25.2892	25.814	5.51E-55	798900000	6	6	6	17.8	49.932	25.9635	26.5687	25.3583	6	3	3	B8N4N0	B8N4N0	1	AFLA_037350	Casein kinase I, putative
26.5552	26.9626	26.6867	27.4741	27.5277	27.1186	3.81E-119	2384000000	6	6	6	45.8	31.578	27.0541	26.7348	27.3735	6	3	3	B8N4V7	B8N4V7	1	AFLA_018160	Coatomer subunit epsilon, putative
28.1031	27.6455	28.1788	28.3631	28.1624	27.6155	1.13E-79	3134000000	6	6	6	59.2	17.288	28.0114	27.9758	28.047	6	3	3	B8N546	B8N546	1	AFLA_020840	Ubiquitin conjugating enzyme (UbcB), putative
25.8436	25.9799	25.8939	26.3265	26.1572	26.0532	3.57E-20	795820000	6	6	6	42.8	29.808	26.0424	25.9058	26.179	6	3	3	B8N5C5	B8N5C5	1	AFLA_022530	Cell polarity protein (Alp11), putative
26.9361	29.3592	29.5347	ND	22.5629	ND	7.60E-94	1734200000	6	6	6	27.6	32.989	27.0982	28.61	22.5629	4	3	1	B8N5N1	B8N5N1	1	AFLA_013740	Acid phosphatase, putative
31.3337	31.3025	31.3355	31.6191	31.5156	31.1533	0	32219000000	6	6	6	84.1	13.728	31.3766	31.3239	31.4293	6	3	3	B8N5W7	B8N5W7	1	AFLA_014600	Profilin
ND	ND	ND	26.244	25.8101	25.9626	2.51E-25	281970000	6	6	6	4.8	200.15	26.0056	ND	26.0056	3	0	3	B8N5Y3	B8N5Y3	1	AFLA_014760	rRNA biogenesis protein RRP5, putative
24.7064	24.2489	24.4356	24.6243	25.7448	24.7903	3.55E-12	269700000	6	6	6	20.7	47.985	24.7584	24.4636	25.0531	6	3	3	B8N6N3	B8N6N3	1	AFLA_015460	Molybdopterin biosynthesis protein, putative
25.5377	26.8076	25.3656	26.355	26.6756	26.2731	2.99E-102	882310000	6	6	6	50	18.197	26.1691	25.9036	26.4346	6	3	3	B8N6N7	B8N6N7	1	AFLA_015500	DUF866 domain protein
27.5294	27.3808	27.6151	27.8462	27.6207	27.4867	9.62E-97	2678800000	6	6	6	28.6	28.881	27.5798	27.5084	27.6512	6	3	3	B8N6S7;B8	B8N6S7	2	AFLA_016800	Thioredoxin, putative
ND	24.0496	ND	24.8849	25.1581	25.9454	3.80E-16	251620000	6	6	6	32.5	33.02	25.0095	24.0496	25.3295	4	1	3	B8N6U6	B8N6U6	1	AFLA_016990	Fibrillarin
29.9556	29.184	29.6202	29.4105	29.7524	29.299	6.16E-272	6904800000	6	6	6	53.5	18.549	29.5369	29.5866	29.4873	6	3	3	B8N728	B8N728	1	AFLA_019610	Carboxypeptidase S1, putative
26.0083	26.074	26.543	26.9992	26.0008	26.0169	9.81E-77	776330000	6	6	6	9	113.7	26.2737	26.2084	26.3389	6	3	3	B8N7C7	B8N7C7	1	AFLA_021490	PAB1 binding protein (Pbp1), putative
25.0031	26.357	25.4455	25.9174	25.2036	25.642	2.49E-19	506600000	6	6	6	8.4	98.488	25.5948	25.6018	25.5877	6	3	3	B8N863	B8N863	1	AFLA_106570	Cullin binding protein CanA, putative
ND	26.1894	ND	27.8371	27.1173	27.0241	7.08E-79	836510000	6	6	6	26.6	54.465	27.042	26.1894	27.3262	4	1	3	B8N8A6	B8N8A6	1	AFLA_107000	Ribosome biogenesis protein (Rrb1), putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
25.0737	25.7411	25.9048	24.8249	24.8293	ND	1.68E-57	485690000	6	6	6	4.7	172.52	25.2748	25.5732	24.8271	5	3	2	B8N8F0	B8N8F0	1	AFLA_107440	Cytoskeleton assembly control protein Sla1, putative
26.3721	25.6571	26.1912	25.437	26.4815	25.3827	4.77E-13	476600000	6	6	6	10.8	85.746	25.9203	26.0735	25.7671	6	3	3	B8N8I6	B8N8I6	1	AFLA_107800	Exo-beta-1,3-glucanase, putative
27.8862	27.2932	27.7578	25.6784	26.0995	25.5335	1.00E-19	1279900000	6	6	6	23.7	46.238	26.7081	27.6457	25.7705	6	3	3	B8N8S4	B8N8S4	1	AFLA_108690	Putative uncharacterized protein
25.7916	25.767	25.7316	26.8642	26.333	26.352	2.13E-17	879910000	6	6	6	30.8	38.043	26.1399	25.7634	26.5164	6	3	3	B8N947	B8N947	1	AFLA_109930	D-lactate dehydrogenase, putative
ND	ND	ND	24.9932	24.3147	24.757	2.02E-14	207020000	6	6	6	7.6	96.177	24.6883	ND	24.6883	3	0	3	B8N9H1	B8N9H1	1	AFLA_111170	Transcription initiation protein spt5
27.5629	27.2541	27.5336	27.7293	27.7684	27.3644	9.85E-158	2023500000	6	6	6	34.8	21.941	27.5354	27.4502	27.6207	6	3	3	B8N9S3	B8N9S3	1	AFLA_112190	Cyclophilin, putative
26.0835	26.0707	26.4005	26.9299	26.7696	26.1903	8.50E-26	982210000	6	6	6	13.1	64.29	26.4074	26.1849	26.6299	6	3	3	B8N9W7	B8N9W7	1	AFLA_112630	KH domain protein
26.9041	26.2042	27.1228	26.5068	26.2605	26.0682	3.17E-21	1019400000	6	6	6	56.2	13.708	26.5111	26.7437	26.2785	6	3	3	B8NA77	B8NA77	1	AFLA_113730	Progesterone binding protein, putative
27.4991	26.6733	27.5759	26.7659	26.9923	26.6204	6.80E-21	1816600000	6	6	6	37.9	35.698	27.0212	27.2495	26.7929	6	3	3	B8NAN1	B8NAN1	1	AFLA_042560	Phytanoyl-CoA dioxygenase family protein
26.714	26.5986	26.7831	25.964	26.6309	26.529	7.43E-26	1084500000	6	6	6	13.7	71.123	26.5366	26.6986	26.3746	6	3	3	B8NB20	B8NB20	1	AFLA_043950	Serine/threonine protein kinase (YPK1), putative
26.3082	26.4897	26.6026	25.3117	24.4765	24.654	7.39E-46	541170000	6	6	6	23.2	68.968	25.6404	26.4668	24.8141	6	3	3	B8NB56	B8NB56	1	AFLA_044310	SH3 domain protein
27.5564	27.4361	27.8102	27.745	27.5571	27.228	4.64E-118	2027900000	6	6	6	38.4	26.092	27.5555	27.6009	27.51	6	3	3	B8NBB8	B8NBB8	1	AFLA_044930	Superoxide dismutase copper chaperone Lys7, putative
25.1518	25.2136	25.6163	25.7486	25.4789	25.3557	6.38E-41	680530000	6	6	6	27.5	27.2	25.4275	25.3273	25.5277	6	3	3	B8NBJ3	B8NBJ3	1	AFLA_045680	GNAT family acetyltransferase, putative
23.364	26.1299	23.6089	26.9919	27.9606	29.1084	3.36E-95	1870400000	6	6	6	57.5	11.353	26.194	24.3676	28.0203	6	3	3	B8NBK4	B8NBK4	1	AFLA_045790	60S ribosomal protein L30, putative
25.0696	25.1637	25.5285	25.9873	25.5397	25.4551	1.45E-21	520390000	6	6	6	11.9	70.047	25.4573	25.254	25.6607	6	3	3	B8NBK5	B8NBK5	1	AFLA_045800	M protein, serotype 2.1, putative
23.0449	24.405	23.819	27.8457	28.768	31.1123	2.13E-67	5185600000	6	6	6	37.5	20.782	26.4991	23.7563	29.242	6	3	3	B8NC19	B8NC19	1	AFLA_047440	60S ribosomal protein L18
24.7306	24.206	24.4476	25.1862	25.2264	24.781	4.33E-18	348110000	6	6	6	14.8	52.992	24.763	24.4614	25.0646	6	3	3	B8NCQ8	B8NCQ8	1	AFLA_041430	Glutamine synthetase, putative
ND	ND	ND	26.0605	24.6033	25.0182	1.94E-13	195150000	6	6	6	9.3	91.575	25.2273	ND	25.2273	3	0	3	B8ND54	B8ND54	1	AFLA_055250	Mitochondrial mRNA processing protein PET127, putative
27.5198	26.0751	27.559	26.3054	25.6585	25.136	2.84E-46	862340000	6	6	6	32.4	24.789	26.3756	27.0513	25.6999	6	3	3	B8ND83	B8ND83	1	AFLA_056440	Putative uncharacterized protein
25.9109	25.6716	25.1527	25.264	25.6561	25.6832	5.03E-20	704710000	6	6	6	49.6	27.18	25.5564	25.5784	25.5344	6	3	3	B8NE06	B8NE06	1	AFLA_057370	Ubiquitin conjugating enzyme (UbcA), putative
25.0391	25.5776	25.7204	26.4626	26.0325	25.7451	5.62E-15	749020000	6	6	6	26.2	41.443	25.7629	25.4457	26.0801	6	3	3	B8NED9	B8NED9	1	AFLA_060480	Phenazine biosynthesis protein, putative
26.4394	23.6856	24.5828	ND	23.3314	24.2174	1.13E-33	787000000	6	6	6	26.3	34.238	24.4513	24.9026	23.7744	5	3	2	B8NEZ5	B8NEZ5	1	AFLA_058590	Dihydrodipicolinate synthetase family protein
26.0062	25.1627	25.4588	24.7066	25.3333	24.3919	1.65E-20	556290000	6	6	6	21	38.576	25.1766	25.5426	24.8106	6	3	3	B8NFE6	B8NFE6	1	AFLA_062800	Aldo-keto reductase, putative
25.1164	25.1785	25.2791	25.6859	24.0894	24.7433	1.16E-17	377070000	6	6	6	30.4	24.559	25.0155	25.1914	24.8395	6	3	3	B8NFJ8	B8NFJ8	1	AFLA_063320	Putative uncharacterized protein
24.4532	24.5154	24.7107	ND	ND	ND	1.94E-14	167190000	6	6	6	7.5	93.992	24.5597	24.5597	ND	3	3	0	B8NFV3	B8NFV3	1	AFLA_133820	Putative uncharacterized protein
26.3113	26.0832	26.852	23.7358	24.2927	23.9389	5.06E-24	454330000	6	6	6	24.6	38.508	25.2023	26.4155	23.9892	6	3	3	B8NFV4	B8NFV4	1	AFLA_133830	Alcohol dehydrogenase, putative
30.509	30.846	30.6419	31.0146	30.9311	30.7148	0	20651000000	6	6	6	65.5	12.024	30.7762	30.6656	30.8868	6	3	3	B8NH30	B8NH30	1	AFLA_132540	Thioredoxin
25.4718	24.5661	25.3817	ND	24.1271	ND	5.20E-14	191080000	6	6	6	17.3	58.227	24.8867	25.1399	24.1271	4	3	1	B8NHI5	B8NHI5	1	AFLA_136790	Thiamine pyrophosphate enzyme, putative
ND	25.3649	ND	24.126	24.2854	24.6248	1.85E-83	1124400000	6	6	6	70.1	18.158	24.6003	25.3649	24.3454	4	1	3	B8NHS0	B8NHS0	1	AFLA_137640	Putative uncharacterized protein
25.1853	25.7337	25.362	26.4278	26.1464	26.1632	2.90E-18	776950000	6	6	6	19.3	51.722	25.8364	25.427	26.2458	6	3	3	B8NIH3	B8NIH3	1	AFLA_067600	Nuclear and cytoplasmic polyadenylated RNA-binding protein pub1
27.6317	27.7096	28.1134	26.5378	26.8942	26.5742	1.02E-57	1332200000	6	6	6	36.1	20.972	27.2435	27.8183	26.6688	6	3	3	B8NIL7;B8N	B8NIL7	2	AFLA_068040	ADP-ribosylation factor, putative
30.1143	29.9889	30.2293	30.8213	30.4838	30.3043	1.89E-214	16596000000	6	6	6	54.5	17.871	30.3236	30.1108	30.5365	6	3	3	B8NIP0	B8NIP0	1	AFLA_068270	Putative uncharacterized protein
25.7608	26.085	25.2	27.2919	26.7199	27.1114	9.02E-40	1356200000	6	6	6	20.2	36.753	26.3615	25.6819	27.0411	6	3	3	B8NIU5	B8NIU5	1	AFLA_069730	HMG box protein, putative
24.1578	24.8368	24.5676	25.8348	25.1753	25.4508	2.50E-16	351690000	6	6	6	13.7	55.939	25.0039	24.5207	25.487	6	3	3	B8NJ01	B8NJ01	1	AFLA_071180	Indoleamine 2,3-dioxygenase family protein
29.3624	29.5049	28.9861	29.2415	29.9595	30.0125	3.25E-165	10654000000	6	6	6	59.4	17.394	29.5111	29.2845	29.7378	6	3	3	B8NJ33	B8NJ33	1	AFLA_071500	Translation initiation inhibitor, putative
27.2996	26.6338	27.3182	26.9954	27.0745	26.5806	3.11E-31	2190300000	6	6	6	42.3	14.649	26.9837	27.0839	26.8835	6	3	3	B8NK85	B8NK85	1	AFLA_089590	Putative uncharacterized protein
27.3586	27.0655	27.3855	27.3025	27.3121	27.1296	3.13E-30	1671100000	6	6	6	48.1	17.269	27.259	27.2699	27.2481	6	3	3	B8NKC0	B8NKC0	1	AFLA_089940	Thioredoxin, putative
23.5891	25.7826	23.3689	26.2898	26.5178	27.2122	2.32E-31	1052100000	6	6	6	38.9	17.264	25.4601	24.2469	26.6733	6	3	3	B8NKG5	B8NKG5	1	AFLA_091310	Eukaryotic translation initiation factor eIF-1A subunit, putative
25.7024	25.9286	25.8745	26.1785	25.8205	25.909	1.42E-52	627520000	6	6	6	12.3	55.099	25.9023	25.8352	25.9693	6	3	3	B8NKP0	B8NKP0	1	AFLA_092060	Golgi to endosome transport protein (Ent3), putative
24.1823	23.6968	24.0574	ND	ND	ND	9.77E-12	196260000	6	6	6	12.3	63.286	23.9788	23.9788	ND	3	3	0	B8NKX5	B8NKX5	1	AFLA_093790	Dihydroxyacetone kinase (DakA), putative
25.9072	25.6168	26.0006	25.7065	25.7056	25.2383	1.43E-29	774150000	6	6	6	13.9	70.711	25.6958	25.8415	25.5501	6	3	3	B8NL86	B8NL86	1	AFLA_089220	Ser/Thr protein phosphatase family
ND	26.0763	ND	26.7548	26.6113	26.3425	8.52E-29	1012400000	6	6	6	43.9	19.124	26.4462	26.0763	26.5695	4	1	3	B8NLE9	B8NLE9	1	AFLA_090760	Ankyrin repeat protein
26.5548	25.952	26.8017	23.0333	23.6757	23.1817	5.62E-25	372200000	6	6	6	19.6	47.21	24.8665	26.4361	23.2969	6	3	3	B8NLF5	B8NLF5	1	AFLA_090820	Aminotransferase, putative
26.6095	27.0756	25.1621	25.9191	26.5948	26.6621	1.04E-32	977730000	6	6	6	27.5	37.348	26.3372	26.2824	26.392	6	3	3	B8NLL9	B8NLL9	1	AFLA_092350	Proteasome regulatory particle subunit (RpnK), putative
26.7066	26.6492	26.8706	27.4958	27.0754	26.7814	3.23E-28	1865000000	6	6	6	14.8	46.883	26.9298	26.7421	27.1175	6	3	3	B8NLP7	B8NLP7	1	AFLA_092630	Cell wall glucanase (Utr2), putative
26.761	26.1014	26.5021	25.4209	25.6554	25.1717	5.77E-45	795190000	6	6	6	15.7	66.631	25.9354	26.4548	25.416	6	3	3	B8NLP8	B8NLP8	1	AFLA_092640	Alkaline phosphatase
29.3735	29.1173	29.4443	29.4	29.3166	28.9543	2.92E-131	6779800000	6	6	6	48.5	18.026	29.2677	29.3117	29.2236	6	3	3	B8NM00	B8NM00	1	AFLA_094560	Peptidyl-prolyl cis-trans isomerase
ND	ND	ND	29.0495	27.8466	27.8035	1.36E-176	1470100000	6	6	6	40.9	27.781	28.2332	ND	28.2332	3	0	3	B8NM09	B8NM09	1	AFLA_094650	60S acidic ribosomal protein P0, putative
26.7108	26.8373	27.1969	28.1702	26.7788	27.4172	1.07E-83	1308700000	6	6	6	50.3	19.467	27.1852	26.915	27.4554	6	3	3	B8NMQ4	B8NMQ4	1	AFLA_126670	Putative uncharacterized protein
27.72	27.6274	27.5761	26.4028	26.0542	26.1356	9.55E-36	1207100000	6	6	6	48.3	18.988	26.9193	27.6412	26.1975	6	3	3	B8NMR6	B8NMR6	1	AFLA_126790	Threonine synthase Thr4, putative
ND	24.2427	ND	ND	27.3854	25.0339	9.84E-48	216900000	6	6	6	41.8	16.611	25.554	24.2427	26.2097	3	1	2	B8NN64	B8NN64	1	AFLA_124980	4-carboxymuconolactone decarboxylase, putative
26.0099	26.0615	26.1738	23.9967	23.8834	23.7887	1.12E-21	405930000	6	6	6	19.3	51.465	24.9857	26.0817	23.8896	6	3	3	B8NNC8	B8NNC8	1	AFLA_127390	Proteasome regulatory particle subunit Rpt5, putative
ND	24.6977	ND	26.8229	26.2715	26.2885	3.05E-25	546960000	6	6	6	6.3	129.33	26.0201	24.6977	26.461	4	1	3	B8NNS5	B8NNS5	1	AFLA_129760	RNA binding protein Jsn1, putative
26.4665	26.4682	26.7477	26.0034	26.06	26.2602	1.43E-21	604750000	6	6	6	12.3	74.252	26.3343	26.5608	26.1078	6	3	3	B8NPE5	B8NPE5	1	AFLA_130170	Actin cortical patch component, putative
27.4659	26.9498	27.681	26.9432	26.7409	26.2745	3.17E-103	1912600000	6	6	6	48.1	17.749	27.0092	27.3656	26.6529	6	3	3	B8NQ08	B8NQ08	1	AFLA_003110	Cyanate hydratase
ND	25.2853	24.9341	25.0504	24.851	24.7061	1.46E-11	308000000	6	6	6	11	76.159	24.9654	25.1097	24.8692	5	2	3	B8NQ20	B8NQ20	1	AFLA_003230	Putative uncharacterized protein
27.8163	28.0056	28.1787	28.0922	27.9324	27.151	2.98E-201	2765300000	6	6	6	43.2	28.276	27.8627	28.0002	27.7252	6	3	3	B8NQH6	B8NQH6	1	AFLA_006580	WW domain protein
26.0487	25.992	26.0117	26.1039	26.0219	25.8436	5.48E-18	796140000	6	6	6	18.9	56.385	26.0036	26.0175	25.9898	6	3	3	B8NQI0	B8NQI0	1	AFLA_006620	Ferrooxidoreductase Fet3, putative
ND	24.373	ND	ND	24.9865	24.7671	4.07E-14	253840000	6	6	6	29.6	36.932	24.7089	24.373	24.8768	3	1	2	B8NQW3	B8NQW3	1	AFLA_003470	Oxidoreductase family, NAD-binding Rossmann fold protein
ND	22.2961	ND	23.7123	23.6736	23.8831	1.04E-107	978650000	6	6	6	40.6	27.435	23.3913	22.2961	23.7563	4	1	3	B8NRH6	B8NRH6	1	AFLA_048810	60S ribosomal protein L8, putative
28.8542	28.7522	28.0519	28.0648	29.1782	28.3322	7.38E-225	2987500000	6	6	6	22.1	33.843	28.5389	28.5527	28.525	6	3	3	B8NRS8	B8NRS8	1	AFLA_050690	Mitochondrial ADP,ATP carrier protein (Ant), putative
26.8831	26.3365	26.8846	27.0014	26.4873	26.7394	1.18E-47	1542600000	6	6	6	31.2	40.221	26.722	26.7014	26.7427	6	3	3	B8NRU2	B8NRU2	1	AFLA_050830	Uridine nucleosidase Urh1, putative
24.6635	24.834	24.7817	25.6317	25.4605	25.3228	1.00E-15	402330000	6	6	6	7.1	112.08	25.1157	24.7597	25.4717	6	3	3	B8NS03	B8NS03	1	AFLA_052340	SNF2 family helicase/ATPase, putative
26.7878	25.8551	26.9402	25.0343	25.172	24.849	1.39E-37	1055000000	6	6	6	27.9	31.227	25.773	26.5277	25.0184	6	3	3	B8NS77	B8NS77	1	AFLA_053990	Class II aldolase/adducin domain protein
22.8022	25.3508	23.9787	23.7678	25.2304	27.6326	4.05E-19	596000000	6	6	6	28.2	22.986	24.7937	24.0439	25.5436	6	3	3	B8NSP9	B8NSP9	1	AFLA_050000	Ribosomal protein L16a
27.0432	27.5732	24.5266	25.3149	26.9901	27.6865	4.41E-36	2651500000	6	6	6	57.8	10.968	26.5224	26.381	26.6638	6	3	3	B8NSR1	B8NSR1	1	AFLA_050120	Glutaredoxin Grx1, putative
23.9152	24.6437	24.0905	25.7343	24.5939	25.6285	1.16E-33	470980000	6	6	6	20.2	45.89	24.7677	24.2165	25.3189	6	3	3	B8NSR2	B8NSR2	1	AFLA_050130	Putative uncharacterized protein
26.1593	25.9331	25.9983	25.7686	25.3139	25.503	2.52E-20	385870000	6	6	6	31.4	42.182	25.7794	26.0302	25.5285	6	3	3	B8NUK7	B8NUK7	1	AFLA_100600	Salicylate hydroxylase, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
30.5672	30.214	30.4143	30.3383	30.4751	29.9023	0	13415000000	6	6	6	22.1	54.876	30.3185	30.3985	30.2385	6	3	3	B8NUL2	B8NUL2	1	AFLA_100650	Serine carboxypeptidase (CpdS), putative
23.6333	25.1184	23.7052	24.3182	25.2907	27.8148	1.16E-110	1014900000	6	6	6	43.7	18.044	24.9801	24.1523	25.8079	6	3	3	B8NUR2	B8NUR2	1	AFLA_101150	60S ribosomal protein L21, putative
24.6225	24.9816	25.099	24.0917	24.29	24.5658	1.31E-17	211270000	6	6	6	11.9	69.182	24.6084	24.9011	24.3158	6	3	3	B8NV31	B8NV31	1	AFLA_103250	Proteasome regulatory particle subunit (RpnC), putative
25.4765	25.4405	24.9528	23.7917	23.7745	24.5541	4.91E-20	224570000	6	6	6	20.8	33.121	24.665	25.2899	24.0401	6	3	3	B8NV71	B8NV71	1	AFLA_103660	Nicotinate-nucleotide pyrophosphorylase [carboxylating]
26.9062	26.6761	26.8829	27.0477	26.1593	26.4921	1.63E-83	1168500000	6	6	6	23.7	44.853	26.6941	26.8217	26.5664	6	3	3	B8NW28	B8NW28	1	AFLA_119560	Pyridoxamine phosphate oxidase, putative
26.2587	24.6902	25.9465	25.8759	26.3323	25.7032	1.47E-56	817180000	6	6	6	15.6	59.389	25.8011	25.6318	25.9705	6	3	3	B8NW87	B8NW87	1	AFLA_118340	Flavin containing polyamine oxidase, putative
25.6281	26.2414	25.8614	26.7557	26.6129	26.3345	1.89E-34	983580000	6	6	6	52.2	20.222	26.239	25.9103	26.5677	6	3	3	B8NWR6	B8NWR6	1	AFLA_121030	GNAT family N-acetyltransferase, putative
24.073	24.0803	24.3586	25.0849	24.1144	24.0134	2.38E-24	537200000	6	6	6	31.5	26.192	24.2874	24.1706	24.4043	6	3	3	B8NXD5	B8NXD5	1	AFLA_007540	Glutathione S-transferase, putative
27.5246	27.2528	27.5787	ND	ND	ND	3.45E-43	826930000	6	6	6	17.5	57.585	27.452	27.452	ND	3	3	0	B8NXS3	B8NXS3	1	AFLA_008930	Acid phosphatase AphA
24.484	24.4644	24.6575	25.1808	24.7694	24.5855	2.27E-11	291760000	6	6	6	14.5	47.521	24.6903	24.5353	24.8452	6	3	3	B8NXT5	B8NXT5	1	AFLA_009050	TPR repeat protein
31.3714	31.1703	31.5189	31.357	31.099	30.8887	3.89E-180	29482000000	6	6	6	48.4	13.315	31.2342	31.3535	31.1149	6	3	3	B8NYC1	B8NYC1	1	AFLA_010910	Peptidyl-prolyl cis-trans isomerase
27.1689	27.4205	27.4682	27.0928	27.6564	27.4058	1.12E-29	1670700000	7	7	6	38.1	23.795	27.3687	27.3525	27.385	6	3	3	B8N9M9	B8N9M9	1	AFLA_111750	RAB GTPase Ypt5, putative
25.6727	25.7962	25.7754	27.1899	26.061	26.2398	8.18E-37	710640000	10	6	6	26	36.237	26.1225	25.7481	26.4969	6	3	3	B8NRM9	B8NRM9	1	AFLA_049340	Aldo/keto reductase, putative
26.0259	24.3479	25.0748	24.6629	24.7582	24.4607	1.23E-74	942670000	7	7	7	17.8	62.965	24.8884	25.1495	24.6273	6	3	3	B8MW63	B8MW63	1	AFLA_074100	Gamma-glutamyltranspeptidase
26.5681	26.4228	26.8037	27.3731	26.8595	26.6298	1.30E-24	1225900000	7	7	7	22.8	44.789	26.7761	26.5982	26.9541	6	3	3	B8MWB2	B8MWB2	1	AFLA_088020	Methionine aminopeptidase
23.4539	25.7857	24.1768	28.5988	28.0599	28.1248	9.71E-45	1580000000	7	7	7	50	33.532	26.3666	24.4721	28.2612	6	3	3	B8MWC5	B8MWC5	1	AFLA_088150	Fe superoxide dismutase, putative
27.5339	27.8598	27.579	28.8519	28.196	27.725	4.63E-76	2430500000	7	7	7	30	43.337	27.9576	27.6576	28.2576	6	3	3	B8MX56	B8MX56	1	AFLA_076430	SUN domain protein (Uth1), putative
28.0614	27.3904	27.8027	27.2696	25.9266	26.8098	8.07E-242	1352000000	7	7	7	30.8	36.099	27.2101	27.7515	26.6687	6	3	3	B8MX58	B8MX58	1	AFLA_076450	Electron transfer flavoprotein alpha subunit, putative
28.3232	28.268	26.4263	25.6425	28.8053	28.3226	1.88E-133	3886400000	7	7	7	38	25.59	27.6313	27.6725	27.5902	6	3	3	B8MY92	B8MY92	1	AFLA_080290	DUTPase (Dut), putative
24.2893	24.9601	ND	24.4505	25.1934	25.0131	3.19E-24	406000000	7	7	7	20.3	45.561	24.7813	24.6247	24.8857	5	2	3	B8MYZ2	B8MYZ2	1	AFLA_082810	Putative uncharacterized protein
28.2277	27.7686	27.8913	26.7257	27.0606	26.3184	5.84E-71	2564400000	7	7	7	25	34.953	27.332	27.9625	26.7016	6	3	3	B8MZ00	B8MZ00	1	AFLA_082890	Ribonuclease T2, putative
26.2491	25.9091	26.1703	25.887	25.8874	25.8077	9.00E-22	788330000	7	7	7	26.4	35.022	25.9851	26.1095	25.8607	6	3	3	B8MZ55	B8MZ55	1	AFLA_083440	26S proteasome-associated ubiquitin C-terminal hydrolase, putative
25.2723	26.2208	26.5198	25.126	24.7949	25.9813	3.47E-85	530390000	7	7	7	18	57.211	25.6525	26.0043	25.3008	6	3	3	B8MZ66	B8MZ66	1	AFLA_083550	Coatomer subunit delta, putative
27.0816	27.3198	27.238	27.9898	27.4693	27.578	4.36E-32	1963900000	7	7	7	21.8	44.288	27.4461	27.2132	27.679	6	3	3	B8MZU4	B8MZU4	1	AFLA_085840	Tubulin-specific chaperone c, putative
24.6825	23.8002	24.2989	ND	23.8022	ND	3.99E-41	477290000	7	7	7	31	44.506	24.146	24.2605	23.8022	4	3	1	B8MZY1	B8MZY1	1	AFLA_086210	Epoxide hydrolase, putative
25.1994	26.7206	25.145	26.8976	26.5523	26.6013	1.73E-27	1020100000	7	7	7	15.8	85.073	26.186	25.6883	26.6837	6	3	3	B8MZZ0	B8MZZ0	1	AFLA_086300	Vacuolar import and degRadation protein, putative
26.0207	26.761	24.5447	26.6292	26.3532	26.892	4.75E-29	1289200000	7	7	7	52.2	19.711	26.2002	25.7755	26.6248	6	3	3	B8N027	B8N027	1	AFLA_086670	Cystathionine beta-synthase (Beta-thionase), putative
26.506	26.4978	26.4176	26.0032	26.0165	25.9175	8.04E-32	938240000	7	7	7	37.3	18.406	26.2264	26.4738	25.9791	6	3	3	B8N0U4	B8N0U4	1	AFLA_026290	Phosphotransmitter protein Ypd1, putative
24.7222	24.1406	24.065	25.1778	25.1181	24.9193	7.42E-14	295960000	7	7	7	22.7	44.372	24.6905	24.3092	25.0717	6	3	3	B8N151	B8N151	1	AFLA_028260	Probable glucan 1,3-beta-glucosidase A
26.8504	26.748	27.1648	27.1292	26.7816	26.737	3.42E-60	1380600000	7	7	7	24.6	54.156	26.9018	26.9211	26.8826	6	3	3	B8N163	B8N163	1	AFLA_028380	Putative uncharacterized protein
27.5867	27.7091	28.0597	26.3333	27.0138	27.2847	6.11E-47	1491000000	7	7	7	46	21.415	27.3312	27.7851	26.8773	6	3	3	B8N1B1	B8N1B1	1	AFLA_029760	Small monomeric GTPase SarA, putative
26.6105	26.2425	26.9951	25.314	24.8182	25.2865	3.59E-22	619630000	7	7	7	10.1	99.561	25.8778	26.616	25.1396	6	3	3	B8N1T0	B8N1T0	1	AFLA_032340	Vacuolar protein sorting-associated protein 35
27.2829	27.3288	27.6603	27.9855	27.7689	27.2832	6.34E-54	2129000000	7	7	7	54.4	16.399	27.5516	27.424	27.6792	6	3	3	B8N238	B8N238	1	AFLA_034320	HIT domain protein
24.9992	25.025	25.0904	23.567	23.9843	24.4912	5.86E-42	1296700000	7	7	7	23.6	27.221	24.5262	25.0382	24.0142	6	3	3	B8N370	B8N370	1	AFLA_026830	40S ribosomal protein S6
27.3096	28.0265	27.8909	24.0772	23.9474	24.4807	1.03E-92	838750000	7	7	7	30.2	40.13	25.9554	27.7424	24.1685	6	3	3	B8N3D7	B8N3D7	1	AFLA_027500	Mannose-1-phosphate guanylyltransferase
23.6866	26.2457	24.1127	29.5226	29.2648	31.3796	5.21E-111	7088100000	7	7	7	22.4	33.628	27.3687	24.6817	30.0557	6	3	3	B8N3M3	B8N3M3	1	AFLA_029260	Ribosomal protein L15
26.6461	27.1429	26.4238	25.3306	26.6077	26.6129	6.84E-34	1627600000	7	7	7	40.3	22.775	26.4607	26.7376	26.1837	6	3	3	B8N3W2	B8N3W2	1	AFLA_031960	40S ribosomal protein S7e
23.2462	ND	23.4192	ND	23.4697	ND	3.99E-28	250890000	7	7	7	16.1	74.805	23.3784	23.3327	23.4697	3	2	1	B8N3Z9	B8N3Z9	1	AFLA_033220	Amidase family protein
24.0525	24.8553	ND	25.7201	26.1245	26.0361	7.28E-21	366760000	7	7	7	7.9	134.05	25.3577	24.4539	25.9602	5	2	3	B8N430	B8N430	1	AFLA_033530	Nuclear mRNA splicing factor, putative
29.0568	29.0745	29.085	27.7126	27.8937	28.364	5.95E-33	3368000000	7	7	7	29.9	24.083	28.5311	29.0721	27.9901	6	3	3	B8N442	B8N442	1	AFLA_033650	GTP-binding nuclear protein Ran, putative
27.2687	27.3031	27.4956	28.1302	27.8696	27.4726	2.78E-62	2160600000	7	7	7	36.2	25.195	27.59	27.3558	27.8241	6	3	3	B8N456	B8N456	1	AFLA_033790	3,4-dihydroxy-2-butanone 4-phosphate synthase
25.8793	25.5736	25.8503	24.517	25.0665	24.9351	1.01E-19	556440000	7	7	7	18.7	56.337	25.3036	25.7677	24.8395	6	3	3	B8N4A3	B8N4A3	1	AFLA_035160	Tyrosine decarboxylase, putative
29.0517	29.102	29.0125	29.077	29.5949	28.8924	3.15E-156	8548600000	7	7	7	63.5	14.54	29.1217	29.0554	29.1881	6	3	3	B8N4D7	B8N4D7	1	AFLA_035500	Cytochrome b5, putative
26.2546	26.6362	26.5141	26.579	26.0514	26.5774	3.66E-46	978800000	7	7	7	23.9	50.078	26.4355	26.4683	26.4026	6	3	3	B8N4V5	B8N4V5	1	AFLA_018140	Mannose-6-phosphate isomerase
25.1241	25.0809	25.4052	27.0942	25.3221	26.3487	9.15E-53	852400000	7	7	7	72.6	14.609	25.7292	25.2034	26.255	6	3	3	B8N5Z6	B8N5Z6	1	AFLA_015800	DUF636 domain protein
25.5063	25.4766	25.7657	26.3762	26.2155	25.974	1.08E-50	882770000	7	7	7	18.6	46.394	25.8857	25.5829	26.1886	6	3	3	B8N684	B8N684	1	AFLA_018480	Cytoskeletal adaptor protein SagA
ND	25.9638	ND	26.6621	26.2812	26.3763	1.46E-20	598920000	7	7	7	30.4	39.721	26.3208	25.9638	26.4399	4	1	3	B8N6Z7	B8N6Z7	1	AFLA_019300	Putative uncharacterized protein
28.9912	28.8129	29.3587	29.2248	29.0058	29.0125	4.18E-137	6115400000	7	7	7	34.9	27.151	29.0676	29.0542	29.081	6	3	3	B8N716	B8N716	1	AFLA_019490	ThiJ/Pfpl family protein
ND	ND	ND	26.3822	26.0895	25.9938	1.89E-14	596520000	7	7	7	13.5	92.143	26.1552	ND	26.1552	3	0	3	B8N7A0	B8N7A0	1	AFLA_021220	tRNA ligase
27.0426	26.8696	27.3962	26.4135	26.8447	26.5761	3.84E-102	1170800000	7	7	7	38.4	27.774	26.8571	27.1028	26.6115	6	3	3	B8N7D0	B8N7D0	1	AFLA_021520	N-acetyltransferase complex ARD1 subunit, putative
28.477	28.4004	28.7757	28.7604	28.0458	28.2822	8.41E-239	4085300000	7	7	7	74.6	14.904	28.4569	28.551	28.3628	6	3	3	B8N7D6	B8N7D6	1	AFLA_021580	Dynein light chain (Tctex1), putative
25.7451	25.1746	25.5782	26.8104	26.6337	26.5377	1.31E-24	976380000	7	7	7	12.4	92.147	26.08	25.4993	26.6606	6	3	3	B8N7E5	B8N7E5	1	AFLA_021670	Probable E3 ubiquitin-protein ligase hulA
25.2052	25.9153	25.4043	26.8968	25.4389	25.567	4.09E-58	443210000	7	7	7	18.4	55.557	25.7379	25.5082	25.9676	6	3	3	B8N9E3	B8N9E3	1	AFLA_110890	FAD-dependent oxygenase, putative
28.0276	28.089	28.2256	28.3473	28.4302	28.0331	1.40E-114	3729900000	7	7	7	37.4	22.613	28.1922	28.1141	28.2702	6	3	3	B8N9T8	B8N9T8	1	AFLA_112340	Proteasome subunit beta type
27.7813	27.7267	28.0254	26.9677	26.7112	26.6381	1.24E-75	1169200000	7	7	7	18.5	64.711	27.3084	27.8445	26.7724	6	3	3	B8NA09	B8NA09	1	AFLA_113050	Asparagine synthetase
26.6061	26.6703	26.6717	27.1267	26.7259	26.7938	2.50E-43	1231600000	7	7	7	31.2	34.465	26.7657	26.6494	26.8821	6	3	3	B8NAU9	B8NAU9	1	AFLA_043240	Prefoldin subunit 3, putative
26.2134	27.1589	26.8407	25.3523	26.1272	25.9333	1.07E-126	1512000000	7	7	7	52	15.817	26.271	26.7377	25.8043	6	3	3	B8NB42	B8NB42	1	AFLA_044170	40S ribosomal protein S11
25.5973	25.5062	25.525	25.7469	25.3687	25.2522	7.57E-21	503810000	7	7	7	30.6	36.561	25.4994	25.5429	25.4559	6	3	3	B8NB55	B8NB55	1	AFLA_044300	SH3 domain protein
25.5655	25.4842	25.3706	ND	25.2558	24.8212	1.06E-51	809280000	7	7	7	19.6	62.144	25.2995	25.4734	25.0385	5	3	2	B8NB71	B8NB71	1	AFLA_044460	Phenylacetyl-CoA ligase, putative
26.8158	27.2267	27.3695	27.1738	26.2515	26.4632	9.29E-73	1624200000	7	7	7	32	32.556	26.8834	27.1374	26.6295	6	3	3	B8NBE2	B8NBE2	1	AFLA_045170	Alpha/beta hydrolase, putative
ND	25.6521	24.0626	25.0049	25.3092	25.4221	6.36E-54	561820000	7	7	7	24.9	33.339	25.0902	24.8573	25.2454	5	2	3	B8NBX2	B8NBX2	1	AFLA_046970	Ribosomal protein L19
ND	24.2859	ND	25.7403	25.9544	27.3903	6.08E-44	542470000	7	7	7	32.2	34.813	25.8427	24.2859	26.3617	4	1	3	B8NDQ5	B8NDQ5	1	AFLA_055460	37S ribosomal protein S9
ND	25.0983	ND	24.7567	24.7496	26.496	1.35E-37	502270000	7	7	7	27.4	52.927	25.2751	25.0983	25.3341	4	1	3	B8NDQ9	B8NDQ9	1	AFLA_055500	SET domain protein
24.665	26.5423	25.0785	26.8649	26.6934	28.7038	5.24E-186	2233400000	7	7	7	43	17.028	26.4247	25.4286	27.4207	6	3	3	B8NDY4	B8NDY4	1	AFLA_056250	Ribosomal protein L14
26.3755	24.6559	24.2406	25.4253	25.9595	27.06	2.57E-32	864390000	7	7	7	39.6	15.129	25.6195	25.0907	26.1483	6	3	3	B8NEA6	B8NEA6	1	AFLA_060150	Ribosomal protein L26
27.7191	27.8476	27.5453	29.2165	28.7802	28.8379	1.55E-178	4158700000	7	7	7	47.9	15.65	28.3244	27.704	28.9449	6	3	3	B8NEG5	B8NEG5	1	AFLA_061630	Single-stranded DNA-binding protein
25.1619	25.1651	25.2908	25.922	25.4693	25.3797	3.42E-47	503800000	7	7	7	15.7	72.065	25.3981	25.2059	25.5903	6	3	3	B8NEQ3	B8NEQ3	1	AFLA_062510	Myosin heavy chain, embryonic smooth muscle isoform, putative
25.5522	ND	25.2896	27.2798	27.4197	26.0914	7.39E-54	656200000	7	7	7	40.5	33.455	26.3266	25.4209	26.9303	5	2	3	B8NF67	B8NF67	1	AFLA_061110	Mono-and diacylglycerol lipase, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
ND	ND	ND	26.3176	26.4487	27.6284	6.27E-88	595050000	7	7	7	45.3	27.389	26.7982	ND	26.7982	3	0	3	B8NFL4	B8NFL4	1	AFLA_131050	Putative uncharacterized protein
27.9475	28.1411	28.1627	28.5307	28.1814	27.9558	1.57E-68	3610700000	7	7	7	62.7	16.274	28.1532	28.0838	28.2226	6	3	3	B8NH12	B8NH12	1	AFLA_132360	Glial factor naturation factor, putative
25.607	25.8158	25.9165	26.6168	25.6867	26.1919	5.76E-22	808370000	7	7	7	19.5	44.23	25.9725	25.7798	26.1651	6	3	3	B8NHC9	B8NHC9	1	AFLA_135340	Acetylornithine aminotransferase
26.2762	26.2972	26.6843	27.0096	26.1375	26.2282	4.44E-50	947160000	7	7	7	22.2	32.652	26.4388	26.4192	26.4584	6	3	3	B8NHP7	B8NHP7	1	AFLA_137410	SAP domain protein, putative
30.6004	30.2041	30.7517	30.0807	30.0009	29.4765	0	12675000000	7	7	7	91.2	15.031	30.1857	30.5187	29.8527	6	3	3	B8NI98	B8NI98	1	AFLA_065940	Glyoxalase family protein
25.695	25.3947	25.5113	26.1359	26.1171	25.8677	3.61E-110	706980000	7	7	7	23.6	47.87	25.7869	25.5336	26.0402	6	3	3	B8NIN1	B8NIN1	1	AFLA_068180	Ethanolamine kinase, putative
25.4296	25.527	25.7162	26.2762	25.9831	25.6361	5.92E-32	991320000	7	7	7	10.5	106.25	25.7614	25.5576	25.9651	6	3	3	B8NIY9	B8NIY9	1	AFLA_070170	Lysosomal alpha-glucosidase, putative
28.1962	28.0889	28.3279	27.7215	27.6136	28.0693	2.45E-44	2368000000	7	7	7	52.6	23.223	28.0029	28.2043	27.8015	6	3	3	B8NJ30	B8NJ30	1	AFLA_071470	Adenine phosphoribosyltransferase 1
28.388	28.4862	28.6209	25.7631	27.8943	26.2536	3.11E-263	1761400000	7	7	7	29.6	46.178	27.5677	28.4984	26.637	6	3	3	B8NJC1	B8NJC1	1	AFLA_065540	Extracellular lipase, putative
26.3516	26.2464	26.6554	26.1868	25.8538	26.0232	4.83E-33	1066800000	7	7	7	24	43.682	26.2195	26.4178	26.0213	6	3	3	B8NJS0	B8NJS0	1	AFLA_068800	Vacuolar ATP synthase subunit c
24.1065	24.1954	24.014	26.7972	24.1295	28.9014	1.50E-36	1432200000	7	7	7	33.1	14.625	25.3573	24.1053	26.6094	6	3	3	B8NJV8	B8NJV8	1	AFLA_069180	60S ribosomal protein L35
25.8559	25.7418	26.0073	26.5532	26.1805	26.0548	1.99E-28	815030000	7	7	7	23	46.047	26.0656	25.8683	26.2629	6	3	3	B8NKG4	B8NKG4	1	AFLA_091300	Chitin biosynthesis protein (ChsS), putative
27.0957	26.8804	27.4387	25.5059	26.5334	26.7248	1.22E-140	1597300000	7	7	7	28	41.309	26.6965	27.1383	26.2547	6	3	3	B8NKS2	B8NKS2	1	AFLA_093260	Oxidoreductase, 2OG-Fe(II) oxygenase family, putative
26.5576	26.5911	26.6473	27.0135	26.9778	26.5111	3.54E-30	1410800000	7	7	7	30.3	30.443	26.7164	26.5987	26.8341	6	3	3	B8NKS3	B8NKS3	1	AFLA_093270	Putative uncharacterized protein
24.3139	24.1193	24.4492	24.4832	24.3617	ND	2.77E-21	364220000	7	7	7	9.8	117.64	24.3455	24.2942	24.4225	5	3	2	B8NLC2	B8NLC2	1	AFLA_090490	Alpha,alpha-trehalose glucohydrolase TreA/Ath1
27.5119	27.3276	27.5834	27.9505	27.481	27.3626	4.04E-26	2242000000	7	7	7	57.7	19.665	27.5362	27.4743	27.598	6	3	3	B8NLP3	B8NLP3	1	AFLA_092590	Peptide methionine sulfoxide reductase
24.4239	23.9972	24.5638	25.1185	24.2233	24.1147	9.21E-13	352130000	7	7	7	24.1	38.345	24.4069	24.3283	24.4855	6	3	3	B8NMD1	B8NMD1	1	AFLA_095630	FAD dependent oxidoreductase superfamily
25.4203	24.7667	24.9653	ND	25.191	25.3015	5.14E-21	529930000	7	7	7	22.8	38.431	25.1289	25.0507	25.2462	5	3	2	B8NP72	B8NP72	1	AFLA_128550	Proline utilization protein PrnX, putative
26.7403	26.707	27.0407	25.7958	26.5548	25.9392	4.69E-45	878770000	7	7	7	23.7	50.16	26.463	26.8294	26.0966	6	3	3	B8NP77	B8NP77	1	AFLA_128600	2-oxoisovalerate dehydrogenase complex alpha subunit, putative
28.5932	28.1313	28.6079	27.1045	26.6726	27.0988	1.49E-19	1965100000	7	7	7	22.9	50.88	27.7014	28.4442	26.9586	6	3	3	B8NQD0	B8NQD0	1	AFLA_006100	HypA-like protein, putative
25.4861	25.6692	25.9784	25.8447	26.3603	25.5619	2.42E-15	664790000	7	7	7	16.9	51.283	25.8168	25.7112	25.9223	6	3	3	B8NQE2	B8NQE2	1	AFLA_006220	Exopolyphosphatase, putative
24.8992	24.5957	24.3498	24.1733	24.5763	24.8615	4.26E-66	593370000	7	7	7	36.6	38.004	24.576	24.6149	24.537	6	3	3	B8NQM7	B8NQM7	1	AFLA_001710	Aldo-keto reductase, putative
26.7136	26.7969	27.4177	27.7727	27.5445	27.5398	3.69E-42	2161300000	7	7	7	24.1	35.104	27.2975	26.9761	27.619	6	3	3	B8NQQ2	B8NQQ2	1	AFLA_001960	Aldehyde dehydrogenase, putative
26.9163	27.3405	26.9055	28.1145	27.7455	27.4106	1.27E-48	2034100000	7	7	7	26.1	48.983	27.4055	27.0541	27.7569	6	3	3	B8NRB1	B8NRB1	1	AFLA_005860	Chromatin assembly factor 1 subunit C, putative
28.2576	27.3629	28.1833	28.4138	27.7323	27.5814	1.28E-123	3703200000	7	7	7	28.7	31.509	27.9219	27.9346	27.9091	6	3	3	B8NSP2	B8NSP2	1	AFLA_049930	Putative uncharacterized protein
27.7424	27.8563	28.0041	27.6829	27.8	27.5335	5.27E-88	2566600000	7	7	7	37.8	29.495	27.7699	27.8676	27.6721	6	3	3	B8NSX2	B8NSX2	1	AFLA_051650	Phosphoserine phosphatase, putative
25.026	25.5751	25.5601	25.2327	25.2855	25.4527	5.72E-29	349790000	7	7	7	29.2	55.59	25.3554	25.3871	25.3237	6	3	3	B8NSX9	B8NSX9	1	AFLA_051720	Ubiquinone biosynthesis monooxgenase (Coq6), putative
26.8072	26.9779	27.0552	25.8018	25.4211	25.3384	4.18E-30	1194700000	7	7	7	18.5	55.226	26.2336	26.9468	25.5204	6	3	3	B8NTG9	B8NTG9	1	AFLA_098090	BAR adaptor protein RVS167, putative
25.59	25.4478	ND	ND	25.7562	ND	2.75E-20	519170000	7	7	7	22	47.268	25.598	25.5189	25.7562	3	2	1	B8NU30	B8NU30	1	AFLA_102010	Class V chitinase, putative
26.3993	26.2132	26.5186	25.9258	26.2332	25.6007	2.10E-45	829710000	7	7	7	17.2	72.541	26.1485	26.3771	25.9199	6	3	3	B8NUZ1	B8NUZ1	1	AFLA_102850	Rho GTPase activator (Rgd1), putative
25.9768	26.2159	26.0774	25.8806	25.8646	25.7656	8.09E-36	878680000	7	7	7	14.9	81.138	25.9635	26.0901	25.837	6	3	3	B8NV84	B8NV84	1	AFLA_103790	Chitin synthase activator (Chs3), putative
26.6561	26.6633	26.5805	26.5472	26.5274	26.4921	7.40E-61	1038500000	7	7	7	19.8	53.852	26.5778	26.6333	26.5222	6	3	3	B8NVU0	B8NVU0	1	AFLA_117770	DnaJ domain protein
26.9453	26.5264	27.2327	26.5633	25.8925	25.7763	3.76E-21	977290000	7	7	7	23.4	41.897	26.4894	26.9015	26.0774	6	3	3	B8NWK8	B8NWK8	1	AFLA_120450	Porphyromonas-type peptidyl-arginine deiminase superfamily
30.4757	29.3644	30.644	28.2283	28.9868	27.9628	7.28E-225	5662100000	7	7	7	20.6	45.559	29.277	30.1613	28.3926	6	3	3	B8NWT9	B8NWT9	1	AFLA_121260	Aspartic-type endopeptidase, putative
25.0876	25.5341	25.1397	26.1357	26.1033	25.2139	5.62E-20	448600000	7	7	7	9.3	127.59	25.5357	25.2538	25.8176	6	3	3	B8NXT9	B8NXT9	1	AFLA_009090	Nuclear serine protease HtrA2/Nma111, putative
ND	25.5224	25.4373	26.2366	25.5118	25.8117	2.23E-20	513890000	7	7	7	30.9	36.288	25.704	25.4799	25.8534	5	2	3	B8NYA7;B8	B8NYA7	2	AFLA_010770	Porphobilinogen deaminase Hem3, putative
29.1326	28.0455	28.7053	27.1815	27.2266	26.9638	8.98E-217	5089300000	7	7	7	16.8	60.796	27.8759	28.6278	27.1239	6	3	3	B8NYN2	B8NYN2	1	AFLA_012020	Carboxypeptidase S1, putative
24.4366	24.9186	24.172	25.3491	25.1931	24.9364	1.27E-14	325120000	7	7	7	6.6	131.93	24.8343	24.5091	25.1595	6	3	3	B8NYP1	B8NYP1	1	AFLA_012110	Cleavage and polyadenylation specificity factor subunit A, putative
28.5103	28.3158	27.5828	25.8779	27.9168	27.7601	3.32E-115	2170200000	7	7	7	48.6	23.448	27.6606	28.1363	27.1849	6	3	3	B8NYQ3	B8NYQ3	1	AFLA_012230	Putative uncharacterized protein
26.108	26.6678	26.3492	25.963	25.4101	25.9749	1.70E-74	726120000	8	7	7	32.2	48.212	26.0788	26.375	25.7827	6	3	3	B8N3P2	B8N3P2	1	AFLA_031260	Proteasome regulatory particle subunit Rpt3, putative
27.58	27.6743	27.7292	26.5414	27.7095	27.1847	1.74E-85	2954200000	8	8	7	39.3	22.303	27.4032	27.6611	27.1452	6	3	3	B8NRE5;B8	B8NRE5	3	AFLA_007120	Secretion related GTPase SrgB/Ypt1
24.4927	25.7907	24.4378	25.7688	26.0326	26.3925	1.77E-23	368090000	8	8	7	14.7	88.797	25.4858	24.907	26.0646	6	3	3	B8NYP7	B8NYP7	1	AFLA_012170	U5 snRNP component Snu114, putative
ND	26.1135	ND	26.7288	28.0275	28.6681	7.62E-21	1644200000	8	8	8	22.4	55.064	27.3845	26.1135	27.8082	4	1	3	B8MW24	B8MW24	1	AFLA_073710	Mitochondrial ribosomal protein DAP3, putative
28.7328	28.6011	28.7791	28.9091	28.9812	28.6233	1.64E-130	5369400000	8	8	8	44	24.89	28.7711	28.7043	28.8379	6	3	3	B8MW52	B8MW52	1	AFLA_073990	Proteasome subunit beta type
25.4293	25.9024	25.5349	26.0053	25.7952	25.6292	1.06E-26	616100000	8	8	8	27.2	45.433	25.7161	25.6222	25.8099	6	3	3	B8MXQ8	B8MXQ8	1	AFLA_078450	COP9 signalosome subunit CsnD
26.9605	26.7912	27.0121	26.9654	26.5104	26.5911	1.17E-14	1509800000	8	8	8	17.6	71.422	26.8051	26.9213	26.689	6	3	3	B8MY40	B8MY40	1	AFLA_079770	Endothelin-converting enzyme
27.6763	28.0819	26.5119	27.6956	27.9974	28.1713	2.76E-196	1910600000	8	8	8	40.1	32.288	27.6891	27.4234	27.9548	6	3	3	B8MY65	B8MY65	1	AFLA_080020	ATP synthase subunit gamma
28.0412	27.8585	28.0499	26.9688	27.6701	27.4672	1.70E-57	2054500000	8	8	8	36.4	38.083	27.676	27.9832	27.3687	6	3	3	B8MYC0	B8MYC0	1	AFLA_080570	F-actin capping protein beta subunit
28.5669	28.484	28.5389	27.1487	26.9053	27.1982	6.52E-129	2120700000	8	8	8	23.3	60.343	27.807	28.5299	27.0841	6	3	3	B8MYN6	B8MYN6	1	AFLA_081750	T-complex protein 1, beta subunit, putative
27.9088	27.7212	27.7313	28.028	28.1667	27.872	1.87E-60	2579300000	8	8	8	34.4	40.11	27.9047	27.7871	28.0223	6	3	3	B8MZ09	B8MZ09	1	AFLA_082980	Dihydroorotase, homodimeric type
25.7221	25.6058	25.7199	25.1548	25.5553	25.4297	7.51E-17	559510000	8	8	8	10.7	110.4	25.5313	25.6826	25.3799	6	3	3	B8N020	B8N020	1	AFLA_086600	Morphogenesis protein (Msb1), putative
30.6911	30.3053	30.705	30.7243	30.4841	30.0783	1.95E-299	15767000000	8	8	8	16.7	93.134	30.498	30.5671	30.4289	6	3	3	B8N0Y3	B8N0Y3	1	AFLA_027580	Iron superoxide dismutase A, putative
29.1861	29.5607	29.5691	ND	22.2598	22.2618	0	3586100000	8	8	8	48	31.217	26.5675	29.4386	22.2608	5	3	2	B8N1G5	B8N1G5	1	AFLA_030300	Putative uncharacterized protein
27.4849	26.9565	27.4624	26.8701	27.0709	26.4882	2.21E-71	1729100000	8	8	8	43.6	34.316	27.0555	27.3013	26.8097	6	3	3	B8N1S7	B8N1S7	1	AFLA_032310	Putative uncharacterized protein
27.6116	27.9371	27.262	26.4254	26.4469	26.1929	3.31E-34	1292200000	8	8	8	20.9	58.992	26.9793	27.6036	26.3551	6	3	3	B8N1U7	B8N1U7	1	AFLA_032510	Galactokinase
26.8634	26.751	26.3391	24.6765	26.3113	26.4246	5.90E-21	753760000	8	8	8	27.4	40.976	26.2276	26.6512	25.8041	6	3	3	B8N223	B8N223	1	AFLA_034170	MAP kinase FUS3/KSS1
27.9311	27.7459	28.1307	28.2078	27.7383	27.8772	1.64E-151	2688900000	8	8	8	27.5	54.829	27.9385	27.9359	27.9411	6	3	3	B8N2F9	B8N2F9	1	AFLA_036440	Alanine aminotransferase, putative
29.9646	29.7931	30.1164	30.4993	30.2858	29.9809	0	12915000000	8	8	8	62.5	21.722	30.1067	29.958	30.2553	6	3	3	B8N2M0	B8N2M0	1	AFLA_037950	6,7-dimethyl-8-ribityllumazine synthase
27.1696	26.876	27.0564	27.1098	27.0934	27.1017	2.08E-39	1770000000	8	8	8	34.6	25.364	27.0678	27.034	27.1016	6	3	3	B8N2W4	B8N2W4	1	AFLA_024880	Putative uncharacterized protein
27.8787	27.697	27.8467	27.1359	27.6935	27.5769	2.20E-167	2410500000	8	8	8	53.7	21.024	27.6381	27.8075	27.4688	6	3	3	B8N2X1	B8N2X1	1	AFLA_024950	ARP2/3 complex subunit Arc18, putative
24.9572	26.7066	26.0434	26.8517	27.2327	28.6217	6.72E-207	4858800000	8	8	8	49	22.811	26.7356	25.9024	27.5687	6	3	3	B8N3J9	B8N3J9	1	AFLA_029020	40S ribosomal protein S8
27.6233	27.813	28.0852	25.8909	26.7012	26.6531	2.71E-130	1247000000	8	8	8	41.5	21.621	27.1278	27.8405	26.4151	6	3	3	B8N4M7	B8N4M7	1	AFLA_037320	Rho GTPase Rho1
ND	22.8816	ND	25.7837	25.3849	26.1485	4.08E-24	287490000	8	8	8	27	51.308	25.0497	22.8816	25.7724	4	1	3	B8N570	B8N570	1	AFLA_021980	30S ribosomal subunit S4, putative
25.2014	25.3644	25.1707	25.2581	25.7515	25.8003	1.27E-19	511180000	8	8	8	7.8	162.01	25.4244	25.2455	25.6033	6	3	3	B8N581	B8N581	1	AFLA_022090	Putative uncharacterized protein
27.2844	26.5787	26.7833	27.2968	27.4228	26.8737	6.95E-26	1619100000	8	8	8	15.1	89.195	27.0399	26.8821	27.1978	6	3	3	B8N584	B8N584	1	AFLA_022120	C-24(28) sterol reductase
26.1869	26.1221	26.6077	24.901	24.8414	24.8386	2.02E-18	699440000	8	8	8	22.1	53.768	25.583	26.3056	24.8603	6	3	3	B8N592	B8N592	1	AFLA_022200	Mitochondrial cytochrome b2, putative
28.7682	28.5607	28.8436	27.7877	28.001	28.2452	2.74E-113	3087400000	8	8	8	20.6	66.965	28.3677	28.7241	28.0113	6	3	3	B8N6G8	B8N6G8	1	AFLA_014810	Prolyl-tRNA synthetase
28.2501	28.1096	28.4332	28.0664	27.9375	27.6296	5.60E-106	3260500000	8	8	8	37.6	38.354	28.0711	28.2643	27.8778	6	3	3	B8N6L6	B8N6L6	1	AFLA_015290	Putative uncharacterized protein

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
26.4696	26.1947	26.3613	26.4043	26.38	26.0665	7.03E-25	940490000	8	8	8	30.1	41.009	26.3127	26.3419	26.2836	6	3	3	B8N6S0	B8N6S0	1	AFLA_016730	Alanine racemase
27.9261	27.0868	27.5735	27.0056	27.7478	27.4758	1.67E-68	2697600000	8	8	8	30.4	32.116	27.4693	27.5288	27.4097	6	3	3	B8N7K8	B8N7K8	1	AFLA_104510	Methyltransferase family protein
27.5016	26.9622	27.6209	26.9626	27.4022	26.856	1.17E-32	1223500000	8	8	8	17.6	64.958	27.2176	27.3616	27.0736	6	3	3	B8N8J0	B8N8J0	1	AFLA_107840	AMP dependent CoA ligase, putative
27.4201	27.8218	27.3277	28.4367	28.1279	27.9184	3.44E-90	3157900000	8	8	8	30.6	34.3	27.8421	27.5232	28.161	6	3	3	B8N9G2	B8N9G2	1	AFLA_111080	AT DNA binding protein (Thy28), putative
24.8427	25.9931	23.1045	26.9402	27.1496	28.6498	1.04E-96	2142800000	8	8	8	45.1	20.059	26.1133	24.6468	27.5799	6	3	3	B8N9R3	B8N9R3	1	AFLA_112090	60S ribosomal protein L11
26.0998	26.7831	25.6439	26.1892	25.7626	26.4492	4.82E-39	875550000	8	8	8	25.9	55.879	26.1546	26.1756	26.1337	6	3	3	B8N9T1	B8N9T1	1	AFLA_112270	Translation initiation factor EF-2 gamma subunit, putative
ND	ND	ND	24.6225	24.5824	26.4286	2.92E-57	203070000	8	8	8	34.1	30.478	25.2112	ND	25.2112	3	0	3	B8N9W4	B8N9W4	1	AFLA_112600	37S ribosomal protein Rsm25
26.1166	25.787	26.2774	ND	24.5586	24.6443	1.41E-24	339310000	8	8	8	11.7	97.024	25.4768	26.0603	24.6014	5	3	2	B8NAA2	B8NAA2	1	AFLA_113980	Cyclin dependent kinase inhibitor Pho81, putative
27.2932	27.2685	27.3302	27.6135	27.3798	27.3567	2.79E-119	1996600000	8	8	8	48.2	24.963	27.3736	27.2973	27.45	6	3	3	B8NAZ4	B8NAZ4	1	AFLA_043690	Phosphoribosylglycinamide formyltransferase, putative
26.3941	25.8713	26.6497	26.1553	25.7728	25.595	1.86E-41	1017600000	8	8	8	34.6	29.692	26.073	26.305	25.841	6	3	3	B8NB70	B8NB70	1	AFLA_044450	Putative uncharacterized protein
29.1028	30.7601	29.3335	32.6169	32.0884	32.3418	7.10E-271	33806000000	8	8	8	95.4	11.087	31.0406	29.7321	32.3491	6	3	3	B8NB77	B8NB77	1	AFLA_044520	60S acidic ribosomal protein P2/allergen Asp F 8
27.4514	27.3232	27.2696	26.4947	27.1227	27.0763	9.44E-101	1332800000	8	8	8	42	25.286	27.123	27.3481	26.8979	6	3	3	B8NBU0	B8NBU0	1	AFLA_046650	Orotidine 5-phosphate decarboxylase
31.6856	31.9602	31.8599	26.905	28.9694	26.4019	3.00E-277	20497000000	8	8	8	27.3	46.686	29.6303	31.8353	27.4254	6	3	3	B8NCF7	B8NCF7	1	AFLA_041320	Acid phosphatase, putative
24.0435	25.8384	23.8402	26.044	27.0887	28.3801	1.33E-44	1379100000	8	8	8	33.6	26.174	25.8725	24.574	27.1709	6	3	3	B8NCW4	B8NCW4	1	AFLA_041990	60S ribosomal protein L17
27.1053	27.4097	27.2218	27.0037	27.1031	26.9692	1.20E-31	1857900000	8	8	8	35.3	39.971	27.1355	27.2456	27.0253	6	3	3	B8ND22	B8ND22	1	AFLA_054930	DUF410 domain protein
27.5696	27.5209	27.4608	27.5964	27.7013	27.6089	7.24E-75	2170700000	8	8	8	51.4	23.558	27.5763	27.5171	27.6355	6	3	3	B8ND51	B8ND51	1	AFLA_055220	Hsp70 nucleotide exchange factor (Fes1), putative
24.2805	25.4493	24.726	26.1025	25.4525	25.7852	1.10E-86	733840000	8	8	8	15.4	81.967	25.2994	24.8186	25.7801	6	3	3	B8NDC1	B8NDC1	1	AFLA_056820	Geranylgeranyl pyrophosphate synthase, putative
27.1145	26.4977	27.4177	26.8417	25.4605	26.0635	1.70E-141	1171500000	8	8	8	40.6	28.162	26.5659	27.01	26.1219	6	3	3	B8NDC4	B8NDC4	1	AFLA_056850	Electron transfer flavoprotein, beta subunit, putative
26.9047	27.4986	27.5333	26.8251	26.5156	26.511	1.26E-60	1611900000	8	8	8	51.7	20.811	26.9647	27.3122	26.6172	6	3	3	B8NDR9	B8NDR9	1	AFLA_055600	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase
24.5838	26.107	26.0179	27.0613	27.2589	25.9318	7.46E-33	557990000	8	8	8	30.5	51.349	26.1601	25.5696	26.7506	6	3	3	B8NEF9	B8NEF9	1	AFLA_060680	Dimethylallyl tryptophan synthase, putative
23.6023	23.8978	ND	24.7605	26.5064	26.4628	8.90E-27	353540000	8	8	8	24.4	51.673	25.046	23.7501	25.9099	5	2	3	B8NFE9;B8	B8NFE9	2	AFLA_062830	Monoxygenase, putative
26.3423	26.424	26.084	26.3251	26.1847	26.758	1.62E-27	1097100000	8	8	8	22.6	45.817	26.353	26.2834	26.4226	6	3	3	B8NFS9	B8NFS9	1	AFLA_133580	Casein kinase I, putative
26.3346	26.6938	26.9119	26.0062	24.9284	25.839	3.98E-117	958350000	8	8	8	35.4	33.553	26.119	26.6468	25.5912	6	3	3	B8NG94	B8NG94	1	AFLA_134340	BAR domain protein
29.1486	29.306	29.3387	30.2225	29.439	29.569	3.71E-57	8671700000	8	8	8	47.3	12.139	29.504	29.2644	29.7435	6	3	3	B8NGN0	B8NGN0	1	AFLA_136570	Cytochrome c
25.9155	25.7134	26.1485	26.0545	26.0459	26.018	1.77E-32	777000000	8	8	8	52.9	26.124	25.9826	25.9258	26.0395	6	3	3	B8NGT1	B8NGT1	1	AFLA_137990	Putative uncharacterized protein
24.2188	ND	24.5313	24.5247	24.3178	24.4041	6.12E-12	226450000	8	8	8	4.8	233.83	24.3993	24.3751	24.4155	5	2	3	B8NH76	B8NH76	1	AFLA_133000	Pre-mRNA splicing factor (Prp8), putative
26.7135	26.4214	26.9891	27.0389	26.8733	26.6074	2.22E-22	1203500000	8	8	8	22.9	44.083	26.7739	26.708	26.8399	6	3	3	B8NH99	B8NH99	1	AFLA_135040	cAMP-dependent protein kinase catalytic subunit PkaC1
27.1881	27.229	26.9464	27.6231	27.2997	27.1359	2.57E-20	1551600000	8	8	8	36.4	34.857	27.237	27.1212	27.3529	6	3	3	B8NIN2	B8NIN2	1	AFLA_068190	CORD and CS domain protein
25.9605	26.0305	26.5172	26.5898	25.9948	26.5531	2.26E-41	702510000	8	8	8	17.7	68.069	26.2743	26.1694	26.3792	6	3	3	B8NIR3	B8NIR3	1	AFLA_069410	RNase L inhibitor of the ABC superfamily, putative
28.6835	28.4808	28.6274	28.4032	28.3094	28.1078	3.56E-140	4252900000	8	8	8	39.8	30.254	28.4353	28.5972	28.2735	6	3	3	B8NIT8	B8NIT8	1	AFLA_069660	TIM-barrel enzyme family protein
25.5998	26.9188	26.6539	24.9304	25.3283	25.1661	1.69E-24	460830000	8	8	8	12.6	103.24	25.7662	26.3908	25.1416	6	3	3	B8NJP5	B8NJP5	1	AFLA_068550	Coatomer subunit beta
29.1533	29.13	29.5422	29.1051	28.8219	28.7253	0	5760700000	8	8	8	61.1	23.675	29.0796	29.2752	28.8841	6	3	3	B8NJR9	B8NJR9	1	AFLA_068790	Adenylyl-sulfate kinase
28.0312	27.6109	28.0529	28.6998	28.2305	28.064	3.03E-106	3353100000	8	8	8	57.6	21.331	28.1149	27.8984	28.3315	6	3	3	B8NKG0	B8NKG0	1	AFLA_091260	Glucosamine 6-phosphate acetyltransferase, putative
28.525	28.6965	28.8165	28.9038	28.5247	28.4833	6.47E-250	4987300000	8	8	8	70.1	15.646	28.6583	28.6793	28.6373	6	3	3	B8NKK9	B8NKK9	1	AFLA_091750	Putative uncharacterized protein
26.923	27.5478	25.7283	27.3678	27.7113	27.8014	1.20E-269	2544200000	8	8	8	39.4	26.044	27.1799	26.733	27.6268	6	3	3	B8NLG2	B8NLG2	1	AFLA_090890	ATP synthase subunit E, putative
25.9852	26.9692	26.1372	ND	25.0444	ND	5.45E-36	543530000	8	8	8	19	62.607	26.034	26.3639	25.0444	4	3	1	B8NM53	B8NM53	1	AFLA_094850	Glucose-methanol-choline (Gmc) oxidoreductase, putative
26.1301	26.3121	26.3937	28.3089	26.9875	28.1553	1.33E-111	3207900000	8	8	8	35.2	25.832	27.0479	26.2786	27.8172	6	3	3	B8NMC5	B8NMC5	1	AFLA_095570	RNA annealing protein Yra1, putative
26.7343	26.6967	27.0616	28.8412	27.5968	27.605	7.51E-88	1492500000	8	8	8	55.5	23.667	27.4226	26.8309	28.0143	6	3	3	B8NMK2	B8NMK2	1	AFLA_124380	Putative uncharacterized protein
26.7217	26.7986	27.1154	28.1803	26.9728	27.3097	2.36E-90	1429400000	8	8	8	38.1	32.663	27.1831	26.8785	27.4876	6	3	3	B8NMQ3	B8NMQ3	1	AFLA_126660	Ankyrin repeat protein
25.4843	27.059	25.5751	29.1277	29.1166	30.8271	2.17E-105	5038200000	8	8	8	47.4	15.612	27.865	26.0395	29.6905	6	3	3	B8NMV9	B8NMV9	1	AFLA_127220	60S ribosomal protein L27
25.4914	25.091	25.217	25.4278	24.9518	25.3517	5.49E-19	483640000	8	8	8	16.5	69.73	25.2551	25.2665	25.2437	6	3	3	B8NNF9	B8NNF9	1	AFLA_127700	VHS domain protein
29.3276	30.1561	30.0761	26.8434	27.7385	29.0403	0	4562800000	8	8	8	52.5	16.407	28.8637	29.8533	27.8741	6	3	3	B8NNY3	B8NNY3	1	AFLA_125890	40S ribosomal protein S17, putative
26.0652	26.3287	26.5943	27.384	26.856	26.6102	2.97E-77	1192500000	8	8	8	33.9	48.828	26.6397	26.3294	26.9501	6	3	3	B8NPF1	B8NPF1	1	AFLA_130230	Heterogeneous nuclear ribonucleoprotein HRP1
26.774	26.4629	26.6242	26.9779	26.8542	26.7788	1.43E-66	1394200000	8	8	8	37	39.99	26.7454	26.6204	26.8703	6	3	3	B8NQ82	B8NQ82	1	AFLA_004730	Ribokinase
28.9775	28.7356	29.1041	29.1623	28.967	28.6709	4.30E-133	8809500000	8	8	8	82.4	12.091	28.9363	28.9391	28.9334	6	3	3	B8NQA5	B8NQA5	1	AFLA_004960	Antibiotic biosynthesis monooxygenase family protein
27.5669	27.5643	27.582	28.0365	27.9766	27.7516	5.66E-97	2670500000	8	8	8	26.9	42.264	27.7463	27.5711	27.9216	6	3	3	B8NQG2	B8NQG2	1	AFLA_006420	Cdc48-dependent protein degradation adaptor protein (Shp1), putative
26.8863	27.6732	25.4149	26.1838	28.2599	28.7769	2.61E-94	1881800000	8	8	8	45.6	32.883	27.1992	26.6582	27.7402	6	3	3	B8NQL8	B8NQL8	1	AFLA_007000	Ubiquinol-cytochrome C reductase complex core protein 2, putative
26.3742	26.4771	26.4455	27.221	26.7905	26.7953	2.95E-48	1324900000	8	8	8	13.8	82.063	26.6839	26.4323	26.9356	6	3	3	B8NRD6	B8NRD6	1	AFLA_007030	RNA binding protein Nrd1, putative
25.4454	25.8663	26.0876	25.5688	25.7416	25.7295	9.01E-14	631530000	8	8	8	9.1	123.55	25.7399	25.7998	25.68	6	3	3	B8NRM5	B8NRM5	1	AFLA_049300	mRNA-nucleus export ATPase (Elf1), putative
25.1363	25.7942	26.1831	25.1131	25.19	25.0811	6.19E-50	1026200000	8	8	8	51.4	16.551	25.4163	25.7046	25.1281	6	3	3	B8NRS4;RE	B8NRS4	2	AFLA_050650	40S ribosomal protein S19
26.3961	25.8252	25.2732	24.0388	25.0335	24.0417	1.05E-34	365740000	8	8	8	13.7	93.414	25.1014	25.8315	24.3713	6	3	3	B8NRX2	B8NRX2	1	AFLA_051140	Probable beta-glucosidase A
27.4052	25.964	26.9021	25.1391	25.4617	25.4711	1.16E-46	802070000	8	8	8	20.3	63.876	26.0572	26.7571	25.3573	6	3	3	B8NS16	B8NS16	1	AFLA_052470	Gamma-glutamyltranspeptidase
25.2158	24.6964	25.4418	24.2689	24.5866	24.0545	6.65E-46	564460000	8	8	8	32	35.307	24.7107	25.118	24.3033	6	3	3	B8NSB2	B8NSB2	1	AFLA_054340	Isoflavone reductase family protein
22.5658	26.0784	22.4432	32.205	31.5464	31.8542	6.41E-114	15300000000	8	8	8	37	16.959	27.7822	23.6958	31.8686	6	3	3	B8NSF1	B8NSF1	1	AFLA_048140	60S ribosomal protein L23
26.1219	26.5092	26.0801	26.0189	26.3537	26.4183	2.60E-32	876970000	8	8	8	37.7	37.895	26.2503	26.2371	26.2636	6	3	3	B8NSG6	B8NSG6	1	AFLA_048290	Homoserine kinase
28.3907	28.7291	28.094	28.4346	28.513	28.2123	3.33E-51	4679900000	8	8	8	21.4	47.095	28.3956	28.4046	28.3866	6	3	3	B8NSI8	B8NSI8	1	AFLA_048510	UV excision repair protein (RadW), putative
24.9142	ND	25.7888	ND	ND	24.1209	4.18E-22	253650000	8	8	8	19	64.237	24.9413	25.3515	24.1209	3	2	1	B8NSW3	B8NSW3	1	AFLA_051560	Vacuolar protein sorting-associated protein Vps5, putative
27.4134	26.9079	27.5756	26.5174	26.4982	26.7314	3.59E-66	1669700000	8	8	8	57.9	18.977	26.9407	27.299	26.5824	6	3	3	B8NT21	B8NT21	1	AFLA_052140	Putative uncharacterized protein
27.8138	28.0584	28.3421	28.169	28.1561	27.7001	3.11E-214	3019100000	8	8	8	47.2	27.811	28.0399	28.0714	28.0084	6	3	3	B8NTC5	B8NTC5	1	AFLA_097650	Putative uncharacterized protein
27.0336	26.5069	25.5586	27.5284	27.8799	27.4949	2.61E-40	1464500000	8	8	8	19.7	56.603	27.0004	26.3664	27.6344	6	3	3	B8NTN4	B8NTN4	1	AFLA_099650	Woronin body major protein, putative
26.0527	26.9299	26.0466	25.655	27.1319	27.1754	4.79E-40	1218400000	8	8	8	30.3	29.222	26.4986	26.3431	26.6541	6	3	3	B8NUP9	B8NUP9	1	AFLA_101020	40S ribosomal protein S4, putative
24.9906	26.8634	24.8734	27.539	27.9401	28.7472	8.77E-122	1242100000	8	8	8	32.1	22.173	26.8256	25.5758	28.0754	6	3	3	B8NUR3	B8NUR3	1	AFLA_101160	40S ribosomal protein S9
24.202	25.3826	25.2595	28.4932	28.5729	31.7348	1.66E-190	9168200000	8	8	8	49.7	16.827	27.2742	24.948	29.6003	6	3	3	B8NV82	B8NV82	1	AFLA_103770	60S ribosomal protein L27a, putative
28.1356	27.6938	28.4309	28.5682	28.3716	27.8983	2.11E-134	3206400000	8	8	8	44.3	24.327	28.1831	28.0867	28.2794	6	3	3	B8NWI9	B8NWI9	1	AFLA_120260	Nitroreductase family protein, putative
ND	27.289	24.3797	24.5292	24.2246	26.2106	1.65E-25	503860000	8	8	8	16.2	63.696	25.3266	25.8344	24.9881	5	2	3	B8NX59	B8NX59	1	AFLA_122470	CobW domain protein
28.2802	28.0487	28.4712	28.4162	28.0859	27.801	1.34E-59	3488300000	8	8	8	73.1	14.415	28.1839	28.2667	28.101	6	3	3	B8NXX3	B8NXX3	1	AFLA_009430	Putative uncharacterized protein
26.3719	25.9972	26.1913	28.9616	28.3642	28.3394	6.27E-83	1576200000	8	8	8	42.8	25.3	27.3709	26.1868	28.5551	6	3	3	B8NYF4	B8NYF4	1	AFLA_011240	Putative uncharacterized protein
27.7807	28.1007	28.1196	27.4027	27.4418	27.7523	1.02E-46	1819400000	8	8	8	38.9	42.898	27.7663	28.0003	27.5323	6	3	3	B8NYK4	B8NYK4	1	AFLA_011740	Cystathionine gamma-lyase

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
24.7262	23.9052	24.7139	23.2626	24.4493	23.6749	5.04E-41	716610000	8	8	8	21.4	61.89	24.122	24.4484	23.7956	6	3	3	B8NYW3	B8NYW3	1	AFLA_114750	Glutamyl-tRNA(Gln) amidotransferase subunit A, putative
27.2769	26.627	26.9924	26.186	26.4715	26.6335	1.92E-58	1343800000	8	8	8	36.7	43.147	26.6979	26.9654	26.4304	6	3	3	B8NYX1	B8NYX1	1	AFLA_114830	Leucine aminopeptidase 1
26.5704	25.9415	26.7763	25.2865	25.3569	24.9457	1.63E-53	1127700000	9	8	8	40.4	35.853	25.8129	26.4294	25.1963	6	3	3	B8NCW5	B8NCW5	1	AFLA_042000	Hydroxyisocaproate dehydrogenase, putative
27.223	27.4057	27.2097	27.1052	27.1357	27.6935	2.00E-45	1506000000	9	9	8	21.5	67.607	27.2955	27.2795	27.3115	6	3	3	B8NRV2	B8NRV2	1	AFLA_050940	Phenylalanyl-tRNA synthetase, beta subunit
28.698	28.4257	28.6848	24.5785	25.8099	26.2733	9.00E-181	1534600000	9	9	8	31	38.786	27.0784	28.6028	25.5539	6	3	3	B8NU27	B8NU27	1	AFLA_101980	Tartrate dehydrogenase, putative
29.7073	29.1086	29.7475	29.5645	29.9077	29.1625	4.53E-279	7252400000	9	9	8	23.2	57.753	29.533	29.5211	29.5449	6	3	3	B8NWI1	B8NWI1	1	AFLA_120180	Pheromone processing carboxypeptidase (Sxa2), putative
26.1558	25.008	26.2948	ND	24.5571	ND	6.50E-26	425410000	10	8	8	19.5	77.093	25.5039	25.8195	24.5571	4	3	1	B8NXN6	B8NXN6	1	AFLA_008560	Alpha-1,2-mannosidase, putative subfamily
26.4242	26.4663	26.6176	24.8548	25.1215	25.396	2.29E-30	570530000	9	9	9	11.2	123.33	25.8134	26.5027	25.1241	6	3	3	B8MWT5	B8MWT5	1	AFLA_088850	Exportin KapK
27.038	26.1168	26.6943	27.4746	28.3382	28.0231	4.35E-125	1791200000	9	9	9	31.1	43.873	27.2808	26.6164	27.9453	6	3	3	B8MWW3	B8MWW3	1	AFLA_075500	Putative uncharacterized protein
25.6277	25.7729	25.7548	26.0617	25.7726	25.7431	5.75E-21	686800000	9	9	9	15.9	73.932	25.7888	25.7185	25.8591	6	3	3	B8MX62	B8MX62	1	AFLA_076490	RSC complex subunit (RSC8), putative
27.4083	27.103	27.4946	27.4711	27.3014	26.8496	1.38E-47	1700600000	9	9	9	22.9	54.547	27.2713	27.3353	27.2074	6	3	3	B8MXQ3	B8MXQ3	1	AFLA_078400	Protein phosphatase PP2A regulatory subunit B
29.388	29.8878	29.6268	30.1338	29.1813	29.7913	6.46E-64	10974000000	9	9	9	34	28.156	29.6682	29.6342	29.7021	6	3	3	B8MY54	B8MY54	1	AFLA_079910	Glutathione peroxidase
29.933	29.5567	29.9825	29.4033	29.25	28.9466	9.84E-299	12499000000	9	9	9	70	21.813	29.512	29.8241	29.2	6	3	3	B8MYC6	B8MYC6	1	AFLA_080630	NADH-quinone oxidoreductase Pst2, putative
ND	26.252	ND	26.2899	27.2576	27.0477	5.58E-37	825290000	9	9	9	22.8	59.662	26.7118	26.252	26.8651	4	1	3	B8MYE7	B8MYE7	1	AFLA_080850	rRNA processing protein Pwp1, putative
31.1654	31.352	31.1639	31.3132	31.5741	31.2783	0	25664000000	9	9	9	48.6	19.708	31.3078	31.2271	31.3885	6	3	3	B8MYW2	B8MYW2	1	AFLA_082510	TCTP family protein
28.556	28.7723	28.7098	29.0356	28.6059	28.5772	1.18E-176	4762700000	9	9	9	51.2	37.506	28.7095	28.6794	28.7395	6	3	3	B8MZA0	B8MZA0	1	AFLA_083890	Oxidoreductase, zinc-binding dehydrogenase family, putative
27.8709	26.9149	27.6301	27.3753	27.388	26.9129	3.41E-97	2627500000	9	9	9	41.1	26.115	27.3487	27.472	27.2254	6	3	3	B8N056	B8N056	1	AFLA_086960	Fumarylacetoacetate hydrolase family protein
ND	26.7416	ND	28.5766	27.9933	28.0206	2.58E-73	1492900000	9	9	9	48.1	32.591	27.833	26.7416	28.1968	4	1	3	B8N156	B8N156	1	AFLA_028310	Putative uncharacterized protein
25.1135	25.8149	25.0732	27.8778	27.2584	27.2274	9.45E-57	1280100000	9	9	9	37.2	44.826	26.3942	25.3339	27.4546	6	3	3	B8N193	B8N193	1	AFLA_029580	Protein phosphatase PP1 regulatory subunit Sds22, putative
28.9272	28.8762	28.9431	29.4529	29.0903	28.8633	3.51E-119	6628900000	9	9	9	51.2	26.863	29.0255	28.9155	29.1355	6	3	3	B8N1K3	B8N1K3	1	AFLA_030680	Microtubule associated protein EB1, putative
26.7256	25.4453	26.3916	26.3714	27.2178	26.6122	1.35E-38	608210000	9	9	9	39.6	34.993	26.4607	26.1875	26.7338	6	3	3	B8N1U2	B8N1U2	1	AFLA_032460	Pterin-4-alpha-carbinolamine dehydratase, putative
24.8973	24.8062	25.3397	23.7746	23.9795	24.4023	5.06E-18	363280000	9	9	9	4.1	266.87	24.5333	25.0144	24.0521	6	3	3	B8N1V7	B8N1V7	1	AFLA_032610	Ccr4-Not transcription complex subunit (NOT1), putative
26.6638	24.4504	26.1949	ND	23.8437	23.7989	1.23E-28	439260000	9	9	9	24.6	54.14	24.9904	25.7697	23.8213	5	3	2	B8N239	B8N239	1	AFLA_034330	Beta-alanine synthase, putative
26.2334	25.5494	26.1793	26.4792	25.8959	25.8796	2.19E-92	869250000	9	9	9	5.5	263.06	26.0362	25.9874	26.0849	6	3	3	B8N2R2	B8N2R2	1	AFLA_023460	Alpha-1,3-glucan synthase Ags1
27.1113	27.3366	27.1478	26.9438	27.1643	27.005	1.58E-69	1549600000	9	9	9	43.4	37.416	27.1181	27.1986	27.0377	6	3	3	B8N3P7	B8N3P7	1	AFLA_031310	ATPase get3
28.3532	28.1042	28.3138	26.9655	27.8848	27.7255	6.16E-296	2885400000	9	9	9	76.2	20.442	27.8912	28.2571	27.5253	6	3	3	B8N3W5	B8N3W5	1	AFLA_031990	Actin-related protein 2/3 complex subunit 5
28.9322	28.8206	28.069	29.1793	29.755	29.6331	0	7643900000	9	9	9	75.9	20.375	29.0649	28.6072	29.5225	6	3	3	B8N4E8	B8N4E8	1	AFLA_035610	DUF967 domain protein
28.0249	27.669	28.0413	29.3862	28.9511	28.8965	1.46E-188	5104600000	9	9	9	24.3	47.589	28.4948	27.9117	29.0779	6	3	3	B8N599	B8N599	1	AFLA_022270	Putative uncharacterized protein
28.5875	28.0726	28.3695	28.4172	28.2394	27.9659	5.94E-173	4742100000	9	9	9	32	54.187	28.2753	28.3432	28.2075	6	3	3	B8N5Q5	B8N5Q5	1	AFLA_013980	Aminopeptidase, putative
28.9281	28.9502	28.9708	29.1397	28.9476	28.8675	7.38E-180	5727900000	9	9	9	45.8	29.718	28.9673	28.9497	28.9849	6	3	3	B8N5R2	B8N5R2	1	AFLA_014050	Pyrroline-5-carboxylate reductase
26.0237	25.4917	25.8928	24.3712	24.1324	25.0155	1.06E-25	344160000	9	9	9	25.7	53.612	25.1546	25.8027	24.5064	6	3	3	B8N5S1	B8N5S1	1	AFLA_014140	Aldehyde dehydrogenase family protein, putative
26.9982	26.9265	27.4386	26.4869	26.2781	26.0048	4.24E-67	904890000	9	9	9	43.5	37.713	26.6888	27.1211	26.2566	6	3	3	B8N5U3	B8N5U3	1	AFLA_014360	Serine/threonine-protein phosphatase
27.315	27.3386	27.2532	27.3002	27.283	27.1756	6.65E-76	2225600000	9	9	9	24.5	56.764	27.2776	27.3023	27.253	6	3	3	B8N6C9	B8N6C9	1	AFLA_018930	Adenylyl cyclase-associated protein
26.2163	26.973	26.8388	ND	25.1804	24.3554	3.00E-26	806380000	9	9	9	14.7	114.12	25.9128	26.676	24.7679	5	3	2	B8N6J1	B8N6J1	1	AFLA_015040	Importin beta-5 subunit, putative
27.3976	27.17	27.5681	27.0276	27.0036	27.117	5.67E-61	1527600000	9	9	9	29.5	45.829	27.214	27.3786	27.0494	6	3	3	B8N6W4	B8N6W4	1	AFLA_017170	Histidinol-phosphate aminotransferase
25.9775	24.5489	25.1404	25.4956	ND	ND	4.68E-25	902590000	9	9	9	31.8	37.43	25.2906	25.2222	25.4956	4	3	1	B8N7P3	B8N7P3	1	AFLA_104860	Leucoanthocyanidin dioxygenase, putative
27.0732	27.7462	26.7706	25.9218	26.3603	26.6054	1.53E-61	1321400000	9	9	9	28.4	48.634	26.7462	27.1967	26.2958	6	3	3	B8N7Y1	B8N7Y1	1	AFLA_105740	Sulfide quinone reductase, putative
28.5607	28.3372	28.4104	28.0868	28.5403	28.307	6.37E-128	4228100000	9	9	9	55.7	29.976	28.3737	28.4361	28.3114	6	3	3	B8N8C6	B8N8C6	1	AFLA_107200	F-actin capping protein alpha subunit, putative
27.7981	27.7389	27.9504	28.4387	27.9156	27.7849	1.23E-94	3297200000	9	9	9	26.9	45.682	27.9378	27.8291	28.0464	6	3	3	B8N8E4	B8N8E4	1	AFLA_107380	PWWP domain protein
28.876	28.7751	29.0208	30.1173	29.6804	29.4315	6.60E-298	6775500000	9	9	9	65.3	26.615	29.3169	28.8906	29.7431	6	3	3	B8N8N3	B8N8N3	1	AFLA_108270	Formyltetrahydrofolate deformylase, putative
26.5995	26.1613	26.7772	26.3228	26.3661	25.9354	2.09E-89	1296800000	9	9	9	37.6	44.286	26.3604	26.5126	26.2081	6	3	3	B8N8P6	B8N8P6	1	AFLA_108410	Dipeptidase
28.1962	28.1793	28.2526	28.9116	28.5588	28.2846	1.02E-71	3741000000	9	9	9	66.9	17.881	28.3972	28.2093	28.585	6	3	3	B8N9D1	B8N9D1	1	AFLA_110770	DUF757 domain protein
26.5948	26.1846	25.9382	25.7734	26.6231	26.715	1.46E-46	1169200000	9	9	9	32.1	34.893	26.3048	26.2392	26.3705	6	3	3	B8N9G0	B8N9G0	1	AFLA_111060	Calcium homeostasis protein Regucalcin, putative
28.7161	28.5528	28.6247	28.5442	28.2729	27.8669	1.42E-169	4479600000	9	9	9	45.5	32.025	28.4296	28.6312	28.228	6	3	3	B8N9L6	B8N9L6	1	AFLA_111620	Succinate-semialdehyde dehydrogenase Uga2, putative
27.2718	27.3962	27.5631	28.0198	27.7546	27.4781	4.35E-73	1972500000	9	9	9	14.3	88.836	27.5806	27.4103	27.7508	6	3	3	B8N9M2	B8N9M2	1	AFLA_111680	Elongation factor G, mitochondrial
27.5955	27.3694	26.8974	26.8051	26.0257	26.3241	1.13E-44	1002100000	9	9	9	25.2	56.896	26.8362	27.2874	26.385	6	3	3	B8N9M6	B8N9M6	1	AFLA_111720	Glycylpeptide N-tetradecanoyltransferase
25.4121	25.2993	25.3371	25.972	25.9951	25.7638	1.17E-40	555670000	9	9	9	25.6	54.956	25.6299	25.3495	25.9103	6	3	3	B8NBM7	B8NBM7	1	AFLA_046020	Thiamine biosynthetic bifunctional enzyme, putative
26.4335	25.491	25.7908	27.5758	27.6132	26.8307	4.65E-41	1316100000	9	9	9	46	36.683	26.6225	25.9051	27.3399	6	3	3	B8NBQ3	B8NBQ3	1	AFLA_046280	Mitochondrial inner membrane nuclease Nuc1, putative
21.9837	ND	21.2545	26.2642	28.8373	25.9388	1.45E-49	683850000	9	9	9	20.6	69.301	24.8557	21.6191	27.0134	5	2	3	B8NC58	B8NC58	1	AFLA_038530	Extracellular metalloproteinase mep
29.8465	29.4004	29.5633	30.7724	30.3249	30.0971	0	13731000000	9	9	9	29.7	43.181	30.0008	29.6034	30.3981	6	3	3	B8NE68	B8NE68	1	AFLA_057990	Purine nucleoside permease, putative
27.3939	27.1583	27.1992	ND	ND	ND	7.84E-34	1066200000	9	9	9	20	74.118	27.2504	27.2504	ND	3	3	0	B8NEP7	B8NEP7	1	AFLA_062450	Sphingomyelin phosphodiesterase, putative
28.1976	28.3527	28.3357	29.1561	28.3469	28.726	8.26E-124	5432700000	9	9	9	48.4	23.642	28.5192	28.2953	28.743	6	3	3	B8NFY1	B8NFY1	1	AFLA_131420	Uridylate kinase Ura6
26.3976	26.7102	26.4817	26.4044	26.2137	25.8388	3.85E-30	976440000	9	9	9	54.3	28.929	26.3411	26.5298	26.1523	6	3	3	B8NG46	B8NG46	1	AFLA_132070	Putative uncharacterized protein
23.9362	24.3008	24.2159	27.7423	27.1664	26.9385	5.42E-31	897210000	9	9	9	58.6	28.548	25.7167	24.151	27.2824	6	3	3	B8NG47	B8NG47	1	AFLA_132080	Small nuclear ribonucleoprotein U2, A
27.0444	27.4633	27.1602	27.4462	26.8801	26.937	2.49E-66	1537200000	9	9	9	42	37.926	27.1552	27.2226	27.0878	6	3	3	B8NG53	B8NG53	1	AFLA_132140	Pantoate--beta-alanine ligase
26.4383	26.296	26.7682	26.2961	26.3221	25.7625	5.72E-26	945030000	9	9	9	67.6	25.538	26.3139	26.5009	26.1269	6	3	3	B8NGB5	B8NGB5	1	AFLA_134550	HD family hydrolase, putative
26.2722	26.4578	26.5559	27.0764	26.7036	26.5637	3.63E-27	1128400000	9	9	9	6.5	160.85	26.6049	26.4287	26.7812	6	3	3	B8NGK9	B8NGK9	1	AFLA_136360	GYF domain protein
27.1028	27.2597	27.4767	27.4066	27.0735	27.1419	5.68E-140	2187900000	9	9	9	55.7	36.758	27.2435	27.2797	27.2073	6	3	3	B8NH13	B8NH13	1	AFLA_132370	Molybdopterin binding domain protein
25.2106	23.8857	24.9155	ND	ND	ND	9.31E-35	554340000	9	9	9	25.1	58.984	24.6706	24.6706	ND	3	3	0	B8NH51	B8NH51	1	AFLA_132750	Putative uncharacterized protein
26.6164	25.5683	25.9143	25.0583	25.3112	24.4372	6.37E-36	704240000	9	9	9	30.2	47.815	25.4843	26.033	24.9356	6	3	3	B8NI96	B8NI96	1	AFLA_065920	Putative uncharacterized protein
27.9706	27.6282	27.835	28.2151	27.8531	27.8589	1.50E-56	3006200000	9	9	9	27.7	44.468	27.8935	27.8113	27.9757	6	3	3	B8NIJ9	B8NIJ9	1	AFLA_067860	Tyrosinase, putative
27.3686	27.1527	27.2065	27.3454	27.6216	27.0497	7.15E-30	1762500000	9	9	9	32.1	55.01	27.2907	27.2426	27.3389	6	3	3	B8NK55	B8NK55	1	AFLA_071040	Nicotinate phosphoribosyltransferase
26.6041	26.7558	26.4309	25.8304	26.7403	27.0106	3.30E-34	1186400000	9	9	9	29.9	43.451	26.562	26.597	26.5271	6	3	3	B8NKK2	B8NKK2	1	AFLA_091680	Putative uncharacterized protein
25.6123	25.7552	26.0544	27.2957	26.4311	26.7925	1.07E-29	933500000	9	9	9	29.9	45.901	26.3236	25.8073	26.8398	6	3	3	B8NKT3	B8NKT3	1	AFLA_093370	Ribonucleotide reductase small subunit RnrA, putative
30.9719	31.2726	30.3977	26.4859	25.8126	26.8714	0	6918600000	9	9	9	69.4	12.309	28.6354	30.8807	26.39	6	3	3	B8NL17	B8NL17	1	AFLA_096010	Putative uncharacterized protein
ND	23.3063	ND	26.8708	25.3825	26.9413	3.30E-21	529130000	9	9	9	21.7	48.134	25.6252	23.3063	26.3982	4	1	3	B8NLT8	B8NLT8	1	AFLA_093940	Mitochondrial large ribosomal subunit YmL35, putative
25.7573	24.722	24.4299	ND	24.7651	ND	0	2817400000	9	9	9	51.5	42.308	24.9186	24.9697	24.7651	4	3	1	B8NLX2	B8NLX2	1	AFLA_094280	Agmatinase, putative
30.0612	30.4324	30.3232	31.0495	30.7715	30.4226	5.67E-117	17396000000	9	9	9	43.6	27.256	30.5101	30.2723	30.7479	6	3	3	B8NMC7	B8NMC7	1	AFLA_095590	Hsp90 binding co-chaperone (Sba1), putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
24.4706	ND	23.7448	23.1135	23.2821	23.2681	5.88E-146	1275600000	9	9	9	24	74.712	23.5758	24.1077	23.2212	5	2	3	B8NMK6	B8NMK6	1	AFLA_124420	Amine oxidase, putative
27.4398	26.1366	27.1386	ND	25.3639	25.216	2.30E-22	594040000	9	9	9	33.2	32.784	26.259	26.905	25.29	5	3	2	B8NMM6	B8NMM6	1	AFLA_126390	Oxidoreductase 2-nitropropane dioxygenase family, putative
26.3284	25.9278	26.2935	27.4734	26.3679	26.6859	1.29E-73	811380000	9	9	9	19.9	59.701	26.5128	26.1832	26.8424	6	3	3	B8NMQ5	B8NMQ5	1	AFLA_126680	WD repeat-containing protein, putative
27.0809	27.5221	27.6769	25.375	25.5023	26.6421	1.93E-43	829610000	9	9	9	21.8	61.088	26.6332	27.4266	25.8398	6	3	3	B8NNG4	B8NNG4	1	AFLA_127750	T-complex protein 1, eta subunit, putative
26.5739	26.5094	26.8578	26.904	26.754	26.6587	2.70E-89	1407300000	9	9	9	31.8	50.501	26.7096	26.647	26.7722	6	3	3	B8NNH4	B8NNH4	1	AFLA_127850	Putative uncharacterized protein
27.2036	27.218	27.1763	26.9306	26.8479	26.875	1.14E-45	1409300000	9	9	9	26.7	53.615	27.0419	27.1993	26.8845	6	3	3	B8NPF4	B8NPF4	1	AFLA_130260	Chromatin remodeling and histone acetyltransferase complexes subunit
26.5499	26.3237	26.6857	25.6398	26.2891	25.9349	6.18E-39	776020000	9	9	9	18.5	74.533	26.2372	26.5198	25.9546	6	3	3	B8NQD2	B8NQD2	1	AFLA_006120	Glutamine dependent NAD+ synthetase, putative
26.2184	25.685	26.1847	25.5746	26.0719	25.429	4.42E-39	777680000	9	9	9	25.5	46.12	25.8606	26.0294	25.6918	6	3	3	B8NQD3	B8NQD3	1	AFLA_006130	NADH pyrophosphatase, putative
26.5596	26.2332	26.3304	25.0633	25.7287	ND	3.41E-24	618910000	9	9	9	12.9	110.1	25.983	26.3744	25.396	5	3	2	B8NQF1	B8NQF1	1	AFLA_006310	Alpha glucosidase II, alpha subunit, putative
28.5815	28.6895	27.9841	26.629	27.0822	27.4071	1.25E-81	1965700000	9	9	9	43	42.286	27.7289	28.4184	27.0394	6	3	3	B8NRK3	B8NRK3	1	AFLA_049080	Biotin synthase, putative
28.158	28.748	28.5399	31.1171	30.8179	30.7315	3.11E-105	9848400000	9	9	9	54.7	16.338	29.6854	28.482	30.8888	6	3	3	B8NRT9	B8NRT9	1	AFLA_050800	40S ribosomal protein S12
25.5952	25.4811	25.0518	25.8773	26.2403	26.2475	7.01E-29	627120000	9	9	9	15	86.695	25.7488	25.376	26.1217	6	3	3	B8NS12	B8NS12	1	AFLA_052430	Alpha,alpha-trehalase TreB/Nth1
27.4927	27.1023	27.3376	28.2291	27.989	27.9544	6.16E-139	2484400000	9	9	9	59	27.683	27.6842	27.3109	28.0575	6	3	3	B8NSD6	B8NSD6	1	AFLA_047890	Cytosine deaminase-uracil phosphoribosyltransferase fusion protein
27.9978	28.2233	28.0157	29.0579	28.7676	28.542	4.77E-194	3766600000	9	9	9	65.6	20.966	28.4341	28.0789	28.7892	6	3	3	B8NSE4	B8NSE4	1	AFLA_048070	Inosine triphosphate pyrophosphatase
29.3487	29.4292	29.426	30.3189	30.0077	29.8381	0	8835300000	9	9	9	51.8	26.568	29.7281	29.4013	30.0549	6	3	3	B8NSI6	B8NSI6	1	AFLA_048490	Translation initiation factor eIF-6, putative
27.9802	27.9511	27.8967	26.959	27.793	27.7546	4.91E-48	2696900000	9	9	9	33.2	45.072	27.7225	27.9427	27.5022	6	3	3	B8NTV8	B8NTV8	1	AFLA_101290	FAD binding domain protein
27.6568	29.5156	28.0315	30.5549	29.107	30.1109	0	21912000000	9	9	9	82.5	16.008	29.1628	28.4013	29.9243	6	3	3	B8NUD8	B8NUD8	1	AFLA_099000	Superoxide dismutase [Cu-Zn]
27.0096	26.7203	26.973	27.018	27.0116	26.6921	5.45E-34	1400800000	9	9	9	58.9	30.67	26.9041	26.9009	26.9072	6	3	3	B8NUM7	B8NUM7	1	AFLA_100800	Dihydrofolate reductase
26.913	26.8535	27.552	26.895	27.2928	26.8856	2.99E-58	1415100000	9	9	9	40.4	36.363	27.0653	27.1062	27.0245	6	3	3	B8NV88	B8NV88	1	AFLA_103830	OTU-like cysteine protease, putative
26.5853	25.3321	26.3839	ND	24.2081	25.2428	4.58E-21	413620000	9	9	9	15.2	68.837	25.5505	26.1004	24.7255	5	3	2	B8NVS5	B8NVS5	1	AFLA_117620	Putative uncharacterized protein
28.2606	28.2075	28.431	28.5715	28.1588	28.2526	9.81E-147	3654100000	9	9	9	56.7	27.707	28.3137	28.2997	28.3276	6	3	3	B8NW54	B8NW54	1	AFLA_118010	Cap binding protein
31.523	31.5693	31.7043	31.773	31.4443	31.3668	0	37124000000	9	9	9	67.8	16.985	31.5634	31.5988	31.528	6	3	3	B8NWC7	B8NWC7	1	AFLA_119640	Cofilin
27.2179	27.5309	27.4566	27.4521	27.7093	27.7831	2.65E-122	2665200000	10	9	9	39.8	39.492	27.525	27.4018	27.6482	6	3	3	B8MVY2	B8MVY2	1	AFLA_073290	Phospho-2-dehydro-3-deoxyheptonate aldolase
26.3901	26.9493	27.0376	25.3939	25.4289	25.8072	2.93E-58	866940000	10	9	9	32.1	43.417	26.1678	26.7923	25.5433	6	3	3	B8NZ22	B8NZ22	1	AFLA_115340	Proteasome regulatory particle subunit Rpt6, putative
26.5489	28.0178	26.4407	27.5041	27.3179	28.3394	1.06E-99	1327100000	11	9	9	39.5	36.003	27.3615	27.0025	27.7205	6	3	3	B8NAL4	B8NAL4	1	AFLA_042390	Glyceraldehyde-3-phosphate dehydrogenase
25.9039	25.4747	25.9253	25.6523	25.7235	25.3025	1.73E-31	809530000	10	10	10	15.9	98.082	25.6637	25.768	25.5594	6	3	3	B8MW10	B8MW10	1	AFLA_073570	RhoGAP and Fes/CIP4 domain protein
27.5873	28.4896	27.8255	27.6639	28.2376	29.0957	1.94E-51	3494100000	10	10	10	62.5	21.888	28.15	27.9675	28.3324	6	3	3	B8MWE7	B8MWE7	1	AFLA_088370	60S ribosomal protein L9, putative
25.1408	25.4607	25.0454	28.6492	27.6807	27.5688	3.13E-49	1832400000	10	10	10	42.5	35.332	26.5909	25.2156	27.9662	6	3	3	B8MWP8	B8MWP8	1	AFLA_075060	Transformer-SR ribonucleoprotein, putative
25.4727	25.8779	25.6321	26.2043	25.5385	25.829	8.76E-18	625290000	10	10	10	11.3	115.13	25.7591	25.6609	25.8572	6	3	3	B8MXA6	B8MXA6	1	AFLA_076930	Importin, putative
27.0387	27.4927	27.2105	28.0182	27.7037	27.4491	3.65E-107	2034000000	10	10	10	48.5	37.292	27.4855	27.2473	27.7237	6	3	3	B8MXS7	B8MXS7	1	AFLA_078640	Methylenetetrahydrofolate dehydrogenase
27.6898	27.4631	27.7298	27.0419	26.5399	26.2644	6.19E-73	1720200000	10	10	10	21.6	78.809	27.1215	27.6276	26.6154	6	3	3	B8MY11	B8MY11	1	AFLA_079480	Oligopeptidase family protein
23.3562	ND	ND	ND	24.0926	23.4825	1.13E-163	2825200000	10	10	10	39.9	39.669	23.6438	23.3562	23.7876	3	1	2	B8MYC9	B8MYC9	1	AFLA_080660	L-asparaginase
27.5941	27.6688	27.4879	26.9265	27.2712	27.2213	1.11E-85	1993400000	10	10	10	55	23.473	27.3616	27.5836	27.1396	6	3	3	B8MYJ0	B8MYJ0	1	AFLA_081280	Ras GTPase Rab11, putative
28.0183	28.2578	28.4668	27.2541	27.4241	28.2946	1.26E-57	2019400000	10	10	10	46.3	23.866	27.9526	28.2477	27.6576	6	3	3	B8MZH2	B8MZH2	1	AFLA_084620	40S ribosomal protein S5, putative
25.8084	25.3847	25.992	26.0731	26.125	25.7027	9.40E-41	772470000	10	10	10	37	46.008	25.8476	25.7283	25.9669	6	3	3	B8N099	B8N099	1	AFLA_087400	Oxysterol binding protein (Osh7), putative
27.2521	27.8733	27.7367	28.7468	28.134	28.0841	3.62E-124	3063400000	10	10	10	16.2	108.76	27.9711	27.6207	28.3216	6	3	3	B8N0T0	B8N0T0	1	AFLA_026150	Alpha-glucosidase AgdA, putative
32.6834	32.3921	32.8424	32.5293	32.4394	32.1095	0	74425000000	10	10	10	75.9	18.17	32.4994	32.6393	32.3594	6	3	3	B8N0Z6	B8N0Z6	1	AFLA_027710	Peptidyl-prolyl cis-trans isomerase
26.7534	25.1558	26.9229	27.8073	29.0443	27.6531	4.01E-172	1995800000	10	10	10	46.7	42.571	27.2228	26.2774	28.1682	6	3	3	B8N106	B8N106	1	AFLA_027810	Alkaline protease 1
27.3813	27.8612	28.0006	28.0411	27.9179	27.8873	2.05E-85	2942000000	10	10	10	84.2	15.75	27.8482	27.7477	27.9487	6	3	3	B8N141	B8N141	1	AFLA_028160	Ubiquitin conjugating enzyme (MmsB), putative
27.6816	28.4468	27.6972	28.7968	28.4861	28.4106	5.75E-100	4177000000	10	10	10	37.6	33.508	28.2532	27.9419	28.5645	6	3	3	B8N174	B8N174	1	AFLA_029390	HMG box protein, putative
28.0493	28.817	28.6483	29.8095	29.5508	29.4891	5.03E-223	5867300000	10	10	10	18.2	89.842	29.0607	28.5049	29.6165	6	3	3	B8N1A6	B8N1A6	1	AFLA_029710	Proliferating cell nuclear antigen
27.6549	29.6594	27.5386	31.7868	31.4011	32.0186	0	23994000000	10	10	10	48.9	33.441	30.0099	28.2843	31.7355	6	3	3	B8N1E9	B8N1E9	1	AFLA_030140	60S ribosomal protein P0
28.1692	27.6615	28.0285	28.0165	28.2607	27.6266	2.47E-171	2883600000	10	10	10	40.1	32.75	27.9605	27.953	27.9679	6	3	3	B8N1Q0	B8N1Q0	1	AFLA_031150	Methylglutaconyl-CoA hydratase, mitochondrial, putative
29.2938	28.7656	29.3662	29.7326	30.2266	29.4078	4.18E-202	6324200000	10	10	10	73.3	24.935	29.4654	29.1418	29.789	6	3	3	B8N1U3	B8N1U3	1	AFLA_032470	Phosphoglycolate phosphatase, putative
25.9119	26.3004	25.9695	26.3194	26.255	26.275	5.71E-58	957470000	10	10	10	28.7	56.957	26.1719	26.0606	26.2832	6	3	3	B8N253	B8N253	1	AFLA_034470	Anthranilate synthase component I, putative
23.0937	23.1333	22.5841	23.7642	23.8914	23.6138	3.53E-82	723620000	10	10	10	35.3	53.556	23.3468	22.9371	23.7565	6	3	3	B8N270	B8N270	1	AFLA_034640	Aminopeptidase Y, putative
27.2501	26.9767	27.0499	26.0868	26.2476	26.1582	3.37E-65	1593500000	10	10	10	75.2	23.447	26.6282	27.0922	26.1642	6	3	3	B8N2U0	B8N2U0	1	AFLA_023740	Glutathione S-transferase, putative
28.0314	27.6405	27.4622	27.5125	27.9142	27.5492	1.07E-48	2399000000	10	10	10	34.4	47.84	27.685	27.7114	27.6586	6	3	3	B8N3A4	B8N3A4	1	AFLA_027170	Kynurenine aminotransferase, putative
26.9463	27.1457	27.033	26.0772	26.3194	26.8347	1.20E-45	1168900000	10	10	10	19.8	100.54	26.726	27.0416	26.4104	6	3	3	B8N3D1	B8N3D1	1	AFLA_027440	Aminotransferase, classes I and II, putative
28.4477	28.7923	28.9595	29.3005	29.2376	28.4568	1.11E-161	4393900000	10	10	10	39.3	37.684	28.8657	28.7331	28.9983	6	3	3	B8N3M8	B8N3M8	1	AFLA_029310	Alcohol dehydrogenase, zinc-containing, putative
27.7275	27.5354	27.8111	27.7869	27.4382	27.2339	3.02E-79	3045700000	10	10	10	54.8	28.662	27.5888	27.6913	27.4863	6	3	3	B8N3U8	B8N3U8	1	AFLA_031820	Glutathione S-transferase GstA
27.5371	27.4639	27.3612	27.8791	27.8076	27.5841	7.21E-161	2421400000	10	10	10	49.3	29.518	27.6055	27.4541	27.7569	6	3	3	B8N4B1	B8N4B1	1	AFLA_035240	Proteasome subunit beta type
29.1103	29.0434	29.1308	29.4369	29.4275	28.9607	1.75E-189	7174000000	10	10	10	52.4	32.871	29.1849	29.0948	29.275	6	3	3	B8N4K7	B8N4K7	1	AFLA_037110	Proteasome subunit beta type
27.2333	27.3622	27.8257	27.4963	26.8434	27.5531	1.33E-62	1537200000	10	10	10	37.9	45.511	27.3857	27.4737	27.2976	6	3	3	B8N4L8	B8N4L8	1	AFLA_037230	Chorismate synthase
26.111	26.7108	26.7251	26.1887	26.6127	26.7839	1.95E-48	1017300000	10	10	10	14.7	113.44	26.522	26.5156	26.5285	6	3	3	B8N4X9	B8N4X9	1	AFLA_018380	Anthranilate synthase multifunctional protein TrpC, putative
25.8269	25.5864	26.0207	26.0754	25.6465	25.4628	6.24E-31	693230000	10	10	10	19.3	76.166	25.7698	25.8113	25.7282	6	3	3	B8N782	B8N782	1	AFLA_020150	Glutamate-cysteine ligase Gcs1, putative
27.5095	27.954	27.8174	28.428	27.2924	27.6503	8.47E-52	2318400000	10	10	10	46.8	34.545	27.7752	27.7603	27.7902	6	3	3	B8N794	B8N794	1	AFLA_021160	Aldehyde reductase (AKR1), putative
29.8249	29.1874	29.4401	28.966	29.7176	28.9005	0	10065000000	10	10	10	31.1	56.806	29.3394	29.4841	29.1947	6	3	3	B8N7M4	B8N7M4	1	AFLA_104670	Serine peptidase, putative
27.6371	27.3904	26.9473	28.2192	27.8226	27.5775	1.97E-119	2381800000	10	10	10	38.1	40.025	27.599	27.3249	27.8731	6	3	3	B8N9C3	B8N9C3	1	AFLA_110690	Cytochrome c peroxidase Ccp1, putative
26.9977	27.0135	27.0628	27.2352	27.3826	27.2445	1.65E-54	1671100000	10	10	10	42.9	38.268	27.156	27.0247	27.2874	6	3	3	B8N9L9	B8N9L9	1	AFLA_111650	Threonine dehydratase, biosynthetic
27.1595	26.7722	26.9721	27.1681	26.9155	26.6952	4.41E-62	1404500000	10	10	10	39.5	34.894	26.9471	26.9679	26.9263	6	3	3	B8NA03	B8NA03	1	AFLA_112990	UBX domain protein, putative
ND	24.8706	ND	24.3483	25.1681	28.095	8.72E-38	792110000	10	10	10	29.7	51.166	25.6205	24.8706	25.8705	4	1	3	B8NB59	B8NB59	1	AFLA_044340	Putative uncharacterized protein
28.2031	28.2063	28.3183	28.5724	28.1859	28.0274	0	3847500000	10	10	10	74.6	13.446	28.2522	28.2426	28.2619	6	3	3	B8NBV7	B8NBV7	1	AFLA_046820	Tubulin-specific chaperone Rbl2, putative
26.4478	26.4271	26.7414	27.3226	26.7489	26.2912	2.80E-35	1545900000	10	10	10	31.3	50.921	26.6631	26.5387	26.7876	6	3	3	B8NCQ6	B8NCQ6	1	AFLA_041410	Aldehyde dehydrogenase family protein, putative
28.107	28.0493	27.5112	26.2774	26.0519	27.5489	0	2545200000	10	10	10	41.4	38.305	27.2576	27.8892	26.6261	6	3	3	B8NEK6	B8NEK6	1	AFLA_062040	Stress protein DDR48, putative
ND	25.6162	ND	27.9471	27.3039	28.3741	7.93E-57	1242300000	10	10	10	35.8	44.771	27.3103	25.6162	27.875	4	1	3	B8NEM2	B8NEM2	1	AFLA_062200	Putative uncharacterized protein
26.601	26.6682	26.6105	26.0039	26.8804	26.869	1.08E-52	1467900000	10	10	10	39.1	44.755	26.6055	26.6266	26.5844	6	3	3	B8NFS1	B8NFS1	1	AFLA_133500	HAD superfamily hydrolase, putative
32.1639	32.1485	32.3163	32.3401	31.7585	31.7189	0	60618000000	10	10	10	78.3	15.607	32.0744	32.2096	31.9392	6	3	3	B8NFW3	B8NFW3	1	AFLA_133920	Acyl CoA binding protein family

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 μg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
29.5625	28.0184	27.4776	23.449	27.4401	26.9855	0	4005700000	10	10	10	64.8	17.23	27.1555	28.3528	25.9582	6	3	3	B8NFW5	B8NFW5	1	AFLA_133940	Putative uncharacterized protein
28.5398	28.9943	28.5614	29.5187	29.6793	29.9326	0	6786200000	10	10	10	33.7	50.769	29.2043	28.6985	29.7102	6	3	3	B8NFY0	B8NFY0	1	AFLA_131410	Eukaryotic translation initiation factor 3 subunit M
28.3709	27.0543	28.0678	24.7124	25.9134	25.6259	4.30E-126	1223100000	10	10	10	24.8	49.624	26.6241	27.831	25.4172	6	3	3	B8NGR8	B8NGR8	1	AFLA_137860	Putative uncharacterized protein
29.7299	29.8576	30.1882	30.1386	29.6164	29.0182	3.65E-201	10950000000	10	10	10	64	22.19	29.7582	29.9253	29.5911	6	3	3	B8NH38	B8NH38	1	AFLA_132620	Rho-gdp dissociation inhibitor
28.1369	28.8069	27.6891	29.3549	28.8318	29.2022	3.24E-88	4952700000	10	10	10	47.3	24.181	28.6703	28.2109	29.1296	6	3	3	B8NHE9	B8NHE9	1	AFLA_135540	ATP synthase oligomycin sensitivity conferral protein, putative
27.031	27.2616	27.3251	27.0203	26.9005	26.5559	3.78E-48	1085600000	10	10	10	49.7	33.105	27.0157	27.2059	26.8256	6	3	3	B8NHH4	B8NHH4	1	AFLA_135790	Vesicular-fusion protein sec17
27.3023	26.4082	27.0373	ND	ND	ND	9.27E-34	411810000	10	10	10	44.3	27.896	26.9159	26.9159	ND	3	3	0	B8NHZ4	B8NHZ4	1	AFLA_139300	AflM/ ver-1/ dehydrogenase/ ketoreductase
28.9716	28.0207	28.7675	28.2535	28.9977	28.5807	1.19E-91	4686800000	10	10	10	45.9	34.031	28.5986	28.5866	28.6107	6	3	3	B8NI45	B8NI45	1	AFLA_064500	Putative uncharacterized protein
28.2423	28.7122	29.085	24.9545	24.7889	ND	7.36E-77	2357000000	10	10	10	37.1	45.706	27.1566	28.6798	24.8717	5	3	2	B8NJ90	B8NJ90	1	AFLA_065230	Glycerophosphoryl diester phosphodiesterase family protein
26.7017	26.4892	26.5721	26.3887	25.9638	26.1563	4.57E-26	1297800000	10	10	10	44.4	26.85	26.3786	26.5877	26.1696	6	3	3	B8NKH2	B8NKH2	1	AFLA_091380	Phosphoglycerate mutase family protein
34.3923	34.2901	34.4957	34.6755	34.4162	34.2054	0	2.4121E+11	10	10	10	60.9	23.525	34.4125	34.3927	34.4323	6	3	3	B8NKN3	B8NKN3	1	AFLA_091990	Peptidyl-prolyl cis-trans isomerase
25.5412	25.4696	25.6703	25.0349	24.9718	24.928	3.99E-49	958000000	10	10	10	68.7	22.593	25.2693	25.5604	24.9782	6	3	3	B8NKR2	B8NKR2	1	AFLA_093160	Rab small monomeric GTPase Rab7, putative
26.7618	26.9321	26.9298	25.2759	26.4928	26.6165	3.09E-62	863230000	10	10	10	31.3	58.513	26.5015	26.8746	26.1284	6	3	3	B8NLJ7	B8NLJ7	1	AFLA_092130	Phenylalanyl-tRNA synthetase beta chain cytoplasmic
27.6746	27.6366	27.5856	27.4693	27.6501	27.5387	1.02E-60	2405200000	10	10	10	38.3	36.547	27.5925	27.6323	27.5527	6	3	3	B8NLR0	B8NLR0	1	AFLA_092760	Hydroxymethylbilane synthase, putative
27.3853	27.1923	27.5371	27.3139	27.1091	26.8883	2.03E-50	1924100000	10	10	10	52	28.36	27.2377	27.3716	27.1038	6	3	3	B8NLT5	B8NLT5	1	AFLA_093910	Hydroxyacylglutathione hydrolase, putative
27.0202	27.1775	25.0673	27.9248	28.5143	28.4419	1.71E-139	2491100000	10	10	10	34.8	55.183	27.3577	26.4217	28.2937	6	3	3	B8NLU0	B8NLU0	1	AFLA_093960	Mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative
27.0719	27.0012	27.182	27.1651	26.7752	26.6	5.51E-215	1590400000	10	10	10	54.1	30.536	26.9659	27.085	26.8468	6	3	3	B8NLW5	B8NLW5	1	AFLA_094210	Chorismate mutase
26.5703	26.9111	26.7797	27.0585	26.6317	26.4837	2.11E-58	1169200000	10	10	10	24.7	60.647	26.7392	26.7537	26.7246	6	3	3	B8NLZ3	B8NLZ3	1	AFLA_094490	Protein phosphatase 2C, putative
27.6446	27.2893	27.6631	27.0792	26.3374	26.4575	1.50E-50	1077900000	10	10	10	25.1	73.215	27.0785	27.5323	26.6247	6	3	3	B8NPH7	B8NPH7	1	AFLA_130490	Ubiquitin carboxyl-terminal hydrolase
27.6516	27.683	27.7681	26.8158	27.012	27.0964	2.66E-142	2300200000	10	10	10	34.5	49.46	27.3378	27.7009	26.9747	6	3	3	B8NQH0	B8NQH0	1	AFLA_006520	CRAL/TRIO domain protein
28.9007	28.0982	28.7444	28.3147	28.7783	28.0788	4.41E-154	4352400000	10	10	10	23.2	63.769	28.4858	28.5811	28.3906	6	3	3	B8NQR5	B8NQR5	1	AFLA_002090	Extracellular serine carboxypeptidase, putative
27.0336	26.9567	27.3388	27.5961	27.4113	27.0659	9.82E-96	1729000000	10	10	10	44.4	30.601	27.2337	27.1097	27.3578	6	3	3	B8NQU8	B8NQU8	1	AFLA_002420	Defective in cullin neddylation protein
28.1406	28.5346	27.3941	27.4538	28.6796	28.7865	0	4684600000	10	10	10	47.4	37.661	28.1649	28.0231	28.3066	6	3	3	B8NQV7	B8NQV7	1	AFLA_002510	Actin monomer binding protein, putative
28.1091	28.2016	27.8831	28.9597	28.7547	28.5487	1.54E-160	4593600000	10	10	10	30.4	53.426	28.4095	28.0646	28.7544	6	3	3	B8NQW0	B8NQW0	1	AFLA_003440	Translation initiation factor 4B
27.1808	27.4449	27.0331	28.0407	27.4833	27.4101	1.19E-88	1967500000	10	10	10	17.5	79.165	27.4321	27.2196	27.6447	6	3	3	B8NRY5	B8NRY5	1	AFLA_051270	DnaJ and TPR domain protein
28.0613	27.7186	27.7672	28.2445	28.2051	27.8184	4.65E-136	2856000000	10	10	10	42.6	40.212	27.9692	27.849	28.0893	6	3	3	B8NS61	B8NS61	1	AFLA_052920	Putative GTP cyclohydrolase 1 type 2
27.1601	28.2393	26.926	26.2897	27.0656	26.8282	7.88E-72	2095200000	10	10	10	37.5	29.21	27.0848	27.4418	26.7278	6	3	3	B8NSD4	B8NSD4	1	AFLA_047870	40S ribosomal protein S1
26.9641	26.7902	27.3241	25.6242	25.0035	24.8382	6.42E-34	1306600000	10	10	10	42.1	30.2	26.0907	27.0261	25.1553	6	3	3	B8NSH8	B8NSH8	1	AFLA_048410	BAR adaptor protein RVS161, putative
26.6751	26.4014	26.4376	26.1367	27.0553	26.8012	1.63E-112	1448100000	10	10	10	28.2	55.205	26.5845	26.5047	26.6644	6	3	3	B8NTJ2	B8NTJ2	1	AFLA_098320	Conserved fungal protein
26.72	26.7596	26.827	26.7548	26.4895	26.3089	1.48E-57	1378300000	10	10	10	33.7	59.093	26.6433	26.7689	26.5177	6	3	3	B8NUB3	B8NUB3	1	AFLA_098750	Serine/threonine-protein phosphatase
27.3612	27.3186	27.2691	26.1597	26.9619	27.0751	7.39E-143	1683800000	10	10	10	36	38.785	27.0243	27.3163	26.7322	6	3	3	B8NW40	B8NW40	1	AFLA_117870	Thiosulfate sulfurtransferase, putative
25.891	25.2812	25.6072	28.0268	27.7626	27.2584	1.02E-158	903530000	10	10	10	24.7	65.47	26.6379	25.5931	27.6826	6	3	3	B8NX52	B8NX52	1	AFLA_122400	Glucoamylase
29.0172	29.2156	29.2831	29.0077	29.1292	30.2064	4.64E-103	5749000000	10	10	10	53.5	17.943	29.3099	29.172	29.4478	6	3	3	B8NXT0	B8NXT0	1	AFLA_009000	Ribosomal protein S13p/S18e
26.7385	24.1602	26.0639	ND	24.2564	23.5686	3.16E-29	328680000	10	10	10	7.5	229.88	24.9575	25.6542	23.9125	5	3	2	B8NY92	B8NY92	1	AFLA_010620	Nonribosomal siderophore peptide synthase Sid2
28.5397	28.0454	28.5776	27.9412	27.8751	27.3917	5.42E-216	3804100000	10	10	10	57.1	28.833	28.0618	28.3875	27.736	6	3	3	B8NYC3	B8NYC3	1	AFLA_010930	Glutathione S-transferase family protein, putative
27.6099	27.6323	27.9004	25.5271	26.7484	27.391	8.78E-105	1352000000	10	10	10	36.7	42.97	27.1348	27.7142	26.5555	6	3	3	B8NYJ6	B8NYJ6	1	AFLA_011660	Putative uncharacterized protein
28.5363	28.5593	28.6057	27.5927	27.3424	27.6235	3.57E-188	2514300000	11	10	10	32.5	59.145	28.0433	28.5671	27.5195	6	3	3	B8MX20	B8MX20	1	AFLA_076070	Septin AspB
24.6715	27.6135	25.6828	25.7539	25.704	26.39	7.41E-82	710000000	11	10	10	31.9	50.409	25.9693	25.9893	25.9493	6	3	3	B8N6T0	B8N6T0	1	AFLA_016830	Tubulin subunit TubB
29.214	29.0908	28.9112	28.246	28.561	28.6292	9.65E-188	6236700000	11	11	10	35	33.833	28.7754	29.072	28.4787	6	3	3	B8NH15	B8NH15	1	AFLA_132390	Oxidoreductase, short chain dehydrogenase/reductase family
27.0641	27.2304	26.7956	26.832	27.364	27.3129	2.32E-32	1031500000	11	10	10	32.8	45.502	27.0999	27.0301	27.1696	6	3	3	B8NQ69	B8NQ69	1	AFLA_004600	Eukaryotic translation initiation factor eIF-4A subunit, putative
28.8926	28.7156	28.3326	26.305	27.13	27.7217	6.06E-213	2246800000	11	11	10	40.6	44.435	27.8496	28.6469	27.0522	6	3	3	B8NRA6	B8NRA6	1	AFLA_005810	Septin
27.3136	27.3843	27.3714	27.258	26.8298	26.6968	4.50E-96	1532800000	11	11	11	44.1	39.208	27.1423	27.3565	26.9282	6	3	3	B8MW92	B8MW92	1	AFLA_087820	Cell wall integrity signaling protein Lsp1/Pil1, putative
28.4386	29.6447	29.1987	28.8978	28.4963	29.6872	1.18E-284	6604600000	11	11	11	61	20.02	29.0605	29.094	29.0271	6	3	3	B8MWG7	B8MWG7	1	AFLA_088570	Putative uncharacterized protein
27.819	26.1508	27.2396	24.6461	26.1348	25.2649	1.23E-43	1406400000	11	11	11	23.2	58.726	26.2092	27.0698	25.3486	6	3	3	B8MWJ5	B8MWJ5	1	AFLA_074520	Probable alpha-galactosidase A
28.2246	28.9514	28.9433	27.2809	27.4956	28.9348	2.42E-101	4598600000	11	11	11	55.2	25.898	28.3051	28.7064	27.9038	6	3	3	B8MWS7	B8MWS7	1	AFLA_088770	Guanylate kinase
29.2062	29.2706	29.304	29.6081	29.6532	29.3257	1.41E-256	8611100000	11	11	11	67.7	30.174	29.3946	29.2603	29.529	6	3	3	B8MX97	B8MX97	1	AFLA_076840	Proteasome subunit alpha type
27.2069	27.6455	27.507	28.1742	27.5475	27.7844	1.74E-45	2443400000	11	11	11	26.3	65.149	27.6442	27.4531	27.8354	6	3	3	B8MYE1	B8MYE1	1	AFLA_080790	TPR domain protein
28.3173	27.8147	28.5981	27.9386	28.3379	27.5058	1.12E-78	3031600000	11	11	11	80.5	26.482	28.0854	28.2434	27.9274	6	3	3	B8MZH5	B8MZH5	1	AFLA_084650	Palmitoyltransferase with autoacylation activity Pfa4, putative
28.232	27.6288	28.1163	27.8616	27.965	27.5995	6.25E-87	2970200000	11	11	11	86.3	16.691	27.9005	27.9924	27.8087	6	3	3	B8MZT0	B8MZT0	1	AFLA_085700	Arsenate reductase (Arc2), putative
25.5472	29.859	25.4268	31.2545	30.5547	30.671	0	11098000000	11	11	11	53.5	34.847	28.8855	26.9444	30.8267	6	3	3	B8MZV8	B8MZV8	1	AFLA_085980	Regulatory protein SUAPRGA1
28.6169	28.857	28.7015	29.1544	28.9949	28.8861	0	5830800000	11	11	11	51.4	31.14	28.8685	28.7251	29.0118	6	3	3	B8MZX7	B8MZX7	1	AFLA_086170	Proteasome regulatory particle subunit (RpnL), putative
27.9208	25.8572	27.8284	28.9999	27.8972	27.8977	5.37E-155	3283800000	11	11	11	48.1	31.082	27.7335	27.2022	28.2649	6	3	3	B8N042	B8N042	1	AFLA_086820	Pyruvate dehydrogenase complex component Pdx1, putative
28.1484	28.073	27.8934	27.3349	27.9873	28.4117	5.04E-51	2758500000	11	11	11	36.7	31.135	27.9748	28.0382	27.9113	6	3	3	B8N083	B8N083	1	AFLA_087240	Glutathione S-transferase, putative
27.4907	27.2237	27.5755	27.2494	27.3031	26.9336	1.48E-34	1627900000	11	11	11	14.3	92.036	27.296	27.43	27.1621	6	3	3	B8N0I3	B8N0I3	1	AFLA_024260	Glycosyl hydrolase, putative
27.7994	27.568	26.4473	25.1214	28.8906	27.9953	6.43E-83	2590500000	11	11	11	35.5	51.803	27.3037	27.2716	27.3358	6	3	3	B8N134	B8N134	1	AFLA_028090	Biotin-dependent 2-oxo acid dehydrogenases acyltransferase, putative
25.7697	27.599	26.5756	28.0485	28.2939	31.267	0	7674800000	11	11	11	38.8	28.509	27.9256	26.6481	29.2031	6	3	3	B8N180	B8N180	1	AFLA_029450	Ribosomal L18ae protein family
27.0488	26.867	27.287	27.4838	27.0796	26.9336	6.21E-58	1555200000	11	11	11	38.4	37.741	27.1166	27.0676	27.1657	6	3	3	B8N1X3	B8N1X3	1	AFLA_032770	Dihydroneopterin aldolase domain protein
28.1631	28.2998	28.0828	26.8054	26.8007	27.102	9.53E-114	1609700000	11	11	11	35.5	48.625	27.5423	28.1819	26.9027	6	3	3	B8N2E0	B8N2E0	1	AFLA_036250	GDP-mannose pyrophosphorylase A
28.777	28.7755	28.9651	29.3158	29.2382	28.9119	3.76E-116	6481000000	11	11	11	60.5	28.673	28.9973	28.8392	29.1553	6	3	3	B8N2L0	B8N2L0	1	AFLA_037850	Proteasome component Prs3, putative
28.0265	27.7956	28.0723	28.2983	27.7982	27.3927	1.15E-166	2960000000	11	11	11	60.4	31.226	27.8973	27.9648	27.8297	6	3	3	B8N2Z4	B8N2Z4	1	AFLA_025180	Cleavage and polyadenylation specific factor 5
24.9364	26.8903	25.6489	26.982	27.3725	27.6486	1.08E-91	1697300000	11	11	11	12.2	118.75	26.5798	25.8252	27.3343	6	3	3	B8N3G3	B8N3G3	1	AFLA_028660	Mitochondrial translation initiation factor IF-2, putative
28.8718	29.1107	29.1454	30.3235	28.3565	29.5861	6.63E-220	5940400000	11	11	11	35.4	31.06	29.2323	29.0426	29.422	6	3	3	B8N3U4	B8N3U4	1	AFLA_031780	Telomere and ribosome associated protein Stm1, putative
32.2693	31.7467	32.375	31.1869	31.3549	30.5972	0	29089000000	11	11	11	79	23.229	31.5883	32.1303	31.0463	6	3	3	B8N419	B8N419	1	AFLA_033420	Superoxide dismutase
28.7698	26.1093	28.1859	ND	25.9447	23.9171	9.92E-95	1708200000	11	11	11	31.6	57.045	26.5854	27.6883	24.9309	5	3	2	B8N4G1	B8N4G1	1	AFLA_036640	PH domain protein
26.6364	26.1658	26.3796	26.5125	26.2588	26.0199	4.07E-65	1106800000	11	11	11	16.8	94.06	26.3288	26.394	26.2637	6	3	3	B8N4S3	B8N4S3	1	AFLA_017820	Putative uncharacterized protein
28.5678	28.3174	28.598	26.8917	28.1015	27.8509	2.58E-103	2966300000	11	11	11	44.5	42.51	28.0546	28.4944	27.6147	6	3	3	B8N5B8	B8N5B8	1	AFLA_022460	Dimeric dihydrodiol dehydrogenase, putative
24.907	ND	ND	24.6361	24.9333	24.0445	4.41E-63	552620000	11	11	11	14.4	115.12	24.6302	24.907	24.538	4	1	3	B8N6J8	B8N6J8	1	AFLA_015110	Putative uncharacterized protein
27.6669	27.186	27.657	27.0583	27.267	27.0131	1.84E-43	1960100000	11	11	11	28.2	51.849	27.308	27.5033	27.1128	6	3	3	B8N6M2	B8N6M2	1	AFLA_015350	Aldehyde dehydrogenase family protein, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
24.1529	ND	ND	27.8637	28.7051	29.0357	2.82E-101	1165500000	11	11	11	42.8	48.89	27.4394	24.1529	28.5349	4	1	3	B8N6Q7	B8N6Q7	1	AFLA_016600	Putative uncharacterized protein
27.9623	27.7317	28.1958	28.1066	27.4013	28.0179	3.51E-78	2727800000	11	11	11	65.5	22.54	27.9026	27.9633	27.8419	6	3	3	B8N7G0	B8N7G0	1	AFLA_021820	Nuclear movement protein NudC
28.4615	28.1866	28.6953	27.7327	27.7942	27.4697	5.94E-172	2759900000	11	11	11	50.6	35.175	28.0567	28.4478	27.6656	6	3	3	B8N8X0	B8N8X0	1	AFLA_109160	Isopentenyl-diphosphate delta-isomerase
27.2188	26.2038	27.1854	25.7308	26.965	26.0822	1.19E-113	1880400000	11	11	11	37.2	39.317	26.5643	26.8693	26.2593	6	3	3	B8N8Y6	B8N8Y6	1	AFLA_109320	3-hydroxyisobutyrate dehydrogenase
28.7436	28.7153	28.8642	29.1197	29.0707	28.5659	0	6995200000	11	11	11	54.5	24.59	28.8465	28.7744	28.9187	6	3	3	B8N940	B8N940	1	AFLA_109860	Translation elongation factor eEF-1B gamma subunit, putative
25.6264	25.802	26.0507	26.1633	25.8833	25.7343	9.38E-28	733040000	11	11	11	12.8	121.52	25.8767	25.8264	25.9269	6	3	3	B8N9V3	B8N9V3	1	AFLA_112490	Ubiquitin fusion degradation protein UfdB, putative
27.3552	27.5535	26.8135	27.237	27.5994	27.87	1.91E-70	2069400000	11	11	11	49.7	35.221	27.4048	27.2407	27.5688	6	3	3	B8N9W8	B8N9W8	1	AFLA_112640	Mitochondrial acetolactate synthase small subunit, putative
29.174	29.0158	28.8141	27.9644	28.0604	28.5295	4.57E-144	3081800000	11	11	11	45.6	34.16	28.593	29.0013	28.1848	6	3	3	B8NA93	B8NA93	1	AFLA_113890	Nuclear pore complex subunit (SEC13), putative
28.3601	26.8915	27.998	26.7248	27.5125	26.7946	4.67E-251	3588600000	11	11	11	34.8	45.012	27.3803	27.7499	27.0107	6	3	3	B8NAS6	B8NAS6	1	AFLA_043010	Formamidase FmdS
25.2142	26.8945	25.4231	26.6549	25.7976	26.4483	1.56E-44	861690000	11	11	11	13.4	108.24	26.0721	25.8439	26.3003	6	3	3	B8NB84	B8NB84	1	AFLA_044590	Nonsense-mediated mRNA decay protein (Nmd5), putative
27.3917	27.28	27.5862	26.7457	26.864	26.513	8.55E-45	1852900000	11	11	11	27.9	76.31	27.0634	27.4193	26.7076	6	3	3	B8NB89	B8NB89	1	AFLA_044640	Fatty acid activator Faa4, putative
29.1133	29.302	29.6337	30.3364	29.9816	29.8557	1.15E-236	9028300000	11	11	11	40.4	31.538	29.7038	29.3497	30.0579	6	3	3	B8NB96	B8NB96	1	AFLA_044710	Eukaryotic translation initiation factor 3 subunit G
ND	ND	ND	28.7561	28.874	28.9034	2.15E-73	2776500000	11	11	11	28.9	46.84	28.8445	ND	28.8445	3	0	3	B8NBM6	B8NBM6	1	AFLA_046010	Eukaryotic translation initiation factor 5, putative
29.066	28.6179	29.0195	27.5769	29.2996	28.7658	8.08E-100	4803300000	11	11	11	60	28.447	28.7243	28.9012	28.5474	6	3	3	B8NBN0	B8NBN0	1	AFLA_046050	GDSL Lipase/Acylhydrolase family protein
27.901	27.7465	27.8827	25.9688	25.4948	27.3738	1.33E-112	2640800000	11	11	11	28.8	51.2	27.0613	27.8434	26.2791	6	3	3	B8NCF1	B8NCF1	1	AFLA_041260	Ribosome associated DnaJ chaperone Zuotin, putative
31.2415	31.4221	31.2081	31.4717	31.3303	31.3609	0	27185000000	11	11	11	80.7	21.804	31.3391	31.2906	31.3876	6	3	3	B8ND65	B8ND65	1	AFLA_056260	Nascent polypeptide-associated complex (NAC) subunit, putative
27.5652	27.348	27.6622	27.3145	27.72	27.2859	1.91E-73	2293600000	11	11	11	32.4	53.407	27.4826	27.5251	27.4401	6	3	3	B8NDA9	B8NDA9	1	AFLA_056700	DUF89 domain protein
26.9472	26.9704	27.1606	26.1495	25.9357	26.2935	6.34E-45	1010400000	11	11	11	33.5	51.609	26.5761	27.026	26.1262	6	3	3	B8NE05	B8NE05	1	AFLA_057360	Proteasome regulatory particle subunit Rpt2, putative
27.3659	27.8983	27.1175	26.1295	26.7437	28.2253	3.62E-164	2684400000	11	11	11	44.9	28.09	27.2467	27.4606	27.0328	6	3	3	B8NGN3	B8NGN3	1	AFLA_136600	GrpE protein homolog
27.8981	27.561	27.3627	26.4963	27.5295	27.0938	1.14E-70	2520500000	11	11	11	49.4	35.675	27.3235	27.6073	27.0398	6	3	3	B8NH43	B8NH43	1	AFLA_132670	Quinone oxidoreductase, putative
30.2867	29.3431	29.9596	29.6112	30.321	29.9887	1.29E-303	6152800000	11	11	11	35	49.232	29.9184	29.8631	29.9736	6	3	3	B8NI11	B8NI11	1	AFLA_139480	Dimethylallyl tryptophan synthase, putative
28.3274	28.6967	28.643	29.2619	28.8204	28.7406	1.27E-175	4537200000	11	11	11	61.8	37.136	28.7483	28.5557	28.941	6	3	3	B8NIB4	B8NIB4	1	AFLA_066100	Putative uncharacterized protein
26.8097	27.2537	26.6784	26.3915	27.4734	27.6952	1.43E-55	1400800000	11	11	11	23.9	68.175	27.0503	26.9139	27.1867	6	3	3	B8NIJ3	B8NIJ3	1	AFLA_067800	Mitochondrial processing peptidase alpha subunit, putative
24.4882	24.1107	24.3653	24.8759	24.3438	24.3216	1.04E-26	555400000	11	11	11	39.7	34.644	24.4176	24.3214	24.5138	6	3	3	B8NIR6	B8NIR6	1	AFLA_069440	Pyridoxal reductase (AKR8), putative
26.455	26.8281	25.014	21.8832	23.3298	24.8371	1.59E-28	889050000	11	11	11	22.9	72.59	24.7245	26.099	23.35	6	3	3	B8NJ06	B8NJ06	1	AFLA_071230	AIF-like mitochondrial oxidoreductase (Nfrl), putative
28.7137	29.4657	28.9845	31.1117	30.4252	30.3548	0	14247000000	11	11	11	33.7	45.881	29.8426	29.0547	30.6306	6	3	3	B8NJ22	B8NJ22	1	AFLA_071390	mRNA binding post-transcriptional regulator (Csx1), putative
28.0855	27.9347	28.1324	28.0031	28.0299	27.8788	1.49E-165	3600400000	11	11	11	54.9	41.418	28.0107	28.0509	27.9706	6	3	3	B8NJN3	B8NJN3	1	AFLA_068430	Adhesion regulating molecule, putative
27.6401	27.4302	27.5353	27.8892	27.5921	27.5686	7.41E-80	2235600000	11	11	11	24.8	53.058	27.6093	27.5352	27.6833	6	3	3	B8NJT6	B8NJT6	1	AFLA_068960	Vacuolar ATP synthase subunit H, putative
27.3562	27.4718	27.672	27.7444	27.5089	27.3292	4.02E-125	2303000000	11	11	11	41.1	42.069	27.5137	27.5	27.5275	6	3	3	B8NLU8	B8NLU8	1	AFLA_094040	CRAL/TRIO domain protein
27.1405	27.7484	26.7986	26.8282	26.9621	27.3414	3.56E-59	1424500000	11	11	11	23.2	85.381	27.1365	27.2292	27.0439	6	3	3	B8NNH3	B8NNH3	1	AFLA_127840	Aconitate hydratase, mitochondrial
25.9903	27.1565	27.0213	27.4792	26.3988	26.8927	1.89E-35	1175900000	11	11	11	51	36.986	26.8231	26.7227	26.9236	6	3	3	B8NNR3	B8NNR3	1	AFLA_129640	Deoxyhypusine hydroxylase
28.3655	28.2076	28.4729	28.0413	27.985	27.7997	1.13E-62	3233900000	11	11	11	48.8	27.327	28.1453	28.3487	27.942	6	3	3	B8NNS3	B8NNS3	1	AFLA_129740	Ubiquitin C-terminal hydrolase L3
32.7408	32.0754	33.0291	34.2271	33.7444	33.4355	0	1.0168E+11	11	11	11	73.9	17.009	33.2087	32.6151	33.8023	6	3	3	B8NQF0	B8NQF0	1	AFLA_006300	Nucleoside diphosphate kinase
28.869	29.0119	29.2465	28.7845	28.593	28.2218	2.23E-145	5203800000	11	11	11	45.7	35.279	28.7878	29.0425	28.5331	6	3	3	B8NQF3	B8NQF3	1	AFLA_006330	Putative uncharacterized protein
29.0322	27.8724	28.7746	28.8759	28.935	28.2733	1.16E-174	3740200000	11	11	11	31.8	42.409	28.6272	28.5597	28.6947	6	3	3	B8NQF5	B8NQF5	1	AFLA_006350	Thioredoxin reductase, putative
27.5605	27.693	28.0566	28.8252	28.3395	28.2816	1.03E-178	3191100000	11	11	11	30.2	57.131	28.1261	27.77	28.4821	6	3	3	B8NQL3	B8NQL3	1	AFLA_006950	NTF2 and RRM domain protein
28.1779	27.9761	28.0916	28.2125	27.7355	27.6329	4.30E-194	2941500000	11	11	11	48.2	39.926	27.9711	28.0819	27.8603	6	3	3	B8NR08	B8NR08	1	AFLA_003920	Cysteine synthase (O-acetylserine (Thiol)-lyase) (Csase)
28.3083	27.3888	27.9708	24.5533	25.1973	24.6251	4.18E-66	1058700000	11	11	11	24.9	61.075	26.3406	27.8893	24.7919	6	3	3	B8NRN4	B8NRN4	1	AFLA_049390	Malate synthase
29.7401	30.0084	26.9682	26.8375	28.9141	29.7173	3.94E-248	6878900000	11	11	11	61.5	24.287	28.6976	28.9055	28.4896	6	3	3	B8NS74	B8NS74	1	AFLA_053060	Peroxiredoxin 5, prdx5, putative
25.9426	26.3472	25.9692	24.0362	25.034	25.7019	4.92E-31	386280000	11	11	11	10.4	171.18	25.5052	26.0863	24.924	6	3	3	B8NSE3	B8NSE3	1	AFLA_048060	Class V myosin (Myo4), putative
27.9041	27.9494	27.7236	27.4684	28.0042	28.0785	5.03E-91	2875000000	11	11	11	35.5	48.572	27.8547	27.8591	27.8503	6	3	3	B8NSF4	B8NSF4	1	AFLA_048170	Peptide chain release factor eRF/aRF, subunit 1
27.6248	27.6693	27.5411	27.0237	26.942	27.463	1.49E-61	2201500000	11	11	11	50.9	29.624	27.3773	27.6117	27.1429	6	3	3	B8NTF4	B8NTF4	1	AFLA_097940	AhpC/TSA family thioredoxin peroxidase, putative
22.251	ND	ND	31.0877	30.4475	30.2058	0	6545600000	11	11	11	21.3	55.822	28.498	22.251	30.5803	4	1	3	B8NTS2	B8NTS2	1	AFLA_100030	Nucleolin protein Nsr1, putative
27.1409	27.0944	27.4723	27.4949	27.222	27.0471	2.97E-59	1683000000	11	11	11	36.3	46.932	27.2452	27.2359	27.2546	6	3	3	B8NUD7	B8NUD7	1	AFLA_098990	Phosphatidylinositol transporter, putative
27.9575	28.0229	28.1907	28.1603	28.5073	28.3953	3.27E-111	3033800000	11	11	11	37.8	48.351	28.2057	28.057	28.3543	6	3	3	B8NUG6	B8NUG6	1	AFLA_099280	3-methylcrotonyl-CoA carboxylase, beta subunit (MccB), putative
27.0483	26.2027	26.9641	25.4121	25.9552	25.2439	2.07E-31	1113700000	11	11	11	28.8	68.621	26.1377	26.7384	25.5371	6	3	3	B8NUU0	B8NUU0	1	AFLA_102340	Oligo-1,6-glucosidase
26.6047	26.4718	26.6402	29.9875	29.3707	29.4766	7.56E-218	4866500000	11	11	11	26.9	57.28	28.0919	26.5722	29.6116	6	3	3	B8NVT9	B8NVT9	1	AFLA_117760	Phytase, putative
26.5088	28.4162	26.6738	27.2548	28.893	29.0281	1.73E-184	2808800000	11	11	11	50.2	28.274	27.7958	27.1996	28.392	6	3	3	B8NW52	B8NW52	1	AFLA_117990	Ribosomal protein S5
28.7506	28.5796	28.9584	28.2771	27.8154	28.005	8.31E-169	3360700000	11	11	11	65.3	24.748	28.3977	28.7629	28.0325	6	3	3	B8NWR2	B8NWR2	1	AFLA_120990	O-methyltransferase, putative
30.2249	30.7322	30.653	31.1985	30.3239	30.5305	1.26E-107	20713000000	11	11	11	78.1	12.539	30.6105	30.5367	30.6843	6	3	3	B8NWS2	B8NWS2	1	AFLA_121090	Putative uncharacterized protein
28.9098	29.9494	29.2548	30.0048	29.5947	29.3861	0	7291500000	11	11	11	80.1	16.359	29.5166	29.3713	29.6619	6	3	3	B8NXA7	B8NXA7	1	AFLA_115930	Putative uncharacterized protein
28.8269	28.9877	29.1688	28.9	28.5238	28.7378	7.42E-149	3896800000	11	11	11	74	22.939	28.8575	28.9945	28.7205	6	3	3	B8NZ08	B8NZ08	1	AFLA_115200	Xanthine-guanine phosphoribosyl transferase Xpt1, putative
27.4425	27.5457	27.8714	27.9061	28.0272	27.8048	3.23E-107	2208200000	12	11	11	88.5	15.333	27.7663	27.6199	27.9127	6	3	3	B8MXA4	B8MXA4	1	AFLA_076910	Cytokinesis EF-hand protein Cdc4, putative
27.5216	27.4002	27.8267	26.6657	26.6355	27.1907	1.94E-44	1538800000	12	12	11	40	46.412	27.2067	27.5829	26.8306	6	3	3	B8N2H2	B8N2H2	1	AFLA_037470	Proteasome regulatory particle subunit Rpt4, putative
26.5135	ND	26.263	25.5239	26.1706	25.4057	2.63E-50	905640000	13	11	11	34.9	54.821	25.9754	26.3883	25.7001	5	2	3	B8NG57	B8NG57	1	AFLA_132180	Aldehyde dehydrogenase ALDH
27.7593	27.9422	28.2911	26.5263	26.9445	26.8421	5.37E-161	1518600000	12	12	12	34.9	58.819	27.3842	27.9975	26.7709	6	3	3	B8MVZ9;B8	B8MVZ9	2	AFLA_073460	Cyclopropane-fatty-acyl-phospholipid synthase, putative
ND	24.6893	ND	27.7882	27.7005	27.4895	8.84E-62	1481300000	12	12	12	25.6	70.64	26.9169	24.6893	27.6594	4	1	3	B8MX19	B8MX19	1	AFLA_076060	Structure-specific recognition protein, putative
26.0566	25.6388	26.1929	25.471	25.4916	25.1616	6.61E-26	705910000	12	12	12	24.7	64.064	25.6687	25.9628	25.3747	6	3	3	B8MXT7	B8MXT7	1	AFLA_078740	2-hydroxyphytanoyl-CoA lyase, putative
25.6146	27.213	25.6213	29.163	28.8006	28.6934	3.16E-135	3137400000	12	12	12	45.2	39.263	27.5177	26.1496	28.8857	6	3	3	B8MXX7	B8MXX7	1	AFLA_079140	Casein kinase, putative
ND	26.1063	ND	26.8891	26.899	26.7029	5.53E-31	944880000	12	12	12	7.1	249.12	26.6493	26.1063	26.8303	4	1	3	B8MY10	B8MY10	1	AFLA_079470	Pre-mRNA splicing helicase, putative
28.12	27.7813	27.1483	26.4408	26.9056	27.4231	4.97E-84	2150900000	12	12	12	42.3	41.189	27.3032	27.6832	26.9232	6	3	3	B8MYP9	B8MYP9	1	AFLA_081880	Branched-chain amino acid aminotransferase
24.2355	24.3556	24.3481	26.9936	26.3974	26.2745	1.57E-34	625330000	12	12	12	19	80.072	25.4341	24.313	26.5551	6	3	3	B8MYY0	B8MYY0	1	AFLA_082690	Pseudouridine synthase TruD/Pus7, putative
27.2568	27.2929	26.3425	25.2458	27.4529	27.2972	9.79E-74	1084900000	12	12	12	18.4	110.69	26.8147	26.9641	26.6653	6	3	3	B8MZM3	B8MZM3	1	AFLA_085130	Sec23/Sec24 family protein
28.6979	27.0843	27.0294	23.4884	27.8147	26.8863	9.37E-133	5669900000	12	12	12	44.6	33.63	26.8335	27.6038	26.0631	6	3	3	B8N0C1	B8N0C1	1	AFLA_087620	NmrA family transcriptional regulator, putative
26.5846	24.4364	24.9779	24.3933	25.274	24.397	7.76E-200	1682600000	12	12	12	34.4	68.812	25.0105	25.333	24.6881	6	3	3	B8N0I7;B8	B8N0I7	2	AFLA_024300	Amidase, putative
30.167	29.9241	29.7695	30.6951	30.6321	30.3861	1.33E-223	13869000000	12	12	12	52.3	36.321	30.2623	29.9535	30.5711	6	3	3	B8N179	B8N179	1	AFLA_029440	NADH-cytochrome b5 reductase, putative
29.8176	29.4798	29.8843	29.8975	29.7694	29.3243	0	9069100000	12	12	12	43	40.766	29.6955	29.7272	29.6638	6	3	3	B8N1F1	B8N1F1	1	AFLA_030160	Uroporphyrinogen decarboxylase
28.3709	28.5521	28.6466	27.7944	27.7945	28.1526	5.53E-153	3436400000	12	12	12	39.1	43.56	28.2185	28.5232	27.9138	6	3	3	B8N227	B8N227	1	AFLA_034210	Proteasome regulatory particle subunit (Rpnl), putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
26.613	26.5319	26.2936	27.229	26.9335	26.6534	1.59E-55	1839600000	12	12	12	41.3	39.105	26.7091	26.4795	26.9386	6	3	3	B8N3B2;B8	B8N3B2	3	AFLA_027250	Aldo-keto reductase, putative
28.4137	28.1668	28.4078	28.5251	28.4755	28.1949	6.14E-146	4365100000	12	12	12	47.4	45.809	28.364	28.3294	28.3985	6	3	3	B8N4P0	B8N4P0	1	AFLA_037450	Probable carboxypeptidase AFLA_037450
30.1375	29.8873	30.3405	29.9129	28.9244	28.9094	1.56E-243	11939000000	12	12	12	53.9	22.745	29.6853	30.1218	29.2489	6	3	3	B8N4Z0	B8N4Z0	1	AFLA_020280	Glycolipid transfer protein HET-C2, putative
30.4773	30.6785	31.061	ND	ND	ND	0	6867000000	12	12	12	45.2	54.633	30.7389	30.7389	ND	3	3	0	B8N7N3	B8N7N3	1	AFLA_104760	Acid phosphatase, putative
27.4366	26.5527	27.5754	26.9192	27.4683	26.6956	2.09E-90	2014000000	12	12	12	30.6	86.874	27.108	27.1882	27.0277	6	3	3	B8N970	B8N970	1	AFLA_110160	Probable dipeptidyl peptidase 4
28.5435	28.2466	28.6285	29.0741	28.7956	28.4571	1.46E-239	4783500000	12	12	12	47.8	40.452	28.6242	28.4729	28.7756	6	3	3	B8N9X0	B8N9X0	1	AFLA_112660	Ornithine carbamoyltransferase
28.3869	28.0221	28.461	29.109	29.0128	28.7585	6.50E-122	3864100000	12	12	12	43.4	48.527	28.6251	28.29	28.9601	6	3	3	B8NA06	B8NA06	1	AFLA_113020	Methionine aminopeptidase 2-1
31.2639	30.9258	31.1038	31.5656	31.1529	30.9727	0	30700000000	12	12	12	33.9	41.463	31.1641	31.0978	31.2304	6	3	3	B8NA16	B8NA16	1	AFLA_113120	GPI-anchored cell wall organization protein Ecm33
30.1199	29.6206	29.9658	31.3308	31.2464	30.7568	0	12793000000	12	12	12	37.3	50.7	30.5067	29.9021	31.1114	6	3	3	B8NAJ8	B8NAJ8	1	AFLA_040430	Tripeptidyl-peptidase (TppA), putative
27.7089	27.7922	27.9017	25.713	26.6241	26.6645	4.01E-66	1080100000	12	12	12	48.9	42.355	27.0674	27.8009	26.3339	6	3	3	B8NCE8	B8NCE8	1	AFLA_041230	Sterol 24-c-methyltransferase, putative
28.8564	28.7507	28.9055	29.2758	29.2494	28.9275	1.91E-255	6462400000	12	12	12	69.5	28.518	28.9942	28.8375	29.1509	6	3	3	B8ND48	B8ND48	1	AFLA_055190	Proteasome subunit alpha type
28.3106	28.3822	28.6723	27.937	27.7628	27.6471	1.06E-196	5150600000	12	12	12	55.3	37.563	28.1187	28.455	27.7823	6	3	3	B8NDF3	B8NDF3	1	AFLA_057140	Nucleoside-diphosphate-sugar epimerase, putative
27.8607	28.5777	27.665	31.2964	31.018	30.7017	0	15549000000	12	12	12	47.7	38.179	29.5199	28.0345	31.0054	6	3	3	B8NDZ3	B8NDZ3	1	AFLA_057240	RNP domain protein
27.4213	27.2599	27.2483	27.4341	27.4184	26.8792	2.85E-61	1816700000	12	12	12	29.8	77.193	27.2769	27.3098	27.2439	6	3	3	B8NF31	B8NF31	1	AFLA_060750	Golgi transport protein Sly1, putative
25.3082	26.4734	24.3608	23.3632	27.2504	26.8756	4.22E-55	1438900000	12	12	12	19.6	100.68	25.6053	25.3808	25.8297	6	3	3	B8NFS3	B8NFS3	1	AFLA_133520	Coatomer subunit gamma
26.4487	26.5103	26.6193	27.4193	27.0837	26.8348	5.83E-57	1204500000	12	12	12	22.1	94.631	26.8194	26.5261	27.1126	6	3	3	B8NH66	B8NH66	1	AFLA_132900	Protein methyltransferase RmtC
28.6814	28.667	28.3523	28.021	28.4408	28.8421	1.85E-82	4350200000	12	12	12	59.4	29.275	28.5007	28.5669	28.4346	6	3	3	B8NHH7	B8NHH7	1	AFLA_135820	Urease accessory protein UreG, putative
23.9401	25.9709	23.0551	31.5357	31.5323	31.5052	3.41E-219	12604000000	12	12	12	51.2	24.222	27.9232	24.3221	31.5244	6	3	3	B8NIL3	B8NIL3	1	AFLA_068000	Ribosomal protein
29.3308	28.1995	29.1126	27.4485	28.1498	27.3178	0	4412500000	12	12	12	55.4	36.305	28.2598	28.881	27.6387	6	3	3	B8NKU8	B8NKU8	1	AFLA_093520	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase, putative
28.0768	26.8643	27.8402	25.4722	26.9822	25.7808	6.27E-102	2312800000	12	12	12	45.3	39.245	26.8361	27.5938	26.0784	6	3	3	B8NKU9	B8NKU9	1	AFLA_093530	Oxidoreductase, 2OG-Fe(II) oxygenase family
29.5172	29.5752	29.6555	28.8765	29.2893	29.3783	0	7008700000	12	12	12	52.4	42.001	29.382	29.5826	29.1814	6	3	3	B8NLS4	B8NLS4	1	AFLA_092900	Oxidative stress protein Svf1, putative
28.7638	28.5992	29.1581	30.2564	29.8949	29.7595	6.06E-129	4273900000	12	12	12	52.9	39.188	29.4053	28.8404	29.9703	6	3	3	B8NMA8	B8NMA8	1	AFLA_095400	Putative uncharacterized protein
25.4914	25.9399	25.8888	27.8545	26.8167	27.0096	6.17E-42	764560000	12	12	12	27.6	74.726	26.5001	25.7734	27.2269	6	3	3	B8NMS3	B8NMS3	1	AFLA_126860	Cell wall cysteine-rich protein
28.3987	28.468	28.1616	28.3834	28.8121	28.7877	9.02E-62	3215500000	12	12	12	43.5	38.926	28.5019	28.3428	28.6611	6	3	3	B8NNC6	B8NNC6	1	AFLA_127370	Histone H4 arginine methyltransferase RmtA
30.1338	29.7205	30.1794	30.222	30.01	29.6534	0	11999000000	12	12	12	53.7	40.3	29.9865	30.0112	29.9618	6	3	3	B8NP67	B8NP67	1	AFLA_128500	5-methylthioadenosine phosphorylase (Meu1), putative
29.2333	29.3433	29.3722	29.6019	29.6174	29.3244	0	8643600000	12	12	12	66.7	28.249	29.4154	29.3163	29.5146	6	3	3	B8NP97	B8NP97	1	AFLA_128800	Proteasome subunit alpha type
27.0102	27.4015	27.5799	25.8473	26.2078	26.9411	6.50E-55	1095300000	12	12	12	20.5	90.96	26.8313	27.3305	26.3321	6	3	3	B8NPE3	B8NPE3	1	AFLA_130150	NAD+ dependent glutamate dehydrogenase, putative
28.7176	29.0195	28.6891	28.7341	29.2342	29.2097	9.32E-245	5369900000	12	12	12	51	43.132	28.934	28.8087	29.0593	6	3	3	B8NPZ5	B8NPZ5	1	AFLA_002980	N,N-dimethylglycine oxidase
22.6655	27.5218	ND	29.6303	29.0205	28.9537	2.43E-194	3685200000	12	12	12	40.2	39.9	27.5584	25.0936	29.2015	5	2	3	B8NR86	B8NR86	1	AFLA_005610	NAP family protein
27.9412	27.6003	27.8132	27.3459	27.3319	27.5037	1.41E-43	2148600000	12	12	12	42.5	42.671	27.5894	27.7849	27.3938	6	3	3	B8NRJ7	B8NRJ7	1	AFLA_049020	Acyl-CoA dehydrogenase family protein
26.7682	26.3033	26.8465	26.6154	26.333	26.1844	1.34E-32	1122400000	12	12	12	23.2	87.809	26.5085	26.6393	26.3776	6	3	3	B8NRK4	B8NRK4	1	AFLA_049090	Onanonoxo-7-onima-8-eninoihtemlysoneda
ND	25.542	ND	26.705	26.7465	28.3192	6.65E-107	1174100000	12	12	12	37.9	44.308	26.8282	25.542	27.2569	4	1	3	B8NRZ7	B8NRZ7	1	AFLA_052280	Putative uncharacterized protein
29.115	29.3796	29.3552	29.7843	29.3474	29.1902	0	7492900000	12	12	12	68.9	18.464	29.3619	29.2833	29.4406	6	3	3	B8NSJ0	B8NSJ0	1	AFLA_048530	E3 ubiquitin ligase complex SCF subunit sconC
29.4624	29.1591	29.51	28.9994	29.2438	28.277	0	5065400000	12	12	12	32	61.962	29.1086	29.3772	28.8401	6	3	3	B8NSW1	B8NSW1	1	AFLA_051540	Calnexin
28.5666	28.3473	28.6828	28.3528	28.6918	28.1819	1.69E-161	3999000000	12	12	12	79.3	27.168	28.4705	28.5322	28.4088	6	3	3	B8NSW2	B8NSW2	1	AFLA_051550	Methylthioribulose-1-phosphate dehydratase
29.7124	29.2528	29.6631	29.1502	28.8272	28.6331	6.31E-223	6238100000	12	12	12	33	67.134	29.2065	29.5427	28.8702	6	3	3	B8NTE9	B8NTE9	1	AFLA_097890	Glycosyl hydrolases family 32 superfamily
27.2817	26.8918	27.2475	26.2324	26.3253	26.5878	2.99E-54	1248900000	12	12	12	20.8	98.489	26.7611	27.1403	26.3818	6	3	3	B8NTJ5	B8NTJ5	1	AFLA_098350	Cysteinyl-tRNA synthetase
27.2506	27.6636	27.7637	26.7944	26.9143	26.8564	1.77E-91	1449600000	12	12	12	34.6	57.591	27.2072	27.5593	26.855	6	3	3	B8NTS0	B8NTS0	1	AFLA_100010	T-complex protein 1 subunit delta
29.1216	29.1883	29.3342	29.7105	29.3107	29.1468	1.79E-181	7385300000	12	12	12	43.9	40.713	29.302	29.2147	29.3893	6	3	3	B8NUA2	B8NUA2	1	AFLA_098640	Isoflavone reductase family protein
31.2828	30.5065	31.0974	30.8257	30.5407	30.4003	0	27945000000	12	12	12	47.9	52.4	30.7756	30.9622	30.5889	6	3	3	B8NUE0	B8NUE0	1	AFLA_099020	Autophagic serine protease Alp2
27.951	27.7486	26.9312	26.7772	27.5898	27.1469	5.58E-113	1718400000	12	12	12	27	77.885	27.3574	27.5436	27.1713	6	3	3	B8NUG3	B8NUG3	1	AFLA_099250	3-methylcrotonyl-CoA carboxylase subunit alpha (MccA), putative
28.7768	28.9158	28.9315	29.0637	29.1805	28.8445	9.81E-273	5889700000	12	12	12	50.4	39.182	28.9521	28.8747	29.0296	6	3	3	B8NUP8;B8	B8NUP8	2	AFLA_101010	Aspartate-semialdehyde dehydrogenase
28.4835	27.9227	28.4483	27.809	27.7853	27.2355	6.02E-258	3123900000	12	12	12	52.1	37.028	27.9474	28.2848	27.6099	6	3	3	B8NV70	B8NV70	1	AFLA_103650	Aldose 1-epimerase, putative
27.3586	27.2435	27.5764	26.8333	27.1283	26.9465	3.20E-165	2105000000	12	12	12	50.9	36.155	27.1811	27.3928	26.9694	6	3	3	B8NVM0	B8NVM0	1	AFLA_117070	Kelch repeat protein
28.4641	27.9995	28.8638	ND	ND	ND	3.55E-141	2031900000	12	12	12	25.9	85.243	28.4425	28.4425	ND	3	3	0	B8NWD3	B8NWD3	1	AFLA_119700	Alpha-1,2-mannosidase family protein
29.251	29.374	29.5637	25.5001	26.539	25.3993	6.16E-154	3265900000	12	12	12	51.7	29.585	27.6045	29.3962	25.8128	6	3	3	B8NWI5	B8NWI5	1	AFLA_120220	Putative uncharacterized protein
27.9591	28.3992	28.2804	29.0102	28.8149	28.5403	1.17E-105	4524500000	12	12	12	40.9	55.471	28.5007	28.2129	28.7885	6	3	3	B8NZ30	B8NZ30	1	AFLA_115420	Ran exchange factor Prp20/Pim1, putative
30.4006	30.1964	30.3432	30.55	30.3813	30.1715	3.01E-193	14524000000	13	12	12	50.2	22.89	30.3405	30.3134	30.3676	6	3	3	B8N2H5	B8N2H5	1	AFLA_037500	14-3-3 protein sigma, gamma, zeta, beta/alpha, putative
28.5074	28.6315	28.3764	28.6857	28.7428	28.6752	4.05E-268	4597400000	13	13	12	34	65.522	28.6032	28.5051	28.7012	6	3	3	B8N7W8	B8N7W8	1	AFLA_105610	Dihydroxy acid dehydratase Ilv3, putative
28.7024	28.6201	28.4277	27.6115	28.6383	28.3568	2.30E-157	4524400000	13	13	12	44.4	48.224	28.3928	28.5834	28.2022	6	3	3	B8NS26	B8NS26	1	AFLA_052570	MAP kinase MpkA
26.2999	29.6218	26.9866	28.3253	28.1745	28.4264	4.88E-219	2405900000	19	12	12	58.7	50.544	27.9724	27.6361	28.3087	6	3	3	B8NJQ2;CC	B8NJQ2	2	AFLA_068620	Tubulin beta, putative
28.2229	30.9296	29.249	28.8973	29.0744	29.4008	0	5882500000	19	19	12	67.6	49.813	29.2957	29.4672	29.1241	6	3	3	B8NSZ1	B8NSZ1	1	AFLA_051840	Tubulin beta subunit
31.2347	31.522	31.6628	32.0215	31.2681	31.2905	0	34587000000	13	13	13	70.8	18.83	31.4999	31.4732	31.5267	6	3	3	B8MW01	B8MW01	1	AFLA_073480	Tropomyosin, putative
28.8675	29.5324	28.8565	29.3126	30.0424	30.2517	0	8667600000	13	13	13	52.8	37.175	29.4772	29.0855	29.8689	6	3	3	B8MWD6	B8MWD6	1	AFLA_088260	Eukaryotic translation initiation factor 3 subunit F
28.2655	28.06	28.2767	28.7301	28.5094	28.2132	9.79E-131	3792500000	13	13	13	49.9	39.699	28.3425	28.2007	28.4842	6	3	3	B8MWG9	B8MWG9	1	AFLA_088590	Nuclear pore complex protein (SonA), putative
28.1102	26.9185	28.1683	25.2873	25.7311	25.3085	2.78E-163	1719700000	13	13	13	39.7	48.158	26.5873	27.7323	25.4423	6	3	3	B8MXJ9	B8MXJ9	1	AFLA_077860	Putative uncharacterized protein
28.8244	28.3057	28.9455	28.7686	29.0056	28.5427	2.25E-152	5893200000	13	13	13	44.4	47.607	28.7321	28.6919	28.7723	6	3	3	B8MZJ2	B8MZJ2	1	AFLA_084820	Acyl-CoA dehydrogenase, putative
27.8553	27.3692	27.9771	26.3163	26.8167	26.3616	1.18E-59	2222900000	13	13	13	53.3	39.312	27.116	27.7339	26.4982	6	3	3	B8N040	B8N040	1	AFLA_086800	Epoxide hydrolase, putative
28.1338	28.2995	28.3453	29.5324	29.2101	28.7956	3.17E-114	3682100000	13	13	13	35.1	54.803	28.7194	28.2595	29.1793	6	3	3	B8N0S9	B8N0S9	1	AFLA_026140	Alpha-amylase, putative
27.3381	27.8089	25.9246	26.8703	27.6546	27.629	5.77E-115	3156600000	13	13	13	28.9	65.77	27.2042	27.0239	27.3846	6	3	3	B8N0T8	B8N0T8	1	AFLA_026230	Putative uncharacterized protein
28.4595	28.6852	28.6641	29.4531	29.0224	29.0883	7.80E-182	5347300000	13	13	13	40.4	50.499	28.8954	28.6029	29.188	6	3	3	B8N0W8;B	B8N0W8	2	AFLA_026530	Homocitrate synthase
29.4915	28.7376	29.1278	29.4753	30.1184	29.3488	0	10329000000	13	13	13	72.4	27.369	29.3832	29.119	29.6475	6	3	3	B8N226	B8N226	1	AFLA_034200	2-heptaprenyl-1,4-naphthoquinone methyltransferase, putative
29.1915	29.2595	29.3329	29.5555	29.4923	29.1495	0	7779100000	13	13	13	57.7	31.719	29.3302	29.2613	29.3991	6	3	3	B8N2L9	B8N2L9	1	AFLA_037940	Proteasome subunit alpha type
28.8744	29.0337	29.1368	29.5637	29.5695	29.256	4.78E-253	6865200000	13	13	13	53.3	36.953	29.239	29.015	29.4631	6	3	3	B8N3C1	B8N3C1	1	AFLA_027340	Aha1 domain family
28.5022	28.545	28.9031	29.6362	29.2044	28.9289	0	7881600000	13	13	13	65.4	35.167	28.9533	28.6501	29.2565	6	3	3	B8N3N6	B8N3N6	1	AFLA_031200	Arginase, putative
32.0802	31.7278	32.1713	31.8526	31.4373	31.3334	0	45544000000	13	13	13	40.1	43.135	31.7671	31.9931	31.5411	6	3	3	B8N3P1	B8N3P1	1	AFLA_031250	Aspartic endopeptidase Pep2
29.919	30.2335	29.9684	30.3359	30.0119	30.4166	0	12388000000	13	13	13	45.2	51.026	30.1475	30.0403	30.2548	6	3	3	B8N3W9;B	B8N3W9	2	AFLA_032030	Hydroxymethylglutaryl-CoA synthase Erg13, putative
28.3033	27.7789	28.1634	27.8509	27.9545	27.7031	7.97E-125	3999300000	13	13	13	57.9	31.788	27.959	28.0819	27.8362	6	3	3	B8N447	B8N447	1	AFLA_033700	Nitrilase family protein (Nit3), putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
28.3494	28.1981	28.3265	28.9871	28.5234	28.4415	3.58E-101	4423600000	13	13	13	46.6	48.762	28.471	28.2913	28.6507	6	3	3	B8N4A8	B8N4A8	1	AFLA_035210	KH domain RNA binding protein
27.7473	28.2246	28.1058	28.2728	27.1348	28.4205	0	11639000000	13	13	13	51.7	35.109	27.9843	28.0259	27.9427	6	3	3	B8N4L2	B8N4L2	1	AFLA_037160	Thiamine thiazole synthase
29.1288	28.8462	29.0149	27.2494	28.6892	28.3151	4.00E-128	4393200000	13	13	13	39.7	43.63	28.5406	28.9966	28.0846	6	3	3	B8N4V0	B8N4V0	1	AFLA_018090	Arp2/3 complex subunit (Arp2), putative
27.2758	27.7095	27.3163	28.3453	27.404	27.3174	9.61E-170	2614100000	13	13	13	59.4	34.977	27.5614	27.4339	27.6889	6	3	3	B8N4Z7	B8N4Z7	1	AFLA_020350	Translation initiation factor 2 alpha subunit, putative
30.7101	31.0353	31.1465	29.4821	29.6741	30.8545	0	13851000000	13	13	13	60.5	32.232	30.4838	30.964	30.0036	6	3	3	B8N513	B8N513	1	AFLA_020510	40S ribosomal protein S0
27.9558	28.2425	28.3691	28.6035	28.5627	28.3674	3.52E-283	3120900000	13	13	13	40.8	52.592	28.3502	28.1891	28.5112	6	3	3	B8N862	B8N862	1	AFLA_106560	Zinc finger protein ZPR1
28.1097	28.3572	28.5269	ND	ND	ND	9.14E-136	1902700000	13	13	13	45.8	51.072	28.3313	28.3313	ND	3	3	0	B8N8U9	B8N8U9	1	AFLA_108950	Histidine acid phosphatase, putative
27.098	27.1001	27.2781	25.5885	26.8723	26.4831	1.02E-64	1026400000	13	13	13	27.5	76.636	26.7367	27.1587	26.3146	6	3	3	B8N8Y9	B8N8Y9	1	AFLA_109350	NADPH--cytochrome P450 reductase
27.7563	27.4405	27.693	27.7248	27.3036	27.4041	2.01E-92	2605900000	13	13	13	51.8	49.825	27.5537	27.6299	27.4775	6	3	3	B8NAA9	B8NAA9	1	AFLA_114050	Phosphoethanolamine
30.3994	30.1849	30.4616	30.9131	30.6539	30.4922	0	17102000000	13	13	13	49.3	40.858	30.5175	30.3486	30.6864	6	3	3	B8NAS9	B8NAS9	1	AFLA_043040	Peptidyl-prolyl cis-trans isomerase Cpr7, putative
27.6638	27.7654	27.1374	26.5763	27.3949	27.1784	9.44E-124	2528900000	13	13	13	49.6	43.479	27.286	27.5222	27.0499	6	3	3	B8NB23	B8NB23	1	AFLA_043980	Mannitol-1-phosphate dehydrogenase
27.1954	26.6764	27.1469	27.0785	26.7873	26.5051	7.61E-46	1592300000	13	13	13	62.8	39.389	26.8983	27.0062	26.7903	6	3	3	B8NB75	B8NB75	1	AFLA_044500	YjeF domain protein
26.3371	27.686	26.2598	29.1467	28.9187	31.1081	0	7273100000	13	13	13	59	29.018	28.2427	26.761	29.7245	6	3	3	B8NCT6	B8NCT6	1	AFLA_041710	60S ribosomal protein L7
27.4302	27.5621	27.4439	27.2789	26.9727	27.1908	7.01E-88	1276400000	13	13	13	15.7	123.24	27.3131	27.4787	27.1475	6	3	3	B8ND30	B8ND30	1	AFLA_055010	Homoaconitase LysF
26.8289	27.1229	27.1376	27.3697	26.9762	26.936	1.24E-39	1428300000	13	13	13	39.7	55.765	27.0619	27.0298	27.0939	6	3	3	B8NDA8	B8NDA8	1	AFLA_056690	Serine/threonine-protein phosphatase
29.8571	29.1201	29.7432	29.5014	29.4465	29.0881	0	9220500000	13	13	13	30.8	67.479	29.4594	29.5735	29.3453	6	3	3	B8NDC0	B8NDC0	1	AFLA_056810	Carboxypeptidase S1, putative
27.8776	27.5449	27.6722	27.6129	27.3851	27.248	1.26E-49	2395700000	13	13	13	49.9	51.881	27.5568	27.6982	27.4153	6	3	3	B8NDV6	B8NDV6	1	AFLA_055970	Fad NAD binding oxidoreductase, putative
27.5562	27.336	27.6308	26.1627	26.2815	27.8608	1.05E-102	2234200000	13	13	13	26.3	69.005	27.138	27.5077	26.7683	6	3	3	B8NE08	B8NE08	1	AFLA_057390	Ribosome biogenesis ABC transporter Arb1, putative
31.5453	30.6777	31.2887	30.1156	30.389	29.8506	0	34357000000	13	13	13	60.6	32.512	30.6445	31.1706	30.1184	6	3	3	B8NE88	B8NE88	1	AFLA_059970	Short-chain dehydrogenase, putative
28.2227	28.0428	28.2575	28.4592	28.5117	27.6592	1.53E-58	2179200000	13	13	13	28.9	77.148	28.1922	28.1743	28.2101	6	3	3	B8NEG1	B8NEG1	1	AFLA_060700	Phenylalanine ammonia-lyase, putative
30.2033	30.1613	30.2539	29.493	29.8965	29.4569	0	12851000000	13	13	13	54.3	28.717	29.9108	30.2062	29.6155	6	3	3	B8NEL2	B8NEL2	1	AFLA_062100	HAD superfamily hydrolase, putative
28.4534	28.6964	28.3108	27.6701	27.4286	27.8608	1.17E-152	2375000000	13	13	13	55.8	40.28	28.07	28.4869	27.6532	6	3	3	B8NEW7;B	B8NEW7	3	AFLA_058310	Formaldehyde dehydrogenase
29.8629	28.9378	29.7072	29.6352	29.4163	29.0887	0	9103100000	13	13	13	33.3	48.268	29.4413	29.5026	29.3801	6	3	3	B8NEY4	B8NEY4	1	AFLA_058480	1,3-beta-glucanosyltransferase Gel1
27.907	27.6253	27.9151	27.5498	27.5697	27.3179	1.32E-87	2563400000	13	13	13	54.8	31.309	27.6475	27.8158	27.4791	6	3	3	B8NF27	B8NF27	1	AFLA_058910	Putative uncharacterized protein
25.1286	27.0756	25.2996	28.6235	28.0097	30.2151	4.97E-212	6160500000	13	13	13	59	21.955	27.392	25.8346	28.9494	6	3	3	B8NIQ5	B8NIQ5	1	AFLA_068420	60S ribosomal protein L6
29.2522	29.1721	29.2353	29.8109	29.4294	29.0735	2.89E-290	8046800000	13	13	13	50.3	40.044	29.3289	29.2198	29.4379	6	3	3	B8NIW7	B8NIW7	1	AFLA_069950	Hsc70 cochaperone (SGT), putative
28.6497	28.5916	28.5968	28.1072	27.6675	27.9693	1.50E-145	2774800000	13	13	13	45.4	44.316	28.2637	28.6127	27.9147	6	3	3	B8NJC4	B8NJC4	1	AFLA_065570	O-methyltransferase family protein
27.1984	27.4049	27.5643	27.1203	26.4259	26.9446	3.49E-77	1952600000	13	13	13	32	63.917	27.1098	27.3892	26.8303	6	3	3	B8NKF3	B8NKF3	1	AFLA_091190	Ubiquitin carboxyl-terminal hydrolase
30.0432	30.5916	28.4419	29.9873	30.6671	30.7458	0	14739000000	13	13	13	48.9	25.169	30.0795	29.6922	30.4667	6	3	3	B8NKJ4	B8NKJ4	1	AFLA_091600	Nascent polypeptide-associated complex (NAC) subunit, putative
29.1742	29.0596	29.0346	27.763	28.6084	28.6717	2.43E-130	5476800000	13	13	13	71.9	26.804	28.7186	29.0895	28.3477	6	3	3	B8NKJ7	B8NKJ7	1	AFLA_091630	Phospholipase, putative
33.5679	33.3696	33.7743	33.6708	33.5444	33.34	1.36E-297	1.4187E+11	13	13	13	83.3	18.618	33.5445	33.5706	33.5184	6	3	3	B8NLH9	B8NLH9	1	AFLA_091060	Allergen Asp F3
26.4672	26.267	26.3713	27.4364	26.9436	26.7724	5.71E-45	1247000000	13	13	13	25.7	83.22	26.7097	26.3685	27.0508	6	3	3	B8NPC5	B8NPC5	1	AFLA_129970	IdgA domain protein
26.8168	26.7511	26.8102	26.8225	26.8147	26.8964	6.34E-60	1263600000	13	13	13	23.8	82.675	26.8186	26.7927	26.8445	6	3	3	B8NQE8	B8NQE8	1	AFLA_006280	Methylenetetrahydrofolate reductase
29.8828	29.0026	29.2597	26.8714	28.5557	28.2561	0	7453400000	13	13	13	71.9	24.841	28.6381	29.3817	27.8944	6	3	3	B8NQY1	B8NQY1	1	AFLA_003650	Uracil phosphoribosyltransferase
29.2912	29.2758	29.3573	29.6065	29.5913	29.2419	6.76E-242	8194800000	13	13	13	68.2	29.218	29.394	29.3081	29.4799	6	3	3	B8NR05	B8NR05	1	AFLA_003890	Proteasome subunit alpha type
28.0144	27.4328	26.3127	24.7141	28.3128	27.3781	3.70E-274	2529800000	13	13	13	37.1	55.616	27.0275	27.2533	26.8017	6	3	3	B8NS30	B8NS30	1	AFLA_052610	Succinyl-CoA:3-ketoacid-coenzyme A transferase (ScoT), putative
29.2096	29.148	29.1852	28.5877	28.4667	28.512	1.72E-125	7327100000	13	13	13	57.8	27.708	28.8515	29.1809	28.5221	6	3	3	B8NSP1	B8NSP1	1	AFLA_049920	Dienelactone hydrolase family protein
28.0677	28.0791	28.2091	27.3758	27.5365	28.102	1.11E-130	2699600000	13	13	13	33.3	57.52	27.895	28.1187	27.6714	6	3	3	B8NUM6	B8NUM6	1	AFLA_100790	Proteasome regulatory particle subunit (RpnE), putative
27.6807	26.8844	27.4597	25.6154	26.598	26.1311	5.76E-112	1730300000	13	13	13	36.2	63.638	26.7282	27.3416	26.1148	6	3	3	B8NUU5	B8NUU5	1	AFLA_102390	Putative uncharacterized protein
28.4736	28.4327	28.6181	26.6911	26.6026	27.0024	3.65E-167	1627200000	13	13	13	30	70.001	27.6368	28.5081	26.7654	6	3	3	B8NW02	B8NW02	1	AFLA_119290	Phosphofructokinase, putative
23.1038	25.9526	ND	27.1897	27.0958	27.1299	0	5828200000	13	13	13	63.5	23.657	26.0944	24.5282	27.1384	5	2	3	B8NXF1	B8NXF1	1	AFLA_007700	Putative uncharacterized protein
29.5131	29.1572	29.5154	28.5767	29.1948	28.6172	1.22E-243	6839300000	15	15	13	73.1	34.609	29.0957	29.3952	28.7963	6	3	3	B8NB66	B8NB66	1	AFLA_044410	Glycerol dehydrogenase, putative
28.9228	29.2674	29.2085	28.8581	28.5737	29.0421	5.77E-154	6212800000	14	14	14	53.2	33.913	28.9788	29.1329	28.8246	6	3	3	B8MWE2	B8MWE2	1	AFLA_088320	Protein phosphatase 2C, putative
27.0145	26.2508	26.8939	27.1476	27.4004	26.8563	1.36E-60	1452000000	14	14	14	27.7	78.204	26.9272	26.7197	27.1348	6	3	3	B8MXD8	B8MXD8	1	AFLA_077250	Acyl-coenzyme A oxidase
30.6074	30.6978	30.6401	30.5276	30.636	30.4917	0	19651000000	14	14	14	85	29.031	30.6001	30.6485	30.5518	6	3	3	B8MYA2	B8MYA2	1	AFLA_080390	6-phosphogluconolactonase, putative
28.8686	28.5818	28.8263	27.5887	28.4868	28.3309	1.32E-100	3756700000	14	14	14	56.9	36.893	28.4472	28.7589	28.1355	6	3	3	B8MYD7	B8MYD7	1	AFLA_080750	ARP2/3 complex 34 kDa subunit , putative
26.6744	26.3781	26.3792	27.6267	27.1758	26.9467	1.82E-71	1228800000	14	14	14	34.3	58.524	26.8635	26.4772	27.2497	6	3	3	B8MZ19	B8MZ19	1	AFLA_083080	Histidine acid phosphatase, putative
28.5865	28.263	28.6471	28.4004	28.5979	27.9759	6.23E-131	4559800000	14	14	14	55.6	38.587	28.4118	28.4989	28.3247	6	3	3	B8N186	B8N186	1	AFLA_029510	Putative uncharacterized protein
30.7689	30.6435	30.3704	30.8793	31.0947	31.0358	0	21739000000	14	14	14	48.1	40.857	30.7988	30.5942	31.0033	6	3	3	B8N1M4	B8N1M4	1	AFLA_030890	Saccharopine dehydrogenase [NAD(+), L-lysine-forming]
29.7565	29.5351	29.7345	28.2198	29.3298	29.02	2.20E-224	7203700000	14	14	14	32.7	76.931	29.2659	29.6754	28.8565	6	3	3	B8N2K3	B8N2K3	1	AFLA_037780	Actin-related protein 2/3 complex subunit 1A, putative
25.4273	25.6466	25.3554	27.0477	26.4854	26.3073	1.87E-36	796050000	14	14	14	9.3	222.86	26.045	25.4765	26.6135	6	3	3	B8N3B6	B8N3B6	1	AFLA_027290	Proteasome activator subunit 4, putative
28.6624	28.3457	27.645	26.2969	27.4885	27.9633	6.25E-148	3811400000	14	14	14	53.8	38.911	27.7336	28.2177	27.2495	6	3	3	B8N3B8	B8N3B8	1	AFLA_027310	Fructose-1,6-bisphosphatase Fbp1, putative
29.4121	29.4334	29.5367	29.8763	29.7697	29.5539	0	9732400000	14	14	14	24.9	74.441	29.597	29.4607	29.7333	6	3	3	B8N3Q2	B8N3Q2	1	AFLA_031360	Proteasome component Prs2, putative
29.8192	30.433	30.2119	31.7608	30.7831	31.0326	2.03E-168	17776000000	14	14	14	42.3	27.787	30.6734	30.1547	31.1922	6	3	3	B8N5B3	B8N5B3	1	AFLA_022410	Coproporphyrinogen III oxidase, putative
28.0977	27.7633	28.2463	27.9569	27.6032	27.3021	1.10E-58	2512900000	14	14	14	47.3	44.465	27.8282	28.0358	27.6207	6	3	3	B8N6K9	B8N6K9	1	AFLA_015220	Cell wall biogenesis protein/glutathione transferase (Gto1), putative
30.1726	29.9134	30.188	30.4563	30.2843	30.0087	1.16E-172	13736000000	14	14	14	65.1	29.12	30.1705	30.0913	30.2497	6	3	3	B8N845	B8N845	1	AFLA_106390	Ribose 5-phosphate isomerase A
27.8269	27.6796	28.1453	27.2091	26.7684	27.1253	3.77E-71	1577700000	14	14	14	33.1	67.5	27.4591	27.884	27.0343	6	3	3	B8N9A0	B8N9A0	1	AFLA_110460	mRNA splicing protein (Prp39), putative
28.8611	28.717	28.5511	28.8052	29.2656	28.9225	7.19E-177	4599000000	14	14	14	48.6	52.321	28.8538	28.7097	28.9978	6	3	3	B8N9E7	B8N9E7	1	AFLA_110930	Phospho-2-dehydro-3-deoxyheptonate aldolase, class II
31.3238	31.164	31.3186	30.6954	30.5148	30.5419	0	27838000000	14	14	14	38.5	37.964	30.9264	31.2688	30.584	6	3	3	B8N9G4	B8N9G4	1	AFLA_111100	Mitochondrial peroxiredoxin Prx1, putative
27.7703	27.5422	27.757	27.5991	27.0392	27.1495	9.81E-60	2699500000	14	14	14	31.4	56.094	27.4762	27.6898	27.2626	6	3	3	B8NA12	B8NA12	1	AFLA_113080	Coenzyme A synthetase, putative
28.7945	28.6895	28.3924	27.4627	28.6848	28.5783	4.05E-300	4460900000	14	14	14	51.9	45.268	28.4337	28.6254	28.2419	6	3	3	B8NA84	B8NA84	1	AFLA_113800	Branched-chain-amino-acid aminotransferase
28.4267	28.9813	28.6962	29.4695	29.4725	29.3522	5.10E-153	4493100000	14	14	14	48.1	54.745	29.0664	28.7014	29.4314	6	3	3	B8NB48	B8NB48	1	AFLA_044230	Eukaryotic translation initiation factor 3 subunit L
28.4739	28.5143	28.4537	28.2156	28.2907	28.3148	2.71E-154	4462800000	14	14	14	55.1	48.429	28.3771	28.4806	28.2737	6	3	3	B8NBC7;B8	B8NBC7	2	AFLA_045020	Aspartate aminotransferase
27.1764	27.5671	27.4203	27.2886	27.7579	27.1847	1.07E-75	2153100000	14	14	14	20.6	91.951	27.3992	27.3879	27.4104	6	3	3	B8NBM2	B8NBM2	1	AFLA_045970	Vacuolar transporter chaperone (Vtc4), putative
28.0897	27.0715	27.7305	27.8045	27.7695	27.455	2.96E-40	2598800000	14	14	14	39.6	54.159	27.6535	27.6306	27.6763	6	3	3	B8NCS4	B8NCS4	1	AFLA_041590	Peroxisomal multifunctional beta-oxidation protein (MFP), putative
28.1201	28.5805	28.2655	28.8366	27.8267	28.0445	1.54E-142	2824300000	14	14	14	39.5	60.701	28.279	28.3221	28.2359	6	3	3	B8NCV5	B8NCV5	1	AFLA_041900	Amidase family protein
28.3063	28.3051	28.2771	27.4922	28.5621	28.238	1.93E-109	3748600000	14	14	14	45.8	56.772	28.1968	28.2962	28.0974	6	3	3	B8ND96	B8ND96	1	AFLA_056570	Glutathione synthetase, putative
28.6859	28.4576	28.7286	28.1449	28.447	28.0302	1.02E-105	3639100000	14	14	14	23.4	84.821	28.4157	28.624	28.2074	6	3	3	B8NEL8	B8NEL8	1	AFLA_062160	Polyubiquitin binding protein (Doa1/Ufd3), putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
29.2627	29.1228	29.3715	29.6414	29.5422	29.0879	4.02E-282	7696600000	14	14	14	57.4	26.541	29.3381	29.2523	29.4238	6	3	3	B8NG73	B8NG73	1	AFLA_134120	Orotate phosphoribosyltransferase
29.8786	29.8806	29.975	30.2909	30.2554	29.8915	0	13129000000	14	14	14	72	26.998	30.0287	29.9114	30.1459	6	3	3	B8NG89	B8NG89	1	AFLA_134290	Proteasome subunit alpha type
27.4202	27.2824	27.5156	27.4891	27.66	27.031	1.07E-43	1912000000	14	14	14	52.2	43.447	27.3997	27.4061	27.3933	6	3	3	B8NGA5	B8NGA5	1	AFLA_134450	Galactose-1-phosphate uridylyltransferase
28.15	28.1727	28.0141	26.8978	27.2082	27.3395	1.12E-84	1790600000	14	14	14	41.9	56.675	27.6304	28.1123	27.1485	6	3	3	B8NGL6	B8NGL6	1	AFLA_136430	V-type ATPase, B subunit, putative
ND	25.2324	23.7138	27.8997	27.4725	28.3479	1.14E-47	1292500000	14	14	14	41.6	46.429	26.5332	24.4731	27.9067	5	2	3	B8NH55	B8NH55	1	AFLA_132790	37S ribosomal protein S5
28.5444	28.1643	27.7992	27.9059	28.9854	28.5686	2.49E-175	3958200000	14	14	14	52.7	58.402	28.328	28.1693	28.4866	6	3	3	B8NHI9	B8NHI9	1	AFLA_136830	Aromatic aminotransferase Aro8, putative
30.9931	29.9319	30.5801	30.4374	31.3834	30.1433	0	10651000000	14	14	14	40.9	50.794	30.5782	30.5017	30.6547	6	3	3	B8NI10	B8NI10	1	AFLA_139470	FAD dependent oxidoreductase, putative
26.1672	25.9073	26.5124	24.8685	26.9671	26.7636	2.56E-35	513140000	14	14	14	5.3	425.47	26.1977	26.1956	26.1997	6	3	3	B8NI12	B8NI12	1	AFLA_139490	Hybrid PKS/NRPS enzyme, putative
28.0905	28.4883	28.4613	28.4385	28.1246	27.8962	2.55E-141	3988500000	14	14	14	47.1	45.979	28.2499	28.3467	28.1531	6	3	3	B8NIA6	B8NIA6	1	AFLA_066020	12-oxophytodienoate reductase, putative
27.0165	27.8364	27.1859	28.9619	28.572	28.6439	1.04E-85	3529900000	14	14	14	40	40.919	28.0361	27.3463	28.7259	6	3	3	B8NIU9	B8NIU9	1	AFLA_069770	Eukaryotic translation initiation factor 3 subunit H
29.7338	29.7434	29.2244	28.5633	29.7077	29.81	0	8400100000	14	14	14	40.6	59.683	29.4638	29.5672	29.3603	6	3	3	B8NKG1	B8NKG1	1	AFLA_091270	Fumarate hydratase, putative
28.4371	28.1215	28.6542	27.7493	28.0981	27.7933	3.37E-136	2644200000	14	14	14	31.8	67.951	28.1423	28.4043	27.8802	6	3	3	B8NKK3	B8NKK3	1	AFLA_091690	Isocitrate lyase
31.5026	31.4475	31.5259	32.0942	31.6625	31.5255	0	36849000000	14	14	14	54.8	40.402	31.6264	31.492	31.7608	6	3	3	B8NL85	B8NL85	1	AFLA_089210	Pyruvate dehydrogenase E1 beta subunit PdbA, putative
25.7445	27.2678	26.3197	28.3839	28.527	28.8851	5.78E-150	4280500000	14	14	14	51.3	44.491	27.5213	26.444	28.5986	6	3	3	B8NPA7	B8NPA7	1	AFLA_128900	3(2),5-bisphosphate nucleotidase
29.6389	29.8917	29.867	30.2805	29.96	29.6952	5.21E-274	11807000000	14	14	14	46.8	39.497	29.8889	29.7992	29.9786	6	3	3	B8NQ72	B8NQ72	1	AFLA_004630	Farnesyl-pyrophosphate synthetase
28.773	27.1468	28.351	26.6922	27.0722	26.269	9.00E-153	4459100000	14	14	14	69.1	37.226	27.384	28.0903	26.6778	6	3	3	B8NQH9	B8NQH9	1	AFLA_006610	Lipase, putative
29.7292	29.0196	29.5281	29.6988	29.578	29.1776	0	9282000000	14	14	14	39.8	55.485	29.4552	29.4256	29.4848	6	3	3	B8NQJ3	B8NQJ3	1	AFLA_006750	Vacuolar aspartyl aminopeptidase Lap4, putative
27.7127	27.6725	27.8061	26.7251	26.7637	27.2277	4.93E-58	1535900000	14	14	14	24.7	67.381	27.318	27.7304	26.9055	6	3	3	B8NRV1	B8NRV1	1	AFLA_050930	Protein phosphotase 2a 65kd regulatory subunit
27.6674	26.616	27.6916	27.0756	27.6936	26.948	3.70E-67	1706900000	14	14	14	35.3	60.04	27.282	27.325	27.2391	6	3	3	B8NS09	B8NS09	1	AFLA_052400	Isocitrate lyase
30.0359	30.3291	28.1636	27.7512	30.0966	30.105	5.72E-291	9383700000	14	14	14	61.5	34.409	29.4136	29.5095	29.3176	6	3	3	B8NSJ8	B8NSJ8	1	AFLA_048610	Succinyl-CoA synthetase alpha subunit, putative
27.688	27.8515	27.508	27.014	26.7886	27.4432	2.31E-107	1930500000	14	14	14	33.7	65.817	27.3822	27.6825	27.0819	6	3	3	B8NSX8	B8NSX8	1	AFLA_051710	Histidyl-tRNA synthetase, mitochondrial
29.1626	27.8117	28.0054	26.983	28.6458	28.0177	0	7717900000	14	14	14	34	66.878	28.1044	28.3266	27.8822	6	3	3	B8NTV3	B8NTV3	1	AFLA_101240	Vacuolar carboxypeptidase Cps1, putative
28.9657	28.0167	29.0284	26.8735	26.5617	26.8887	2.76E-140	3077700000	14	14	14	73.6	30.978	27.7225	28.6703	26.7746	6	3	3	B8NWD0	B8NWD0	1	AFLA_119670	Glycogen branching enzyme GbeA, putative
30.4785	31.2405	30.8284	31.7485	31.4104	31.2272	0	25994000000	14	14	14	73.8	17.013	31.1556	30.8491	31.462	6	3	3	B8N0R7	B8N0R7	1	AFLA_026020	Calmodulin
26.5334	25.9159	26.4778	26.1315	26.6638	25.9766	7.33E-105	1644400000	16	16	14	27.5	89.135	26.2832	26.309	26.2573	6	3	3	B8NLD2	B8NLD2	1	AFLA_090590	Alpha-1,2-mannosidase, putative subfamily
29.4852	29.2469	29.5067	29.2942	29.2526	28.8682	2.17E-183	7353100000	15	15	15	69	31.585	29.2756	29.4129	29.1383	6	3	3	B8MWQ7	B8MWQ7	1	AFLA_075150	Esterase, putative
31.0504	28.501	30.8224	32.0083	31.0273	31.0268	0	26089000000	15	15	15	50.1	51.618	30.7394	30.1246	31.3541	6	3	3	B8MX81	B8MX81	1	AFLA_076680	Pyruvate dehydrogenase complex, dihydrolipoamide acetyltransferase
28.887	28.7737	28.9638	28.358	28.1641	28.091	2.03E-178	3579500000	15	15	15	47	53.991	28.5396	28.8748	28.2044	6	3	3	B8N038	B8N038	1	AFLA_086780	Aspartyl aminopeptidase
27.923	27.1299	27.8706	26.4529	26.6188	26.2468	2.68E-44	1822800000	15	15	15	20	123.51	27.0403	27.6412	26.4395	6	3	3	B8N050	B8N050	1	AFLA_086900	Alpha-mannosidase
29.0099	29.0858	29.275	29.5799	29.192	29.0622	3.95E-246	7483700000	15	15	15	52.5	45.843	29.2008	29.1236	29.278	6	3	3	B8N1L8	B8N1L8	1	AFLA_030830	Oxysterol binding protein (Osh5), putative
29.6293	29.3459	29.7148	29.9012	29.5639	29.2735	6.03E-290	9225900000	15	15	15	47.1	45.104	29.5714	29.5633	29.5795	6	3	3	B8N1Y3	B8N1Y3	1	AFLA_032870	cAMP-dependent protein kinase regulatory subunit
28.3541	28.3662	28.5577	28.7658	27.9214	27.9411	2.72E-113	3119200000	15	15	15	47.4	53.28	28.3177	28.426	28.2094	6	3	3	B8N244	B8N244	1	AFLA_034380	Catalase, putative
28.9424	29.0069	29.3698	29.3207	28.7793	28.5449	1.89E-297	6335400000	15	15	15	58.7	31.301	28.994	29.1064	28.8816	6	3	3	B8N293	B8N293	1	AFLA_035780	Putative uncharacterized protein
29.201	28.6814	29.2378	28.8774	29.0273	28.4474	8.87E-193	5080200000	15	15	15	43.4	50.269	28.912	29.0401	28.784	6	3	3	B8N4A2	B8N4A2	1	AFLA_035150	Proline iminopeptidase
27.6628	27.7277	27.7075	27.8576	27.4881	27.598	5.19E-53	2277000000	15	15	15	22.2	104.41	27.6736	27.6993	27.6479	6	3	3	B8N4D8	B8N4D8	1	AFLA_035510	RNA binding effector protein Scp160, putative
28.5679	28.6713	28.8629	28.216	27.8176	27.7412	1.98E-78	2373200000	15	15	15	31.4	58.973	28.3128	28.7007	27.9249	6	3	3	B8N538	B8N538	1	AFLA_020760	T-complex protein 1, gamma subunit (Cct3), putative
28.6595	28.9144	28.6553	27.6894	28.1169	28.6127	0	3777400000	15	15	15	73.2	39.705	28.4414	28.7431	28.1397	6	3	3	B8N5C0	B8N5C0	1	AFLA_022480	26S proteasome regulatory particle subunit Rpn8, putative
26.3561	26.7248	26.7438	26.7313	25.8108	26.7967	6.72E-33	895300000	15	15	15	22.7	91.568	26.5273	26.6083	26.4463	6	3	3	B8N732;B8	B8N732	2	AFLA_019650	Phosphoketolase, putative
28.6976	28.8681	28.0236	28.9753	29.0914	29.102	2.10E-218	5414500000	15	15	15	44.5	46.039	28.793	28.5297	29.0562	6	3	3	B8N7T9	B8N7T9	1	AFLA_105320	Phosphoserine aminotransferase
29.185	29.0548	29.4415	29.2688	29.1698	28.9503	0	6962900000	15	15	15	81.2	32.366	29.1784	29.2271	29.1296	6	3	3	B8N831	B8N831	1	AFLA_106250	HAD superfamily hydrolase, putative
27.636	27.4241	27.6389	26.8571	26.7085	27.0361	2.15E-146	3305500000	15	15	15	57.1	39.009	27.2168	27.5663	26.8672	6	3	3	B8N888	B8N888	1	AFLA_106820	FAD dependent oxidoreductase superfamily
31.2718	30.929	31.3241	30.7861	30.9444	30.4321	0	24607000000	15	15	15	60.2	36.511	30.9479	31.175	30.7209	6	3	3	B8N894	B8N894	1	AFLA_106880	Aldehyde reductase (AKR1), putative
29.293	29.135	29.629	29.1507	29.1943	28.7482	2.86E-84	7078500000	15	15	15	69.9	31.27	29.1917	29.3523	29.0311	6	3	3	B8NAY6	B8NAY6	1	AFLA_043610	Enoyl-CoA hydratase/isomerase family protein
28.7695	28.1984	27.1873	26.5397	28.1136	27.7801	3.27E-163	4728000000	15	15	15	61.4	36.746	27.7648	28.0517	27.4778	6	3	3	B8NB58;RE	B8NB58	2	AFLA_044330	Ketoreductase
28.3644	27.9254	28.4983	28.5363	28.3073	28.0029	6.97E-126	3603600000	15	15	15	67.4	34.641	28.2724	28.2627	28.2822	6	3	3	B8NCZ7	B8NCZ7	1	AFLA_054680	Purine nucleoside phosphorylase
29.0726	28.8335	28.7762	28.0045	28.0485	28.2763	1.02E-143	3487600000	15	15	15	35.3	63.847	28.5019	28.8941	28.1098	6	3	3	B8ND10	B8ND10	1	AFLA_054810	Transcriptional repressor TupA/RocA, putative
28.1119	27.9039	27.8763	28.034	27.7091	27.8079	1.91E-166	3693300000	15	15	15	43.7	45.218	27.9072	27.964	27.8503	6	3	3	B8ND13	B8ND13	1	AFLA_054840	Glycogen synthase kinase (Skp1), putative
26.7533	25.5417	26.4857	25.5496	26.1434	25.5979	7.76E-114	1141400000	15	15	15	29.7	76.548	26.0119	26.2602	25.7637	6	3	3	B8NE30	B8NE30	1	AFLA_057610	Amine oxidase
29.4982	29.2397	29.4199	30.1971	30.0264	29.788	0	10026000000	15	15	15	63	38.309	29.6949	29.3859	30.0038	6	3	3	B8NFQ0	B8NFQ0	1	AFLA_133290	KH domain RNA-binding protein
27.7518	27.5812	27.9011	26.5741	26.026	26.8691	1.26E-57	1721300000	15	15	15	27.4	83.676	27.1172	27.7447	26.4898	6	3	3	B8NG70	B8NG70	1	AFLA_134090	3-isopropylmalate dehydratase
28.2851	28.2928	28.6821	25.9202	26.464	27.2608	4.35E-111	3400500000	15	15	15	34.6	69.076	27.4842	28.42	26.5483	6	3	3	B8NG74	B8NG74	1	AFLA_134130	Methylenetetrahydrofolate reductase
28.7846	28.7452	28.9488	29.5229	29.6834	29.3859	3.93E-245	7398300000	15	15	15	70.4	34.384	29.1785	28.8262	29.5308	6	3	3	B8NGP4	B8NGP4	1	AFLA_136710	Putative uncharacterized protein
28.84	28.9046	28.2267	27.7465	29.4932	29.4235	7.65E-129	5783700000	15	15	15	44.1	42.417	28.7724	28.6571	28.8877	6	3	3	B8NKA1	B8NKA1	1	AFLA_089750	Tyrosyl-tRNA synthetase
29.1568	29.2891	29.3623	29.048	28.8694	28.9729	8.19E-116	5925400000	15	15	15	44.2	49.499	29.1164	29.2694	28.9634	6	3	3	B8NKH6	B8NKH6	1	AFLA_091420	ATP dependent RNA helicase (Sub2), putative
28.9961	28.8494	28.1587	27.5707	29.1018	29.1032	7.15E-138	6060000000	15	15	15	28.8	75.166	28.63	28.6681	28.5919	6	3	3	B8NNN2	B8NNN2	1	AFLA_129330	Putative uncharacterized protein
27.1172	27.4705	26.8942	27.9503	27.8383	27.247	3.54E-66	2125100000	15	15	15	22.4	114.45	27.4196	27.1607	27.6785	6	3	3	B8NP92	B8NP92	1	AFLA_128750	Assimilatory sulfite reductase
27.0923	27.271	26.7133	25.8514	26.8546	26.7732	1.73E-86	991070000	15	15	15	46	59.97	26.7593	27.0255	26.4931	6	3	3	B8NR20	B8NR20	1	AFLA_004040	Actin interacting protein 2
29.0383	28.5438	28.3232	27.2195	26.6986	27.2977	7.49E-147	2504300000	15	15	15	49.7	46.991	27.8535	28.6351	27.0719	6	3	3	B8NRD7	B8NRD7	1	AFLA_007040	Homocysteine synthase CysD
ND	ND	ND	29.0699	27.1217	27.7928	2.41E-95	1508300000	15	15	15	41.8	54.862	27.9948	ND	27.9948	3	0	3	B8NSF7	B8NSF7	1	AFLA_048200	Pseudouridylate synthase family protein
31.1559	31.0593	31.275	31.5358	31.4394	31.0653	0	29935000000	15	15	15	70.8	37.894	31.2551	31.1634	31.3468	6	3	3	B8NSY4	B8NSY4	1	AFLA_051770	Thioredoxin reductase
27.4023	27.8993	27.9142	26.1872	26.3186	26.8903	1.73E-61	1457100000	15	15	15	38.3	48.944	27.102	27.7386	26.4654	6	3	3	B8NTR9	B8NTR9	1	AFLA_100000	Proteasome regulatory particle subunit Rpt1, putative
28.1653	28.1261	27.0583	26.9212	28.5062	28.1602	8.67E-193	3428900000	15	15	15	62.3	34.153	27.8229	27.7832	27.8625	6	3	3	B8NTT7	B8NTT7	1	AFLA_100180	Phosphoribosyl-aminoimidazole-succinocarboxamide synthase
28.328	28.2265	28.5795	28.5992	28.0222	27.8297	2.53E-142	3835100000	15	15	15	45.4	56.078	28.2642	28.378	28.1504	6	3	3	B8NX84	B8NX84	1	AFLA_122720	Actin binding protein, putative
28.6824	28.2691	28.0821	27.2766	29.1241	28.3778	1.21E-147	3925600000	15	15	15	53.5	45.738	28.302	28.3445	28.2595	6	3	3	B8NXL2	B8NXL2	1	AFLA_008310	Acetyl-CoA-acetyltransferase, putative
31.2076	30.5382	31.2034	23.2472	24.9281	21.7891	0	17906000000	15	15	15	45.7	55.696	27.1523	30.9831	23.3215	6	3	3	B8NYI6	B8NYI6	1	AFLA_011560	Phosphatidylglycerol specific phospholipase, putative
24.0902	24.9937	22.4161	28.4665	28.8838	31.9358	0	9387500000	15	15	15	47.3	25.677	26.7977	23.8333	29.762	6	3	3	B8NYZ9	B8NYZ9	1	AFLA_115110	60S ribosomal protein L13
29.2571	28.8542	29.3176	29.3594	29.1571	28.808	6.29E-254	6333700000	16	16	15	67	36.418	29.1256	29.143	29.1082	6	3	3	B8N4G3	B8N4G3	1	AFLA_036660	Lactoylglutathione lyase
29.4343	29.3744	29.4296	29.8397	29.5073	29.2462	0	8690200000	16	16	16	14.6	152.65	29.4719	29.4128	29.531	6	3	3	B8MW29	B8MW29	1	AFLA_073760	DNA mismatch repair protein Msh3

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
29.6091	29.5849	29.6297	30.2582	30.0721	29.7372	0	9964800000	16	16	16	70	41.427	29.8152	29.6079	30.0225	6	3	3	B8MWH2	B8MWH2	1	AFLA_088620	UPF0160 domain protein MYG1, putative
27.6952	27.7061	27.8412	27.3069	27.0295	26.8359	1.72E-91	3224500000	16	16	16	47.7	42.38	27.4025	27.7475	27.0574	6	3	3	B8MZF5	B8MZF5	1	AFLA_084450	Putative uncharacterized protein
28.9771	29.1814	29.2457	30.4519	30.245	29.9669	8.51E-265	9694000000	16	16	16	70.7	37.317	29.678	29.1347	30.2213	6	3	3	B8N002	B8N002	1	AFLA_086420	Eukaryotic translation initiation factor 3 subunit I
31.8417	30.6692	31.7101	31.3848	31.6441	31.2144	0	20240000000	16	16	16	62.4	35.991	31.4107	31.407	31.4144	6	3	3	B8N1C0	B8N1C0	1	AFLA_029850	Cysteine-rich secreted protein
30.5511	30.9987	30.884	31.7361	31.0289	31.179	0	26126000000	16	16	16	42.4	51.72	31.063	30.8112	31.3147	6	3	3	B8N1C3	B8N1C3	1	AFLA_029880	FAD dependent oxidoreductase, putative
24.0768	26.0663	24.4939	31.8432	31.2079	31.948	0	14554000000	16	16	16	46.6	29.318	28.2727	24.879	31.6664	6	3	3	B8N204	B8N204	1	AFLA_033980	Cytosolic large ribosomal subunit protein L7A
27.7015	28.0294	27.9979	24.6576	27.8949	26.5443	8.29E-107	2098100000	16	16	16	46.2	45.34	27.1376	27.9096	26.3656	6	3	3	B8N2C6	B8N2C6	1	AFLA_036110	4-hydroxyphenylpyruvate dioxygenase
28.8334	28.9626	29.2116	28.5194	28.1029	28.4682	1.04E-168	3075200000	16	16	16	49.2	42.061	28.683	29.0026	28.3635	6	3	3	B8N2L6	B8N2L6	1	AFLA_037910	NAD(+)-isocitrate dehydrogenase subunit I
29.6158	29.4187	29.6804	29.1853	29.1966	29.1652	0	6467100000	16	16	16	62.4	38.059	29.377	29.5716	29.1824	6	3	3	B8N426	B8N426	1	AFLA_033490	Nitrilase
27.2068	26.9982	27.4746	27.412	27.0462	27.2039	7.59E-38	1619100000	16	16	16	29.9	76.816	27.2236	27.2265	27.2207	6	3	3	B8N551	B8N551	1	AFLA_020890	Clathrin-coated vesiclec protein (Bud7), putative
26.9532	28.195	26.8465	32.6452	32.1099	32.7152	0	22761000000	16	16	16	60.7	34.613	29.9108	27.3316	32.4901	6	3	3	B8N6A6	B8N6A6	1	AFLA_018700	60S ribosomal protein L5, putative
31.4406	31.2902	31.5725	31.3911	31.0816	30.9452	0	30865000000	16	16	16	72.6	28.46	31.2869	31.4344	31.1393	6	3	3	B8N6P5	B8N6P5	1	AFLA_015580	Sorbitol/xylulose reductase Sou1-like, putative
28.2452	28.7554	26.6771	27.9878	28.5883	29.0775	2.18E-110	3138000000	16	16	16	48.2	53.17	28.2219	27.8926	28.5512	6	3	3	B8N6U8	B8N6U8	1	AFLA_017010	Mitochondrial processing peptidase beta subunit, putative
31.0392	30.3698	31.0182	30.4231	30.2722	29.7922	0	20505000000	16	16	16	71.5	41.597	30.4858	30.8091	30.1625	6	3	3	B8N7E8	B8N7E8	1	AFLA_021700	Aminotransferase, class V, putative
28.3414	28.2654	28.6136	28.8371	28.5342	28.2705	2.73E-182	4002500000	16	16	16	46.3	49.785	28.477	28.4068	28.5473	6	3	3	B8N886	B8N886	1	AFLA_106800	Guanine deaminase, putative
28.6168	28.9255	28.8715	29.5938	29.3481	29.013	8.64E-267	6440700000	16	16	16	70.1	35.782	29.0614	28.8046	29.3183	6	3	3	B8N9C1	B8N9C1	1	AFLA_110670	Thioredoxin, putative
30.4551	30.279	30.5147	30.5989	30.3629	30.0235	0	16334000000	16	16	16	68.7	34.911	30.3724	30.4163	30.3284	6	3	3	B8N9D5	B8N9D5	1	AFLA_110810	Possible apospory-associated protein c
23.0214	26.6168	ND	28.0278	27.8104	27.5331	1.43E-147	2179600000	16	16	16	18.5	117.67	26.6019	24.8191	27.7904	5	2	3	B8N9S7	B8N9S7	1	AFLA_112230	Zinc metalloprotease, putative
28.4298	28.0704	28.1475	25.4156	26.327	26.4284	9.96E-100	1272700000	16	16	16	30.3	95.646	27.1365	28.2159	26.057	6	3	3	B8NA29	B8NA29	1	AFLA_113250	Ribonucleoside-diphosphate reductase
26.7056	26.2681	26.526	27.8954	27.7115	27.4668	1.18E-63	1890900000	16	16	16	39.6	75.183	27.0956	26.4999	27.6912	6	3	3	B8NDM0	B8NDM0	1	AFLA_059590	Amine oxidase
26.3566	24.4661	26.2371	24.7404	24.4873	24.1668	8.57E-107	1557800000	16	16	16	51.5	50.833	25.0757	25.6866	24.4648	6	3	3	B8NJE0	B8NJE0	1	AFLA_065730	Guanine deaminase, putative
28.9396	28.8616	28.8698	28.7062	28.1192	28.496	6.98E-171	4716800000	16	16	16	42.4	58.657	28.6654	28.8904	28.4405	6	3	3	B8NNC4	B8NNC4	1	AFLA_127350	N-acetylglucosamine-phosphate mutase
30.0918	29.9068	30.0493	30.3533	30.0515	29.8807	0	13345000000	16	16	16	38.8	58.683	30.0556	30.016	30.0952	6	3	3	B8NNP3	B8NNP3	1	AFLA_129440	1,3-beta-glucanosyltransferase, putative
28.6041	28.5996	28.5686	28.6617	28.6285	28.6801	4.82E-175	4653700000	16	16	16	34.3	69.117	28.6238	28.5908	28.6568	6	3	3	B8NNT0	B8NNT0	1	AFLA_129810	Cytoplasmic asparaginyl-tRNA synthetase, putative
27.4301	26.7852	27.3458	27.092	27.4665	26.6013	1.24E-60	1853800000	16	16	16	48.6	55.467	27.1201	27.187	27.0533	6	3	3	B8NQY6	B8NQY6	1	AFLA_003700	Mitochondrial cytochrome b2, putative
28.4964	28.5268	28.7728	28.4078	28.4853	28.2965	8.14E-102	4239500000	16	16	16	50.8	44.623	28.4976	28.5987	28.3965	6	3	3	B8NSB3	B8NSB3	1	AFLA_054350	Actin-binding protein Fragmin, putative
23.9178	28.9374	ND	30.332	30.1348	29.8205	3.86E-298	7926700000	16	16	16	50.8	46.086	28.6285	26.4276	30.0958	5	2	3	B8NTS5	B8NTS5	1	AFLA_100060	Ran GTPase activating protein 1 (RNA1 protein)
28.731	28.4755	28.1593	28.171	28.6852	27.3556	8.64E-271	2493200000	16	16	16	25.6	93.812	28.2629	28.4553	28.0706	6	3	3	B8NTT0;B8	B8NTT0	2	AFLA_100110	Plasma membrane H+-ATPase Pma1
29.4028	29.6485	29.6939	30.357	29.7244	29.7253	0	10327000000	16	16	16	51.2	54.684	29.7586	29.5817	29.9356	6	3	3	B8NTU4	B8NTU4	1	AFLA_100250	Catalase
28.7814	28.7027	28.9248	29.7535	29.3945	29.1693	0	5943600000	16	16	16	37.1	74.988	29.121	28.803	29.4391	6	3	3	B8NV47	B8NV47	1	AFLA_103410	Eukaryotic translation initiation factor subunit eIF2A, putative
29.5663	29.659	29.5048	29.9527	29.8466	29.7064	4.39E-286	9453800000	16	16	16	41.5	50.724	29.706	29.5767	29.8352	6	3	3	B8NVA6	B8NVA6	1	AFLA_104010	Dihydrolipoamide succinyltransferase, putative
29.252	29.4631	29.1826	28.9997	29.1597	29.3362	1.13E-278	6924900000	17	17	16	67.3	40.626	29.2322	29.2992	29.1652	6	3	3	B8MYJ8	B8MYJ8	1	AFLA_081360	Phospho-2-dehydro-3-deoxyheptonate aldolase
31.1071	31.5143	30.8405	30.7399	31.2424	31.759	0	18100000000	17	17	16	44.9	49.384	31.2005	31.154	31.2471	6	3	3	B8N054	B8N054	1	AFLA_086940	Eukaryotic translation initiation factor 4, putative
29.356	28.9317	29.3573	28.7336	29.2081	28.7044	1.69E-271	7466500000	17	17	16	71.6	36.684	29.0485	29.215	28.882	6	3	3	B8N110;B8	B8N110	2	AFLA_027850	Glyoxylate reductase
26.869	27.2798	26.9244	26.6695	26.3997	27.0892	7.66E-183	2303600000	17	17	16	34.3	77.514	26.8719	27.0244	26.7195	6	3	3	B8NQ64	B8NQ64	1	AFLA_004550	Vacuolar dynamin-like GTPase VpsA, putative
31.3248	31.1205	31.3043	31.9321	31.5222	31.4409	0	31054000000	18	18	16	46.4	45.451	31.4408	31.2499	31.6317	6	3	3	B8N7H4	B8N7H4	1	AFLA_021960	Pyruvate dehydrogenase E1 component alpha subunit, putative
31.3372	31.4682	31.8578	28.9102	28.9998	29.6467	0	15560000000	19	19	16	68.8	41.639	30.37	31.5544	29.1855	6	3	3	B8ND52;C0	B8ND52	2	AFLA_055230	Actin Act1
27.7612	27.7629	27.8679	28.2476	28.253	28.0941	4.08E-246	3137600000	17	17	17	50.1	46.285	27.9978	27.7974	28.1982	6	3	3	B8MXB5	B8MXB5	1	AFLA_077020	DNA damage-inducible v-SNARE binding protein Ddi1, putative
29.6515	29.2175	28.5987	27.696	28.3083	28.5268	1.33E-252	3931500000	17	17	17	55.2	58.058	28.6665	29.1559	28.177	6	3	3	B8MXQ1	B8MXQ1	1	AFLA_078380	Acetyl-coA hydrolase Ach1, putative
28.177	27.3815	27.8567	25.4994	26.1262	26.0051	2.80E-169	2576800000	17	17	17	43.6	54.228	26.841	27.8051	25.8769	6	3	3	B8MXR1	B8MXR1	1	AFLA_078480	Cysteine protease, putative
25.82	27.3519	26.1068	28.881	28.5719	28.0493	6.12E-64	2390300000	17	17	17	46.6	61.121	27.4635	26.4262	28.5007	6	3	3	B8MY33	B8MY33	1	AFLA_079700	Protein arginine methyltransferase RmtB
28.6586	28.5283	28.4118	29.8007	29.6774	29.3352	0	6231300000	17	17	17	40.7	85.922	29.0687	28.5329	29.6044	6	3	3	B8N077	B8N077	1	AFLA_087170	Extracellular serine-rich protein, putative
30.1918	30.0204	30.3354	31.2358	31.1597	30.7244	0	14414000000	17	17	17	36.2	62.627	30.6112	30.1825	31.04	6	3	3	B8N177	B8N177	1	AFLA_029420	Dipeptidyl-peptidase II, putative
27.9058	28.1345	28.0964	27.3913	27.5956	27.7905	2.33E-192	2698700000	17	17	17	45.4	54.247	27.819	28.0455	27.5925	6	3	3	B8N2F8	B8N2F8	1	AFLA_036430	Proteasome regulatory particle subunit (RpnG), putative
31.9766	31.8356	31.9009	32.4328	32.2132	31.8508	0	49907000000	17	17	17	65	38.725	32.035	31.9044	32.1656	6	3	3	B8N4T3	B8N4T3	1	AFLA_017920	Spermidine synthase
30.4979	30.3719	30.4562	30.9175	30.5205	30.4239	6.69E-201	17408000000	17	17	17	59.3	28.463	30.5313	30.442	30.6206	6	3	3	B8N5B9	B8N5B9	1	AFLA_022470	Adenylate kinase, putative
27.5993	27.7058	27.6285	27.6887	28.1337	28.017	9.31E-79	2488300000	17	17	17	23.4	117.4	27.7955	27.6446	27.9465	6	3	3	B8N9P4	B8N9P4	1	AFLA_111900	Pitrilysin family metalloprotease (Cym1), putative
29.2481	28.7796	29.0738	29.3118	29.2372	28.8185	0	6527100000	17	17	17	52.9	39.319	29.0782	29.0338	29.1225	6	3	3	B8NA87	B8NA87	1	AFLA_113830	Dipeptidyl peptidase, putative
28.846	28.8279	28.7478	29.0593	28.9722	28.6311	3.09E-170	5986500000	17	17	17	36.5	75.74	28.8474	28.8072	28.8875	6	3	3	B8NC08	B8NC08	1	AFLA_047330	Leukotriene A4 hydrolase
27.8845	27.8858	27.9055	27.2088	27.0952	27.7045	3.80E-86	2517400000	17	17	17	25.3	108.39	27.614	27.8919	27.3362	6	3	3	B8NDT9	B8NDT9	1	AFLA_055800	Chromosome segregation protein Cse1, putative
31.2988	31.0409	30.7557	28.8237	29.5684	30.0034	0	10520000000	17	17	17	65.8	39.876	30.2485	31.0318	29.4652	6	3	3	B8NE10	B8NE10	1	AFLA_057410	NAD binding Rossmann fold oxidoreductase, putative
29.1378	28.5605	29.0777	28.9548	29.1422	28.5426	9.36E-204	5157100000	17	17	17	56.9	48.016	28.9026	28.9253	28.8799	6	3	3	B8NEG2	B8NEG2	1	AFLA_060710	Toxin biosynthesis protein, putative
28.31	28.688	27.8161	27.9537	29.183	28.7759	5.38E-152	4497500000	17	17	17	44.1	49.068	28.4545	28.2714	28.6375	6	3	3	B8NEP1	B8NEP1	1	AFLA_062390	Tryptophanyl-tRNA synthetase
28.6603	28.6991	27.6516	27.9383	28.8399	28.6408	3.54E-170	4820600000	17	17	17	52.4	53.32	28.405	28.337	28.473	6	3	3	B8NEZ3	B8NEZ3	1	AFLA_058570	ATP dependent RNA helicase (Dbp5), putative
27.0379	27.1098	27.3009	27.9356	27.4031	27.381	1.53E-139	2150000000	17	17	17	14.4	160.35	27.3614	27.1495	27.5732	6	3	3	B8NFM7	B8NFM7	1	AFLA_131280	Actin cortical patch assembly protein Pan1, putative
29.4282	29.2092	29.3976	27.9801	28.8564	28.7737	9.88E-287	5437000000	17	17	17	61.4	47.205	28.9409	29.345	28.5367	6	3	3	B8NH60	B8NH60	1	AFLA_132840	Arp2/3 complex subunit (Arp3), putative
28.4868	28.7319	28.664	27.7165	27.8256	27.7729	6.35E-197	3129300000	17	17	17	25.8	100.98	28.1996	28.6276	27.7717	6	3	3	B8NLQ7	B8NLQ7	1	AFLA_092730	26S proteasome regulatory subunit Mts4, putative
33.3557	33.3774	33.4197	33.9122	33.4349	33.3542	0	1.3792E+11	17	17	17	82.5	27.414	33.4757	33.3843	33.5671	6	3	3	B8NM07	B8NM07	1	AFLA_094630	Triosephosphate isomerase
29.0139	28.9505	29.1822	29.2876	30.0583	29.4645	4.15E-153	7491000000	17	17	17	49.5	46.755	29.3261	29.0489	29.6034	6	3	3	B8NUG5	B8NUG5	1	AFLA_099270	Isovaleryl-CoA dehydrogenase IvdA, putative
27.681	28.5362	28.684	29.2906	26.913	28.2114	8.81E-275	2533300000	17	17	17	39.6	64.187	28.2194	28.3004	28.1383	6	3	3	B8NXS1	B8NXS1	1	AFLA_008910	Putative uncharacterized protein
23.7121	26.2417	ND	26.0684	27.0555	26.6614	3.96E-159	2970200000	18	18	17	61.9	45.256	25.9478	24.9769	26.5951	5	2	3	B8MXE0;B8	B8MXE0	2	AFLA_077270	NADH-dependent flavin oxidoreductase, putative
29.3558	29.3362	28.6049	28.2908	29.3187	29.6265	1.04E-248	6666500000	18	17	17	56.7	58.462	29.0888	29.0989	29.0787	6	3	3	B8NBY3	B8NBY3	1	AFLA_047080	Serine hydroxymethyltransferase
31.9259	33.2536	31.895	32.8411	32.8268	33.8689	0	91883000000	19	19	17	72.5	36.3	32.7686	32.3582	33.1789	6	3	3	B8N2Y6;B8	B8N2Y6	2	AFLA_025100	Glyceraldehyde-3-phosphate dehydrogenase
30.2849	30.8327	30.5984	30.3138	29.5812	29.644	0	14792000000	19	17	17	61.3	43.173	30.2092	30.572	29.8463	6	3	3	B8NWM6	B8NWM6	1	AFLA_120630	Glyoxylate/hydroxypyruvate reductase, putative
29.6967	28.9821	29.5747	27.8585	28.2383	27.6753	3.92E-148	5497700000	18	18	18	33.6	67.874	28.6709	29.4178	27.924	6	3	3	B8MXQ5	B8MXQ5	1	AFLA_078420	Fumarate reductase Osm1, putative
26.9887	27.593	27.8855	27.9107	27.2531	27.5485	9.43E-254	3064900000	18	18	18	19.8	132.4	27.5299	27.4891	27.5708	6	3	3	B8MYF5	B8MYF5	1	AFLA_080930	EF hand domain protein
30.1239	29.8511	30.177	30.4022	30.3478	29.9507	0	13952000000	18	18	18	51.1	60.985	30.1421	30.0507	30.2336	6	3	3	B8MZ48	B8MZ48	1	AFLA_083370	Glutathione oxidoreductase Glr1, putative
30.4051	30.5968	30.7967	24.6763	24.4754	ND	0	8350700000	18	18	18	48.1	69.417	28.19	30.5995	24.5758	5	3	2	B8MZ53	B8MZ53	1	AFLA_083420	Non-hemolytic phospholipase C, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
28.4946	29.0986	28.0124	28.5307	28.6239	29.0827	1.79E-128	5048200000	18	18	18	51.2	46.282	28.6405	28.5352	28.7458	6	3	3	B8MZA3	B8MZA3	1	AFLA_083920	Adenylosuccinate synthetase
28.4682	28.4711	28.6807	28.977	28.6544	28.4889	7.35E-163	4354200000	18	18	18	49.7	54.675	28.6234	28.54	28.7068	6	3	3	B8N0R3	B8N0R3	1	AFLA_025980	Hsp90 co-chaperone Cdc37
29.6257	28.9697	29.7412	28.2078	29.7635	28.4271	0	10084000000	18	18	18	68.4	46.876	29.1225	29.4455	28.7995	6	3	3	B8N2C3	B8N2C3	1	AFLA_036080	Fumarylacetoacetate hydrolase FahA
28.6682	28.1211	28.804	27.2209	28.653	27.4139	0	5697700000	18	18	18	79.7	50.35	28.1469	28.5311	27.7626	6	3	3	B8N2C4	B8N2C4	1	AFLA_036090	Homogentisate 1,2-dioxygenase (HmgA), putative
25.8957	24.9732	25.5027	24.9726	25.0852	24.6372	4.74E-44	1013500000	18	18	18	23.7	127.12	25.1778	25.4572	24.8983	6	3	3	B8N3A7	B8N3A7	1	AFLA_027200	Xanthine dehydrogenase HxA, putative
30.7534	30.8573	30.3784	29.4699	30.2979	30.279	0	14279000000	18	18	18	57.1	41.862	30.3393	30.663	30.0156	6	3	3	B8N6C1	B8N6C1	1	AFLA_018850	Isocitrate dehydrogenase, NAD-dependent
27.9755	27.9569	28.1941	28.1052	28.9438	28.2853	4.57E-188	4720100000	18	18	18	51.8	44.839	28.2435	28.0422	28.4448	6	3	3	B8N6I5	B8N6I5	1	AFLA_014980	Putative uncharacterized protein
27.8532	27.7988	27.858	27.9512	27.8015	27.5718	1.06E-94	2604800000	18	18	18	44.3	61.895	27.8058	27.8367	27.7748	6	3	3	B8N846	B8N846	1	AFLA_106400	Ubiquitin-like activating enzyme (UlaA), putative
29.9784	29.8807	29.8165	27.6484	27.9745	29.333	0	8331400000	18	18	18	55.5	60.75	29.1053	29.8919	28.3186	6	3	3	B8NAW4	B8NAW4	1	AFLA_043390	Hsp70 chaperone (BiP), putative
29.6962	28.8295	29.5526	30.4517	30.6445	29.9859	0	7839300000	18	18	18	40.9	65.01	29.8601	29.3594	30.3607	6	3	3	B8NCH3	B8NCH3	1	AFLA_038790	Adenosine deaminase family protein
29.0085	29.0219	29.1061	29.7586	29.4607	29.2112	0	6736700000	18	18	18	33	86.584	29.2612	29.0455	29.4769	6	3	3	B8ND53	B8ND53	1	AFLA_055240	Bifunctional purine biosynthetic protein Ade1, putative
27.3669	27.4825	27.3862	28.0062	27.9186	27.5202	3.49E-129	2175500000	18	18	18	33.3	92.748	27.6134	27.4118	27.815	6	3	3	B8NDV7	B8NDV7	1	AFLA_055980	Mannosyl-oligosaccharide glucosidase, putative
29.66	29.2016	29.6959	29.6667	30.1261	29.4573	0	11223000000	18	18	18	25.2	105.17	29.6346	29.5191	29.75	6	3	3	B8NEE0	B8NEE0	1	AFLA_060490	Pyridine nucleotide-disulphide oxidoreductase family protein
29.5689	29.2855	29.6569	26.0028	26.627	26.3952	9.13E-198	2628100000	18	18	18	59.9	59.652	27.9227	29.5038	26.3417	6	3	3	B8NEF7	B8NEF7	1	AFLA_060660	AMP-binding enzyme, putative
ND	27.7042	ND	28.7309	28.3179	28.4313	2.81E-140	2848100000	18	18	18	40.2	72.33	28.2961	27.7042	28.4934	4	1	3	B8NG06	B8NG06	1	AFLA_131670	Oxidoreductase, putative
28.7083	28.786	28.8005	28.2655	28.175	28.4323	3.01E-286	3961000000	18	18	18	24.7	135.79	28.5279	28.7649	28.2909	6	3	3	B8NGG2	B8NGG2	1	AFLA_135890	Protein transport protein (SEC31), putative
31.0269	30.9558	31.0215	31.566	31.3653	31.0732	0	26431000000	18	18	18	48.3	63.572	31.1681	31.0014	31.3348	6	3	3	B8NPM2	B8NPM2	1	AFLA_000860	Tripeptidyl peptidase A
32.0177	31.7017	32.1035	30.4464	30.8191	30.9166	0	32846000000	18	18	18	71.7	38.503	31.3342	31.941	30.7273	6	3	3	B8NRH9	B8NRH9	1	AFLA_048840	Adenosine kinase, putative
30.1553	30.6224	30.5633	30.0457	30.6481	31.4453	0	14505000000	18	18	18	76.7	29.23	30.58	30.447	30.713	6	3	3	B8NRV3	B8NRV3	1	AFLA_050950	40S ribosomal protein S3, putative
31.9303	31.5526	32.119	31.031	31.3163	31.1672	0	22749000000	18	18	18	54.9	41.944	31.5194	31.8673	31.1715	6	3	3	B8NT00	B8NT00	1	AFLA_051930	Glutamine synthetase
30.0113	29.8087	30.0592	28.9119	28.7821	28.3441	3.03E-283	6762200000	18	18	18	80.5	23.726	29.3195	29.9597	28.6794	6	3	3	B8NW05	B8NW05	1	AFLA_119330	Glutathione-S-transferase theta, GST, putative
31.208	31.6407	31.2929	30.7078	30.3101	31.0976	0	18255000000	18	18	18	78.1	25.65	31.0428	31.3805	30.7052	6	3	3	B8NW18	B8NW18	1	AFLA_119460	UDP-glucose 4-epimerase
28.9737	29.4526	29.4926	29.9106	28.3256	29.3002	0	6029000000	18	18	18	67.2	40.803	29.2426	29.3063	29.1788	6	3	3	B8NYP6	B8NYP6	1	AFLA_012160	Acetyl-CoA acetyltransferase, putative
28.8198	30.9873	29.2874	29.7139	29.3899	29.7294	0	7564600000	19	19	18	66.7	50.168	29.6546	29.6982	29.611	6	3	3	B8MYF4	B8MYF4	1	AFLA_080920	Tubulin alpha-1 subunit
28.0664	28.3864	26.8746	26.7358	28.5429	28.3997	3.65E-189	3816700000	19	18	18	54.1	53.051	27.8343	27.7758	27.8928	6	3	3	B8NE43	B8NE43	1	AFLA_057740	Aldehyde dehydrogenase, putative
30.8642	31.7342	29.1324	28.2606	31.6635	31.8738	0	30328000000	20	18	18	81	34.679	30.5881	30.5769	30.5993	6	3	3	B8ND04	B8ND04	1	AFLA_054750	Malate dehydrogenase, NAD-dependent
28.8835	26.1335	27.8222	24.6929	26.5349	25.7359	0	4480200000	19	19	19	44.8	65.751	26.6338	27.6131	25.6545	6	3	3	B8MVT0	B8MVT0	1	AFLA_072770	Pyrroline-5-carboxylate dehydrogenase, putative
29.656	29.6841	28.5915	27.5673	30.0283	29.8388	1.39E-168	10830000000	19	19	19	48.1	41.263	29.2277	29.3105	29.1448	6	3	3	B8MWA5	B8MWA5	1	AFLA_087950	Isocitrate dehydrogenase LysB
28.8295	28.8622	28.9726	29.1473	28.4397	29.2855	8.94E-169	5126200000	19	19	19	37.9	86.1	28.9228	28.8881	28.9575	6	3	3	B8N0K5	B8N0K5	1	AFLA_024480	6-phosphofructokinase
27.819	28.4095	28.0873	28.0338	28.3096	28.3518	2.35E-74	3210600000	19	19	19	40.8	78.714	28.1685	28.1053	28.2317	6	3	3	B8N1I0	B8N1I0	1	AFLA_030450	Trehalose synthase (Ccg-9), putative
28.8331	28.9361	28.6478	28.2459	28.6621	28.4484	1.10E-203	4756900000	19	19	19	36.9	99.543	28.6289	28.8057	28.4521	6	3	3	B8N222	B8N222	1	AFLA_034160	Protein transport protein Sec24, putative
31.8821	32.8029	32.5121	32.4606	31.8902	33.3178	0	1.1324E+11	19	19	19	54.3	47.406	32.4776	32.399	32.5562	6	3	3	B8N2H3	B8N2H3	1	AFLA_037480	Enolase/allergen Asp F 22
28.9148	28.5482	28.7759	28.1159	27.4062	28.3812	9.36E-275	3423800000	19	19	19	34.8	99.725	28.357	28.7463	27.9678	6	3	3	B8N691	B8N691	1	AFLA_018550	Glycogen phosphorylase GlpV/Gph1, putative
28.0394	28.4263	28.4601	27.5076	27.2109	27.7658	7.15E-110	2341100000	19	19	19	21.9	124.65	27.9017	28.3086	27.4947	6	3	3	B8N9H5	B8N9H5	1	AFLA_111210	26S proteasome regulatory subunit Rpn2, putative
31.542	30.7733	31.4543	31.0081	30.8997	30.8065	0	42557000000	19	19	19	68.2	34.24	31.0807	31.2566	30.9048	6	3	3	B8NB34	B8NB34	1	AFLA_044090	Uricase
30.9651	30.6917	31.006	30.5585	30.0258	30.8341	0	23651000000	19	19	19	55	44.422	30.6802	30.8876	30.4728	6	3	3	B8NEC1	B8NEC1	1	AFLA_060300	Ketol-acid reductoisomerase
28.9853	27.8255	28.9432	26.3702	26.7361	26.7345	1.56E-143	3585800000	19	19	19	64.8	49.534	27.5991	28.5847	26.6136	6	3	3	B8NEZ4	B8NEZ4	1	AFLA_058580	GTP cyclohydrolase II, putative
28.5159	28.7314	28.5263	30.7169	30.1721	29.9446	3.18E-292	9134400000	19	19	19	52.9	42.938	29.4345	28.5912	30.2779	6	3	3	B8NID1	B8NID1	1	AFLA_066270	RNA-binding La domain protein
29.8845	30.0616	30.0217	31.1838	30.4413	30.4208	0	15625000000	19	19	19	50.7	51.545	30.3356	29.9893	30.682	6	3	3	B8NJS4	B8NJS4	1	AFLA_068840	Aminomethyltransferase
27.9865	27.8345	27.6562	28.1232	28.1003	27.8841	1.71E-181	2902000000	19	19	19	19.8	166.52	27.9308	27.8257	28.0359	6	3	3	B8NK51	B8NK51	1	AFLA_071000	Membrane bound C2 domain protein (Vp115), putative
30.0836	29.9282	30.1069	29.1614	28.7143	28.9247	3.29E-233	6368100000	19	19	19	65.2	43.248	29.4865	30.0396	28.9335	6	3	3	B8NKM2	B8NKM2	1	AFLA_091880	Septin AspA, putative
30.3824	29.9764	30.2922	30.6863	30.3487	30.068	1.52E-218	12966000000	19	19	19	59.6	39.916	30.2923	30.217	30.3677	6	3	3	B8NKS4	B8NKS4	1	AFLA_093280	Disulfide isomerase (TigA), putative
33.6612	33.0043	33.7397	31.5068	32.4885	31.673	0	59219000000	19	19	19	63.9	42.313	32.6789	33.4684	31.8894	6	3	3	B8NLY9	B8NLY9	1	AFLA_094450	Aspartic protease pep1
30.1579	29.4498	30.2414	29.3625	29.9893	29.1411	0	10585000000	19	19	19	49.9	51.656	29.7237	29.9497	29.4976	6	3	3	B8NRM4	B8NRM4	1	AFLA_049290	Citrate synthase
28.9383	28.8314	28.235	23.9514	27.4304	27.1008	1.33E-125	2943400000	19	19	19	53.4	51.594	27.4146	28.6682	26.1609	6	3	3	B8NRR9	B8NRR9	1	AFLA_050600	Betaine-aldehyde dehydrogenase, putative
29.4796	29.351	29.4516	28.0603	29.8261	29.5242	9.53E-274	7493700000	19	19	19	53.5	62.412	29.2821	29.4274	29.1369	6	3	3	B8NSU4	B8NSU4	1	AFLA_051370	Phosphoribosyl-aminoimidazole carboxylase
31.8173	31.9064	32.1702	30.2639	30.3564	30.7327	0	19643000000	19	19	19	81.3	35.017	31.2078	31.9646	30.451	6	3	3	B8NT05	B8NT05	1	AFLA_051980	G-protein complex beta subunit CpcB
30.7382	30.2395	30.692	29.6723	29.7247	29.5598	0	17127000000	19	19	19	40	60.878	30.1044	30.5565	29.6522	6	3	3	B8NXS9	B8NXS9	1	AFLA_008990	Carboxypeptidase Y homolog A
30.8957	32.3896	31.5792	31.3685	29.9644	31.4999	0	28436000000	19	19	19	78	37.057	31.2829	31.6215	30.9443	6	3	3	P41747	P41747	1	AFLA_048690	Alcohol dehydrogenase 1
26.9281	25.7028	26.6883	28.799	29.1028	29.0029	6.77E-158	4747400000	20	19	19	44.4	78.235	27.704	26.4397	28.9683	6	3	3	B8MVZ8	B8MVZ8	1	AFLA_073450	Amine oxidase
29.5913	29.0279	29.6538	29.3132	29.7268	28.9719	2.65E-298	8437600000	20	20	19	47.7	64.283	29.3808	29.4243	29.3373	6	3	3	B8NK82;B8	B8NK82	2	AFLA_089560	Pyruvate decarboxylase, putative
30.1405	29.3996	29.5339	27.6879	28.6578	28.7071	3.22E-230	6894600000	22	22	19	51.2	54.164	29.0211	29.6913	28.3509	6	3	3	B8N9G1	B8N9G1	1	AFLA_111070	Aldehyde dehydrogenase, putative
27.7027	28.3008	27.9201	28.8059	28.6496	28.5284	0	4914300000	20	20	20	23.7	135.61	28.3179	27.9745	28.6613	6	3	3	B8MZV1	B8MZV1	1	AFLA_085910	Coatomer subunit alpha, putative
29.0742	29.7164	28.6879	28.8959	30.4994	30.5282	0	9176100000	20	20	20	59.9	51.591	29.567	29.1595	29.9745	6	3	3	B8N3P5	B8N3P5	1	AFLA_031290	Eukaryotic translation initiation factor 3 subunit E
30.4699	30.6983	30.902	30.4372	30.1581	30.281	0	16381000000	20	20	20	75.4	36.716	30.4911	30.6901	30.2921	6	3	3	B8N3Y7	B8N3Y7	1	AFLA_033100	Phosphatidylinositol transporter, putative
29.2476	29.1443	29.1727	28.5239	29.1788	28.9231	2.76E-292	5414200000	20	20	20	42.1	71.002	29.0317	29.1882	28.8753	6	3	3	B8N672	B8N672	1	AFLA_016560	Methionyl-tRNA synthetase
28.7525	28.446	28.7853	26.7223	27.8627	26.8638	4.74E-149	2848000000	20	20	20	32.9	95.766	27.9055	28.6613	27.1496	6	3	3	B8N6M3	B8N6M3	1	AFLA_015360	N-methyltransferase, putative
28.434	27.8919	28.4972	26.8236	26.8637	26.5376	6.59E-122	2759600000	20	20	20	26.7	109.87	27.508	28.2744	26.7416	6	3	3	B8N6V7	B8N6V7	1	AFLA_017100	Probable beta-galactosidase A
29.7141	29.5133	29.8192	30.1948	29.9577	29.669	0	12309000000	20	20	20	52	56.251	29.8113	29.6822	29.9405	6	3	3	B8NAJ3	B8NAJ3	1	AFLA_040380	Mannitol dehydrogenase, putative
30.1724	29.1662	29.9649	29.15	29.7041	29.0607	0	14133000000	20	20	20	58.4	49.457	29.5364	29.7678	29.305	6	3	3	B8NAS7	B8NAS7	1	AFLA_043020	Fructosyl amine:oxygen oxidoreductase
27.7042	28.3601	27.8425	28.0278	28.3163	28.3015	3.15E-104	3040700000	20	20	20	37.6	90.789	28.0921	27.9689	28.2152	6	3	3	B8NB25	B8NB25	1	AFLA_044000	COPI vesicle coat beta subunit, putative
30.976	31.0592	31.157	31.0454	31.3298	31.0009	0	22427000000	20	20	20	84.2	32.984	31.0947	31.0641	31.1254	6	3	3	B8NEJ0	B8NEJ0	1	AFLA_061880	Pyridoxine biosynthesis protein
25.3013	27.1083	25.7695	26.718	26.6202	27.7622	0	3047100000	20	20	20	43.6	44.346	26.5466	26.0597	27.0335	6	3	3	B8NGD4	B8NGD4	1	AFLA_134740	60S ribosomal protein L3
28.2971	28.3507	28.2936	27.1382	27.4422	27.6996	1.97E-119	2745800000	20	20	20	28.8	117.83	27.8702	28.3138	27.4267	6	3	3	B8NHE8	B8NHE8	1	AFLA_135530	Putative uncharacterized protein
30.6238	31.2689	31.0482	30.1448	29.541	31.0704	0	14335000000	20	20	20	76.7	42.482	30.6162	30.9803	30.252	6	3	3	B8NJU1	B8NJU1	1	AFLA_069010	S-adenosylmethionine synthase
26.0462	27.6351	26.0537	26.4154	26.5802	27.0862	4.14E-58	1297300000	20	20	20	25.5	121.58	26.6361	26.5784	26.6939	6	3	3	B8NNH1	B8NNH1	1	AFLA_127820	Importin beta-3 subunit, putative
30.2966	30.6894	29.5872	29.8285	29.8691	30.3793	3.47E-296	10951000000	20	20	20	56.5	43.9	30.1083	30.191	30.0256	6	3	3	B8NPW4	B8NPW4	1	AFLA_002670	Curved DNA-binding protein (42 kDa protein)
28.8274	28.414	28.8854	28.2264	29.0053	27.6421	1.53E-197	2947900000	20	20	20	23.9	145.25	28.5001	28.7089	28.2913	6	3	3	B8NQ19	B8NQ19	1	AFLA_003220	Phospholipase D (PLD), putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
28.2712	28.9268	28.6635	29.269	27.8711	29.2279	0	22304000000	20	20	20	69.9	38.243	28.7049	28.6205	28.7893	6	3	3	B8NQ74	B8NQ74	1	AFLA_004650	Thiamine biosynthesis protein (Nmt1), putative
32.3402	32.5036	32.1469	30.4747	31.899	31.9218	0	43847000000	20	20	20	50.6	52.027	31.881	32.3302	31.4318	6	3	3	B8NRD5	B8NRD5	1	AFLA_007020	Citrate synthase
30.4224	30.3384	30.5097	31.0941	30.8642	30.5805	0	17938000000	20	20	20	52.9	54.024	30.6349	30.4235	30.8463	6	3	3	B8NSD9	B8NSD9	1	AFLA_048020	D-3-phosphoglycerate dehydrogenase
30.1435	29.5682	30.1115	29.3743	29.4809	29.1331	0	11990000000	20	20	20	45.2	63.699	29.6352	29.941	29.3294	6	3	3	B8NSW0	B8NSW0	1	AFLA_051530	Methylmalonate-semialdehyde dehydrogenase, putative
28.1929	28.0144	28.0984	28.0832	28.077	27.8403	2.26E-162	2548100000	20	20	20	43.7	71.038	28.051	28.1019	28.0002	6	3	3	B8NTR8	B8NTR8	1	AFLA_099990	Succinate dehydrogenase subunit Sdh1, putative
28.1773	27.9402	27.734	29.1202	29.2728	29.2978	1.54E-195	4507900000	21	21	20	34	71.973	28.5904	27.9505	29.2302	6	3	3	B8N9S2	B8N9S2	1	AFLA_112180	ATP dependent RNA helicase (Dbp1), putative
34.022	33.9689	34.1126	34.6528	34.233	34.1349	0	2.2401E+11	22	22	20	65	44.515	34.1874	34.0345	34.3402	6	3	3	B8MX84	B8MX84	1	AFLA_076710	Malate dehydrogenase, NAD-dependent
32.5774	32.7101	32.7419	31.3573	31.1938	30.7745	0	48745000000	22	22	20	72.3	40.145	31.8925	32.6765	31.1085	6	3	3	B8ND35	B8ND35	1	AFLA_055060	NAD-dependent formate dehydrogenase AciA/Fdh
32.5649	32.3903	32.6407	32.6672	32.4023	32.1514	0	75019000000	23	23	20	75.7	36.931	32.4695	32.532	32.407	6	3	3	B8N0Z8	B8N0Z8	1	AFLA_027730	Glycerol dehydrogenase (GldB), putative
32.13	32.0569	32.1841	32.5961	32.3445	32.1804	0	58731000000	21	21	21	59	43.623	32.2487	32.1237	32.3737	6	3	3	B8N031	B8N031	1	AFLA_086710	Inorganic diphosphatase, putative
28.062	27.9631	28.2443	27.1019	27.7762	27.8381	4.91E-127	2310500000	21	21	21	18.8	171.28	27.8309	28.0898	27.5721	6	3	3	B8N4Q9	B8N4Q9	1	AFLA_01768	Pentafunctional AROM polypeptide
27.0812	27.4301	27.5482	29.4396	28.1841	28.3483	3.05E-293	4364500000	21	21	21	42.1	53.022	28.0052	27.3532	28.6573	6	3	3	B8N6W0	B8N6W0	1	AFLA_017130	Nuclear segregation protein (Bfr1), putative
31.1759	31.1787	31.1932	31.9391	31.6809	31.4302	0	26292000000	21	21	21	57.1	46.804	31.433	31.1826	31.6834	6	3	3	B8N8L6	B8N8L6	1	AFLA_108100	Argininosuccinate synthase
30.0909	31.37	30.58	30.8806	30.9533	31.5969	0	21136000000	21	21	21	63	45.963	30.912	30.6803	31.1436	6	3	3	B8NAG7	B8NAG7	1	AFLA_040120	Flavohemoprotein
30.2607	30.4466	30.3774	31.424	31.4339	31.0155	0	23393000000	21	21	21	75.1	44.378	30.8264	30.3616	31.2911	6	3	3	B8NB44	B8NB44	1	AFLA_044190	Branched-chain-amino-acid aminotransferase
30.0132	30.2431	30.2615	29.2331	29.3943	29.7253	0	9167500000	21	21	21	54.6	48.308	29.8117	30.1726	29.4509	6	3	3	B8NJL5	B8NJL5	1	AFLA_067360	Elongation factor Tu
33.092	33.3367	33.3705	33.3339	33.11	33.4774	0	1.0814E+11	21	21	21	53.3	50.067	33.2868	33.2664	33.3071	6	3	3	B8NLF1	B8NLF1	1	AFLA_090780	Elongation factor 1-alpha
29.5766	29.6043	29.3718	29.2298	29.6849	29.5176	0	8550800000	21	21	21	59.5	54.003	29.4975	29.5176	29.4774	6	3	3	B8NSD8	B8NSD8	1	AFLA_048010	Seryl-tRNA synthetase
24.4524	27.1175	24.9524	27.9413	27.4587	27.3341	1.23E-76	1804000000	21	21	21	20.7	163.73	26.5427	25.5074	27.578	6	3	3	B8NV55	B8NV55	1	AFLA_103490	Transcription elongation factor SPT6, putative
30.395	30.692	29.9194	29.6977	30.1613	30.4698	0	11036000000	21	21	21	54.8	53.189	30.2225	30.3355	30.1096	6	3	3	B8NZ05	B8NZ05	1	AFLA_115170	Succinyl-CoA synthetase beta subunit, putative
29.4404	29.4558	29.3034	29.1018	29.5222	29.2356	0	7800500000	24	24	21	51	77.75	29.3432	29.3999	29.2865	6	3	3	B8NGL5;B8	B8NGL5	2	AFLA_136420	Bifunctional tryptophan synthase TRPB
30.0308	29.5501	29.9909	29.6225	29.8644	29.4182	0	9245900000	22	22	22	47.7	67.541	29.7462	29.8573	29.635	6	3	3	B8MXV3	B8MXV3	1	AFLA_078900	Beta-hexosaminidase
29.804	29.8833	29.9164	29.513	29.6323	29.4292	0	7022200000	22	22	22	48	85.571	29.6964	29.8679	29.5248	6	3	3	B8MY76	B8MY76	1	AFLA_080130	Protein transport protein Sec23, putative
28.5128	28.8752	29.1036	28.9137	28.6532	28.4329	2.67E-132	4283300000	22	22	22	33.3	96.049	28.7486	28.8306	28.6666	6	3	3	B8MZ86	B8MZ86	1	AFLA_083750	Importin beta-1 subunit
28.0897	28.2665	28.124	27.966	28.1692	28.1322	2.74E-157	3624600000	22	22	22	32.9	102.84	28.1246	28.1601	28.0891	6	3	3	B8MZF6	B8MZF6	1	AFLA_084460	Heat shock protein Hsp98/Hsp104/ClpA, putative
28.123	28.0982	28.234	28.8134	28.6291	28.1137	4.11E-98	3149600000	22	22	22	30.5	107.67	28.3352	28.1517	28.5187	6	3	3	B8MZG9	B8MZG9	1	AFLA_084590	Hsp70 family chaperone Lhs1/Orp150, putative
29.9532	30.3078	30.109	29.7346	29.7462	29.7533	0	9305800000	22	22	22	50.7	68.796	29.934	30.1233	29.7447	6	3	3	B8N2E2	B8N2E2	1	AFLA_036270	Lysine--tRNA ligase
28.5283	28.1119	28.4912	28.4003	28.4799	28.0311	3.40E-194	3831100000	22	22	22	33.9	88.211	28.3404	28.3771	28.3038	6	3	3	B8N597	B8N597	1	AFLA_022250	SPX domain protein
27.1928	27.4758	27.5296	28.0465	27.7766	27.8345	3.37E-94	2340700000	22	22	22	29.4	117.53	27.6426	27.3994	27.8859	6	3	3	B8N5D9	B8N5D9	1	AFLA_022670	Transcription elongation complex subunit (Cdc68)
29.6948	30.1397	29.8874	30.2745	30.1177	30.0987	0	14404000000	22	22	22	42.7	60.722	30.0355	29.9073	30.1637	6	3	3	B8N5X8	B8N5X8	1	AFLA_014710	Importin subunit alpha
30.3035	30.3268	30.3609	30.7355	30.6606	30.5275	0	16294000000	22	22	22	66.6	46.844	30.4858	30.3304	30.6412	6	3	3	B8N6I0	B8N6I0	1	AFLA_014930	Cofactor for methionyl-and glutamyl-tRNA synthetase, putative
28.4831	28.8392	28.4155	27.5066	28.0124	28.6922	5.07E-137	3494800000	22	22	22	36.2	99.235	28.3248	28.5793	28.0704	6	3	3	B8N6U3	B8N6U3	1	AFLA_016960	Acetylglutamate kinase, putative
29.697	29.6608	29.8422	29.7196	29.5969	29.4035	0	9915100000	22	22	22	53.8	68.258	29.6534	29.7333	29.5734	6	3	3	B8N7U5	B8N7U5	1	AFLA_105380	Coronin
29.6079	29.8954	29.7616	30.7311	30.4858	30.1403	0	12357000000	22	22	22	68.4	50.261	30.1037	29.755	30.4524	6	3	3	B8N997;B8	B8N997	2	AFLA_110430	L-ornithine aminotransferase Car2, putative
29.4552	29.5923	29.8085	30.045	29.6451	29.6199	0	10310000000	22	22	22	62.4	53.168	29.6943	29.6187	29.77	6	3	3	B8NKR8	B8NKR8	1	AFLA_093220	Ran-specific GTPase-activating protein 1, putative
28.9032	28.852	28.9598	28.9654	28.3871	28.4584	3.71E-204	4191800000	22	22	22	37	82.649	28.7543	28.905	28.6036	6	3	3	B8NS24;B8	B8NS24	2	AFLA_052550	Threonyl-tRNA synthetase, putative
31.2231	31.5312	31.6988	31.3471	30.5222	30.9168	0	26351000000	22	22	22	44.8	57.15	31.2065	31.4844	30.9287	6	3	3	B8NSS6	B8NSS6	1	AFLA_050270	Conserved lysine-rich protein, putative
33.0853	33.0071	33.0564	33.2604	33.0513	32.7564	0	94550000000	23	23	22	74.8	26.869	33.0361	33.0496	33.0227	6	3	3	B8NLM9	B8NLM9	1	AFLA_092450	14-3-3 family protein ArtA, putative
29.3373	29.2101	29.359	28.3986	28.3408	29.1551	4.36E-152	5910800000	23	23	23	29.3	119.42	28.9668	29.3021	28.6315	6	3	3	B8MXX8	B8MXX8	1	AFLA_079150	Valyl-tRNA synthetase
30.2358	30.0299	29.9113	29.9549	30.2536	29.9677	0	13497000000	23	23	23	75.3	38.934	30.0589	30.059	30.0588	6	3	3	B8N1N2	B8N1N2	1	AFLA_030970	Homoserine dehydrogenase
28.6221	28.7612	28.7582	29.3338	29.3697	29.1108	3.22E-254	6122000000	23	23	23	40.7	92.27	28.9926	28.7139	29.2714	6	3	3	B8N416	B8N416	1	AFLA_033390	Phosphoribosyl-AMP cyclohydrolase, putative
27.2625	27.2779	27.5707	27.901	27.527	27.4358	2.13E-106	2053700000	23	23	23	17.2	227.08	27.4958	27.3704	27.6213	6	3	3	B8N458	B8N458	1	AFLA_033810	Filament-forming protein (Tpr/p270), putative
30.6311	30.5955	30.5287	29.5362	30.704	30.4066	0	16729000000	23	23	23	80.9	43.129	30.4004	30.5851	30.2156	6	3	3	B8N9X6	B8N9X6	1	AFLA_112720	Diphosphomevalonate decarboxylase
30.2866	30.1416	30.2037	30.3982	30.5369	30.3354	0	15467000000	23	23	23	59	72.825	30.3171	30.2107	30.4235	6	3	3	B8NEI6	B8NEI6	1	AFLA_061840	Probable Xaa-Pro aminopeptidase P
29.0001	28.5915	28.9218	28.212	27.8716	27.9307	5.18E-236	3454100000	23	23	23	43.6	76.132	28.4213	28.8378	28.0047	6	3	3	B8NQ65	B8NQ65	1	AFLA_004560	Vacuolar ATP synthase catalytic subunit A, putative
30.9782	30.4755	31.003	29.8387	29.6012	29.7963	0	10108000000	23	23	23	58.6	57.696	30.2822	30.8189	29.7454	6	3	3	B8NUL4	B8NUL4	1	AFLA_100670	ATP sulphurylase
29.5006	29.4084	29.7175	29.6837	29.6291	29.2454	0	6741500000	24	24	24	42.4	95.892	29.5308	29.5421	29.5194	6	3	3	B8MX77	B8MX77	1	AFLA_076640	Phospholipase PldA, putative
31.0364	31.3042	30.7184	31.9236	31.3743	31.5873	0	31598000000	24	24	24	68.9	52.838	31.324	31.0197	31.6284	6	3	3	B8N0Z7	B8N0Z7	1	AFLA_027720	Phosphatidyl synthase
29.2005	28.8745	29.174	27.3826	27.7533	27.8067	6.49E-120	3784100000	24	24	24	42.7	78.924	28.3653	29.083	27.6475	6	3	3	B8N394	B8N394	1	AFLA_027070	Acetyl-coenzyme A synthetase FacA
30.0491	30.1826	30.2498	30.1989	30.2143	29.985	0	13602000000	24	24	24	70.4	49.295	30.1466	30.1605	30.1327	6	3	3	B8N3C2	B8N3C2	1	AFLA_027350	Saccharopine dehydrogenase Lys9, putative
32.6965	32.8332	32.5763	31.9432	32.2385	32.4386	0	74293000000	24	24	24	62.8	52.764	32.4544	32.702	32.2067	6	3	3	B8N841	B8N841	1	AFLA_106350	ATP citrate lyase subunit (Acl), putatibe
28.9284	28.1016	28.8025	27.2918	28.3957	27.9053	1.71E-107	2644400000	24	24	24	48	69.275	28.2376	28.6108	27.8643	6	3	3	B8N980	B8N980	1	AFLA_110260	Flavin-binding monooxygenase-like protein
29.6594	29.6263	29.8682	28.3848	28.9527	29.5561	0	8710700000	24	24	24	51.7	62.104	29.3413	29.718	28.9645	6	3	3	B8NFS0	B8NFS0	1	AFLA_133490	Aspartyl-tRNA synthetase Dps1, putative
26.251	28.354	27.3915	29.7928	29.9731	33.1616	0	23102000000	24	24	24	71	40.245	29.154	27.3321	30.9758	6	3	3	B8NR98	B8NR98	1	AFLA_005730	60S ribosomal protein L4, putative
29.7333	30.5726	29.599	31.7998	31.3102	31.3224	0	28863000000	24	24	24	58.8	46.314	30.7229	29.9683	31.4775	6	3	3	B8NSE2	B8NSE2	1	AFLA_048050	Nucleosome assembly protein Nap1, putative
30.6652	30.5232	30.7486	31.0986	30.8325	30.6296	0	18181000000	24	24	24	62.3	52.019	30.7496	30.6457	30.8536	6	3	3	B8NTR5	B8NTR5	1	AFLA_099960	Argininosuccinate lyase
30.5208	30.4376	30.5841	30.2949	29.908	29.7231	0	11353000000	24	24	24	54.6	70.783	30.2447	30.5142	29.9753	6	3	3	B8NU07	B8NU07	1	AFLA_101780	NADH-cytochrome B5 reductase, putative
30.7365	30.9257	30.5409	30.892	29.7197	30.5174	0	13930000000	25	25	24	67.2	51.863	30.5554	30.7344	30.3763	6	3	3	B8MZQ2	B8MZQ2	1	AFLA_085420	Serine hydroxymethyltransferase
28.8681	28.9412	28.3396	28.3398	29.2107	28.9125	1.31E-183	4391100000	25	25	24	29.2	135.59	28.7687	28.7163	28.821	6	3	3	B8NIP7	B8NIP7	1	AFLA_068340	Cell wall biogenesis protein phosphatase Ssd1, putative
32.3781	32.1119	32.5069	31.0716	31.6606	31.2724	0	51939000000	25	25	24	63.4	58.659	31.8336	32.3323	31.3349	6	3	3	B8NXR9	B8NXR9	1	AFLA_008890	Glutamate decarboxylase
31.2907	31.5536	30.9858	31.9242	31.3934	31.7011	0	29157000000	25	25	25	51.3	59.938	31.4748	31.2767	31.6729	6	3	3	B8MXS8	B8MXS8	1	AFLA_078650	ATP synthase subunit alpha
27.9842	27.7522	27.4089	26.3634	27.1923	27.5224	7.08E-96	1504000000	25	25	25	27.2	137.48	27.3706	27.7151	27.026	6	3	3	B8MY03	B8MY03	1	AFLA_079400	NRPS-like enzyme, putative
27.9836	27.6246	27.8408	28.0521	28.1388	27.6413	1.01E-130	2779000000	25	25	25	23.8	172.72	27.8802	27.8163	27.944	6	3	3	B8MYJ6	B8MYJ6	1	AFLA_081340	Glycogen debranching enzyme Gdb1, putative
32.4804	32.7264	32.8473	ND	26.7839	ND	0	31018000000	25	25	25	57.4	52.758	31.2095	32.6847	26.7839	4	3	1	B8N5M5	B8N5M5	1	AFLA_013680	Phosphatidylglycerol specific phospholipase C, putative
27.966	28.6591	27.9608	29.0203	28.4951	28.8474	2.46E-180	5414900000	25	25	25	52.1	72.837	28.4915	28.1953	28.7876	6	3	3	B8NBU9	B8NBU9	1	AFLA_046740	Malic enzyme
30.5294	30.1609	30.688	30.6267	30.8119	30.236	0	17315000000	25	25	25	66.4	51.607	30.5088	30.4594	30.5582	6	3	3	B8NC10	B8NC10	1	AFLA_047350	Probable Xaa-Pro aminopeptidase pepP
29.3466	29.2192	29.7215	29.4947	29.3809	29.3437	5.28E-171	6824400000	25	25	25	46.9	71.048	29.4178	29.4291	29.4065	6	3	3	B8NEF6	B8NEF6	1	AFLA_060650	Glutaminyl-tRNA synthetase
31.1604	32.0637	31.5419	32.8831	32.0653	32.2713	0	52847000000	25	25	25	57.8	58.35	31.9976	31.5887	32.4065	6	3	3	B8NEV1	B8NEV1	1	AFLA_058150	Myo-inositol-phosphate synthase, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
29.1294	29.9221	29.3136	31.0943	30.9359	30.7796	0	16584000000	25	25	25	56.4	64.887	30.1958	29.455	30.9366	6	3	3	B8NFY6	B8NFY6	1	AFLA_131470	Eukaryotic translation initiation factor 3 subunit D
32.0065	31.7712	32.1627	30.9929	31.3808	30.9212	0	35620000000	25	25	25	47.3	79.838	31.5392	31.9801	31.0983	6	3	3	B8NLE2	B8NLE2	1	AFLA_090690	Mycelial catalase Cat1
30.3224	30.4508	30.5482	32.1031	31.7451	31.4522	0	25047000000	25	25	25	71.2	58.021	31.1036	30.4405	31.7668	6	3	3	B8NLJ4	B8NLJ4	1	AFLA_092100	Inosine-5-monophosphate dehydrogenase
31.0895	31.7275	30.5784	31.8141	31.8517	32.1448	0	31955000000	25	25	25	74.3	55.402	31.5343	31.1318	31.9368	6	3	3	B8NWC9	B8NWC9	1	AFLA_119660	ATP synthase subunit beta
33.6978	33.8812	33.7753	34.2949	33.7784	33.9318	0	1.9695E+11	26	26	26	86.5	39.721	33.8932	33.7848	34.0017	6	3	3	B8N1M8	B8N1M8	1	AFLA_030930	Fructose-bisphosphate aldolase, class II
30.4633	31.0873	30.9247	ND	26.4187	ND	0	10584000000	26	26	26	51.8	72.622	29.7235	30.8251	26.4187	4	3	1	B8N747	B8N747	1	AFLA_019800	Extracellular phytase, putative
30.8092	30.3106	30.9624	30.491	30.5289	30.1814	0	28987000000	26	26	26	68.8	48.57	30.5473	30.6941	30.4004	6	3	3	B8N8D0	B8N8D0	1	AFLA_107240	Fructosyl amine: oxygen oxidoreductase
25.0543	28.729	25.341	29.107	27.7706	28.5814	6.40E-183	2952800000	26	26	26	34.9	120.48	27.4305	26.3747	28.4863	6	3	3	B8NIY2	B8NIY2	1	AFLA_070100	Importin beta-4 subunit, putative
27.9842	27.9067	27.9401	28.4462	28.3122	28.063	5.15E-126	3664600000	26	26	26	24.8	158.99	28.1087	27.9437	28.2738	6	3	3	B8NRB0	B8NRB0	1	AFLA_005850	Exonuclease Kem1, putative
33.6399	33.3429	33.6585	33.7764	33.4969	33.2053	0	1.5063E+11	26	26	26	63.3	35.496	33.52	33.5471	33.4929	6	3	3	B8NUD9	B8NUD9	1	AFLA_099010	Transaldolase
29.0833	28.55	29.1294	29.0944	29.3292	28.8723	0	12298000000	27	27	26	66.8	75.372	29.0097	28.9209	29.0986	6	3	3	B8N268	B8N268	1	AFLA_034620	Amine oxidase
29.0759	29.5046	29.1179	27.8318	29.24	29.2254	1.44E-270	6155900000	27	27	27	31.1	112	28.9993	29.2328	28.7657	6	3	3	B8N001	B8N001	1	AFLA_086410	C1 tetrahydrofolate synthase, putative
29.8218	29.7082	29.9615	29.1514	29.3991	29.3306	3.51E-197	7272200000	27	27	27	38.6	94.875	29.5621	29.8305	29.2937	6	3	3	B8N118	B8N118	1	AFLA_027930	N-terminal acetyltransferase catalytic subunit Nat1, putative
28.5547	29.2533	28.4641	29.8281	30.0947	30.3769	0	8406800000	27	27	27	31.3	119.79	29.4286	28.7574	30.0999	6	3	3	B8N1D8	B8N1D8	1	AFLA_030030	Eukaryotic translation initiation factor 3 subunit A
30.4941	29.2956	30.0317	28.3679	28.5435	28.6508	0	12789000000	27	27	27	65.2	66.547	29.2306	29.9405	28.5207	6	3	3	B8N2F2	B8N2F2	1	AFLA_036370	Phosphoenolpyruvate carboxykinase AcuF
33.6382	34.3713	33.7505	34.1979	33.6069	34.3583	0	1.6984E+11	27	27	27	79.6	62.926	33.9872	33.92	34.0544	6	3	3	B8N3S3	B8N3S3	1	AFLA_031570	Pyruvate decarboxylase PdcA, putative
31.6722	31.7069	31.9473	32.7804	32.8505	32.2706	0	57716000000	27	27	27	52.7	80.383	32.2047	31.7755	32.6338	6	3	3	B8NBM3	B8NBM3	1	AFLA_045980	Probable dipeptidyl-peptidase 5
31.0017	30.8272	31.0388	31.4773	31.1317	30.8782	0	28415000000	27	27	27	67.1	62.341	31.0592	30.9559	31.1624	6	3	3	B8NP70	B8NP70	1	AFLA_128530	Delta-1-pyrroline-5-carboxylate dehydrogenase PrnC
31.5271	31.4905	31.631	31.9755	31.658	31.4599	0	41247000000	27	27	27	65.9	54.147	31.6236	31.5495	31.6978	6	3	3	B8NPD5	B8NPD5	1	AFLA_130070	Hexokinase Kxk, putative
29.9153	30.5054	29.9421	32.5608	32.0475	31.7601	0	31267000000	28	28	28	37.4	77.339	31.1219	30.1209	32.1228	6	3	3	B8N3I8	B8N3I8	1	AFLA_028910	Polyadenylate-binding protein
29.727	29.9218	29.7238	28.472	29.0972	29.5112	2.97E-232	6668700000	28	28	28	32.5	138.73	29.4088	29.7909	29.0268	6	3	3	B8N3V1	B8N3V1	1	AFLA_031850	Clustered mitochondria protein homolog
32.0829	32.1431	32.239	32.5867	32.3761	32.0937	0	57078000000	28	28	28	65.2	59.368	32.2536	32.155	32.3522	6	3	3	B8N562;B8	B8N562	2	AFLA_021000	Putative uncharacterized protein
32.7002	31.9566	32.6462	31.5833	32.4423	31.6925	0	43532000000	28	28	28	74.8	53.981	32.1702	32.4344	31.906	6	3	3	B8N8T4	B8N8T4	1	AFLA_108790	Aldehyde dehydrogenase AldA, putative
34.6773	34.1098	34.6513	34.5815	34.4956	34.139	0	2.9008E+11	28	28	28	81.7	49.333	34.4424	34.4795	34.4054	6	3	3	B8NA36	B8NA36	1	AFLA_113320	Glutamate dehydrogenase
32.317	31.7128	32.2584	32.5902	32.3343	32.1446	0	51902000000	28	28	28	68	54.614	32.2262	32.0961	32.3564	6	3	3	B8NAT6	B8NAT6	1	AFLA_043110	Dihydrolipoyl dehydrogenase
30.4815	30.5958	30.45	28.9848	30.624	30.6428	0	13905000000	28	28	28	76.9	57.188	30.2965	30.5091	30.0839	6	3	3	B8NBZ9	B8NBZ9	1	AFLA_047240	Cystathionine beta-synthase, putative
30.1958	30.1184	30.2671	30.0571	29.9255	30.003	0	14454000000	28	28	28	68.6	53.664	30.0945	30.1938	29.9952	6	3	3	B8NC16	B8NC16	1	AFLA_047410	Actin-bundling protein Sac6, putative
31.4783	31.4094	29.6433	29.0614	31.1243	31.0549	0	30559000000	28	28	28	69.1	57.221	30.6286	30.8437	30.4135	6	3	3	B8NDA6	B8NDA6	1	AFLA_056670	4-aminobutyrate transaminase GatA
29.7371	29.8126	29.7444	30.4145	30.4809	30.2866	0	11615000000	28	28	28	69.9	59.793	30.0793	29.7647	30.394	6	3	3	B8NGS7	B8NGS7	1	AFLA_137950	GMP synthase
32.8046	32.4682	32.9765	33.0149	33.3176	32.8389	0	95172000000	28	28	28	84.2	33.487	32.9034	32.7498	33.0571	6	3	3	B8NIV7;B8	B8NIV7	2	AFLA_069850	Glycerol dehydrogenase Gcy1, putative
30.4735	30.2552	30.5841	31.719	31.4242	31.1226	0	23632000000	28	28	28	70.6	43.579	30.9298	30.4376	31.4219	6	3	3	B8NIW4	B8NIW4	1	AFLA_069920	GTP-binding protein YchF
29.4082	29.6294	29.0463	29.4813	29.5438	29.444	0	8388600000	28	28	28	60.5	62.245	29.4255	29.3613	29.4897	6	3	3	B8NJ76	B8NJ76	1	AFLA_065080	Phosphoglucomutase, putative
32.8988	32.7434	32.5289	31.7359	32.4188	32.1154	0	64423000000	28	28	28	67.1	56.313	32.4069	32.7237	32.09	6	3	3	B8NK50	B8NK50	1	AFLA_070990	UTP-glucose-1-phosphate uridylyltransferase Ugp1, putative
30.6818	30.5166	30.732	31.222	30.9052	30.6648	0	20933000000	28	28	28	52.5	64.085	30.7871	30.6435	30.9307	6	3	3	B8NK52	B8NK52	1	AFLA_071010	Heat shock protein (Sti1), putative
32.2874	32.0743	32.2977	32.5369	32.5346	32.031	0	49916000000	28	28	28	62.5	56.397	32.2936	32.2198	32.3675	6	3	3	B8NPF9	B8NPF9	1	AFLA_130310	Protein disulfide isomerase Pdi1, putative
29.8683	29.6892	29.9805	28.9362	29.5592	30.0765	0	9271500000	28	28	28	45.9	80.408	29.685	29.846	29.524	6	3	3	B8NSH4	B8NSH4	1	AFLA_048370	Glycyl-tRNA synthetase
30.7638	30.9399	31.0096	30.3501	30.7178	31.07	0	20571000000	28	28	28	78.2	52.912	30.8085	30.9044	30.7126	6	3	3	B8NV99	B8NV99	1	AFLA_103940	Glutamate carboxypeptidase, putative
31.9459	32.1854	32.1063	31.6294	31.8172	31.766	0	42764000000	29	29	28	69.5	47.224	31.9084	32.0792	31.7375	6	3	3	B8N0W2	B8N0W2	1	AFLA_026470	Aspartate aminotransferase
30.6216	30.3212	30.6829	30.3597	30.3356	29.8559	0	15551000000	29	29	29	52	81.691	30.3628	30.5419	30.1837	6	3	3	B8MXA2	B8MXA2	1	AFLA_076890	Metallopeptidase MepB
30.9727	30.7923	29.5782	29.8935	30.8564	30.607	1.35E-248	18034000000	29	29	29	55.3	55.825	30.45	30.4478	30.4523	6	3	3	B8N000	B8N000	1	AFLA_086400	Isocitrate dehydrogenase [NADP]
30.5907	30.3792	30.7523	27.722	28.03	28.4819	0	6044300000	29	29	29	49.4	77.127	29.326	30.574	28.078	6	3	3	B8N2M1	B8N2M1	1	AFLA_037960	Glucosamine-fructose-6-phosphate aminotransferase
31.2551	30.872	31.3376	29.686	30.1192	30.0659	0	18418000000	29	29	29	58.9	61.708	30.5559	31.1549	29.957	6	3	3	B8ND74	B8ND74	1	AFLA_056350	2-methylcitrate dehydratase, putative
29.9015	29.8227	30.0028	30.5489	30.4803	30.0917	0	13096000000	30	30	30	57.5	71.114	30.1413	29.909	30.3736	6	3	3	B8MZH6	B8MZH6	1	AFLA_084660	2-isopropylmalate synthase
29.8474	31.2995	29.8228	30.0797	31.3097	31.6595	0	25842000000	30	30	30	52.1	73.449	30.6698	30.3232	31.0163	6	3	3	B8N4E9	B8N4E9	1	AFLA_035620	Hsp70 chaperone BiP/Kar2, putative
28.9099	29.1619	29.2775	30.1645	29.6157	29.5545	4.26E-298	8160200000	30	30	30	24.3	147.79	29.4473	29.1164	29.7782	6	3	3	B8NBF8	B8NBF8	1	AFLA_045330	Eukaryotic translation initiation factor subunit eIF-4F, putative
28.8484	28.8912	29.0915	30.3041	28.7331	29.1247	5.12E-241	5970200000	30	30	30	57	83.859	29.1655	28.9437	29.3873	6	3	3	B8NDX6	B8NDX6	1	AFLA_056170	Catalase
30.4349	30.6375	29.6151	30.5233	31.0223	31.0038	0	18473000000	30	30	30	61.6	54.349	30.5395	30.2292	30.8498	6	3	3	B8NGE1	B8NGE1	1	AFLA_134810	Adenylosuccinate lyase Ade13, putative
29.8007	31.4713	30.0415	30.3067	30.0528	31.6012	0	33308000000	30	30	30	68.6	44.369	30.5457	30.4379	30.6536	6	3	3	B8NIQ9	B8NIQ9	1	AFLA_069370	Phosphoglycerate kinase
32.1695	32.189	30.9593	30.4513	32.0223	31.784	0	49623000000	30	30	30	79.1	56.165	31.5959	31.7726	31.4192	6	3	3	B8NJ18	B8NJ18	1	AFLA_071350	UDP-N-acetylglucosamine pyrophosphorylase
28.4329	28.214	28.3361	28.6109	28.4024	28.1359	2.69E-126	3663200000	30	30	30	36.6	128.71	28.3554	28.3277	28.3831	6	3	3	B8NRC2	B8NRC2	1	AFLA_005970	Ubiquitin carboxyl-terminal hydrolase
31.678	32.1114	31.5955	31.2228	31.3994	32.1106	0	38900000000	31	31	31	66.9	58.086	31.6863	31.7949	31.5776	6	3	3	B8MWA0	B8MWA0	1	AFLA_087900	Pyruvate kinase
32.7151	32.928	32.9236	33.6643	33.5401	33.2346	0	1.0898E+11	31	31	31	68.8	46.388	33.1676	32.8556	33.4797	6	3	3	B8NDQ4	B8NDQ4	1	AFLA_055450	Translation elongation factor eEF-1 subunit gamma, putative
32.0202	32.0003	31.9196	31.1852	31.7862	31.5926	0	44598000000	31	31	31	79	52.207	31.7507	31.98	31.5213	6	3	3	B8NFX0	B8NFX0	1	AFLA_133990	Secretory pathway gdp dissociation inhibitor
33.763	33.5798	33.8334	33.0187	32.8991	32.7482	0	1.0761E+11	31	31	31	61.5	48.931	33.307	33.7254	32.8886	6	3	3	B8NIT1	B8NIT1	1	AFLA_069590	Adenosylhomocysteinase
31.363	31.2381	31.1206	30.4594	31.6502	31.3662	0	31002000000	32	32	32	72.3	65.045	31.1996	31.2406	31.1586	6	3	3	B8N9R9	B8N9R9	1	AFLA_112150	Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP
29.56	29.1671	29.6965	29.4947	29.3828	29.0178	0	8728700000	32	32	32	62.2	72.633	29.3865	29.4745	29.2984	6	3	3	B8NHB9	B8NHB9	1	AFLA_135240	Carnitine acetyl transferase
30.5271	30.4069	30.6088	30.4793	30.0002	30.1135	0	11584000000	32	32	32	55.6	83.973	30.356	30.5143	30.1977	6	3	3	B8NQF7	B8NQF7	1	AFLA_006370	Glutamyl-tRNA synthetase
31.8144	32.1227	31.8367	31.3179	30.9935	31.5462	0	44453000000	33	33	33	73.5	60.356	31.6052	31.9246	31.2858	6	3	3	B8N1K6	B8N1K6	1	AFLA_030710	Phosphoglucomutase PgmA
28.1194	27.9036	27.4165	ND	22.6214	23.1733	0	7458900000	33	33	33	42.9	113.65	25.8468	27.8132	22.8973	5	3	2	B8NE90	B8NE90	1	AFLA_059990	O-methyltransferase, putative
29.725	29.7188	29.7874	29.8809	29.323	29.5905	5.24E-278	10119000000	34	34	34	41	127.63	29.671	29.7438	29.5982	6	3	3	B8NV28	B8NV28	1	AFLA_103220	Cytoskeleton assembly control protein Sla2, putative
29.2838	29.901	29.8932	29.3846	29.1042	29.5072	0	7297600000	36	36	34	42.9	138.64	29.5123	29.6927	29.332	6	3	3	B8NXH1;B8	B8NXH1	2	AFLA_007900	5-oxo-L-prolinase, putative
31.2607	31.4791	31.1176	32.0927	32.0123	32.3242	0	46383000000	35	35	35	58.3	72.467	31.7144	31.2858	32.1431	6	3	3	B8NB87	B8NB87	1	AFLA_044620	Mitochondrial Hsp70 chaperone (Ssc70), putative
33.006	33.088	33.2209	33.5295	32.9949	32.9356	0	1.1172E+11	35	35	35	69.4	61.213	33.1292	33.105	33.1533	6	3	3	B8NBA7	B8NBA7	1	AFLA_044820	Glucose-6-phosphate isomerase
28.969	29.5514	29.0615	30.1277	30.4737	30.6868	0	11251000000	35	35	35	47.2	97.164	29.8117	29.194	30.4294	6	3	3	B8NCT8	B8NCT8	1	AFLA_041730	Eukaryotic translation initiation factor 3 subunit C
30.5824	30.7913	30.8506	31.9195	31.7439	31.4699	0	27148000000	36	36	36	60.1	84.29	31.2263	30.7414	31.7111	6	3	3	B8MYK4	B8MYK4	1	AFLA_081430	Eukaryotic translation initiation factor 3 subunit B
29.8965	29.8035	29.8088	30.387	30.1472	29.7996	0	11564000000	36	36	36	42.7	130.32	29.9738	29.8363	30.1113	6	3	3	B8N3B0	B8N3B0	1	AFLA_027230	Alpha-aminoadipate reductase Lys2, putative
33.1925	33.0055	33.2408	32.7822	33.1682	32.8982	0	1.0372E+11	36	36	36	75.8	54.216	33.0479	33.1462	32.9495	6	3	3	B8N4I0	B8N4I0	1	AFLA_036840	6-phosphogluconate dehydrogenase, decarboxylating
27.3321	28.3381	27.8625	29.7347	29.5288	29.3284	1.16E-281	5543100000	36	36	36	54.7	97.885	28.6874	27.8443	29.5306	6	3	3	B8N6V6	B8N6V6	1	AFLA_017090	Methyltransferase (Ncl1), putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID (ORF)	Protein Function
29.7322	29.8975	29.6229	29.3302	30.2442	29.9366	0	9003400000	36	36	36	48.7	147.49	29.794	29.7509	29.837	6	3	3	B8NQA1	B8NQA1	1	AFLA_004920	Phosphoribosylformylglycinamidine synthase
32.1627	32.5732	32.338	33.2	32.5726	32.8781	0	77739000000	37	37	37	82.7	57.288	32.6207	32.358	32.8835	6	3	3	B8MZQ0	B8MZQ0	1	AFLA_085400	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent
33.9045	33.7489	33.9995	34.0502	33.8966	33.5411	0	1.8309E+11	37	37	37	64.6	74.803	33.8568	33.8843	33.8293	6	3	3	B8N4T2	B8N4T2	1	AFLA_017910	Transketolase
29.8283	30.05	29.4194	28.6938	29.9098	29.9054	0	8515300000	38	38	38	50	124.24	29.6345	29.7659	29.503	6	3	3	B8N4R2	B8N4R2	1	AFLA_017710	Isoleucyl-tRNA synthetase ,cytoplasmic
31.4931	30.9698	31.1742	29.8247	30.1413	30.4402	0	17011000000	38	38	38	42.2	131.2	30.6739	31.2124	30.1354	6	3	3	B8N9R6	B8N9R6	1	AFLA_112120	Pyruvate carboxylase
31.4198	31.5297	31.1396	31.2758	30.9437	31.2847	0	26177000000	38	38	38	56.5	116.05	31.2655	31.363	31.1681	6	3	3	B8NCU9	B8NCU9	1	AFLA_041840	Glycine dehydrogenase
33.4995	33.6191	33.2363	33.4024	33.5662	33.975	0	1.4977E+11	38	38	38	44.2	96.549	33.5497	33.4516	33.6478	6	3	3	B8NYQ1	B8NYQ1	1	AFLA_012200	Hsp70 chaperone (HscA), putative
29.6844	29.3089	29.725	29.4625	29.3286	28.9754	0	8610100000	39	39	39	46.3	134.5	29.4141	29.5728	29.2555	6	3	3	B8N2Z3	B8N2Z3	1	AFLA_025170	A-pheromone processing metallopeptidase Ste23
34.0112	34.0645	33.8435	34.3849	34.4799	34.3065	0	2.1721E+11	39	39	39	65.1	69.704	34.1818	33.9731	34.3905	6	3	3	B8N5B0	B8N5B0	1	AFLA_022380	Molecular chaperone Hsp70
31.5545	31.1482	31.5804	31.3683	31.1436	30.9415	0	30946000000	40	40	40	73.7	57.904	31.2894	31.4277	31.1511	6	3	3	B8N022	B8N022	1	AFLA_086620	Glucose-6-phosphate 1-dehydrogenase
30.6184	30.6472	30.7379	29.8915	29.7847	30.1399	0	12130000000	40	40	40	47.4	126.92	30.3033	30.6678	29.9387	6	3	3	B8N248	B8N248	1	AFLA_034420	Leucyl-tRNA synthetase
29.0453	29.3963	28.9941	28.0798	28.6054	28.7521	8.99E-181	4204300000	41	40	40	21.5	279.52	28.8122	29.1452	28.4791	6	3	3	B8N8V0	B8N8V0	1	AFLA_108960	Bifunctional pyrimidine biosynthesis protein (PyrABCN), putative
31.1146	31.1361	30.9873	30.4746	30.6031	30.7728	0	24412000000	41	41	41	58.9	114.85	30.8481	31.0793	30.6168	6	3	3	B8N6L0	B8N6L0	1	AFLA_015230	Poly(A)+ RNA transport protein (UbaA), putative
30.253	30.1834	30.4308	30.9096	30.6262	30.2289	0	16046000000	41	41	41	64.3	79.759	30.4387	30.2891	30.5883	6	3	3	B8NGS8	B8NGS8	1	AFLA_137960	Arginyl-tRNA synthetase
31.7007	31.2455	31.8012	31.657	31.7632	31.2767	0	38543000000	41	41	41	55.5	99.049	31.574	31.5825	31.5656	6	3	3	B8NRE7	B8NRE7	1	AFLA_007140	Aminopeptidase, putative
32.2183	32.4268	32.4332	33.3307	32.9836	32.7544	0	74761000000	42	42	42	78.6	62.213	32.6912	32.3594	33.0229	6	3	3	B8NBK0	B8NBK0	1	AFLA_045750	Antigenic mitochondrial protein HSP60, putative
30.3686	30.4978	30.5495	30.8334	30.3644	30.163	0	14777000000	42	42	42	38.9	131.45	30.4628	30.472	30.4536	6	3	3	B8NP45	B8NP45	1	AFLA_128280	M protein repeat protein
30.3679	30.8961	30.4185	29.7857	31.4549	31.4347	0	27929000000	44	44	44	65.2	90.553	30.7263	30.5608	30.8918	6	3	3	B8NQU3	B8NQU3	1	AFLA_002370	Cell division control protein Cdc48
29.5729	29.4736	29.5086	28.403	29.1482	28.9513	0	6157200000	45	45	45	32.1	233.2	29.1763	29.5184	28.8342	6	3	3	B8N5A6	B8N5A6	1	AFLA_022340	Glutamate synthase Glt1, putative
32.381	32.3648	32.4895	33.0522	32.9699	32.6248	0	64800000000	45	45	45	64.7	79.792	32.6471	32.4118	32.8823	6	3	3	B8NL13	B8NL13	1	AFLA_095970	Hsp70 chaperone Hsp88
32.9475	32.907	32.7759	31.8417	32.9248	32.8286	0	92218000000	46	46	46	71.6	85.596	32.7043	32.8768	32.5317	6	3	3	B8N211	B8N211	1	AFLA_034050	Mitochondrial aconitate hydratase, putative
33.0993	32.7139	33.0851	32.9086	32.8598	32.461	0	95074000000	48	48	48	57.8	106.78	32.8546	32.9661	32.7432	6	3	3	B8N9B4	B8N9B4	1	AFLA_110600	Aminopeptidase
33.3726	33.4249	33.5916	33.3654	33.3414	33.1933	0	1.0129E+11	50	50	50	62.8	79.631	33.3815	33.463	33.3	6	3	3	B8NQL4	B8NQL4	1	AFLA_006960	Molecular chaperone and allergen Mod-E/Hsp90/Hsp1
30.388	30.5115	30.7913	29.567	29.8252	30.4088	0	12390000000	52	52	52	45.7	199.56	30.2487	30.5636	29.9337	6	3	3	B8N9R7	B8N9R7	1	AFLA_112130	Clathrin heavy chain
31.0906	31.3736	30.6269	31.0646	31.6436	31.59	0	33235000000	53	53	52	60.1	129.3	31.2316	31.0304	31.4328	6	3	3	B8NB80	B8NB80	1	AFLA_044550	Carbamoyl-phosphate synthase, large subunit
29.1398	29.3639	29.2243	29.9699	29.7067	29.4168	0	9033900000	53	53	53	52.4	167.27	29.4702	29.2427	29.6978	6	3	3	B8N6M9	B8N6M9	1	AFLA_015420	Sulfite reductase, putative
34.4655	34.3765	34.0718	32.9566	33.7757	33.7585	0	1.7991E+11	55	55	55	75.6	87.163	33.9008	34.3046	33.4969	6	3	3	B8N9V1	B8N9V1	1	AFLA_112470	Cobalamin-independent methionine synthase MetH/D
34.492	34.6353	34.1843	33.6423	34.8952	34.6871	0	2.7021E+11	59	59	58	68.2	94.226	34.4227	34.4372	34.4082	6	3	3	B8NGN7	B8NGN7	1	AFLA_136640	Translation elongation factor EF-2 subunit, putative
32.7015	33.1785	32.2671	32.0643	33.1828	33.3952	0	90854000000	62	62	62	74.4	117.9	32.7982	32.7157	32.8808	6	3	3	B8MX73	B8MX73	1	AFLA_076600	Translation elongation factor eEF-3, putative
32.4156	32.8302	32.4269	32.6239	32.725	32.3689	0	52322000000	80	80	79	56.6	204.29	32.5651	32.5576	32.5726	6	3	3	B8NL81	B8NL81	1	AFLA_089170	Fatty acid synthase alpha subunit FasA
32.1971	32.0647	32.3483	30.5036	30.943	31.4773	0	31931000000	85	85	85	56	236.61	31.589	32.2034	30.9746	6	3	3	B8NBR1	B8NBR1	1	AFLA_046360	Acetyl-CoA carboxylase, putative
33.075	33.4761	33.0352	33.2332	33.356	32.9881	0	86246000000	99	99	99	66.4	232.14	33.1939	33.1954	33.1924	6	3	3	B8NL80	B8NL80	1	AFLA_089160	Fatty acid synthase beta subunit, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

B. Quantitative results

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	t-test p value	Log2 (t-test Difference)	Fold Change (Treated v Control)	Protein IDs	Majority protein IDs	Proteins	Gene Name (ORF)	Protein Function
22,5658	26,0784	22,4432	32,205	31,5464	31,8542	6,41E-114	1,53E+10	8	8	8	37	16,959	27,7822	23,6958	31,8686	6	3	3	0,002482	8,17274	288,5625	B8NSF1	B8NSF1	1	AFLA_048140	60S ribosomal protein L23
23,9401	25,9709	23,0551	31,5357	31,5323	31,5052	3,41E-219	1,26E+10	12	12	12	51,2	24,222	27,9232	24,3221	31,5244	6	3	3	0,001128	7,20233	147,27105	B8NIL3	B8NIL3	1	AFLA_068000	Ribosomal protein
24,0768	26,0663	24,4939	31,8432	31,2079	31,948	0	1,46E+10	16	16	16	46,6	29,318	28,2727	24,879	31,6664	6	3	3	0,000471	6,78736	110,45845	B8N204	B8N204	1	AFLA_033980	Cytosolic large ribosomal subunit protein L7A
24,0902	24,9937	22,4161	28,4665	28,8838	31,9358	0	9,39E+09	15	15	15	47,3	25,677	26,7977	23,8333	29,762	6	3	3	0,011149	5,9287	60,913918	B8NYZ9	B8NYZ9	1	AFLA_115110	60S ribosomal protein L13
23,0449	24,405	23,819	27,8457	28,768	31,1123	2,13E-67	5,19E+09	6	6	6	37,5	20,782	26,4991	23,7563	29,242	6	3	3	0,006387	5,48572	44,809105	B8NC19	B8NC19	1	AFLA_047440	60S ribosomal protein L18
21,9837	ND	21,2545	26,2642	28,8373	25,9388	1,45E-49	6,84E+08	9	9	9	20,6	69,301	24,8557	21,6191	27,0134	5	2	3	0,021214	5,39431	42,058048	B8NC58	B8NC58	1	AFLA_038530	Extracellular metalloproteinase mep
23,6866	26,2457	24,1127	29,5226	29,2648	31,3796	5,21E-111	7,09E+09	7	7	7	22,4	33,628	27,3687	24,6817	30,0557	6	3	3	0,006542	5,37401	41,470398	B8N3M3	B8N3M3	1	AFLA_029260	Ribosomal protein L15
26,9532	28,195	26,8465	32,6452	32,1099	32,7152	0	2,28E+10	16	16	16	60,7	34,613	29,9108	27,3316	32,4901	6	3	3	0,000402	5,15855	35,717272	B8N6A6	B8N6A6	1	AFLA_018700	60S ribosomal protein L5, putative
24,202	25,3826	25,2595	28,4932	28,5729	31,7348	1,66E-190	9,17E+09	8	8	8	49,7	16,827	27,2742	24,948	29,6003	6	3	3	0,014706	4,65226	25,146052	B8NV82	B8NV82	1	AFLA_103770	60S ribosomal protein L27a, putative
25,3748	25,9619	24,8813	29,2348	29,7716	30,8372	1,23E-47	8,01E+09	5	5	5	35,8	17,937	27,6769	25,406	29,9478	6	3	3	0,0013	4,54181	23,292765	B8MY77	B8MY77	1	AFLA_080140	60S ribosomal protein L12
23,4539	25,7857	24,1768	28,5988	28,0599	28,1248	9,71E-45	1,58E+09	7	7	7	50	33,532	26,3666	24,4721	28,2612	6	3	3	0,005932	3,78906	13,823586	B8MWC5	B8MWC5	1	AFLA_088150	Fe superoxide dismutase, putative
25,2702	26,7664	25,5753	30,6179	28,2592	30,0702	2,21E-42	8,56E+09	6	6	6	46	14,147	27,7599	25,8706	29,6491	6	3	3	0,011122	3,77847	13,722486	B8MY51	B8MY51	1	AFLA_079880	60S ribosomal protein L22, putative
23,364	26,1299	23,6089	26,9919	27,9606	29,1084	3,36E-95	1,87E+09	6	6	6	57,5	11,353	26,194	24,3676	28,0203	6	3	3	0,02733	3,65272	12,577035	B8NBK4	B8NBK4	1	AFLA_045790	60S ribosomal protein L30, putative
25,4843	27,059	25,5751	29,1277	29,1166	30,8271	2,17E-105	5,04E+09	8	8	8	47,4	15,612	27,865	26,0395	29,6905	6	3	3	0,008779	3,65102	12,562224	B8NMV9	B8NMV9	1	AFLA_127220	60S ribosomal protein L27
26,251	28,354	27,3915	29,7928	29,9731	33,1616	0	2,31E+10	24	24	24	71	40,245	29,154	27,3321	30,9758	6	3	3	0,043626	3,64371	12,498733	B8NR98	B8NR98	1	AFLA_005730	60S ribosomal protein L4, putative
27,6549	29,6594	27,5386	31,7868	31,4011	32,0186	0	2,4E+10	10	10	10	48,9	33,441	30,0099	28,2843	31,7355	6	3	3	0,008338	3,45117	10,937188	B8N1E9	B8N1E9	1	AFLA_030140	60S ribosomal protein P0
ND	25,2324	23,7138	27,8997	27,4725	28,3479	1,14E-47	1,29E+09	14	14	14	41,6	46,429	26,5332	24,4731	27,9067	5	2	3	0,013415	3,43363	10,805021	B8NH55	B8NH55	1	AFLA_132790	37S ribosomal protein S5
24,1789	24,4578	24,2882	28,132	27,5781	27,482	1,56E-64	1,32E+09	5	5	5	35,5	19,836	26,0195	24,3083	27,7307	6	3	3	9,65E-05	3,4224	10,721241	B8N9R2	B8N9R2	1	AFLA_112080	Small nuclear ribonucleoprotein SmB, putative
23,9362	24,3008	24,2159	27,7423	27,1664	26,9385	5,42E-31	8,97E+08	9	9	9	58,6	28,548	25,7167	24,151	27,2824	6	3	3	0,000286	3,13146	8,7632135	B8NG47	B8NG47	1	AFLA_132080	Small nuclear ribonucleoprotein U2, A
25,1286	27,0756	25,2996	28,6235	28,0097	30,2151	4,97E-212	6,16E+09	13	13	13	59	21,955	27,392	25,8346	28,9494	6	3	3	0,026268	3,11482	8,6627195	B8NIQ5	B8NIQ5	1	AFLA_068420	60S ribosomal protein L6
23,8302	22,8528	22,9213	26,4737	26,8975	25,53	1,65E-12	4,8E+08	5	5	5	28	28,345	24,7509	23,2014	26,3004	6	3	3	0,003771	3,09896	8,568009	B8NI48	B8NI48	1	AFLA_064530	Glutathione S-transferase GliG-like, putative
26,6047	26,4718	26,6402	29,9875	29,3707	29,4766	7,56E-218	4,87E+09	11	11	11	26,9	57,28	28,0919	26,5722	29,6116	6	3	3	0,000103	3,03937	8,2213197	B8NVT9	B8NVT9	1	AFLA_117760	Phytase, putative
24,5312	25,089	24,6235	28,0923	27,6383	27,6195	3,73E-15	1,53E+09	4	4	4	36,2	12,867	26,2657	24,7479	27,7834	6	3	3	0,000196	3,03548	8,1991821	B8N0U1	B8N0U1	1	AFLA_026260	Small nuclear ribonucleoprotein SmD3, putative
24,6455	25,3102	24,4675	28,2423	27,6382	27,5605	6,53E-94	1,41E+09	3	3	3	45,5	13,43	26,3107	24,8077	27,8136	6	3	3	0,000853	3,00592	8,0328949	B8N488	B8N488	1	AFLA_035010	Small nuclear ribonucleoprotein SmD1, putative
27,8607	28,5777	27,665	31,2964	31,018	30,7017	0	1,55E+10	12	12	12	47,7	38,179	29,5199	28,0345	31,0054	6	3	3	0,000807	2,97094	7,8404692	B8NDZ3	B8NDZ3	1	AFLA_057240	RNP domain protein
26,3371	27,686	26,2598	29,1467	28,9187	31,1081	0	7,27E+09	13	13	13	59	29,018	28,2427	26,761	29,7245	6	3	3	0,023822	2,96357	7,8005184	B8NCT6	B8NCT6	1	AFLA_041710	60S ribosomal protein L7
24,8427	25,9931	23,1045	26,9402	27,1496	28,6498	1,04E-96	2,14E+09	8	8	8	45,1	20,059	26,1133	24,6468	27,5799	6	3	3	0,042357	2,9331	7,6374975	B8N9R3	B8N9R3	1	AFLA_112090	60S ribosomal protein L11
22,3087	23,2391	ND	26,0933	25,3263	25,481	6,01E-09	2,21E+08	2	2	2	14,2	18,42	24,4897	22,7739	25,6335	5	2	3	0,008392	2,85957	7,2579897	B8N3C6	B8N3C6	1	AFLA_027390	Ubiquinol-cytochrome c reductase complex 17 kd protein
25,1408	25,4607	25,0454	28,6492	27,6807	27,5688	3,13E-49	1,83E+09	10	10	10	42,5	35,332	26,5909	25,2156	27,9662	6	3	3	0,001666	2,75061	6,7300163	B8MWP8	B8MWP8	1	AFLA_075060	Transformer-SR ribonucleoprotein, putative
25,6146	27,213	25,6213	29,163	28,8006	28,6934	3,16E-135	3,14E+09	12	12	12	45,2	39,263	27,5177	26,1496	28,8857	6	3	3	0,007643	2,73608	6,6625756	B8MXX7	B8MXX7	1	AFLA_079140	Casein kinase, putative
24,2945	25,0195	24,672	27,7502	27,4408	26,7852	2,77E-48	9,75E+08	5	5	5	21,7	36,186	25,9937	24,662	27,3254	6	3	3	0,001657	2,66335	6,3350236	B8NEL6	B8NEL6	1	AFLA_062140	RNA binding protein, putative
28,2846	29,8689	28,099	31,4298	31,1463	31,5532	3,90E-184	1,5E+10	5	5	5	27,8	24,904	30,0636	28,7508	31,3764	6	3	3	0,010251	2,6256	6,1714094	B8NNH5	B8NNH5	1	AFLA_127860	60S acidic ribosomal protein P1
29,1028	30,7601	29,3335	32,6169	32,0884	32,3418	7,10E-271	3,38E+10	8	8	8	95,4	11,087	31,0406	29,7321	32,3491	6	3	3	0,008378	2,61693	6,134433	B8NB77	B8NB77	1	AFLA_044520	60S acidic ribosomal protein P2/allergen Asp F 8
24,0435	25,8384	23,8402	26,044	27,0887	28,3801	1,33E-44	1,38E+09	8	8	8	33,6	26,174	25,8725	24,574	27,1709	6	3	3	0,048763	2,59687	6,0497268	B8NCW4	B8NCW4	1	AFLA_041990	60S ribosomal protein L17
26,9281	25,7028	26,6883	28,799	29,1028	29,0029	6,77E-158	4,75E+09	20	19	19	44,4	78,235	27,704	26,4397	28,9683	6	3	3	0,002793	2,52853	5,7698347	B8MVZ8	B8MVZ8	1	AFLA_073450	Amine oxidase
24,9906	26,8634	24,8734	27,539	27,9401	28,7472	8,77E-122	1,24E+09	8	8	8	32,1	22,173	26,8256	25,5758	28,0754	6	3	3	0,027384	2,49963	5,6554037	B8NUR3	B8NUR3	1	AFLA_101160	40S ribosomal protein S9
24,6982	26,138	26,0523	27,2356	28,0557	29,0843	4,10E-59	4,76E+09	5	5	5	61,5	11,246	26,8774	25,6295	28,1252	6	3	3	0,024509	2,49569	5,6399798	B8N837	B8N837	1	AFLA_106310	Chaperonin, putative
23,9707	23,2133	23,685	26,1592	25,8527	26,1392	2,20E-30	5,46E+08	3	3	3	40	14,692	24,8367	23,623	26,0504	6	3	3	0,000555	2,42738	5,3791566	B8MZR4	B8MZR4	1	AFLA_085540	Putative uncharacterized protein
23,5891	25,7826	23,3689	26,2898	26,5178	27,2122	2,32E-31	1,05E+09	6	6	6	38,9	17,264	25,4601	24,2469	26,6733	6	3	3	0,041432	2,42638	5,3754294	B8NKG5	B8NKG5	1	AFLA_091310	Eukaryotic translation initiation factor eIF-1A subunit, putative
28,158	28,748	28,5399	31,1171	30,8179	30,7315	3,11E-105	9,85E+09	9	9	9	54,7	16,338	29,6854	28,482	30,8888	6	3	3	0,000322	2,40684	5,3031149	B8NRT9	B8NRT9	1	AFLA_050800	40S ribosomal protein S12
26,3719	25,9972	26,1913	28,9616	28,3642	28,3394	6,27E-83	1,58E+09	8	8	8	42,8	25,3	27,3709	26,1868	28,5551	6	3	3	0,000505	2,36827	5,1632162	B8NYF4	B8NYF4	1	AFLA_011240	Putative uncharacterized protein
24,3081	23,8873	ND	26,7158	26,7285	25,8303	1,44E-34	5,42E+08	3	3	3	33,8	18,242	25,494	24,0977	26,4248	5	2	3	0,011179	2,32719	5,0182697	B8NPY8	B8NPY8	1	AFLA_002910	Putative uncharacterized protein
23,2724	23,9284	ND	26,0393	25,806	25,7442	1,12E-19	3,75E+08	3	3	3	31,4	13,537	24,9581	23,6004	25,8632	5	2	3	0,003586	2,26274	4,7990206	B8NGE7	B8NGE7	1	AFLA_134870	U6 snRNA-associated Sm-like protein LSM4, putative
24,2355	24,3556	24,3481	26,9936	26,3974	26,2745	1,57E-34	6,25E+08	12	12	12	19	80,072	25,4341	24,313	26,5551	6	3	3	0,000574	2,2421	4,7308519	B8MYY0	B8MYY0	1	AFLA_082690	Pseudouridine synthase TruD/Pus7, putative
28,358	29,3064	28,5144	31,1727	31,0251	30,6844	7,69E-293	1,6E+10	4	4	4	40,2	13,622	29,8435	28,7262	30,9607	6	3	3	0,002406	2,23448	4,7059305	B8N014	B8N014	1	AFLA_086540	Glycine-rich RNA-binding protein, putative
25,7445	27,2678	26,3197	28,3839	28,527	28,8851	5,78E-150	4,28E+09	14	14	14	51,3	44,491	27,5213	26,444	28,5986	6	3	3	0,010034	2,15466	4,452637	B8NPA7	B8NPA7	1	AFLA_128900	3(2),5-bisphosphate nucleotidase
25,1135	25,8149	25,0732	27,8778	27,2584	27,2274	9,45E-57	1,28E+09	9	9	9	37,2	44,826	26,3942	25,3339	27,4546	6	3	3	0,002712	2,12066	4,3489285	B8N193	B8N193	1	AFLA_029580	Protein phosphatase PP1 regulatory subunit Sds22, putative
23,8958	24,4893	23,1051	26,5757	25,2608	25,933	1,19E-52	5,25E+08	4	4	4	11,9	51,306	24,8766	23,8301	25,9231	6	3	3	0,019257	2,09308	4,2665797	B8NP37	B8NP37	1	AFLA_128200	FK506-binding protein
25,891	25,2812	25,6072	28,0268	27,7626	27,2584	1,02E-158	9,04E+08	10	10	10	24,7	65,47	26,6379	25,5931	27,6826	6	3	3	0,001869	2,08947	4,255917	B8NX52	B8NX52	1	AFLA_122400	Glucoamylase
23,9961	24,1342	23,982	26,8974	25,2004	26,2606	1,16E-10	3,28E+08	3	3	3	11,2	47,213	25,0785	24,0374	26,1195	6	3	3	0,013844	2,08203	4,2340256	B8NG30	B8NG30	1	AFLA_131910	Putative uncharacterized protein
25,82	27,3519	26,1068	28,881	28,5719	28,0493	6,12E-64	2,39E+09	17	17	17	46,6	61,121	27,4635	26,4262	28,5007	6	3	3	0,017242	2,07446	4,2118673	B8MY33	B8MY33	1	AFLA_079700	Protein arginine methyltransferase RmtB
26,2695	25,0851	25,6125	27,4554	27,4601	28,0962	3,57E-58	1,58E+09	6	6	6	56,9	14,737	26,6632	25,6557	27,6706	6	3	3	0,007514	2,01485	4,0413856	B8MZ85	B8MZ85	1	AFLA_083740	40S ribosomal protein S22
29,9153	30,5054	29,9421	32,5608	32,0475	31,7601	0	3,13E+10	28	28	28	37,4	77,339	31,1219	30,1209	32,1228	6	3	3	0,002723	2,00187	4,0051881	B8N3I8	B8N3I8	1	AFLA_028910	Polyadenylate-binding protein
24,4583	ND	23,9482	26,2005	26,3324	25,9285	4,68E-24	6,58E+08	4	4	4	7,2	98,636	25,3736	24,2033	26,1538	5	2	3	0,004101	1,95057	3,8652722	B8N3F7	B8N3F7	1	AFLA_028600	DNA replication licensing factor Mcm3, putative
24,0357	23,7704	23,8196	26,1905	25,7139	25,5371	3,05E-10	4,05E+08	3	3	3	34,7	11,23	24,8445	23,8752	25,8138	6	3	3	0,000786	1,93859	3,8333082	B8N5Y8	B8N5Y8	1	AFLA_015720	Small nuclear ribonucleoprotein (LSM2), putative
ND	23,754	23,6204	26,0716	25,4269	25,1568	1,76E-24	2,39E+08	3	3	3	8	61,824	24,8059	23,6872	25,5518	5	2	3	0,013321	1,86457	3,6415938	B8MXP5	B8MXP5	1	AFLA_078320	Probable beta-glucosidase btgE
ND	25,1565	24,5391	26,8323	26,1376	26,9394	1,88E-28	6,22E+08	3	3	3	29,3	10,128	25,921	24,8478	26,6364	5	2	3	0,02053	1,78865	3,4549145	B8NPV3	B8NPV3	1	AFLA_002560	60S ribosomal protein L37a
23,3134	24,8807	24,3306	26,603	25,4331	25,852	2,24E-34	3,02E+08	4	4	4	26,1	24,268	25,0688	24,1749	25,9627	6	3	3	0,035454	1,78779	3,4528556	B8NJ19	B8NJ19	1	AFLA_071360	Zinc knuckle nucleic acid binding protein, putative
29,783	30,1972	29,8885	31,8998	31,7801	31,4349	3,46E-217	2,2E+10	4	4	4	48,8	13,13	30,8306	29,9562	31,7049	6	3	3	0,000724	1,74872	3,3606027	B8NI7	B8NI7	1	AFLA_107810	Heterogeneous nuclear ribonucleoprotein G, putative
24,957	25,2156	25,2829	27,1739	26,8009	26,6866	1,05E-65	8,47E+08	3	3	3	39,6	10,908	26,0195	25,1519	26,8871	6	3	3	0,000614	1,73529	3,3294641	B8NKW0	B8NKW0	1	AFLA_093640	U6 small nuclear ribonucleoprotein (Lsm3), putative
25,4538	24,6882	23,9493	27,0254	26,5576	25,5933	3,36E-17	5,16E+08	2	2	2	20,9	20,307	25,5446	24,6971	26,3921	6	3	3	0,048807	1,69496	3,2376791	B8MX51	B8MX51	1	AFLA_076380	Mitochondrial intermembrane space protein Mia40
28,5159	28,7314	28,5263	30,7169	30,1721	29,9446	3,18E-292	9,13E+09	19	19	19	52,9	42,938	29,4345	28,5912	30,2779	6	3	3	0,002147	1,68666	3,2191058	B8NID1	B8NID1	1	AFLA_066270	RNA-binding La domain protein
27,3321	28,3381	27,8625	29,7347	29,5288	29,3284	1,16E-281	5,54E+09	36	36	36	54,7	97,885	28,6874	27,8443	29,5306	6	3	3	0,005761	1,68638	3,2184811	B8N6V6	B8N6V6	1	AFLA_017090	Methyltransferase (Ncl1), putative
24,3751	24,7244	24,5717	26,497	26,17	25,869	5,73E-14	5,41E+08	2	2	2	16,5	14,216	25,3679	24,5571	26,1787	6	3	3	0,00145	1,6216	3,0771612	B8NCX5	B8NCX5	1	AFLA_042100	Small nuclear ribonucleoprotein (LSM7), putative
28,7137	29,4657	28,9845	31,1117	30,4252	30,3548	0	1,42E+10	11	11	11	33,7	45,881	29,8426	29,0547	30,6306	6	3	3	0,008487	1,57591	2,9812348	B8NJ22	B8NJ22	1	AFLA_071390	mRNA binding post-transcriptional regulator (Csx1), putative
23,341	22,7728	23,3438	25,4263	24,7211	23,9863	4,80E-09	1,43E+08	4	4	4	6,5	78,912	23,9319	23,1525	24,7112	6	3	3	0,027012	1,55871	2,9459031	B8NBL5	B8NBL5	1	AFLA_045900	Phenylalanine ammonia-lyase
24,344	25,6892	24,8043	26,936	26,6547	25,8786	5,80E-25	4,36E+08	5	5	5	16,1	51,057	25,7178	24,9458	26,4898	6	3	3	0,037919	1,54395	2,9159177	B8NTD8	B8NTD8	1	AFLA_097780	Isoamyl alcohol oxidase, putative
26,1301	26,3121	26,3937	28,3089	26,9875	28,1553	1,33E-111	3,21E+09	8	8	8	35,2	25,832	27,0479	26,2786	27,8172	6	3	3	0,022258	1,53859	2,9051044	B8NMC5	B8NMC5	1	AFLA_095570	RNA annealing protein Yra1, putative
29,7333	30,5726	29,599	31,7998	31,3102	31,3224	0	2,89E+10	24	24	24	58,8	46,314	30,7229	29,9683	31,4775	6	3	3	0,011888	1,50917	2,8464623	B8NSE2	B8NSE2	1	AFLA_048050	Nucleosome assembly protein Nap1, putative
24,0525	24,8553	ND	25,7201	26,1245	26,0361	7,28E-21	3,67E+08	7	7	7	7,9	134,05	25,3577	24,4539	25,9602	5	2	3	0,021122	1,50633	2,8408645	B8N430	B8N430	1	AFLA_033530	Nuclear mRNA splicing factor, putative
29,1294	29,9221	29,3136	31,0943	30,9359	30,7796	0	1,66E+10	25	25	25	56,4	64,887	30,1958	29,455	30,9366	6	3	3	0,004441	1,48156	2,7925053	B8NFY6	B8NFY6	1	AFLA_131470	Eukaryotic translation initiation factor 3 subunit D
25,0661	25,8104	25,2924	27,4119	26,5955	26,5292	1,35E-16	6,25E+08	5	5	5	11,4	80,83	26,1176	25,3897	26,8455	6	3	3	0,015451	1,45587	2,7432194	B8NRF2	B8NRF2	1	AFLA_007190	NADH-ubiquinone oxidoreductase, subunit G, putative
25,4914	25,9399	25,8888	27,8545	26,8167	27,0096	6,17E-42	7,65E+08	12	12	12	27,6	74,726	26,5001	25,7734	27,2269	6	3	3	0,014062	1,45352	2,7387546	B8NMS3	B8NMS3	1	AFLA_126860	Cell wall cysteine-rich protein

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

B. Quantitative results

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	t-test p value	Log2 (t-test Difference)	Fold Change (Treated v Control)	Protein IDs	Majority protein IDs	Proteins	Gene Name (ORF)	Protein Function
ND	23,7209	23,6006	25,2691	25,4516	24,62	4,99E-13	2,26E+08	4	4	4	9,4	60,765	24,5324	23,6607	25,1135	5	2	3	0,021522	1,45281	2,7374071	B8NPT7	B8NPT7	1	AFLA_001510	Glutamyl-tRNA(Gln) amidotransferase subunit A, putative
26,4335	25,491	25,7908	27,5758	27,6132	26,8307	4,65E-41	1,32E+09	9	9	9	46	36,683	26,6225	25,9051	27,3399	6	3	3	0,019025	1,43483	2,7035031	B8NBQ3	B8NBQ3	1	AFLA_046280	Mitochondrial inner membrane nuclease Nuc1, putative
27,0165	27,8364	27,1859	28,9619	28,572	28,6439	1,04E-85	3,53E+09	14	14	14	40	40,919	28,0361	27,3463	28,7259	6	3	3	0,007604	1,37968	2,6021065	B8NIU9	B8NIU9	1	AFLA_069770	Eukaryotic translation initiation factor 3 subunit H
23,1143	23,0302	22,8771	24,5874	24,4753	24,0446	6,42E-14	1,76E+08	4	4	4	5,8	78,653	23,6881	23,0072	24,3691	6	3	3	0,001616	1,36189	2,5702167	B8NPX8	B8NPX8	1	AFLA_002810	tRNA nucleotidyltransferase
25,7608	26,085	25,2	27,2919	26,7199	27,1114	9,02E-40	1,36E+09	6	6	6	20,2	36,753	26,3615	25,6819	27,0411	6	3	3	0,011674	1,35912	2,5652866	B8NIU5	B8NIU5	1	AFLA_069730	HMG box protein, putative
28,5547	29,2533	28,4641	29,8281	30,0947	30,3769	0	8,41E+09	27	27	27	31,3	119,79	29,4286	28,7574	30,0999	6	3	3	0,010463	1,34255	2,5359917	B8N1D8	B8N1D8	1	AFLA_030030	Eukaryotic translation initiation factor 3 subunit A
27,038	26,1168	26,6943	27,4746	28,3382	28,0231	4,35E-125	1,79E+09	9	9	9	31,1	43,873	27,2808	26,6164	27,9453	6	3	3	0,022658	1,32888	2,5120758	B8MWW3	B8MWW3	1	AFLA_075500	Putative uncharacterized protein
30,3224	30,4508	30,5482	32,1031	31,7451	31,4522	0	2,5E+10	25	25	25	71,2	58,021	31,1036	30,4405	31,7668	6	3	3	0,002645	1,32634	2,507657	B8NLI4	B8NLI4	1	AFLA_092100	Inosine-5-monophosphate dehydrogenase
27,0812	27,4301	27,5482	29,4396	28,1841	28,3483	3,05E-293	4,36E+09	21	21	21	42,1	53,022	28,0052	27,3532	28,6573	6	3	3	0,035577	1,30414	2,4693648	B8N6W0	B8N6W0	1	AFLA_017130	Nuclear segregation protein (Bfr1), putative
28,1773	27,9402	27,734	29,1202	29,2728	29,2978	1,54E-195	4,51E+09	21	21	20	34	71,973	28,5904	27,9505	29,2302	6	3	3	0,000786	1,27979	2,4280363	B8N9S2	B8N9S2	1	AFLA_112180	ATP dependent RNA helicase (Dbp1), putative
27,0336	26,5069	25,5586	27,5284	27,8799	27,4949	2,61E-40	1,46E+09	8	8	8	19,7	56,603	27,0004	26,3664	27,6344	6	3	3	0,047565	1,268	2,4082748	B8NTN4	B8NTN4	1	AFLA_099650	Woronin body major protein, putative
27,7191	27,8476	27,5453	29,2165	28,7802	28,8379	1,55E-178	4,16E+09	7	7	7	47,9	15,65	28,3244	27,704	28,9449	6	3	3	0,001579	1,24085	2,3633774	B8NEG5	B8NEG5	1	AFLA_061630	Single-stranded DNA-binding protein
28,969	29,5514	29,0615	30,1277	30,4737	30,6868	0	1,13E+10	35	35	35	47,2	97,164	29,8117	29,194	30,4294	6	3	3	0,00709	1,23543	2,3545151	B8NCT8	B8NCT8	1	AFLA_041730	Eukaryotic translation initiation factor 3 subunit C
24,4519	24,7774	24,4817	26,2713	25,6092	25,4945	5,21E-13	3,71E+08	5	5	5	10,9	64,216	25,181	24,5703	25,7917	6	3	3	0,009764	1,22135	2,331648	B8MZ71	B8MZ71	1	AFLA_083600	RNA splicing factor (Pad-1), putative
30,1199	29,6206	29,9658	31,3308	31,2464	30,7568	0	1,28E+10	12	12	12	37,3	50,7	30,5067	29,9021	31,1114	6	3	3	0,006458	1,20927	2,3122061	B8NAJ8	B8NAJ8	1	AFLA_040430	Tripeptidyl-peptidase (TppA), putative
26,7056	26,2681	26,526	27,8954	27,7115	27,4668	1,18E-63	1,89E+09	16	16	16	39,6	75,183	27,0956	26,4999	27,6912	6	3	3	0,002568	1,19134	2,2836475	B8NDM0	B8NDM0	1	AFLA_059590	Amine oxidase
32,7408	32,0754	33,0291	34,2271	33,7444	33,4355	0	1,02E+11	11	11	11	73,9	17,009	33,2087	32,6151	33,8023	6	3	3	0,031136	1,18725	2,2771826	B8NQF0	B8NQF0	1	AFLA_006300	Nucleoside diphosphate kinase
28,0249	27,669	28,0413	29,3862	28,9511	28,8965	1,46E-188	5,1E+09	9	9	9	24,3	47,589	28,4948	27,9117	29,0779	6	3	3	0,004071	1,16618	2,2441669	B8N599	B8N599	1	AFLA_022270	Putative uncharacterized protein
25,7451	25,1746	25,5782	26,8104	26,6337	26,5377	1,31E-24	9,76E+08	7	7	7	12,4	92,147	26,08	25,4993	26,6606	6	3	3	0,003437	1,16132	2,2366197	B8N7E5	B8N7E5	1	AFLA_021670	Probable E3 ubiquitin-protein ligase hulA
25,4273	25,6466	25,3554	27,0477	26,4854	26,3073	1,87E-36	7,96E+08	14	14	14	9,3	222,86	26,045	25,4765	26,6135	6	3	3	0,009015	1,13699	2,1992171	B8N3B6	B8N3B6	1	AFLA_027290	Proteasome activator subunit 4, putative
28,7638	28,5992	29,1581	30,2564	29,8949	29,7595	6,06E-129	4,27E+09	12	12	12	52,9	39,188	29,4053	28,8404	29,9703	6	3	3	0,007086	1,12991	2,1884509	B8NMA8	B8NMA8	1	AFLA_095400	Putative uncharacterized protein
28,0493	28,817	28,6483	29,8095	29,5508	29,4891	5,03E-223	5,87E+09	10	10	10	18,2	89,842	29,0607	28,5049	29,6165	6	3	3	0,011708	1,1116	2,1608516	B8N1A6	B8N1A6	1	AFLA_029710	Proliferating cell nuclear antigen
24,4549	24,243	24,4866	25,8581	25,4225	25,2344	1,84E-31	4,09E+08	4	4	4	43,8	12,738	24,9499	24,3948	25,505	6	3	3	0,005149	1,11014	2,1586659	B8N6L9	B8N6L9	1	AFLA_015320	Transcription initiation factor IIA subunit 2
23,4882	24,0452	ND	24,5042	25,2211	24,8671	1,38E-12	1,94E+08	5	5	5	8	87,029	24,4252	23,7667	24,8641	5	2	3	0,047729	1,09741	2,1397022	B8NH67	B8NH67	1	AFLA_132910	Pre-mRNA splicing factor RNA helicase (Prp43), putative
28,9771	29,1814	29,2457	30,4519	30,245	29,9669	8,51E-265	9,69E+09	16	16	16	70,7	37,317	29,678	29,1347	30,2213	6	3	3	0,002582	1,08653	2,1236264	B8N002	B8N002	1	AFLA_086420	Eukaryotic translation initiation factor 3 subunit I
28,6586	28,5283	28,4118	29,8007	29,6774	29,3352	0	6,23E+09	17	17	17	40,7	85,922	29,0687	28,5329	29,6044	6	3	3	0,002378	1,07153	2,101661	B8N077	B8N077	1	AFLA_087170	Extracellular serine-rich protein, putative
29,8192	30,433	30,2119	31,7608	30,7831	31,0326	2,03E-168	1,78E+10	14	14	14	42,3	27,787	30,6734	30,1547	31,1922	6	3	3	0,039271	1,03746	2,0526107	B8N5B3	B8N5B3	1	AFLA_022410	Coproporphyrinogen III oxidase, putative
25,6123	25,7552	26,0544	27,2957	26,4311	26,7925	1,07E-29	9,34E+08	9	9	9	29,9	45,901	26,3236	25,8073	26,8398	6	3	3	0,021684	1,03247	2,0455233	B8NKT3	B8NKT3	1	AFLA_093370	Ribonucleotide reductase small subunit RnrA, putative
25,3897	25,2474	25,1497	26,4078	25,7468	26,6976	6,46E-14	7,27E+08	5	5	5	23	24,979	25,7732	25,2623	26,2841	6	3	3	0,024336	1,0218	2,0304507	B8NP93	B8NP93	1	AFLA_128760	Putative uncharacterized protein
28,5398	28,9943	28,5614	29,5187	29,6793	29,9326	0	6,79E+09	10	10	10	33,7	50,769	29,2043	28,6985	29,7102	6	3	3	0,006086	1,01169	2,0162716	B8NFY0	B8NFY0	1	AFLA_131410	Eukaryotic translation initiation factor 3 subunit M
29,6962	28,8295	29,5526	30,4517	30,6445	29,9859	0	7,84E+09	18	18	18	40,9	65,01	29,8601	29,3594	30,3607	6	3	3	0,039271	1,00129	2,0017891	B8NCH3	B8NCH3	1	AFLA_038790	Adenosine deaminase family protein
31,2076	30,5382	31,2034	23,2472	24,9281	21,7891	0	1,79E+10	15	15	15	45,7	55,696	27,1523	30,9831	23,3215	6	3	3	0,001202	-7,6616	-202,475	B8NYI6	B8NYI6	1	AFLA_011560	Phosphatidylglycerol specific phospholipase, putative
29,1861	29,5607	29,5691	ND	22,2598	22,2618	0	3,59E+09	8	8	8	48	31,217	26,5675	29,4386	22,2608	5	3	2	2,58E-05	-7,17783	-144,79119	B8N1G5	B8N1G5	1	AFLA_030300	Putative uncharacterized protein
30,4051	30,5968	30,7967	24,6763	24,4754	ND	0	8,35E+09	18	18	18	48,1	69,417	28,19	30,5995	24,5758	5	3	2	4,44E-05	-6,0237	-65,060049	B8MZ53	B8MZ53	1	AFLA_083420	Non-hemolytic phospholipase C, putative
30,6399	30,4815	30,99	24,6733	27,6946	24,5637	5,34E-125	1,05E+10	5	5	5	15,1	49,097	28,1738	30,7038	25,6439	6	3	3	0,008158	-5,05994	-33,357517	B8NRS0	B8NRS0	1	AFLA_050610	Acid phosphatase PHOa
28,1194	27,9036	27,4165	ND	22,6214	23,1733	0	7,46E+09	33	33	33	42,9	113,65	25,8468	27,8132	22,8973	5	3	2	0,000706	-4,91583	-30,186467	B8NE90	B8NE90	1	AFLA_059990	O-methyltransferase, putative
30,9719	31,2726	30,3977	26,4859	25,8126	26,8714	0	6,92E+09	9	9	9	69,4	12,309	28,6354	30,8807	26,39	6	3	3	0,000365	-4,49078	-22,48327	B8NL17	B8NL17	1	AFLA_096010	Putative uncharacterized protein
31,6856	31,9602	31,8599	26,905	28,9694	26,4019	3,00E-277	2,05E+10	8	8	8	27,3	46,686	29,6303	31,8353	27,4254	6	3	3	0,005041	-4,40985	-21,256763	B8NCF7	B8NCF7	1	AFLA_041320	Acid phosphatase, putative
28,2423	28,7122	29,085	24,9545	24,7889	ND	7,36E-77	2,36E+09	10	10	10	37,1	45,706	27,1566	28,6798	24,8717	5	3	2	0,001285	-3,80815	-14,007718	B8NJ90	B8NJ90	1	AFLA_065230	Glycerophosphoryl diester phosphodiesterase family protein
27,891	27,916	28,1707	24,1296	24,3819	ND	4,15E-67	1,19E+09	5	5	5	22,3	39,792	26,4979	27,9926	24,2558	5	3	2	0,000139	-3,73683	-13,33208	B8NJU9	B8NJU9	1	AFLA_069090	GPI anchored protein, putative
29,251	29,374	29,5637	25,5001	26,539	25,3993	6,16E-154	3,27E+09	12	12	12	51,7	29,585	27,6045	29,3962	25,8128	6	3	3	0,000673	-3,58348	-11,987675	B8NWI5	B8NWI5	1	AFLA_120220	Putative uncharacterized protein
27,3096	28,0265	27,8909	24,0772	23,9474	24,4807	1,03E-92	8,39E+08	7	7	7	30,2	40,13	25,9554	27,7424	24,1685	6	3	3	0,000195	-3,57392	-11,908502	B8N3D7	B8N3D7	1	AFLA_027500	Mannose-1-phosphate guanylyltransferase
29,5689	29,2855	29,6569	26,0028	26,627	26,3952	9,13E-198	2,63E+09	18	18	18	59,9	59,652	27,9227	29,5038	26,3417	6	3	3	0,000122	-3,16212	-8,9514413	B8NEF7	B8NEF7	1	AFLA_060660	AMP-binding enzyme, putative
26,5548	25,952	26,8017	23,0333	23,6757	23,1817	5,62E-25	3,72E+08	6	6	6	19,6	47,21	24,8665	26,4361	23,2969	6	3	3	0,000594	-3,13923	-8,8105373	B8NLF5	B8NLF5	1	AFLA_090820	Aminotransferase, putative
28,3083	27,3888	27,9708	24,5533	25,1973	24,6251	4,18E-66	1,06E+09	11	11	11	24,9	61,075	26,3406	27,8893	24,7919	6	3	3	0,000779	-3,09742	-8,558868	B8NRN4	B8NRN4	1	AFLA_049390	Malate synthase
28,698	28,4257	28,6848	24,5785	25,8099	26,2733	9,00E-181	1,53E+09	9	9	8	31	38,786	27,0784	28,6028	25,5539	6	3	3	0,004033	-3,0489	-8,275807	B8NU27	B8NU27	1	AFLA_101980	Tartrate dehydrogenase, putative
25,7962	26,0402	26,5884	23,381	22,909	23,4103	2,12E-14	3,3E+08	5	5	5	13,2	64,473	24,6875	26,1416	23,2334	6	3	3	0,00052	-2,90816	-7,506602	B8NYH6	B8NYH6	1	AFLA_011460	GMC oxidoreductase, putative
28,0365	26,4064	28,305	24,346	24,8803	24,8003	2,27E-12	9,02E+08	2	2	2	29,9	11,998	26,1291	27,5826	24,6755	6	3	3	0,009181	-2,90708	-7,5009847	B8NVS7	B8NVS7	1	AFLA_117640	CipC-like antibiotic stress responsive protein
29,1609	28,3438	29,1752	25,9654	26,8606	26,0383	8,12E-79	4,28E+09	5	5	5	28	31,386	27,5907	28,8933	26,2881	6	3	3	0,002799	-2,60519	-6,0847163	B8NUA8	B8NUA8	1	AFLA_098700	Carbonyl reductase, putative
27,2664	26,5575	26,5364	ND	24,1803	24,2028	2,15E-58	5,39E+08	5	5	5	32,5	21,151	25,7487	26,7868	24,1916	5	3	2	0,003569	-2,59518	-6,0426442	B8NMV8	B8NMV8	1	AFLA_127210	Pathogenesis associated protein Cap20, putative
30,5907	30,3792	30,7523	27,722	28,03	28,4819	0	6,04E+09	29	29	29	49,4	77,127	29,326	30,574	28,078	6	3	3	0,000529	-2,4961	-5,6415829	B8N2M1	B8N2M1	1	AFLA_037960	Glucosamine-fructose-6-phosphate aminotransferase
26,3113	26,0832	26,852	23,7358	24,2927	23,9389	5,06E-24	4,54E+08	6	6	6	24,6	38,508	25,2023	26,4155	23,9892	6	3	3	0,000977	-2,42632	-5,3752058	B8NFV4	B8NFV4	1	AFLA_133830	Alcohol dehydrogenase, putative
28,3709	27,0543	28,0678	24,7124	25,9134	25,6259	4,30E-126	1,22E+09	10	10	10	24,8	49,624	26,6241	27,831	25,4172	6	3	3	0,010941	-2,41385	-5,3289452	B8NGR8	B8NGR8	1	AFLA_137860	Putative uncharacterized protein
31,3372	31,4682	31,8578	28,9102	28,9998	29,6467	0	1,56E+10	19	19	16	68,8	41,639	30,37	31,5544	29,1855	6	3	3	0,001066	-2,36889	-5,1654355	B8ND52;C(	B8ND52	2	AFLA_055230	Actin Act1
28,5542	28,7296	27,6592	25,6828	25,027	27,1667	6,29E-48	2,59E+09	3	3	3	36,8	7,6649	27,1366	28,3143	25,9589	6	3	3	0,030021	-2,35548	-5,1176447	B8MZ58	B8MZ58	1	AFLA_083470	Ribosomal protein S28e
28,1102	26,9185	28,1683	25,2873	25,7311	25,3085	2,78E-163	1,72E+09	13	13	13	39,7	48,158	26,5873	27,7323	25,4423	6	3	3	0,00609	-2,29005	-4,8907306	B8MXJ9	B8MXJ9	1	AFLA_077860	Putative uncharacterized protein
26,5478	26,6741	26,5436	24,6836	24,1216	24,2545	1,19E-34	8,95E+08	2	2	2	38,5	8,7148	25,4709	26,5885	24,3532	6	3	3	0,000216	-2,23526	-4,7084754	B8NIX3	B8NIX3	1	AFLA_070010	Putative uncharacterized protein
26,0099	26,0615	26,1738	23,9967	23,8834	23,7887	1,12E-21	4,06E+08	6	6	6	19,3	51,465	24,9857	26,0817	23,8896	6	3	3	9,15E-06	-2,19212	-4,5697651	B8NNC8	B8NNC8	1	AFLA_127390	Proteasome regulatory particle subunit Rpt5, putative
28,4298	28,0704	28,1475	25,4156	26,327	26,4284	9,96E-100	1,27E+09	16	16	16	30,3	95,646	27,1365	28,2159	26,057	6	3	3	0,003154	-2,15892	-4,4658042	B8NA29	B8NA29	1	AFLA_113250	Ribonucleoside-diphosphate reductase
27,4608	27,0168	27,579	25,171	25,137	25,5272	2,10E-38	7,85E+08	8	8	5	22,8	53,831	26,3153	27,3522	25,2784	6	3	3	0,00061	-2,07383	-4,2100285	B8NOC2	B8NOC2	1	AFLA_087630	Alpha,alpha-trehalose-phosphate synthase subunit, putative
25,4471	24,9986	25,2789	ND	23,2206	23,1716	1,09E-13	1,46E+08	4	4	4	16,3	42,727	24,4234	25,2415	23,1961	5	3	2	0,001233	-2,04545	-4,1280201	B8MXB2	B8MXB2	1	AFLA_076990	Alpha-ketoglutarate-dependent taurine dioxygenase
24,2385	24,6617	26,4202	23,03	22,9392	23,3998	6,60E-17	2,32E+08	4	4	4	9,8	64,728	24,1149	25,1068	23,123	6	3	3	0,043852	-1,9838	-3,9553353	B8NWT6	B8NWT6	1	AFLA_121230	L-amino acid oxidase LaoA
29,3276	30,1561	30,0761	26,8434	27,7385	29,0403	0	4,56E+09	8	8	8	52,5	16,407	28,8637	29,8533	27,8741	6	3	3	0,045582	-1,9792	-3,9427439	B8NNY3	B8NNY3	1	AFLA_125890	40S ribosomal protein S17, putative
28,9853	27,8255	28,9432	26,3702	26,7361	26,7345	1,56E-143	3,59E+09	19	19	19	64,8	49,534	27,5991	28,5847	26,6136	6	3	3	0,007804	-1,97106	-3,9205607	B8NEZ4	B8NEZ4	1	AFLA_058580	GTP cyclohydrolase II, putative
26,8905	25,4141	26,3417	24,0966	24,3649	24,3178	2,12E-10	3,3E+08	2	2	2	10,7	28,721	25,2376	26,2155	24,2598	6	3	3	0,01118	-1,95568	-3,8789872	B8NKD1	B8NKD1	1	AFLA_090060	Aspergillopepsin, putative
28,177	27,3815	27,8567	25,4994	26,1262	26,0051	2,80E-169	2,58E+09	17	17	17	43,6	54,228	26,841	27,8051	25,8769	6	3	3	0,003029	-1,92815	-3,8056688	B8MXR1	B8MXR1	1	AFLA_078480	Cysteine protease, putative
25,2891	24,8598	25,3465	23,1746	23,3628	23,2114	2,21E-11	2,47E+08	5	5	5	19,9	36,327	24,2073	25,1651	23,2496	6	3	3	0,000307	-1,91556	-3,7726022	B8MZF4	B8MZF4	1	AFLA_084440	Autophagy protein Atg27, putative
26,2163	26,973	26,8388	ND	25,1804	24,3554	3,00E-26	8,06E+08	9	9	9	14,7	114,12	25,9128	26,676	24,7679	5	3	2	0,021304	-1,90814	-3,753249	B8N6J1	B8N6J1	1	AFLA_015040	Importin beta-5 subunit, putative
28,9657	28,0167	29,0284	26,8735	26,5617	26,8887	2,76E-140	3,08E+09	14	14	14	73,6	30,978	27,7225	28,6703	26,7746	6	3	3	0,005301	-1,89568	-3,7209732	B8NWD0	B8NWD0	1	AFLA_119670	Glycogen branching enzyme GbeA, putative
27,8862	27,2932	27,7578	25,6784	26,0995	25,5335	1,00E-19	1,28E+09	6	6	6	23,7	46,238	26,7081	27,6457	25,7705	6	3	3	0,001627	-1,87526	-3,6686773	B8N8S4	B8N8S4	1	AFLA_108690	Putative uncharacterized protein
28,2851	28,2928	28,6821	25,9202	26,464	27,2608	4,35E-111	3,4E+09	15	15	15	34,6	69,076	27,4842	28,42	26,5483	6	3	3	0,010366	-1,87166	-3,6595341	B8NG74	B8NG74	1	AFLA_134130	Methylenetetrahydrofolate reductase
26,9641	26,7902	27,3241	25,6242	25,0035	24,8382	6,42E-34	1,31E+09	10	10	10	42,1	30,2	26,0907	27,0261	25,1553	6	3	3	0,002833	-1,87083	-3,6574294	B8NSH8	B8NSH8	1	AFLA_048410	BAR adaptor protein RVS161, putative
28,388	28,4862	28,6209	25,7631	27,8943	26,2536	3,11E-263	1,76E+09	7	7	7	29,6	46,178	27,5677	28,4984	26,637	6	3	3	0,045341	-1,86138	-3,6335506	B8NJC1	B8NJC1	1	AFLA_065540	Extracellular lipase, putative

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

B. Quantitative results

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	t-test p value	Log2 (t-test Difference)	Fold Change (Treated v Control)	Protein IDs	Majority protein IDs	Proteins	Gene Name (ORF)	Protein Function
24,6884	24,3438	24,7058	ND	22,53	23,012	5,31E-08	92711000	3	3	3	8,7	76,204	23,856	24,5793	22,771	5	3	2	0,004584	-1,80833	-3,5023664	B8NU2	B8NU2	1	AFLA_067790	Acetoacetyl-CoA synthase
30,4757	29,3644	30,644	28,2283	28,9868	27,9628	7,28E-225	5,66E+09	7	7	7	20,6	45,559	29,277	30,1613	28,3926	6	3	3	0,024881	-1,76871	-3,4074914	B8NWT9	B8NWT9	1	AFLA_121260	Aspartic-type endopeptidase, putative
28,4736	28,4327	28,6181	26,6911	26,6026	27,0024	3,65E-167	1,63E+09	13	13	13	30	70,001	27,6368	28,5081	26,7654	6	3	3	0,0002	-1,74278	-3,3467946	B8NW02	B8NW02	1	AFLA_119290	Phosphofructokinase, putative
25,9836	25,5913	25,7085	23,5698	24,3497	24,2394	1,34E-43	6,93E+08	2	2	2	19,3	14,322	24,9071	25,7612	24,053	6	3	3	0,003195	-1,7082	-3,2675289	B8N5T3	B8N5T3	1	AFLA_014260	Conidial hydrophobin RodB/HypB
26,7312	25,1897	26,54	24,3202	24,9068	24,2464	7,60E-34	7,23E+08	5	5	5	36,5	21,537	25,3224	26,1536	24,4911	6	3	3	0,034595	-1,66247	-3,1655803	B8NEU7	B8NEU7	1	AFLA_058110	Cupin domain protein
28,1167	27,2719	28,2162	26,0075	26,5409	26,0745	4,77E-44	3,53E+09	4	4	4	59,8	11,573	27,0379	27,8683	26,2076	6	3	3	0,008421	-1,66063	-3,1615455	B8N8S9	B8N8S9	1	AFLA_108740	Putative uncharacterized protein
26,3082	26,4897	26,6026	25,3117	24,4765	24,654	7,39E-46	5,41E+08	6	6	6	23,2	68,968	25,6404	26,4668	24,8141	6	3	3	0,003516	-1,65277	-3,1443678	B8NB56	B8NB56	1	AFLA_044310	SH3 domain protein
25,5475	23,929	25,4198	23,4287	22,934	23,7272	1,08E-06	2,07E+08	4	4	4	8,8	61,463	24,1644	24,9655	23,3633	6	3	3	0,04796	-1,60216	-3,0359752	B8ND16	B8ND16	1	AFLA_054870	6-phosphofructo-2-kinase, putative
28,8926	28,7156	28,3326	26,305	27,13	27,7217	6,06E-213	2,25E+09	11	11	10	40,6	44,435	27,8496	28,6469	27,0522	6	3	3	0,02273	-1,59468	-3,0202752	B8NRA6	B8NRA6	1	AFLA_005810	Septin
27,0809	27,5221	27,6769	25,375	25,5023	26,6421	1,93E-43	8,3E+08	9	9	9	21,8	61,088	26,6332	27,4266	25,8398	6	3	3	0,022731	-1,58683	-3,0038859	B8NNG4	B8NNG4	1	AFLA_127750	T-complex protein 1, eta subunit, putative
33,6612	33,0043	33,7397	31,5068	32,4885	31,673	0	5,92E+10	19	19	19	63,9	42,313	32,6789	33,4684	31,8894	6	3	3	0,014528	-1,57898	-2,9875855	B8NLY9	B8NLY9	1	AFLA_094450	Aspartic protease pep1
29,9784	29,8807	29,8165	27,6484	27,9745	29,333	0	8,33E+09	18	18	18	55,5	60,75	29,1053	29,8919	28,3186	6	3	3	0,038506	-1,57326	-2,9757638	B8NAW4	B8NAW4	1	AFLA_043390	Hsp70 chaperone (BiP), putative
32,5774	32,7101	32,7419	31,3573	31,1938	30,7745	0	4,87E+10	22	22	20	72,3	40,145	31,8925	32,6765	31,1085	6	3	3	0,000971	-1,56794	-2,9648107	B8ND35	B8ND35	1	AFLA_055060	NAD-dependent formate dehydrogenase AciA/Fdh
31,2988	31,0409	30,7557	28,8237	29,5684	30,0034	0	1,05E+10	17	17	17	65,8	39,876	30,2485	31,0318	29,4652	6	3	3	0,014386	-1,56665	-2,9621609	B8NE10	B8NE10	1	AFLA_057410	NAD binding Rossmann fold oxidoreductase, putative
29,0383	28,5438	28,3232	27,2195	26,6986	27,2977	7,49E-147	2,5E+09	15	15	15	49,7	46,991	27,8535	28,6351	27,0719	6	3	3	0,005241	-1,56319	-2,9550653	B8NRD7	B8NRD7	1	AFLA_007040	Homocysteine synthase CysD
28,434	27,8919	28,4972	26,8236	26,8637	26,5376	6,59E-122	2,76E+09	20	20	20	26,7	109,87	27,508	28,2744	26,7416	6	3	3	0,00215	-1,53272	-2,8933082	B8NV7	B8NV7	1	AFLA_017100	Probable beta-galactosidase A
26,1672	25,3221	26,2864	24,26	24,525	24,3925	8,16E-26	2,97E+08	4	4	4	22,4	24,037	25,1589	25,9252	24,3925	6	3	3	0,008062	-1,53269	-2,893248	B8N3Y9	B8N3Y9	1	AFLA_033120	BAP31 domain protein, putative
25,8288	25,9462	26,0024	24,6161	24,3117	24,2985	2,04E-11	3,29E+08	3	3	3	29,2	21,547	25,1673	25,9258	24,4087	6	3	3	0,000195	-1,51706	-2,8620721	B8N8D6	B8N8D6	1	AFLA_107300	3-hydroxyanthranilate 3,4-dioxygenase Bna1, putative
31,8173	31,9064	32,1702	30,2639	30,3564	30,7327	0	1,96E+10	19	19	19	81,3	35,017	31,2078	31,9646	30,451	6	3	3	0,001055	-1,51364	-2,8552954	B8NT05	B8NT05	1	AFLA_051980	G-protein complex beta subunit CpcB
28,7525	28,446	28,7853	26,7223	27,8627	26,8638	4,74E-149	2,85E+09	20	20	20	32,9	95,766	27,9055	28,6613	27,1496	6	3	3	0,015686	-1,51168	-2,8514189	B8N6M3	B8N6M3	1	AFLA_015360	N-methyltransferase, putative
26,7878	25,8551	26,9402	25,0343	25,172	24,849	1,39E-37	1,06E+09	6	6	6	27,9	31,227	25,773	26,5277	25,0184	6	3	3	0,012751	-1,5093	-2,8467188	B8NS77	B8NS77	1	AFLA_053990	Class II aldolase/adducin domain protein
29,1326	28,0455	28,7053	27,1815	27,2266	26,9638	8,98E-217	5,09E+09	7	7	7	16,8	60,796	27,8759	28,6278	27,1239	6	3	3	0,009982	-1,50387	-2,8360245	B8NYN2	B8NYN2	1	AFLA_012020	Carboxypeptidase S1, putative
25,6401	25,7277	26,2243	23,9146	24,87	24,3063	1,15E-26	2,81E+08	4	4	4	10,5	52,195	25,1138	25,864	24,3637	6	3	3	0,010624	-1,50036	-2,829133	B8NEJ4	B8NEJ4	1	AFLA_061920	Protein transport protein Sec61 alpha subunit, putative
25,9168	25,2018	26,3455	24,2391	24,5226	24,2063	9,65E-25	4,59E+08	5	5	5	33,8	29,098	25,072	25,8214	24,3227	6	3	3	0,012626	-1,49869	-2,82586	B8MZS0	B8MZS0	1	AFLA_085600	Putative uncharacterized protein
29,6967	28,9821	29,5747	27,8585	28,2383	27,6753	3,92E-148	5,5E+09	18	18	18	33,6	67,874	28,6709	29,4178	27,924	6	3	3	0,005649	-1,49381	-2,8163175	B8MXQ5	B8MXQ5	1	AFLA_078420	Fumarate reductase Osm1, putative
28,5932	28,1313	28,6079	27,1045	26,6726	27,0988	1,49E-19	1,97E+09	7	7	7	22,9	50,88	27,7014	28,4442	26,9586	6	3	3	0,002183	-1,48553	-2,8002002	B8NQD0	B8NQD0	1	AFLA_006100	HypA-like protein, putative
26,6105	26,2425	26,9951	25,314	24,8182	25,2865	3,59E-22	6,2E+08	7	7	7	10,1	99,561	25,8778	26,616	25,1396	6	3	3	0,005466	-1,47644	-2,7826125	B8N1T0	B8N1T0	1	AFLA_032340	Vacuolar protein sorting-associated protein 35
26,6429	25,9136	26,6531	24,4014	25,3806	25,0228	1,88E-57	9,1E+08	6	6	4	17,3	51,944	25,6691	26,4032	24,9349	6	3	3	0,017546	-1,46829	-2,7669374	B8MXA1	B8MXA1	1	AFLA_076880	Stearic acid desaturase (SdeA), putative
27,7089	27,7922	27,9017	25,713	26,6241	26,6645	4,01E-66	1,08E+09	12	12	12	48,9	42,355	27,0674	27,8009	26,3339	6	3	3	0,009676	-1,46706	-2,7645794	B8NCE8	B8NCE8	1	AFLA_041230	Sterol 24-c-methyltransferase, putative
26,3961	25,8252	25,2732	24,0388	25,0335	24,0417	1,05E-34	3,66E+08	8	8	8	13,7	93,414	25,1014	25,8315	24,3713	6	3	3	0,034473	-1,46017	-2,7514078	B8NRX2	B8NRX2	1	AFLA_051140	Probable beta-glucosidase A
26,1166	25,787	26,2774	ND	24,5586	24,6443	1,41E-24	3,39E+08	8	8	8	11,7	97,024	25,4768	26,0603	24,6014	5	3	2	0,004522	-1,4589	-2,7489868	B8NAA2	B8NAA2	1	AFLA_113980	Cyclin dependent kinase inhibitor Pho81, putative
28,5669	28,484	28,5389	27,1487	26,9053	27,1982	6,52E-129	2,12E+09	8	8	8	23,3	60,343	27,807	28,5299	27,0841	6	3	3	0,000103	-1,44584	-2,7242139	B8MYN6	B8MYN6	1	AFLA_081750	T-complex protein 1, beta subunit, putative
26,1061	26,2782	26,3073	ND	24,348	25,2223	1,04E-20	4,42E+08	3	3	3	27	26,851	25,6524	26,2305	24,7851	5	3	2	0,02307	-1,44539	-2,7233643	B8NUN1	B8NUN1	1	AFLA_100840	Pyridoxamine phosphate oxidase, putative
26,1869	26,1221	26,6077	24,901	24,8414	24,8386	2,02E-18	6,99E+08	8	8	8	22,1	53,768	25,583	26,3056	24,8603	6	3	3	0,000711	-1,44521	-2,7230246	B8N592	B8N592	1	AFLA_022200	Mitochondrial cytochrome b2, putative
27,72	27,6274	27,5761	26,4028	26,0542	26,1356	9,55E-36	1,21E+09	6	6	6	48,3	18,988	26,9193	27,6412	26,1975	6	3	3	0,000219	-1,44365	-2,7200817	B8NMR6	B8NMR6	1	AFLA_126790	Threonine synthase Thr4, putative
29,2005	28,8745	29,174	27,3826	27,7533	27,8067	6,49E-120	3,78E+09	24	24	24	42,7	78,924	28,3653	29,083	27,6475	6	3	3	0,001064	-1,43545	-2,7046652	B8N394	B8N394	1	AFLA_027070	Acetyl-coenzyme A synthetase FacA
26,8072	26,9779	27,0552	25,8018	25,4211	25,3384	4,18E-30	1,19E+09	7	7	7	18,5	55,226	26,2336	26,9468	25,5204	6	3	3	0,000884	-1,42635	-2,6876588	B8NTG9	B8NTG9	1	AFLA_098090	BAR adaptor protein RVS167, putative
27,6233	27,813	28,0852	25,8909	26,7012	26,6531	2,71E-130	1,25E+09	8	8	8	41,5	21,621	27,1278	27,8405	26,4151	6	3	3	0,008418	-1,42542	-2,6859268	B8N4M7	B8N4M7	1	AFLA_037320	Rho GTPase Rho1
30,4941	29,2956	30,0317	28,3679	28,5435	28,6508	0	1,28E+10	27	27	27	65,2	66,547	29,2306	29,9405	28,5207	6	3	3	0,016683	-1,41978	-2,6754471	B8N2F2	B8N2F2	1	AFLA_036370	Phosphoenolpyruvate carboxykinase AcuF
27,4052	25,964	26,9021	25,1391	25,4617	25,4711	1,16E-46	8,02E+08	8	8	8	20,3	63,876	26,0572	26,7571	25,3573	6	3	3	0,032609	-1,3998	-2,63865	B8NS16	B8NS16	1	AFLA_052470	Gamma-glutamyltranspeptidase
25,1504	26,2197	26,2552	24,4404	24,3679	24,6698	6,07E-27	2,91E+08	3	3	3	7,6	58,844	25,1839	25,8751	24,4927	6	3	3	0,020856	-1,38239	-2,6069989	B8MZN7	B8MZN7	1	AFLA_085270	T-complex protein 1, zeta subunit, putative
28,5815	28,6895	27,9841	26,629	27,0822	27,4071	1,25E-81	1,97E+09	9	9	9	43	42,286	27,7289	28,4184	27,0394	6	3	3	0,011859	-1,37896	-2,6008082	B8NRK3	B8NRK3	1	AFLA_049080	Biotin synthase, putative
26,4242	26,4663	26,6176	24,8548	25,1215	25,396	2,29E-30	5,71E+08	9	9	9	11,2	123,33	25,8134	26,5027	25,1241	6	3	3	0,001172	-1,37862	-2,6001953	B8MWT5	B8MWT5	1	AFLA_088850	Exportin KapK
26,4378	25,828	26,5436	24,1394	25,6115	24,9921	6,08E-24	6,67E+08	5	5	5	24,3	39,966	25,5921	26,2698	24,9143	6	3	3	0,048061	-1,35547	-2,5588046	B8NU58	B8NU58	1	AFLA_097300	Putative uncharacterized protein
30,1405	29,3996	29,5339	27,6879	28,6578	28,7071	3,22E-230	6,89E+09	22	22	19	51,2	54,164	29,0211	29,6913	28,3509	6	3	3	0,029117	-1,34041	-2,5322327	B8N9G1	B8N9G1	1	AFLA_111070	Aldehyde dehydrogenase, putative
24,6378	24,1401	24,8011	22,5672	23,9778	23,0192	2,68E-16	1,34E+08	4	4	4	11,2	46,831	23,8572	24,5263	23,1881	6	3	3	0,043969	-1,33825	-2,5284443	B8NA14	B8NA14	1	AFLA_113100	N-glycosyl-transferase
26,0237	25,4917	25,8928	24,3712	24,1324	25,0155	1,06E-25	3,44E+08	9	9	9	25,7	53,612	25,1546	25,8027	24,5064	6	3	3	0,013675	-1,29635	-2,4560671	B8NSS1	B8NSS1	1	AFLA_014140	Aldehyde dehydrogenase family protein, putative
30,0113	29,8087	30,0592	28,9119	28,7821	28,3441	3,03E-283	6,76E+09	18	18	18	80,5	23,726	29,3195	29,9597	28,6794	6	3	3	0,002437	-1,28039	-2,4290463	B8NW05	B8NW05	1	AFLA_119330	Glutathione-S-transferase theta, GST, putative
28,1631	28,2998	28,0828	26,8054	26,8007	27,102	9,53E-114	1,61E+09	11	11	11	35,5	48,625	27,5423	28,1819	26,9027	6	3	3	0,000412	-1,2792	-2,4270436	B8N2E0	B8N2E0	1	AFLA_036250	GDP-mannose pyrophosphorylase A
27,4023	27,8993	27,9142	26,1872	26,3186	26,8903	1,73E-61	1,46E+09	15	15	15	38,3	48,944	27,102	27,7386	26,4654	6	3	3	0,00964	-1,27325	-2,4170545	B8NTR9	B8NTR9	1	AFLA_100000	Proteasome regulatory particle subunit Rpt1, putative
26,6417	26,2687	26,7883	25,5704	25,0942	25,2423	1,01E-21	4,58E+08	3	3	3	26,3	15,049	25,9343	26,5662	25,3023	6	3	3	0,003777	-1,26397	-2,4015569	B8N418	B8N418	1	AFLA_033410	Putative uncharacterized protein
28,2277	27,7686	27,8913	26,7257	27,0606	26,3184	5,84E-71	2,56E+09	7	7	7	25	34,953	27,332	27,9625	26,7016	6	3	3	0,007762	-1,26091	-2,3964685	B8MZ00	B8MZ00	1	AFLA_082890	Ribonuclease T2, putative
27,7518	27,5812	27,9011	26,5741	26,026	26,8691	1,26E-57	1,72E+09	15	15	15	27,4	83,676	27,1172	27,7447	26,4898	6	3	3	0,008917	-1,25493	-2,3865557	B8NG70	B8NG70	1	AFLA_134090	3-isopropylmalate dehydratase
25,4765	25,4405	24,9528	23,7917	23,7745	24,5541	4,91E-20	2,25E+08	6	6	6	20,8	33,121	24,665	25,2899	24,0401	6	3	3	0,015306	-1,24978	-2,3780516	B8NV71	B8NV71	1	AFLA_103660	Nicotinate-nucleotide pyrophosphorylase [carboxylating]
25,5998	26,9188	26,6539	24,9304	25,3283	25,1661	1,69E-24	4,61E+08	8	8	8	12,6	103,24	25,7662	26,3908	25,1416	6	3	3	0,040696	-1,24926	-2,3771946	B8NJP5	B8NJP5	1	AFLA_068550	Coatomer subunit beta
26,3901	26,9493	27,0376	25,3939	25,4289	25,8072	2,93E-58	8,67E+08	10	9	9	32,1	43,417	26,1678	26,7923	25,5433	6	3	3	0,006699	-1,24901	-2,3767827	B8NZ22	B8NZ22	1	AFLA_115340	Proteasome regulatory particle subunit Rpt6, putative
27,6116	27,9371	27,262	26,4254	26,4469	26,1929	3,31E-34	1,29E+09	8	8	8	20,9	58,992	26,9793	27,6036	26,3551	6	3	3	0,004099	-1,24848	-2,3759097	B8N1U7	B8N1U7	1	AFLA_032510	Galactokinase
29,3308	28,1995	29,1126	27,4485	28,1498	27,3178	0	4,41E+09	12	12	12	55,4	36,305	28,2598	28,881	27,6387	6	3	3	0,045267	-1,24228	-2,3657211	B8NKU8	B8NKU8	1	AFLA_093520	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase, putative
27,8553	27,3692	27,9771	26,3163	26,8167	26,3616	1,18E-59	2,22E+09	13	13	13	53,3	39,312	27,116	27,7339	26,4982	6	3	3	0,00726	-1,23566	-2,3548905	B8N040	B8N040	1	AFLA_086800	Epoxide hydrolase, putative
26,5704	25,9415	26,7763	25,2865	25,3569	24,9457	1,63E-53	1,13E+09	9	8	8	40,4	35,853	25,8129	26,4294	25,1963	6	3	3	0,01185	-1,23308	-2,350683	B8NCW5	B8NCW5	1	AFLA_042000	Hydroxyisocaproate dehydrogenase, putative
32,1971	32,0647	32,3483	30,5036	30,943	31,4773	0	3,19E+10	85	85	85	56	236,61	31,589	32,2034	30,9746	6	3	3	0,013799	-1,22873	-2,3436059	B8NBR1	B8NBR1	1	AFLA_046360	Acetyl-CoA carboxylase, putative
27,6807	26,8844	27,4597	25,6154	26,598	26,1311	5,76E-112	1,73E+09	13	13	13	36,2	63,638	26,7282	27,3416	26,1148	6	3	3	0,029491	-1,22674	-2,3403755	B8NUU5	B8NUU5	1	AFLA_102390	Putative uncharacterized protein
27,7593	27,9422	28,2911	26,5263	26,9445	26,8421	5,37E-161	1,52E+09	12	12	12	34,9	58,819	27,3842	27,9975	26,7709	6	3	3	0,003611	-1,2266	-2,3401484	B8MVZ9;B	B8MVZ9	2	AFLA_073460	Cyclopropane-fatty-acyl-phospholipid synthase, putative
32,0177	31,7017	32,1035	30,4464	30,8191	30,9166	0	3,28E+10	18	18	18	71,7	38,503	31,3342	31,941	30,7273	6	3	3	0,002982	-1,21362	-2,3191884	B8NRH9	B8NRH9	1	AFLA_048840	Adenosine kinase, putative
26,6823	26,48	26,5437	24,9716	25,2892	25,814	5,51E-55	7,99E+08	6	6	6	17,8	49,932	25,9635	26,5687	25,3583	6	3	3	0,008722	-1,2104	-2,3140179	B8N4N0	B8N4N0	1	AFLA_037350	Casein kinase I, putative
27,923	27,1299	27,8706	26,4529	26,6188	26,2468	2,68E-44	1,82E+09	15	15	15	20	123,51	27,0403	27,6412	26,4395	6	3	3	0,012389	-1,20166	-2,3000417	B8N050	B8N050	1	AFLA_086900	Alpha-mannosidase
27,0483	26,2027	26,9641	25,4121	25,9552	25,2439	2,07E-31	1,11E+09	11	11	11	28,8	68,621	26,1377	26,7384	25,5371	6	3	3	0,025095	-1,20129	-2,2994519	B8NUU0	B8NUU0	1	AFLA_102340	Oligo-1,6-glucosidase
31,2551	30,872	31,3376	29,686	30,1192	30,0659	0	1,84E+10	29	29	29	58,9	61,708	30,5559	31,1549	29,957	6	3	3	0,003762	-1,19786	-2,2939914	B8ND74	B8ND74	1	AFLA_056350	2-methylcitrate dehydratase, putative
26,0415	25,6339	26,6244	24,7234	25,1363	24,8848	1,19E-19	5,14E+08	4	4	4	39,2	17,83	25,5074	26,0999	24,9148	6	3	3	0,019028	-1,18508	-2,27376	B8NUF7	B8NUF7	1	AFLA_099190	Putative uncharacterized protein
25,0862	26,3599	26,0631	24,95	24,4859	24,5296	3,09E-13	3,46E+08	6	6	6	24,9	44,186	25,2458	25,8364	24,6552	6	3	3	0,045681	-1,18124	-2,267716	B8MWG2	B8MWG2	1	AFLA_088520	CUE domain protein, putative
27,6317	27,7096	28,1134	26,5378	26,8942	26,5742	1,02E-57	1,33E+09	6	6	6	36,1	20,972	27,2435	27,8183	26,6688	6	3	3	0,003578	-1,14951	-2,2183854	B8NIL7;B8	B8NIL7	2	AFLA_068040	ADP-ribosylation factor, putative
30,0836	29,9282	30,1069	29,1614	28,7143	28,9247	3,29E-233	6,37E+09	19	19	19	65,2	43,248	29,4865	30,0396	28,9335	6	3	3	0,001418	-1,10607	-2,1525847	B8NKM2	B8NKM2	1	AFLA_091880	Septin AspA, putative
25,9084	25,4734	26,3552	25,0423	24,5201	24,8919	1,39E-12	3,17E+08	2	2	2	7,5	33,809	25,3652	25,9123	24,8181	6	3	3	0,02139	-1,0942	-2,1349466	B8N008	B8N008	1	AFLA_086480	Translational initiation factor 2 beta

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

B. Quantitative results

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	t-test p value	Log2 (t-test Difference)	Fold Change (Treated v Control)	Protein IDs	Majority protein IDs	Proteins	Gene Name (ORF)	Protein Function
32,2693	31,7467	32,375	31,1869	31,3549	30,5972	0	2,91E+10	11	11	11	79	23,229	31,5883	32,1303	31,0463	6	3	3	0,022695	-1,084	-2,1199056	B8N419	B8N419	1	AFLA_033420	Superoxide dismutase
29,0568	29,0745	29,085	27,7126	27,8937	28,364	5,95E-33	3,37E+09	7	7	7	29,9	24,083	28,5311	29,0721	27,9901	6	3	3	0,005095	-1,08198	-2,1169394	B8N442	B8N442	1	AFLA_033650	GTP-binding nuclear protein Ran, putative
31,4931	30,9698	31,1742	29,8247	30,1413	30,4402	0	1,7E+10	38	38	38	42,2	131,2	30,6739	31,2124	30,1354	6	3	3	0,010012	-1,07698	-2,1096154	B8N9R6	B8N9R6	1	AFLA_112120	Pyruvate carboxylase
30,9782	30,4755	31,003	29,8387	29,6012	29,7963	0	1,01E+10	23	23	23	58,6	57,696	30,2822	30,8189	29,7454	6	3	3	0,004544	-1,07349	-2,1045182	B8NUL4	B8NUL4	1	AFLA_100670	ATP sulphurylase
27,7813	27,7267	28,0254	26,9677	26,7112	26,6381	1,24E-75	1,17E+09	7	7	7	18,5	64,711	27,3084	27,8445	26,7724	6	3	3	0,00139	-1,07211	-2,1025061	B8NA09	B8NA09	1	AFLA_113050	Asparagine synthetase
25,4197	26,2736	25,9741	24,5942	24,8852	25,0204	3,64E-10	5,6E+08	4	4	4	23,4	25,648	25,3612	25,8891	24,8333	6	3	3	0,01958	-1,05587	-2,0789715	B8MX61	B8MX61	1	AFLA_076480	Glutathione S-transferase, putative
26,3346	26,6938	26,9119	26,0062	24,9284	25,839	3,98E-117	9,58E+08	8	8	8	35,4	33,553	26,119	26,6468	25,5912	6	3	3	0,048005	-1,05561	-2,0785969	B8NG94	B8NG94	1	AFLA_134340	BAR domain protein
31,5453	30,6777	31,2887	30,1156	30,389	29,8506	0	3,44E+10	13	13	13	60,6	32,512	30,6445	31,1706	30,1184	6	3	3	0,024898	-1,05219	-2,0736753	B8NE88	B8NE88	1	AFLA_059970	Short-chain dehydrogenase, putative
28,5363	28,5593	28,6057	27,5927	27,3424	27,6235	3,57E-188	2,51E+09	11	10	10	32,5	59,145	28,0433	28,5671	27,5195	6	3	3	0,00033	-1,04755	-2,0670166	B8MX20	B8MX20	1	AFLA_076070	Septin AspB
26,761	26,1014	26,5021	25,4209	25,6554	25,1717	5,77E-45	7,95E+08	6	6	6	15,7	66,631	25,9354	26,4548	25,416	6	3	3	0,0119	-1,03884	-2,054575	B8NLP8	B8NLP8	1	AFLA_092640	Alkaline phosphatase
24,9992	25,025	25,0904	23,567	23,9843	24,4912	5,86E-42	1,3E+09	7	7	7	23,6	27,221	24,5262	25,0382	24,0142	6	3	3	0,018899	-1,02401	-2,0335634	B8N370	B8N370	1	AFLA_026830	40S ribosomal protein S6
27,6898	27,4631	27,7298	27,0419	26,5399	26,2644	6,19E-73	1,72E+09	10	10	10	21,6	78,809	27,1215	27,6276	26,6154	6	3	3	0,01394	-1,01217	-2,0169426	B8MY11	B8MY11	1	AFLA_079480	Oligopeptidase family protein

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 μg/ml PgAFP and untreated control.

C. Qualitative differences

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	t-test p value	Log2 (t-test Difference)	Fold Change (Treated v Control)	Protein IDs	Majority protein IDs	Proteins	Gene Name (ORF)	Protein Function
ND	ND	ND	28,7561	28,874	28,9034	2,15E-73	2,78E+09	11	11	11	28,9	46,84	28,8445	ND	28,8445	3	0	3	N/A	N/A	Detected in Treated only	B8NBM6	B8NBM6	1	AFLA_046010	Eukaryotic translation initiation factor 5, putative
ND	ND	ND	28,5085	28,2485	28,1437	8,31E-75	1,78E+09	2	2	2	10,8	25,563	28,3002	ND	28,3002	3	0	3	N/A	N/A	Detected in Treated only	B8NC17	B8NC17	1	AFLA_047420	Putative uncharacterized protein
ND	ND	ND	29,0495	27,8466	27,8035	1,36E-176	1,47E+09	6	6	6	40,9	27,781	28,2332	ND	28,2332	3	0	3	N/A	N/A	Detected in Treated only	B8NM09	B8NM09	1	AFLA_094650	60S acidic ribosomal protein P0, putative
ND	ND	ND	29,0699	27,1217	27,7928	2,41E-95	1,51E+09	15	15	15	41,8	54,862	27,9948	ND	27,9948	3	0	3	N/A	N/A	Detected in Treated only	B8NSF7	B8NSF7	1	AFLA_048200	Pseudouridylate synthase family protein
ND	ND	ND	28,115	27,873	27,5837	6,47E-11	1,52E+09	3	3	3	16,3	11,278	27,8572	ND	27,8572	3	0	3	N/A	N/A	Detected in Treated only	B8NS34	B8NS34	1	AFLA_052650	Putative uncharacterized protein
ND	ND	ND	27,5426	ND	27,1176	2,65E-06	4,45E+08	4	4	4	1,5	266,76	27,3301	ND	27,3301	2	0	2	N/A	N/A	Detected in Treated only	B8NDF2	B8NDF2	1	AFLA_057130	THO complex component (Rlr1), putative
ND	ND	ND	27,282	27,1296	26,954	4,28E-09	9,42E+08	2	2	2	17,6	19,894	27,1219	ND	27,1219	3	0	3	N/A	N/A	Detected in Treated only	B8NS36	B8NS36	1	AFLA_052670	RNA recognition motif (Rrm) domain containing protein, putative
ND	ND	ND	27,0827	26,7843	27,2357	1,65E-58	6,32E+08	4	4	4	64,1	11,564	27,0343	ND	27,0343	3	0	3	N/A	N/A	Detected in Treated only	B8NEM0	B8NEM0	1	AFLA_062180	37S ribosomal protein S16
ND	ND	ND	26,3176	26,4487	27,6284	6,27E-88	5,95E+08	7	7	7	45,3	27,389	26,7982	ND	26,7982	3	0	3	N/A	N/A	Detected in Treated only	B8NFL4	B8NFL4	1	AFLA_131050	Putative uncharacterized protein
ND	ND	ND	26,9555	26,5675	25,8458	3,80E-25	5,2E+08	3	3	3	42,6	13,05	26,4563	ND	26,4563	3	0	3	N/A	N/A	Detected in Treated only	B8NKX6	B8NKX6	1	AFLA_093800	Small nuclear ribonucleoprotein SmD2, putative
ND	ND	ND	26,3398	ND	26,338	5,36E-28	9,43E+08	4	4	4	20,6	16,934	26,3389	ND	26,3389	2	0	2	N/A	N/A	Detected in Treated only	B8N003	B8N003	1	AFLA_086430	Coactivator bridging factor 1 (Mbf1), putative
ND	ND	ND	26,332	ND	26,2352	1,47E-72	1E+09	5	5	5	34,4	14,925	26,2836	ND	26,2836	2	0	2	N/A	N/A	Detected in Treated only	B8NQW4	B8NQW4	1	AFLA_003480	60S ribosomal protein L32
ND	ND	ND	25,8494	25,2845	27,498	6,81E-24	1,35E+09	6	6	6	37,4	14,069	26,2106	ND	26,2106	3	0	3	N/A	N/A	Detected in Treated only	B8N446	B8N446	1	AFLA_033690	60S ribosomal protein L31e
ND	ND	ND	26,3822	26,0895	25,9938	1,89E-14	5,97E+08	7	7	7	13,5	92,143	26,1552	ND	26,1552	3	0	3	N/A	N/A	Detected in Treated only	B8N7A0	B8N7A0	1	AFLA_021220	tRNA ligase
ND	ND	ND	26,244	25,8101	25,9626	2,51E-25	2,82E+08	6	6	6	4,8	200,15	26,0056	ND	26,0056	3	0	3	N/A	N/A	Detected in Treated only	B8N5Y3	B8N5Y3	1	AFLA_014760	rRNA biogenesis protein RRP5, putative
ND	ND	ND	26,0785	ND	25,601	9,87E-39	2,56E+08	4	4	4	8,1	89,01	25,8397	ND	25,8397	2	0	2	N/A	N/A	Detected in Treated only	B8NNR8	B8NNR8	1	AFLA_129690	Cell division control protein (Cdc5), putative
ND	ND	ND	25,5396	ND	25,7866	1,06E-14	2,82E+08	5	5	5	17,6	41,092	25,6631	ND	25,6631	2	0	2	N/A	N/A	Detected in Treated only	B8NU88	B8NU88	1	AFLA_098500	Putative uncharacterized protein
ND	ND	ND	26,3981	24,8133	25,5339	1,23E-16	4,5E+08	4	4	4	13,3	35,184	25,5818	ND	25,5818	3	0	3	N/A	N/A	Detected in Treated only	B8N1X2	B8N1X2	1	AFLA_032760	Pre-RNA splicing factor Srp2, putative
ND	ND	ND	25,5376	25,5403	25,4022	1,02E-05	4,04E+08	2	2	2	26	20,449	25,4934	ND	25,4934	3	0	3	N/A	N/A	Detected in Treated only	B8NBS0	B8NBS0	1	AFLA_046450	Small subunit of nuclear cap-binding protein complex
ND	ND	ND	25,2458	24,8686	26,0363	1,95E-20	1,78E+08	4	4	4	11,9	44,244	25,3836	ND	25,3836	3	0	3	N/A	N/A	Detected in Treated only	B8N6D2	B8N6D2	1	AFLA_018960	60S ribosomal protein L3
ND	ND	ND	25,1286	25,4973	ND	5,00E-18	2,24E+08	5	5	5	12,1	60,752	25,3129	ND	25,3129	2	0	2	N/A	N/A	Detected in Treated only	B8MWW4	B8MWW4	1	AFLA_075510	General amidase, putative
ND	ND	ND	25,8987	24,7135	25,2262	2,24E-15	2,57E+08	5	5	5	13,1	67,022	25,2795	ND	25,2795	3	0	3	N/A	N/A	Detected in Treated only	B8N3F9	B8N3F9	1	AFLA_028620	Signal recognition particle subunit SRP68
ND	ND	ND	26,0605	24,6033	25,0182	1,94E-13	1,95E+08	6	6	6	9,3	91,575	25,2273	ND	25,2273	3	0	3	N/A	N/A	Detected in Treated only	B8ND54	B8ND54	1	AFLA_055250	Mitochondrial mRNA processing protein PET127, putative
ND	ND	ND	25,4241	25,0097	25,2198	8,32E-38	4,71E+08	4	4	4	39,7	21,287	25,2178	ND	25,2178	3	0	3	N/A	N/A	Detected in Treated only	B8NX71	B8NX71	1	AFLA_122590	RNA binding protein Tma22, putative
ND	ND	ND	24,6225	24,5824	26,4286	2,92E-57	2,03E+08	8	8	8	34,1	30,478	25,2112	ND	25,2112	3	0	3	N/A	N/A	Detected in Treated only	B8N9W4	B8N9W4	1	AFLA_112600	37S ribosomal protein Rsm25
ND	ND	ND	25,5252	25,2387	24,8165	7,79E-15	1,95E+08	5	5	5	7,7	81,936	25,1934	ND	25,1934	3	0	3	N/A	N/A	Detected in Treated only	B8NA76	B8NA76	1	AFLA_113720	Ribosome biogenesis (Nop4), putative
ND	ND	ND	25,3344	24,8987	25,0469	2,05E-09	1,54E+08	4	4	4	10,9	37,363	25,0933	ND	25,0933	3	0	3	N/A	N/A	Detected in Treated only	B8MXX9	B8MXX9	1	AFLA_079160	Ribosome biogenesis protein, putative
ND	ND	ND	25,2676	24,8993	ND	2,71E-07	1,59E+08	2	2	2	9,9	29,157	25,0835	ND	25,0835	2	0	2	N/A	N/A	Detected in Treated only	B8NTQ5	B8NTQ5	1	AFLA_099860	Pre-mRNA splicing factor, putative
ND	ND	ND	25,1738	25,0094	24,8386	5,86E-09	2,32E+08	4	4	4	11,3	53,513	25,0072	ND	25,0072	3	0	3	N/A	N/A	Detected in Treated only	B8NJ17	B8NJ17	1	AFLA_071340	Cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative
ND	ND	ND	25,4157	24,5721	ND	2,33E-07	2,12E+08	5	5	5	5,1	158,06	24,9939	ND	24,9939	2	0	2	N/A	N/A	Detected in Treated only	B8NYY7	B8NYY7	1	AFLA_114990	DEAD helicases superfamily protein (Aquarius), putative
ND	ND	ND	24,2902	24,5375	26,1045	5,56E-13	1,99E+08	4	4	4	10,5	48,761	24,9774	ND	24,9774	3	0	3	N/A	N/A	Detected in Treated only	H9CNZ7	H9CNZ7	1	AFLA_m0250	Ribosomal protein S5
ND	ND	ND	24,9814	ND	24,9224	1,56E-08	2,67E+08	2	2	2	20,7	16,051	24,9519	ND	24,9519	2	0	2	N/A	N/A	Detected in Treated only	B8NEW9	B8NEW9	1	AFLA_058330	Mitochondrial intermembrane space translocase subunit Tim9, putative
ND	ND	ND	24,6159	25,5624	24,5391	3,58E-08	4,2E+08	3	3	3	42,6	11,061	24,9058	ND	24,9058	3	0	3	N/A	N/A	Detected in Treated only	B8N199	B8N199	1	AFLA_029640	Dynein light chain type 1, putative
ND	ND	ND	24,8615	25,3914	24,3905	3,40E-12	3,02E+08	4	4	4	39,6	16,977	24,8811	ND	24,8811	3	0	3	N/A	N/A	Detected in Treated only	B8N729	B8N729	1	AFLA_019620	Putative uncharacterized protein
ND	ND	ND	26,4722	23,4352	24,7111	2,38E-19	2,75E+08	2	2	2	14,3	24,904	24,8728	ND	24,8728	3	0	3	N/A	N/A	Detected in Treated only	B8N4S4	B8N4S4	1	AFLA_017830	Small nuclear ribonucleoprotein complex protein Nhp2, putative
ND	ND	ND	25,5993	24,1112	ND	3,52E-06	1,29E+08	3	3	3	23,3	24,593	24,8553	ND	24,8553	2	0	2	N/A	N/A	Detected in Treated only	B8NNR4	B8NNR4	1	AFLA_129650	NADH-ubiquinone oxidoreductase 18 kDa subunit, putative
ND	ND	ND	24,9201	24,78	ND	4,12E-06	2,13E+08	2	2	2	6	56,002	24,85	ND	24,85	2	0	2	N/A	N/A	Detected in Treated only	B8NIS7	B8NIS7	1	AFLA_069550	Pre-mRNA splicing factor (Prp31), putative
ND	ND	ND	24,88	24,7236	ND	3,80E-05	3,07E+08	2	2	2	3,5	80,926	24,8018	ND	24,8018	2	0	2	N/A	N/A	Detected in Treated only	B8NP31	B8NP31	1	AFLA_128140	Sister chromatid separation protein (Src1), putative
ND	ND	ND	24,9932	24,3147	24,757	2,02E-14	2,07E+08	6	6	6	7,6	96,177	24,6883	ND	24,6883	3	0	3	N/A	N/A	Detected in Treated only	B8N9H1	B8N9H1	1	AFLA_111170	Transcription initiation protein spt5
ND	ND	ND	24,4254	24,867	24,7292	5,14E-10	4,09E+08	5	5	5	11	74,691	24,6739	ND	24,6739	3	0	3	N/A	N/A	Detected in Treated only	B8NBF0	B8NBF0	1	AFLA_045250	Biotin apo-protein ligase, putative
ND	ND	ND	25,5238	23,7559	24,6062	3,55E-11	1,61E+08	4	4	4	10,3	71,219	24,6287	ND	24,6287	3	0	3	N/A	N/A	Detected in Treated only	B8N0T4	B8N0T4	1	AFLA_026190	Signal recognition particle subunit SRP72
ND	ND	ND	ND	24,6262	24,45	1,17E-08	1,78E+08	4	4	4	7,6	71,548	24,5381	ND	24,5381	2	0	2	N/A	N/A	Detected in Treated only	B8NNH8	B8NNH8	1	AFLA_127890	Protein phophatase 2C family protein
ND	ND	ND	24,6922	ND	24,162	4,80E-07	55628000	2	2	2	6,1	36,444	24,4271	ND	24,4271	2	0	2	N/A	N/A	Detected in Treated only	B8NJP3	B8NJP3	1	AFLA_068530	Ribosomal RNA processing protein, putative
ND	ND	ND	24,7219	24,1242	24,2864	3,07E-09	1,83E+08	3	3	3	9,6	55,155	24,3775	ND	24,3775	3	0	3	N/A	N/A	Detected in Treated only	B8N4A4	B8N4A4	1	AFLA_035170	Kelch repeats protein, putative
ND	ND	ND	24,2854	24,4757	24,3477	2,24E-10	1,71E+08	5	5	5	5,8	102,45	24,3696	ND	24,3696	3	0	3	N/A	N/A	Detected in Treated only	B8NXL0	B8NXL0	1	AFLA_008290	Kinesin family protein (KinA), putative
ND	ND	ND	24,2478	24,2413	ND	4,17E-06	93864000	2	2	2	5,8	40,69	24,2446	ND	24,2446	2	0	2	N/A	N/A	Detected in Treated only	B8MZQ8	B8MZQ8	1	AFLA_085480	Cell wall glucanase, putative
ND	ND	ND	24,8791	23,822	23,9469	1,45E-10	1,28E+08	3	3	3	5,8	73,65	24,216	ND	24,216	3	0	3	N/A	N/A	Detected in Treated only	B8NFA3	B8NFA3	1	AFLA_061470	DSB repair complex subunit Ku70, putative
ND	ND	ND	ND	24,8735	23,5532	6,37E-06	2,14E+08	3	3	3	20,4	21,449	24,2133	ND	24,2133	2	0	2	N/A	N/A	Detected in Treated only	B8N1K7	B8N1K7	1	AFLA_030720	RNA exonuclease Rex2, putative
ND	ND	ND	23,9788	25,069	23,579	2,82E-08	1,92E+08	5	5	5	22,6	27,235	24,209	ND	24,209	3	0	3	N/A	N/A	Detected in Treated only	B8NM17	B8NM17	1	AFLA_094730	Exosome complex subunit Csl4, putative
ND	ND	ND	24,3069	ND	23,8656	6,59E-05	1,85E+08	3	3	3	3,9	105,37	24,0863	ND	24,0863	2	0	2	N/A	N/A	Detected in Treated only	B8NBM4	B8NBM4	1	AFLA_045990	DNA ligase
ND	ND	ND	24,4461	23,8885	23,8563	1,00E-06	1,47E+08	3	3	3	4,9	96,417	24,0636	ND	24,0636	3	0	3	N/A	N/A	Detected in Treated only	B8MYW6	B8MYW6	1	AFLA_082550	Cleavage and polyadenylation specifity factor, 73 kDa subunit
ND	ND	ND	24,5665	23,7097	23,9068	9,79E-10	1,46E+08	2	2	2	6,1	63,38	24,061	ND	24,061	3	0	3	N/A	N/A	Detected in Treated only	B8N507	B8N507	1	AFLA_020450	Nucleolar protein nop5
ND	ND	ND	24,7525	23,3429	ND	3,69E-05	1,21E+08	2	2	2	4,5	71,725	24,0477	ND	24,0477	2	0	2	N/A	N/A	Detected in Treated only	B8NID3	B8NID3	1	AFLA_066290	RNA binding protein Ligatin/Tma64, putative
ND	ND	ND	24,2677	23,9925	23,6545	9,65E-08	1,15E+08	4	4	4	19,8	46,735	23,9716	ND	23,9716	3	0	3	N/A	N/A	Detected in Treated only	B8N3Q7	B8N3Q7	1	AFLA_031410	Ribonuclease T2 family, putative
ND	ND	ND	22,8028	24,0298	24,7857	3,86E-08	63141000	4	4	4	11,5	45,78	23,8728	ND	23,8728	3	0	3	N/A	N/A	Detected in Treated only	B8NN65	B8NN65	1	AFLA_124990	Putative uncharacterized protein
ND	ND	ND	24,4364	23,3329	23,5753	1,31E-09	1,66E+08	4	4	4	10,4	62,23	23,7815	ND	23,7815	3	0	3	N/A	N/A	Detected in Treated only	B8N9I7	B8N9I7	1	AFLA_111330	Aspartyl-tRNA synthetase, putative
ND	ND	ND	23,6404	ND	23,4405	6,99E-09	1,15E+08	4	4	4	5,2	100,79	23,5405	ND	23,5405	2	0	2	N/A	N/A	Detected in Treated only	B8MY66	B8MY66	1	AFLA_080030	Topoisomerase I
ND	ND	ND	23,7677	23,3192	23,4335	0,0001001	79670000	2	2	2	3,5	83,606	23,5068	ND	23,5068	3	0	3	N/A	N/A	Detected in Treated only	B8NFR7	B8NFR7	1	AFLA_133460	Ku family DNA helicase, putative
ND	ND	ND	23,5683	23,3992	ND	1,81E-10	2,57E+08	3	3	3	9,2	52,445	23,4837	ND	23,4837	2	0	2	N/A	N/A	Detected in Treated only	B8MZJ4	B8MZJ4	1	AFLA_084840	Putative uncharacterized protein
ND	ND	ND	23,4807	23,3685	23,4433	0,0001907	84988000	2	2	2	2,3	114,51	23,4309	ND	23,4309	3	0	3	N/A	N/A	Detected in Treated only	B8N789	B8N789	1	AFLA_021110	Histone transcription regulator Hir1, putative
ND	ND	ND	23,5114	ND	23,3465	1,28E-05	1,12E+08	2	2	2	23,6	23,229	23,4289	ND	23,4289	2	0	2	N/A	N/A	Detected in Treated only	B8N3G2	B8N3G2	1	AFLA_028650	Rhodanese domain protein
ND	ND	ND	23,8836	ND	22,9423	5,24E-05	35752000	3	3	3	8,4	43,459	23,413	ND	23,413	2	0	2	N/A	N/A	Detected in Treated only	B8N225	B8N225	1	AFLA_034190	NADH-ubiquinone oxidoreductase 39 kDa subunit, putative
ND	ND	ND	ND	23,3996	23,0914	8,66E-05	24332000	2	2	2	0,5	578,43	23,2455	ND	23,2455	2	0	2	N/A	N/A	Detected in Treated only	B8NJX3	B8NJX3	1	AFLA_069330	Nonribosomal peptide synthase Pes1
ND	ND	ND	23,726	22,6377	ND	2,12E-12	1,52E+08	4	4	4	5,3	90,123	23,1819	ND	23,1819	2	0	2	N/A	N/A	Detected in Treated only	B8N5B4	B8N5B4	1	AFLA_022420	Microtubule binding protein HOOK3, putative
ND	ND	ND	23,1051	21,7938	23,197	3,13E-12	1,08E+08	4	4	4	15,8	20,056	22,6986	ND	22,6986	3	0	3	N/A	N/A	Detected in Treated only	B8N234	B8N234	1	AFLA_034280	40S ribosomal protein S29, putative
ND	ND	ND	22,6757	ND	22,489	0,0001006	1,02E+08	2	2	2	3,8	49,076	22,5823	ND	22,5823	2	0	2	N/A	N/A	Detected in Treated only	B8NNC0	B8NNC0	1	AFLA_127310	CAIB/BAIF family enzyme
ND	ND	ND	21,8022	22,2551	22,729	3,76E-24	9,86E+08	4	4	4	31,5	9,9816	22,2621	ND	22,2621	3	0	3	N/A	N/A	Detected in Treated only	B8MZ16	B8MZ16	1	AFLA_083050	40S ribosomal protein S25, putative
30,4773	30,6785	31,061	ND	ND	ND	0	6,87E+09	12	12	12	45,2	54,633	30,7389	30,7389	ND	3	3	0	N/A	N/A	Detected in Control only	B8N7N3	B8N7N3	1	AFLA_104760	Acid phosphatase, putative
28,4641	27,9995	28,8638	ND	ND	ND	3,55E-141	2,03E+09	12	12	12	25,9	85,243	28,4425	28,4425	ND	3	3	0	N/A	N/A	Detected in Control only	B8NWD3	B8NWD3	1	AFLA_119700	Alpha-1,2-mannosidase family protein
28,1097	28,3572	28,5269	ND	ND	ND	9,14E-136	1,9E+09	13	13	13	45,8	51,072	28,3313	28,3313	ND	3	3	0	N/A	N/A	Detected in Control only	B8N8U9	B8N8U9	1	AFLA_108950	Histidine acid phosphatase, putative
27,5246	27,2528	27,5787	ND	ND	ND	3,45E-43	8,27E+08	6	6	6	17,5	57,585	27,452	27,452	ND	3	3	0	N/A	N/A	Detected in Control only	B8NXS3	B8NXS3	1	AFLA_008930	Acid phosphatase AphA
27,3939	27,1583	27,1992	ND	ND	ND	7,84E-34	1,07E+09	9	9	9	20	74,118	27,2504	27,2504	ND	3	3	0	N/A	N/A	Detected in Control only	B8NEP7	B8NEP7	1	AFLA_062450	Sphingomyelin phosphodiesterase, putative
27,132	26,8571	26,9685	ND	ND	ND	1,35E-58	8,57E+08	6	6	6	21,6	50,64	26,9859	26,9859	ND	3	3	0	N/A	N/A	Detected in Control only	B8MZU5	B8MZU5	1	AFLA_085850	Putative uncharacterized protein
27,3023	26,4082	27,0373	ND	ND	ND	9,27E-34	4,12E+08	10	10	10	44,3	27,896	26,9159	26,9159	ND	3	3	0	N/A	N/A	Detected in Control only	B8NHZ4	B8NHZ4	1	AFLA_139300	AflM/ ver-1/ dehydrogenase/ ketoreductase
26,628	25,4141	27,3624	ND	ND	ND	2,45E-29	3,74E+08	5	5	5	31	23,258	26,4681	26,4681	ND	3	3	0	N/A	N/A	Detected in Control only	B8N5H5	B8N5H5	1	AFLA_013180	Williams-beuren syndrome chromosome region, putative
27,2294	25,8868	26,1972	ND	ND	ND	4,18E-06	4,89E+08	2	2	2	48,5	13,96	26,4378	26,4378	ND	3	3	0	N/A	N/A	Detected in Control only	B8NCN3	B8NCN3	1	AFLA_039400	Extracellular guanyl-specific ribonuclease RntA
26,0558	26,2309	26,7575	ND	ND	ND	1,79E-89	6,5E+08	6	6	6	23,4	38,608	26,348	26,348	ND	3	3	0	N/A	N/A	Detected in Control only	B8MZ75	B8MZ75	1	AFLA_083640	3-isopropylmalate dehydrogenase
26,7987	25,4721	26,7275	ND	ND	ND	5,20E-32	4,36E+08	5	5	5	31,5	34,269	26,3328	26,3328	ND	3	3	0	N/A	N/A	Detected in Control only	B8NN48;R(	B8NN48	2	AFLA_124820	Putative uncharacterized protein

Supplementary Table S1. Data on proteins obtained from label-free proteomics from *A. flavus* treated with 10 µg/ml PgAFP and untreated control.

C. Qualitative differences

Log2 LFQ intensity *A. flavus* Control 1	Log2 LFQ intensity *A. flavus* Control 2	Log2 LFQ intensity *A. flavus* Control 3	Log2 LFQ intensity *A. flavus* Treated 1	Log2 LFQ intensity *A. flavus* Treated 2	Log2 LFQ intensity *A. flavus* Treated 3	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *A. flavus* Control)	Log2 (Mean *A. flavus* Treated)	Valid values	Valid values *A. flavus* Control	Valid values *A. flavus* Treated	t-test p value	Log2 (t-test Difference)	Fold Change (Treated v Control)	Protein IDs	Majority protein IDs	Proteins	Gene Name (ORF)	Protein Function
25,1161	26,2974	26,7108	ND	ND	ND	3,31E-26	2,66E+08	4	4	4	17,4	47,811	26,0414	26,0414	ND	3	3	0	N/A	N/A	Detected in Control only	B8NQZ7	B8NQZ7	1	AFLA_003810	Endonuclease/exonuclease/phosphatase family protein
25,6771	25,8896	25,9286	ND	ND	ND	5,94E-35	2,16E+08	3	3	3	10,8	42,861	25,8318	25,8318	ND	3	3	0	N/A	N/A	Detected in Control only	B8NWU6	B8NWU6	1	AFLA_121330	Methyltransferase LaeA-like, putative
25,7019	25,5029	25,7986	ND	ND	ND	1,44E-16	4,62E+08	2	2	2	15,8	23,454	25,6678	25,6678	ND	3	3	0	N/A	N/A	Detected in Control only	B8NH69	B8NH69	1	AFLA_132930	Secretory pathway protein Ssp120, putative
25,3604	ND	25,8738	ND	ND	ND	3,79E-09	2,35E+08	3	3	3	21,7	28,058	25,6171	25,6171	ND	2	2	0	N/A	N/A	Detected in Control only	B8NU84	B8NU84	1	AFLA_098460	Putative uncharacterized protein
25,5437	25,5817	25,5485	ND	ND	ND	1,41E-06	1,57E+08	3	3	3	25,8	24,386	25,558	25,558	ND	3	3	0	N/A	N/A	Detected in Control only	B8N718	B8N718	1	AFLA_019510	Putative uncharacterized protein
25,4561	25,4021	25,4864	ND	ND	ND	9,03E-11	1,7E+08	3	3	3	9,5	63,659	25,4482	25,4482	ND	3	3	0	N/A	N/A	Detected in Control only	B8ND72	B8ND72	1	AFLA_056330	Amidophosphoribosyltransferase
ND	25,2238	25,6194	ND	ND	ND	6,39E-08	2,85E+08	2	2	2	5,9	50,604	25,4216	25,4216	ND	2	2	0	N/A	N/A	Detected in Control only	B8NCN0	B8NCN0	1	AFLA_039370	Acid phosphatase, putative
25,5832	ND	25,2405	ND	ND	ND	3,39E-07	2,07E+08	2	2	2	4,4	58,265	25,4119	25,4119	ND	2	2	0	N/A	N/A	Detected in Control only	B8NWK2	B8NWK2	1	AFLA_120390	Putative uncharacterized protein
25,8756	24,8715	25,4305	ND	ND	ND	4,94E-16	4,11E+08	5	5	5	10,1	92,445	25,3925	25,3925	ND	3	3	0	N/A	N/A	Detected in Control only	B8N3U2	B8N3U2	1	AFLA_031760	Glutaminase, putative
25,3237	ND	25,0587	ND	ND	ND	5,03E-05	1,54E+08	2	2	2	14,3	26,709	25,1912	25,1912	ND	2	2	0	N/A	N/A	Detected in Control only	B8NYA9	B8NYA9	1	AFLA_010790	Elongation factor 1 gamma, putative
24,8557	25,4268	25,2504	ND	ND	ND	4,43E-09	1,3E+08	4	4	4	11,1	51,434	25,1776	25,1776	ND	3	3	0	N/A	N/A	Detected in Control only	B8NUL7	B8NUL7	1	AFLA_100700	Phosphoserine phosphatase
25,3291	24,6886	25,4192	ND	ND	ND	1,67E-09	1,71E+08	3	3	3	23,5	25,272	25,1456	25,1456	ND	3	3	0	N/A	N/A	Detected in Control only	B8N097	B8N097	1	AFLA_087380	Isochorismatase family hydrolase, putative
25,0333	ND	25,2148	ND	ND	ND	9,35E-17	2,48E+08	4	4	4	28,2	27,56	25,1241	25,1241	ND	2	2	0	N/A	N/A	Detected in Control only	B8NGD5	B8NGD5	1	AFLA_134750	Putative uncharacterized protein
25,1511	ND	24,9424	ND	ND	ND	3,16E-18	2,78E+08	4	4	4	38,9	21,849	25,0468	25,0468	ND	2	2	0	N/A	N/A	Detected in Control only	B8NX75	B8NX75	1	AFLA_122630	Cytidine deaminase, putative
24,8195	ND	25,2616	ND	ND	ND	3,11E-07	2,46E+08	2	2	2	40,9	12,007	25,0405	25,0405	ND	2	2	0	N/A	N/A	Detected in Control only	B8NS13	B8NS13	1	AFLA_052440	Putative uncharacterized protein
24,5036	25,4728	24,9027	ND	ND	ND	6,66E-10	2,03E+08	5	5	5	17,3	49,641	24,9597	24,9597	ND	3	3	0	N/A	N/A	Detected in Control only	B8N362	B8N362	1	AFLA_026750	AAA family ATPase Pontin, putative
24,8815	ND	24,882	ND	ND	ND	3,07E-24	4,62E+08	6	6	6	37,8	25,614	24,8818	24,8818	ND	2	2	0	N/A	N/A	Detected in Control only	B8N2C2	B8N2C2	1	AFLA_036070	Maleylacetoacetate isomerase MaiA
24,4243	25,0286	25,0861	ND	ND	ND	1,49E-07	1,22E+08	2	2	2	15,1	21,403	24,8463	24,8463	ND	3	3	0	N/A	N/A	Detected in Control only	B8NPB9	B8NPB9	1	AFLA_129910	Rho GTPase ModA, putative
24,9549	24,5646	ND	ND	ND	ND	8,71E-16	1,67E+08	3	3	3	12,8	40,381	24,7598	24,7598	ND	2	2	0	N/A	N/A	Detected in Control only	B8NUG2	B8NUG2	1	AFLA_099240	D-arabinitol dehydrogenase ArbD, putative
25,0913	24,2916	24,8085	ND	ND	ND	4,57E-06	89030000	3	3	3	6,4	70,264	24,7305	24,7305	ND	3	3	0	N/A	N/A	Detected in Control only	B8NHY3	B8NHY3	1	AFLA_139190	AflK/ vbs/ VERB synthase
24,9194	24,6262	24,4684	ND	ND	ND	5,68E-06	2,12E+08	3	3	3	9,6	47,944	24,6713	24,6713	ND	3	3	0	N/A	N/A	Detected in Control only	B8N0U8	B8N0U8	1	AFLA_026330	CaaX farnesyltransferase beta subunit Ram1
25,2106	23,8857	24,9155	ND	ND	ND	9,31E-35	5,54E+08	9	9	9	25,1	58,984	24,6706	24,6706	ND	3	3	0	N/A	N/A	Detected in Control only	B8NH51	B8NH51	1	AFLA_132750	Putative uncharacterized protein
24,6148	24,6797	24,6545	ND	ND	ND	3,89E-09	1,17E+08	4	4	4	10,3	55,533	24,6497	24,6497	ND	3	3	0	N/A	N/A	Detected in Control only	B8NJL7	B8NJL7	1	AFLA_067380	Nucleoside diphosphatase Gda1
24,295	24,643	24,9455	ND	ND	ND	2,61E-12	2,65E+08	5	5	5	9,6	70,731	24,6278	24,6278	ND	3	3	0	N/A	N/A	Detected in Control only	B8N802	B8N802	1	AFLA_105960	Autophagy protein Atg20, putative
24,5787	ND	24,665	ND	ND	ND	6,18E-10	1,6E+08	2	2	2	18,7	23,738	24,6218	24,6218	ND	2	2	0	N/A	N/A	Detected in Control only	B8N2G6	B8N2G6	1	AFLA_036510	Methionine-R-sulfoxide reductase SelR, putative
24,7493	24,7008	24,4039	ND	ND	ND	4,21E-12	1,21E+08	3	3	3	13,3	45,392	24,618	24,618	ND	3	3	0	N/A	N/A	Detected in Control only	B8NUR6	B8NUR6	1	AFLA_102090	Phosphopantothenate-cysteine ligase, putative
24,5028	23,8533	25,3767	ND	ND	ND	1,55E-06	2E+08	3	3	3	3,1	109,68	24,5776	24,5776	ND	3	3	0	N/A	N/A	Detected in Control only	B8N6H2	B8N6H2	1	AFLA_014850	Phosphatidylethanolamine N-methyltransferase
24,4532	24,5154	24,7107	ND	ND	ND	1,94E-14	1,67E+08	6	6	6	7,5	93,992	24,5597	24,5597	ND	3	3	0	N/A	N/A	Detected in Control only	B8NFV3	B8NFV3	1	AFLA_133820	Putative uncharacterized protein
24,7422	ND	24,3633	ND	ND	ND	2,41E-16	1,65E+08	5	5	5	12,6	54,048	24,5528	24,5528	ND	2	2	0	N/A	N/A	Detected in Control only	B8NY90	B8NY90	1	AFLA_010600	Siderophore biosynthesis acetylase AceI, putative
24,5054	ND	24,5812	ND	ND	ND	5,54E-21	2,77E+08	4	4	4	11,2	49,272	24,5433	24,5433	ND	2	2	0	N/A	N/A	Detected in Control only	B8NGI3	B8NGI3	1	AFLA_136100	GATA transcription factor (AreB), putative
24,9032	23,9219	24,7713	ND	ND	ND	7,72E-08	83524000	3	3	3	9	62,227	24,5321	24,5321	ND	3	3	0	N/A	N/A	Detected in Control only	B8N4H4	B8N4H4	1	AFLA_036780	General amidase GmdA, putative
24,4559	24,2561	24,7613	ND	ND	ND	9,66E-15	79467000	5	5	5	5,6	94,76	24,4911	24,4911	ND	3	3	0	N/A	N/A	Detected in Control only	B8NGD3	B8NGD3	1	AFLA_134730	Transcriptional corepressor Cyc8, putative
24,5011	24,3422	24,6287	ND	ND	ND	4,02E-07	84066000	2	2	2	17,1	18,542	24,4907	24,4907	ND	3	3	0	N/A	N/A	Detected in Control only	B8N1R8	B8N1R8	1	AFLA_032220	DNA damage response protein (Dap1), putative
24,6483	ND	24,3231	ND	ND	ND	8,25E-26	2,24E+08	3	3	3	19	35,133	24,4857	24,4857	ND	2	2	0	N/A	N/A	Detected in Control only	B8NES9	B8NES9	1	AFLA_063660	Polysaccharide deacetylase family protein
24,6503	24,0151	24,6808	ND	ND	ND	3,80E-13	2,2E+08	3	3	3	6,4	57,774	24,4487	24,4487	ND	3	3	0	N/A	N/A	Detected in Control only	B8NGK6	B8NGK6	1	AFLA_136330	Exoenzymes regulatory protein aepA, putative
24,3397	ND	24,5075	ND	ND	ND	7,19E-07	1,4E+08	3	3	3	8,3	56,279	24,4236	24,4236	ND	2	2	0	N/A	N/A	Detected in Control only	B8NCH7	B8NCH7	1	AFLA_038840	Putative uncharacterized protein
24,268	24,5173	24,421	ND	ND	ND	9,22E-08	1,6E+08	4	4	4	6	86,491	24,4021	24,4021	ND	3	3	0	N/A	N/A	Detected in Control only	B8N5W5	B8N5W5	1	AFLA_014580	Chromatin remodeling complex subunit (Arp5), putative
24,3499	24,5857	24,0748	ND	ND	ND	1,68E-08	2,65E+08	4	4	4	6,2	106,32	24,3368	24,3368	ND	3	3	0	N/A	N/A	Detected in Control only	B8NV56	B8NV56	1	AFLA_103500	Oxysterol binding protein (Osh3), putative
24,7482	23,9083	ND	ND	ND	ND	2,32E-07	58024000	3	3	3	7,3	59,897	24,3283	24,3283	ND	2	2	0	N/A	N/A	Detected in Control only	B8N5D1	B8N5D1	1	AFLA_022590	YdiU domain protein
ND	24,7991	23,712	ND	ND	ND	1,08E-05	1,31E+08	3	3	3	10,2	29,815	24,2556	24,2556	ND	2	2	0	N/A	N/A	Detected in Control only	B8N535	B8N535	1	AFLA_020730	Putative uncharacterized protein
ND	23,6015	24,7384	ND	ND	ND	1,73E-06	58775000	2	2	2	8,5	36,25	24,17	24,17	ND	2	2	0	N/A	N/A	Detected in Control only	B8MVP1	B8MVP1	1	AFLA_072380	Putative uncharacterized protein
24,6475	ND	23,5511	ND	ND	ND	1,32E-07	98556000	3	3	3	5,3	98,644	24,0993	24,0993	ND	2	2	0	N/A	N/A	Detected in Control only	B8N6B6	B8N6B6	1	AFLA_018800	Nitrite reductase NiiA
ND	24,1064	23,9833	ND	ND	ND	3,10E-05	1,81E+08	2	2	2	3,5	66,297	24,0448	24,0448	ND	2	2	0	N/A	N/A	Detected in Control only	B8NPG9	B8NPG9	1	AFLA_130410	Autophagy ubiquitin-activating enzyme ApgG, putative
25,2788	22,9302	23,8493	ND	ND	ND	2,15E-16	1,04E+08	4	3	3	11	46,976	24,0194	24,0194	ND	3	3	0	N/A	N/A	Detected in Control only	B8N3I4	B8N3I4	1	AFLA_028870	Aspartate aminotransferase
23,7617	24,1553	24,0473	ND	ND	ND	3,08E-05	1,59E+08	2	2	2	3,1	81,025	23,9881	23,9881	ND	3	3	0	N/A	N/A	Detected in Control only	B8NQT8	B8NQT8	1	AFLA_002320	Sorting nexin Mvp1
24,1823	23,6968	24,0574	ND	ND	ND	9,77E-12	1,96E+08	6	6	6	12,3	63,286	23,9788	23,9788	ND	3	3	0	N/A	N/A	Detected in Control only	B8NKX5	B8NKX5	1	AFLA_093790	Dihydroxyacetone kinase (DakA), putative
23,746	24,1488	ND	ND	ND	ND	2,17E-13	1,58E+08	4	4	4	6,4	106,31	23,9474	23,9474	ND	2	2	0	N/A	N/A	Detected in Control only	B8NVZ7	B8NVZ7	1	AFLA_119250	DNA replication licensing factor Mcm6, putative
24,098	23,2303	24,0718	ND	ND	ND	0,0001783	1,75E+08	2	2	2	6,4	44,19	23,8	23,8	ND	3	3	0	N/A	N/A	Detected in Control only	B8N521	B8N521	1	AFLA_020590	Aldose 1-epimerase, putative
ND	23,4891	23,8834	ND	ND	ND	4,05E-10	1,25E+08	3	3	3	8,1	56,561	23,6863	23,6863	ND	2	2	0	N/A	N/A	Detected in Control only	B8N9T7	B8N9T7	1	AFLA_112330	SnRNP assembly factor, putative
23,7298	23,5731	23,3884	ND	ND	ND	1,08E-06	1,03E+08	2	2	2	4	68,226	23,5638	23,5638	ND	3	3	0	N/A	N/A	Detected in Control only	B8MXU4	B8MXU4	1	AFLA_078810	Oxidoreductin
23,6767	23,4087	ND	ND	ND	ND	7,02E-05	89201000	2	2	2	9,5	34,601	23,5427	23,5427	ND	2	2	0	N/A	N/A	Detected in Control only	B8MYK0	B8MYK0	1	AFLA_081380	Cytochrome C1/Cyt1, putative
23,9958	23,0399	ND	ND	ND	ND	1,42E-13	1,48E+08	3	3	3	18,1	31,57	23,5178	23,5178	ND	2	2	0	N/A	N/A	Detected in Control only	B8MVS8	B8MVS8	1	AFLA_072750	Pyrroline-5-carboxylate reductase, putative
22,7811	ND	23,9363	ND	ND	ND	1,57E-09	1,08E+08	3	3	3	10	32,46	23,3587	23,3587	ND	2	2	0	N/A	N/A	Detected in Control only	B8MWF3	B8MWF3	1	AFLA_088430	Protein kinase activator (Mob2), putative
23,8674	23,0727	23,1278	ND	ND	ND	8,57E-07	1,12E+08	3	3	3	8,8	52,116	23,356	23,356	ND	3	3	0	N/A	N/A	Detected in Control only	B8NP48	B8NP48	1	AFLA_128310	Phosphotyrosyl phosphatase activator
22,9732	23,7292	ND	ND	ND	ND	1,21E-05	1,01E+08	3	3	3	7,4	56,208	23,3512	23,3512	ND	2	2	0	N/A	N/A	Detected in Control only	B8N0B4	B8N0B4	1	AFLA_087550	Serine/threonine-protein phosphatase
ND	22,9611	22,9827	ND	ND	ND	3,81E-05	65771000	3	3	3	8,5	47,582	22,9719	22,9719	ND	2	2	0	N/A	N/A	Detected in Control only	B8NKP9	B8NKP9	1	AFLA_093030	Serine/threonine-protein phosphatase
ND	22,7278	22,9617	ND	ND	ND	9,36E-06	37583000	2	2	2	3,4	62,629	22,8447	22,8447	ND	2	2	0	N/A	N/A	Detected in Control only	B8NND4	B8NND4	1	AFLA_127450	Nuclear localization protein NPL6, putative
22,8023	ND	22,631	ND	ND	ND	2,19E-35	2,71E+08	5	5	5	15	52,932	22,7167	22,7167	ND	2	2	0	N/A	N/A	Detected in Control only	B8NAC3	B8NAC3	1	AFLA_039680	Putative uncharacterized protein

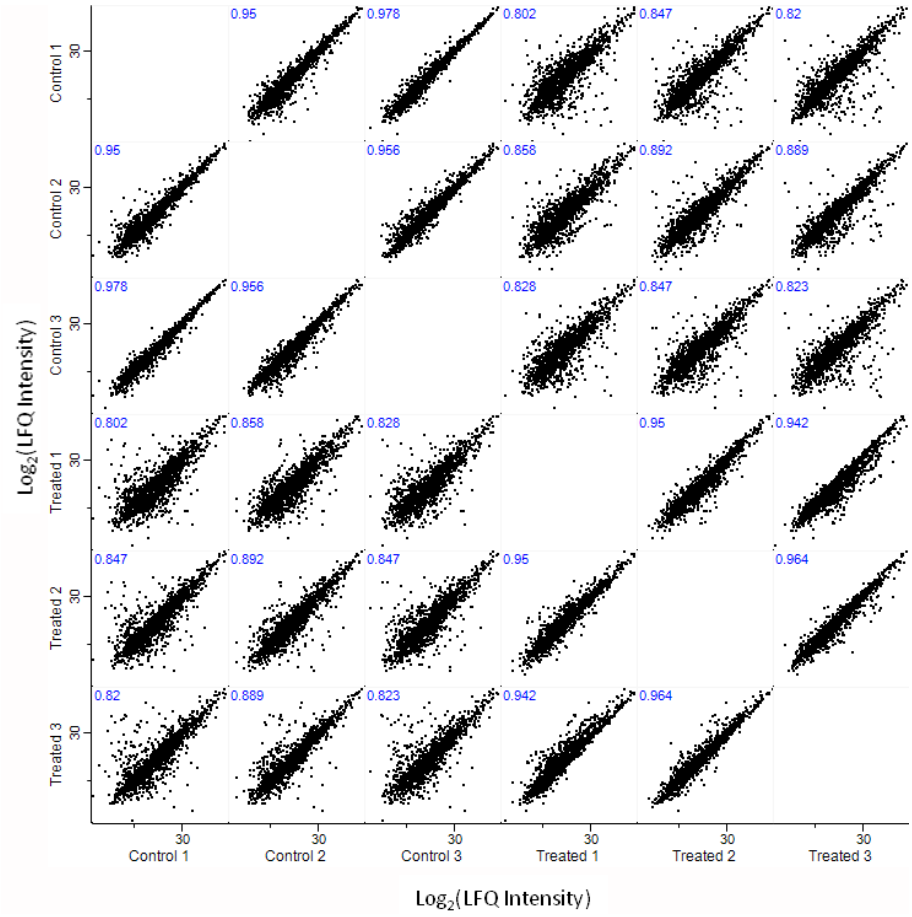
Supplementary Table S2. Data on proteins whose relative abundance was affected by 10 μg/ml PgAFP in *A. flavus* reaching over 1.5 fold change in 2D-PAGE.

Protein name	*p*- value	Fold Change	% coverage	Unique peptides	Score	tMr (Da)	Protein accesion (GI)	Gene
Enolase/allergen Asp F 22	0.00003141	↑3.5	15	4	177	47434	238488036	AFLA_037480
Molecular chaperone and allergen Mod-E/Hsp90/Hsp1	0.000003077	↑3.3	19	10	491	79640	238503321	AFLA_006960
Poly(A)+ RNA transport protein (UbaA), putative	0.001	↑2.3	14	8	340	115238	238488611	AFLA_015230
60S acidic ribosomal protein P0	0.0005509	↑2.2	40	7	382	33420	238486572	AFLA_030140
Translation elongation factor EF-2 subunit, putative	0.0001213	↑1.9	12	8	501	94681	238496883	AFLA_136640
Hsp70 chaperone (HscA), putative	0.004	↑1.7	9	3	178	96833	238508549	AFLA_012200
Hsp70 chaperone (HscA), putative	0.005	↑1.7	19	12	521	96833	238508549	AFLA_012200
Mitochondrial-processing peptidase subunit beta	0.0008611	↑1.7	31	13	866	53195	238488967	AFLA_017010
Cys-Gly metallodipeptidase dug1	0.002	↑1.7	26	8	395	53164	238506124	AFLA_103940
Glutathione synthetase	0.003	↑1.6	13	3	134	57079	238494330	AFLA_056570
Pyruvate decarboxylase	0.005	↑1.6	65	22	1260	63457	238486858	AFLA_031570
Phosphoglucomutase	0.006	↑1.6	8	4	237	62379	238497666	AFLA_065080
Conserved hypothetical protein	0.003	↑1.5	7	3	148	59673	238489765	AFLA_021000
L-xylulose reductase	0.0001245	↓3.6	16	3	199	31595	238505028	AFLA_098700
Conserved hypothetical protein	0.0002845	↓2.4	5	2	109	59673	238489765	AFLA_021000
Actin Act1	0.000061	↓2.2	39	11	562	41910	238494062	AFLA_055230
Septin AspA, putative	0.0003508	↓2	8	2	118	43393	238499547	AFLA_091880
Short-chain dehydrogenase, putative	0.001	↓2	37	7	322	32620	238495010	AFLA_059970
Metallopeptidase MepB	0.005	↓1.9	12	4	167	81812	238482735	AFLA_076890
Pyruvate carboxylase	0.006	↓1.9	3	4	190	131917	238491688	AFLA_112120
Elongation factor 3	0.045	↓1.8	23	16	857	118573	238482677	AFLA_076600
Acetate--CoA ligase	0.006	↓1.7	6	3	98	79217	238485958	AFLA_027070
Aspartyl-tRNA synthetase, cytoplasmic	0.008	↓1.7	17	6	349	62180	238496255	AFLA_133490
Pyruvate carboxylase	0.036	↓1.7	3	3	143	131917	238491688	AFLA_112120
Pyruvate carboxylase	0.032	↓1.7	9	7	313	131917	238491688	AFLA_112120
Autophagic serine protease Alp2	0.021	↓1.6	8	2	104	52539	238505092	AFLA_099020

Supplementary Table S3: Summary of Pearson correlation values for label-free quantitative analysis of *A. flavus* response to PgAFP treatment, as displayed in supplementary Fig. S1.

Pearson Correlation Values	**Control[1]**	**Treated[2]**	**Control v Treated[3]**
Number of values	3	3	9
Mean	0.9613	0.952	0.8451
Std. Deviation	0.01474	0.01114	0.03076
Std. Error	0.008511	0.006429	0.01025

[1]Each biological replicate from the control group, cross-compared. [2]Each biological replicate from the PgAFP treated group, cross-compared. [3]Each biological replicate from the PgAFP treated group compared to each biological replicate from the control group.



Supplementary Fig. S1: Multi-scatter plot demonstrating correlation between all samples included in LFQ proteomics analyses. Blue values included in each box indicate respective Pearson correlation values.

IV.4. Estudio del mecanismo de resistencia frente a PgAFP en mohos

Increased chitin biosynthesis contributes to the resistance of Penicillium polonicum *against the antifungal protein PgAFP*

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APPLIED MICROBIAL AND CELL PHYSIOLOGY

Increased chitin biosynthesis contributes to the resistance of *Penicillium polonicum* against the antifungal protein PgAFP

Josué Delgado[1] · **Rebecca A. Owens**[2] · **Sean Doyle**[2] · **Miguel A. Asensio**[1] · **Félix Núñez**[1]

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Abstract Antifungal proteins from molds have been proposed as a valuable tool against unwanted molds, but the resistance of some fungi limits their use. Resistance to antimicrobial peptides has been suggested to be due to lack of interaction with the mold or to a successful response. The antifungal protein PgAFP produced by *Penicillium chrysogenum* inhibits the growth of various ascomycetes, but not *Penicillium polonicum*. To study the basis for resistance to this antifungal protein, localization of PgAFP and metabolic, structural, and morphological changes were investigated in *P. polonicum*. PgAFP bound the outer layer of *P. polonicum* but not regenerated chitin, suggesting an interaction with specific molecules. Comparative two-dimensional gel electrophoresis (2D-PAGE) and comparative quantitative proteomics revealed changes in the relative abundance of several proteins from ribosome, spliceosome, metabolic, and biosynthesis of secondary metabolite pathways. The proteome changes and an altered permeability reveal an active reaction of *P. polonicum* to PgAFP. The successful response of the resistant mold seems to be based on the higher abundance of protein Rho GTPase Rho1 that would lead to the increased chitin deposition via cell wall integrity (CWI) signaling pathway. Thus, combined treatment with chitinases could provide a complementary means to combat resistance to antifungal proteins.

Keywords Antifungal proteins · Proteomics · Resistance · *Penicillium polonicum* · Chitin · Cell wall integrity pathway

Introduction

The antifungal protein PgAFP produced by the strain *Penicillium chrysogenum* CECT 20922 (formerly RP42C) is within a group of small, highly basic and low molecular mass proteins (Rodríguez-Martín et al. 2010). PgAFP inhibits various pathogenic and spoilage ascomycetes of interest in foods, including strains of various *Aspergillus* spp., such as *A. carbonarius*, *A. flavus*, *A. ochraceus*, *A. fumigatus*, and *A. tubingensis*, as well as *Penicillium* spp., such as *P. commune*, *P. restrictum*, *P. nalgiovense*, and *P. chrysogenum* (Delgado et al. 2015a). However, *Penicillium polonicum* and the PgAFP-producer strain of *P. chrysogenum* were not inhibited by PgAFP.

Other antifungal proteins produced by ascomycetes are PAF from *P. chrysogenum* Q176 (Marx et al. 1995), Pc-Arctin from *P. chrysogenum* A096 (Chen et al. 2013), BP from *Penicillium brevicompactum* (Seibold et al. 2011), AFP and AFP_{NN5353} from *Aspergillus giganteus* (Nakaya et al. 1990; Binder et al. 2011), Anafp from *Aspergillus niger* (Gun Lee et al. 1999), AcAFP and AcAMP from *Aspergillus clavatus* (Skouri-Gargouri and Gargouri 2008; Hajji et al. 2010), FPAP from *Fusarium polyphialidicum* (Galgóczy et al. 2013b), and NFAP from *Neosartorya fischeri* (Kovács et al. 2011). Mechanisms of action of antifungal proteins from molds have been described as multifactorial, where membrane permeabilization, changes in actin distribution, chitin biosynthesis inhibition, destabilization of cell wall,

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✉ Miguel A. Asensio
masensio@unex.es

[1] Food Hygiene and Safety, Institute of Meat Products, University of Extremadura, Cáceres, Spain

[2] Department of Biology, Maynooth University, Maynooth, Co., Kildare, Ireland

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and oxidative stress lead to apoptosis (Leiter et al. 2005; Moreno et al. 2006; Hagen et al. 2007; Binder et al. 2010; Virágh et al. 2015; Delgado et al. 2015b). AFP binds chitin, inhibits chitin biosynthesis, permeabilizes the cell membrane, and penetrates into the cell and binds nucleic acids (Liu et al. 2002; Moreno et al. 2006; Hagen et al. 2007), and AcAFP also binds chitin altering cell wall (Skouri-Gargouri et al. 2009), whereas PAF, NFAP, and PgAFP lead to apoptosis mediated by G-protein signaling (Binder et al. 2010, 2015; Virágh et al. 2015; Delgado et al. 2015b). Both PAF and NFAP activate the cAMP/protein kinase A pathway via G-protein signaling (Leiter et al. 2005; Virágh et al. 2015) and PgAFP provoked a lower amount G-protein subunit β CpcB (Delgado et al. 2015b).

However, the defensive strategies of resistant molds are poorly described. The lack of electrostatic affinity or receptors in cell surfaces has been suggested as the cause of the resistance to antimicrobial peptides (Yeaman and Yount 2003). PgAFP does not bind to the producer strain *P. chrysogenum* CECT 20922 that withstands at least 312 μg/ml (Delgado et al. 2015a, b). The lack of interaction between antifungal proteins and mold surface results in the absence of major metabolic responses in the resistant fungi. Another successful strategy of resistant fungi to counteract AFP is chitin synthesis stimulation (Ouedraogo et al. 2011). The latter strategy implies interaction with the resistant fungus and active metabolic response to the antifungal protein. Thus, studying the mechanisms involved in the resistance requires in-depth investigation of the metabolic response of resistant fungi to antifungal proteins.

Comparative proteomic analysis is a powerful tool to study metabolic changes at the molecular level (Kim et al. 2007). Two-dimensional gel electrophoresis (2D-PAGE) has the ability to separate complete proteins including those with post-translational modifications, but only a small percentage of the whole proteome is revealed (Görg et al. 2009). On the other hand, comparative quantitative proteomics is able to identify proteins not detectable by 2D-PAGE. These two techniques have been used to complementarily evaluate the effect of PgAFP on the proteins involved in signaling pathways and selecting adequate tests to study the metabolic response in molds (Delgado et al. 2015b). In addition, localization of the antifungal protein in non-sensitive molds can give valuable information on the possible interaction at the surface or inside the cell. Given that antifungal proteins provoke oxidative stress leading to apoptosis in sensitive mold, knowing the extent of these two phenomena in resistant molds would contribute to clarify the defense mechanism.

To study the effect of PgAFP on resistant molds, *P. polonicum* was chosen because it was the only resistant ascomycete known, apart from the PgAFP-producer *P. crhysogenum* CECT 20922 (Delgado et al. 2015a). *A. niger* has been used as sensitive control with various antifungal proteins (Kaiserer et al. 2003; Hagen et al. 2007; Kovács et al. 2011). *A. tubingensis* CECT 20932, formerly *A. niger* An261, has been used in the present work as sensitive control because it is the closest species to *A. niger* known to be sensitive to PgAFP (Delgado et al. 2015a).

The aim of this work was to investigate the effect of PgAFP on the proteome profile and selected characteristics to disclose the resistance response of *P. polonicum*. Localization of PgAFP was studied for a better understanding of the interaction with *P. polonicum*. This knowledge would allow designing new strategies to maximize the inhibition effect and spectra of PgAFP in molds.

Material and methods

Strains

In vitro tests were carried out with three molds isolated from dry-cured ham available from the Spanish Type Culture Collection (CECT, Valencia, Spain): *P. chrysogenum* CECT 20922, *P. polonicum* CECT 20933, and *A. tubingensis* CECT 20932.

Purification of PgAFP

PgAFP was obtained from *P. chrysogenum* CECT 20922 grown in potato dextrose broth (PDB, Scharlab, Barcelona, Spain) pH 4.5, at 25 °C for 21 days, as described previously (Acosta et al. 2009). To get cell-free medium, mycelium was removed by filtering through Miracloth (Calbiochem, Darmstadt, Germany) and the culture medium was filtered through a nitrocellulose 0.22 μm pore size (Sartorius, Goettingen, Germany). Cell-free media were applied to an ÄKTA FPLC with a cationic exchange column HiTrap SP HP (Amersham Biosciences, Uppsala, Sweden) with 20 mM sodium acetate, pH 4.5. Adsorbed proteins were eluted with 20 mM sodium acetate buffer (pH 4.5) containing 1 M NaCl and detected at 214 nm. The fraction containing PgAFP protein was then gel filtered on a HiLoad 26/60 Superdex 75 column for FPLC (Amersham Biosciences, Uppsala, Sweden) using 50 mM sodium phosphate buffer, pH 7 containing 0.15 M NaCl as elution buffer. PgAFP concentration in a pooled stock solution was measured by Lowry method (Lowry et al. 1951), sterilized through 0.22 μm acetate cellulose filters (Fisher Scientific), and stored at −20 °C until use.

Effect of PgAFP on mold growth

As a preliminary test, to confirm the known effect of PgAFP on growth of both sensitive and resistant molds in malt extract broth (Delgado et al. 2015a), *P. polonicum* and *A. tubingensis*

were grown in PDB treated with PgAFP in the whole range of concentrations used in this work (0 to 75 μg/ml) for 96 h.

Proteomics

To obtain the protein extracts, *P. polonicum* CECT 20933 was cultured in triplicate in 50 ml of PDB, at 25 °C with continuous shaking at 200 rpm in either presence (10 μg/ml) or absence of PgAFP. Mycelia were harvested, filtered, washed, and lysed as previously described (Carberry et al. 2006). Mycelial lysates were centrifuged to remove cell debris and the subsequent supernatant precipitated with TCA/acetone (Carpentier et al. 2005). The following two proteomic analyses were carried out from these precipitated lysates, similar to the procedure described by Delgado et al. (2015b).

Two-dimensional electrophoresis For protein separation by 2D-PAGE, resuspended extracts containing 250 μg of protein were loaded onto Immobiline Dry strips (IPG strip; Amersham Biosciences) in the pH range 4–7, followed by electrofocusing and electrophoresis as described previously (Carberry et al. 2006). Gels obtained from 3 biological replicates and 2 technical replicates per treatment were stained and analyzed using Progenesis™ SameSpot software (TotalLab, Newcastle, UK) as previously described (O'Keeffe et al. 2013; Collins et al. 2013; Owens et al. 2014). Spot intensities were normalized in Progenesis SameSpots software (Delgado et al. 2015b). Protein spots showing differences ($p < 0.05$, fold change ≥1.5) were excised, destained, and in-gel trypsin digested (Shevchenko et al. 2007). Then, samples were sonicated and the digested supernatant was dried, resuspended in 0.1 % formic acid, and filtered through 0.22 μm cellulose spin-filters according to Delgado et al. (2015b).

The samples were loaded onto a Zorbax 300 SB C-18 Nano-HPLC Chip and analyzed by a 6340 Model Ion Trap LC-Mass Spectrometer (Agilent Technologies, Dublin, Ireland) using electrospray ionization. The eluted peptides were ionized and analyzed by mass spectrometry. MS^n analysis was carried out on the three most abundant peptide precursor ions at each time point, as selected automatically by the mass spectrometer. MASCOT MS/MS Ion search, NCBI (National Centre for Biotechnology Information, www.ncbi.nlm.nih.gov/guide/proteins/) database and KEGG (Kioto Encyclopedia of Genes and Genome, www.genome.jp/kegg/) were used for protein identification and function, also BLAST® protein was employed to find orthologous proteins.

Label-free proteomics Proteins precipitated from three biological replicates were resuspended in 8 M urea, dithiothreitol reduced and iodoacetic acid alkylated (Collins et al. 2013), and trypsin digested. Digested samples were desalted using C18 ZipTips® (Millipore, Darmstadt, Germany). One microgram from each digest was analyzed via a Thermo Scientific Q-Exactive mass spectrometer coupled to a Dionex RSLCnano (Thermo Scientific, Waltham, MA, USA). Data was collected using a Top15 method for MS/MS scans (Dolan et al. 2014; O'Keeffe et al. 2014). Comparative proteome abundance and data analysis was performed using MaxQuant software (Version 1.3.0.5; www.maxquant.org/downloads.htm) (Cox and Mann 2008), with Andromeda used for database searching and Perseus (Version 1.4.1.3) used to organize the data, as per Delgado et al. (2015b). Data were searched against a *P. chrysogenum* database from Uniprot (www.uniprot.org; March 2014). In the absence of sequenced *P. polonicum* or any other species from Section *Fasciculata* (Houbraken and Samson 2011), *P. chrysogenum* also from subgenus *Penicillium* was chosen for comparison. Quantitative analysis was performed using a *t* test. Due to the high sensitivity and larger dynamic range of the gel-free proteomics analyses, only proteins with a *p* value <0.05 and fold change ≥2 were included in the quantitative results (Dolan et al. 2014; O'Keeffe et al. 2014). Qualitative analysis was also performed, to detect proteins that were found in at least 2 replicates of a particular sample, but undetectable in the comparison sample. Blast2GO analysis was utilized to further elucidate putative functions of proteins identified with abundance changes (Conesa et al. 2005).

Hyphal morphology

P. polonicum and *A. tubingensis* were grown on tubes containing 300 μl of PDB at 25 °C for 24 h in either the presence (75 μg/ml) or absence of PgAFP. Mycelia were collected by centrifugation and observed on a microscope Eclipse E200 equipped with a digital camera DS-Fi2 (Nikon, Tokyo, Japan).

Metabolic tests

To study the response to PgAFP, various metabolic tests were performed as described previously (Delgado et al. 2015b). For this, the resistant *P. polonicum* (c.a. 5×10^5 conidia per ml) was cultured in PDB at 25 °C for 24 h in static conditions with and without PgAFP. To rule out even potential weak effects, the highest concentration of 75 μg/ml PgAFP was used. Additionally, to study the effect on membrane permeability throughout a wide concentration range of PgAFP (i.e., 75, 37.5, 18.75, 9.38, 4.69, 2.34, 1.17, and 0 μg/ml) were assayed.

To test membrane permeability, cultures in microtiter plates were supplemented with SYTOX Green (Molecular Probes, Eugene, OR, USA) at a final concentration of 0.2 μM. The fluorescence emitted was measured at 10, 30, and 210 min.

Metabolic activity was assessed by FUN-1 staining. Grown mycelia was washed with 10 mM HEPES (pH 7.5) before staining with 100 μl FUN-1 (Molecular Probes, Eugene, OR, USA) for 30 min at 25 °C as described previously (Kaiserer et al. 2003). Stained hyphae were visualized and

photographed by fluorescence microscopy. Induction of reactive oxygen species (ROS) production was evaluated using 20 μM 2′, 7′ dichlorofluorescein diacetate (Molecular Probes, Eugene, OR, USA) according to Kaiserer et al. (2003) and observed by fluorescence microscopy.

Membrane integrity was assessed by the acridine orange/ethidium bromide (AO/EB) double staining. Hyphae were stained with 4 μg/ml of AO/EB (Sigma-Aldrich, St. Louis, MO, USA), incubated for 30 min, washed, and observed by fluorescence microscopy.

To distinguish between necrotic, late apoptotic, and viable cells, the Apoptosis Detection Kit (Sigma-Aldrich, St. Louis, MO, USA), composed by Annexin V-fluorescein isothiocyanate/propidium iodide (AnV-FITC/PI), was used according to manufacturer's instructions.

For each of these metabolic tests, the sensitive *A. tubingensis* was used as a positive control to confirm the effect of PgAFP in the various assays.

Chitin staining

Conidia of *P. polonicum* were inoculated on 10 ml PDB in a Petri dish containing a coverglass and incubated in the presence (75 μg/ml) and absence of PgAFP at 25 °C for 24 h. Mycelium was fixed, stained for 5 min with fluorescent brightener 28 (Sigma-Aldrich, St. Louis, MO, USA), and then washed, to visualize chitin (Harris et al. 1994) in a fluorescence microscope with an excitation wavelength of 387/11 nm.

Effect of PgAFP combined with chitinase on *P. polonicum* growth

Four different batches were prepared by pouring the reagents onto 15 ml potato dextrose agar plates made with PDB (Scharlab, Barcelona, Spain) and 20 g/l bacteriological agar (Scharlab, Barcelona) as follows: (a) 2.5 ml of 600 μg/ml PgAFP in phosphate elution buffer and 0.1 ml PBS, (b) 2.5 ml of phosphate elution buffer and 0.1 ml of ≥60 units/ml chitinase from *Streptomyces griseus* (Sigma-Aldrich, St. Louis, MO, USA) in PBS, (c) and 2.5 ml of 600 μg/ml PgAFP in phosphate elution buffer and 0.1 ml of ≥60 units/ml chitinase from *S. griseus* (Sigma-Aldrich, St. Louis, MO, USA) in PBS, and (d) 2.5 ml of phosphate elution buffer and 0.1 ml PBS as control samples. Every plate was surface three-point inoculated with 10 μl of a suspension containing 10^4 conidia and incubated at 25 °C for 168 h. The diameter of the colonies were measured every 24 h. To elucidate whether the combined treatment of PgAFP and chitinase has an additive or synergistic effect, the expected efficacy of this combination was determined by the Abbott formula and the interaction ratio as described by Moreno et al. (2003). Interaction ratios between 0.5 and 1.5 are considered to be additive interactions, and ratios over 1.5 are considered to be synergistic interactions.

Chitin-binding ability of PgAFP

Regenerated chitin was prepared as previously described (Souza et al. 2009), using chitin powder from crab shells (Sigma-Aldrich, St. Louis, MO, USA) added to concentrated HCl with vigorous stirring, filtered, and precipitated with ethanol 95 %. The precipitate was filtered and washed with water until neutral pH. Chitin-PgAFP binding assay was carried out as described by Liu et al. (2002). Briefly, three different amounts of PgAFP were mixed with 4 mg of regenerated chitin in a 0.5 ml 0.1 M Tris-HCl pH 7.4, 0.15 M NaCl buffer, incubated in ice for 1 h with stirring every 15 min. After incubation, samples were centrifuged and the quantity of protein contained in the supernatant was measured by the method described by Lowry (Lowry et al. 1951).

PgAFP localization

PgAFP was labeled by DareBio S.L. (Elche, Spain) as described previously (Delgado et al. 2015b). For this, 100 μl of 20 mM fluorescein isothiocyanate (FITC; Anaspec, Fremont, CA, USA) in dimethylsulfoxide was added to 4 ml of PgAFP (369 μg/ml) and left for 8 h at room temperature in the dark. Then, 100 μl of 0.8 M Tris-HCl pH 8 were added and dialyzed against PBS.

P. polonicum and *A. tubingensis* were grown in PDB in the presence of 20 μg/ml PgAFP-FITC for 24 h at 25 °C. Hyphae were washed twice with PBS and visualized by fluorescence microscopy with excitation wavelength of 482/35 nm.

Statistical analysis

Statistical analyses were performed with the IBM SPSS v.22 (www-03.ibm.com/software/products/es/spss-stats-standard). Growth inhibition and membrane permeability data were tested for normality (Kolmogorov–Smirnov with Lilliefors correction) and homoscedasticity (Levene's test). Given that these data were non-normally distributed, mean values were compared using non-parametric Kruskal–Wallis test. To compare treatments in pairs, Mann–Whitney *U* test was applied ($p < 0.05$).

Results

As expected, PgAFP showed no effect ($p > 0.05$) on *P. polonicum* grown in PDB in the whole range of

concentrations tested. *A. tubingensis* growth was affected ($p < 0.05$) from 4.7 μg/ml PgAFP at 48 h (data not shown).

Effect on proteome

2D-PAGE comparative proteomic analysis, in the presence or absence of 10 μg/ml of PgAFP, showed 37 spots with differences ($p < 0.05$) over 1.5-fold change in relative abundance between treated and untreated *P. polonicum*. The abundance in treated samples was higher (1.5–3-fold) in 9 spots and lower (1.5–4.1-fold) in the remaining 27 proteins, including 2 spots from separate isoforms (Table S1 in the Supplementary Material).

Comparative label-free quantitative proteomic analysis showed a total of 918 proteins from *P. polonicum*, 93 of them displayed altered relative abundance ($p < 0.05$) over twofold change with PgAFP treatment (Table S2 in the Supplementary Material). Thirty eight proteins were found in higher amounts (2–12.4-fold) in treated samples, 19 were only detected in treated samples, 25 were obtained in lower amounts (2–663-fold) following treatment, and 11 were only detected in non-treated samples (Table S2 in the Supplementary Material).

Eight of the nine proteins found in higher amounts in treated samples by 2D-PAGE were also detected by label-free proteomic analyses, with six of them showing similar increases in both methods (Tables S1 and S2 in the Supplementary Material). Also 26 of the 27 proteins found in lower relative abundance in treated *P. polonicum* by 2D-PAGE were also detected by label-free proteomics. However, only 16 of them were also detected at a lower relative abundance in the latter.

According to KEGG pathway analysis, most of the 57 proteins from label-free proteomics with higher relative abundance or only detected in treated *P. polonicum* were ribosomal and spliceosomal proteins (39 %), or involved in biosynthesis of secondary metabolites and metabolic pathways (14 %), such as pyruvate decarboxylase, pyrimidine biosynthesis, glycerol kinase, and asparagine synthetase (Table 1). The remaining proteins with higher relative abundance or only detected in treated samples were distributed across various pathways, such as Rho GTPase Rho1 involved in MAPK signaling pathway and, interestingly, glucosamine-6-phosphate *N*-acetyltransferase involved in chitin biosynthesis. Additionally, the antifungal protein PgAFP was detected in each of the triplicate treated sample, but not in any non-treated sample. Most of the proteins found in lower quantity or only detected in non-treated samples were related to biosynthesis of secondary metabolites and metabolic pathways (33 %), including phosphoglucomutase, and glucose 6-phosphate isomerase related to glycolysis and gluconeogenesis (Table 1). Only limited changes in stress-related proteins, including glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and heat shock proteins, were found in treated *P. polonicum* (Tables S1 and S2 in the Supplementary Material).

SYTOX green uptake

Upon PgAFP exposure up to 4.7 μg/ml, a 7 (±3.4) % increase (±standard error) in fluorescence was observed in *P. polonicum* ($p < 0.05$) at 210 min after SYTOX Green addition (Fig. 1). Fluorescence at intermediate PgAFP concentrations (9.37–18.75 μg/ml) did not differ from untreated control ($p > 0.05$), while concentrations higher than 18.75 μg/ml decreased ($p < 0.05$) permeability below the levels of untreated samples, being the fluorescence values up to 21 (±7.1) % lower at 210 min after SYTOX Green addition. On the other hand, the sensitive *A. tubingensis* showed a high increase of permeability ($p < 0.05$) at all PgAFP concentrations assayed (Fig. 1), reaching with 9.37–18.75 μg/ml over 110 (±9.8–15) % fluorescence higher than in the untreated control.

Hyphal morphology and FUN-1 staining

PgAFP exposure provoked no morphological change on either *P. polonicum* or the sensitive *A. tubingensis* (data not shown). To know whether PgAFP affects the metabolic activity, the viability was evaluated with FUN-1 using *A. tubingensis* as sensitive control. The FUN-1 metabolic staining showed red intravacuolar stains in both treated and untreated *P. polonicum* revealing no reduction in the metabolic activity (Fig. 2). Conversely, intravacuolar red stains were not observed in PgAFP-treated *A. tubingensis*, revealing a lower metabolic activity.

Chitin staining

To study the effect of PgAFP on chitin deposition on the resistant mold, the quantity of chitin was estimated by staining with fluorescent brightener 28. The observed fluorescence indicated a higher chitin deposition in the cell wall of treated than in non-treated *P. polonicum* (Fig. 3).

Effect of PgAFP-chitinase combined treatment on *P. polonicum* growth

For the whole incubation time, no statistically significant difference was found among growth of the untreated control and *P. polonicum* treated only with PgAFP (Fig. 4). Chitinase treatment reduced growth compared to control batch. Growth of *P. polonicum* treated with

Table 1 Selected proteins whose relative abundance was affected by PgAFP in *Penicillium polonicum* reaching over 2.0-fold change in label-free proteomics (LFP) analysis or 1.5-fold change in 2D-PAGE. Data are given according to four groups of metabolic pathways

Proteins involved in pathways	Fold change	Detection method
Ribosomal and spliceosomal proteins		
Pc12g05940 40s ribosomal protein s13	T	LFP
Pc13g01870 60s ribosomal protein l16	T	LFP
Pc16g04770 formin binding protein	T	LFP
Pc20g10480 small nuclear ribonucleoprotein	T	LFP
Pc22g08360 pre-mrna branch site protein p14	T	LFP
Pc20g00680 60s ribosomal protein l23	+11.16	LFP
Pc20g13260 ribosomal protein l14	+6.32	LFP
Pc13g02890 60s ribosomal protein l27	+5.32	LFP
Pc13g05540 60s ribosomal protein l18	+4.17	LFP
Pc18g04110 60s ribosomal protein l34	+4.05	LFP
Pc22g02060 60s ribosomal protein l8	+3.88	LFP
Pc21g16520 60s ribosomal protein l4	+3.83	LFP
Pc16g14740 40s ribosomal protein s22	+3.21	LFP
Pc16g09160 60s ribosomal protein l15	+3.14	LFP
Pc22g00880 40s ribosomal protein s18	+2.73	LFP
Pc21g18200 60s ribosomal protein	+2.51	LFP
Pc16g12990 60s ribosomal protein l17	+2.47	LFP
Pc13g07190 60s ribosomal protein l11	+2.32	LFP
Pc13g05920 60s ribosomal protein l7	+2.21	LFP
Pc20g03340 60s ribosomal protein l33	+2.19	LFP
Pc13g06740 60s ribosomal protein l13	+2.06	LFP
Pc20g02900 40s ribosomal protein s4	+2.02	LFP
Biosynthesis of secondary metabolites and metabolic pathway		
Pc21g21940 bifunctional pyrimidine biosynthesis protein	T	LFP
Pc22g06070 glycerol kinase	T	LFP
Pc22g17940 asparagine synthetase	T	LFP
Pc22g23800 glucosamine 6-phosphate N-acetyl transferase[a]	T	LFP
Pc21g15760 glutamyl-trna synthetase	+12.44	LFP
Pc20g07710 sulfate adenylyltransferase	+6.9	LFP
Pc22g07020 nitrilase	+3.49	LFP
Pc18g01490 pyruvate decarboxylase	+2.01	LFP
Phosphoglucomutase	−2	2D-PAGE
Pc16g05080 adenosylhomocysteinase	−2	LFP
Pc12g05750 d-xylulose kinase	−2.31	LFP
Pc21g04710 phospho-2-dehydro-3-deoxyheptonate aldolase	−2.52	LFP
Pc22g19440 aspartate aminotransferase	−2.58	LFP
Pc21g03190 glycerate dehydrogenase	−2.66	LFP
Pc22g02810 methylmalonate-semialdehyde dehydrogenase	−3.05	LFP
Pc22g19730 glucose-6-phosphate isomerase	−3.49	LFP
Pc15g01900 putative oligo-glucosidase	−6.9	LFP
Pc15g01880 phosphatidylglycerol specific phospholipase	−633	LFP
Pc13g03600 thiamine biosynthetic bifunctional	NT	LFP
Pc14g00170 phosphatidylglycerol specific	NT	LFP
Pc22g24860 aldehyde dehydrogenase	NT	LFP
CWI pathway		
Pc22g23800 glucosamine-6-phosphate N-acetyl transferase[a]	NT	LFP
Pc14g01930 protein Rho gtpase rho1	+9.04	LFP
Pc21g11950 UDP-N-acetylglucosamine pyrophosphorylase	−2	2D-PAGE
UDP-glucose 4-epimerase	−1.5	2D-PAGE
Gamma-actin act	−1.6	2D-PAGE

T protein only detected in treated samples, *NT* protein only detected in non-treated samples

[a] Protein involved in more than one pathway

combined PgAFP and chitinase was the lowest ($p < 0.05$). The interaction ratios between these antifungal compounds at 96 and 120 h incubation were 1.93 and 1.70, respectively. Thus, the slower growth in

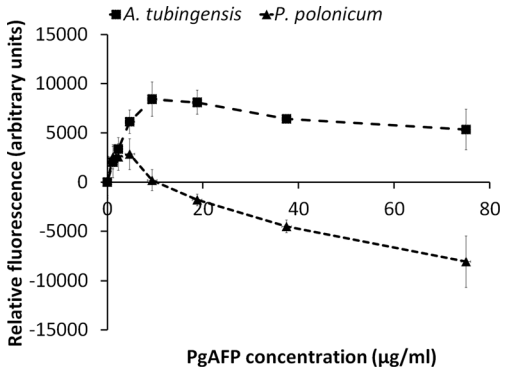

Fig. 1 SYTOX Green uptake with different concentrations of PgAFP on *P. polonicum* and *A. tubingensis* at 24 h (*bars* represent standard deviation of the mean)

the combined treatment is attributed to a synergistic effect of chitinase and PgAFP.

PgAFP localization

PgAFP localization was investigated in *P. polonicum* by incubation with FITC-labeled PgAFP. *P. polonicum* showed green fluorescence only bound to the outer layer (Fig. 5). However, the labeled protein was found both inside the hyphae and bound to the outer layer in *A. tubingensis*, revealing that PgAFP had entered *A. tubingensis*.

Chitin-PgAFP binding assay

Given that PgAFP was located at the outer layer of *P. polonicum*, a chitin-binding assay was performed. When PgAFP was added to a solution of regenerated chitin, over 91 % of the antifungal protein was recovered from the supernatant after incubation, even at the lowest concentration tested (146 µg/ml). Thus, PgAFP does not specifically bind to regenerated chitin.

Effect on oxidative status and viability

To test the influence of PgAFP on ROS production, staining with 2′, 7′ dichlorofluorescein diacetate was used. Both treated and untreated *P. polonicum* showed similar levels of emitted fluorescence (data not shown), revealing that PgAFP does not increase ROS in the resistant *P. polonicum*. The effect of PgAFP on membrane integrity was evaluated by AO/EB double staining. EB was taken only by PgAFP-treated *A. tubingensis*, showing orange hyphae, while non-treated *A. tubingensis* and both treated and non-treated *P. polonicum* only showed green hyphae due to AO uptake (Fig. 6). These results reveal that *P. polonicum* membrane was not compromised by PgAFP, which is the opposite to *A. tubingensis*. The evaluation of apoptosis or necrosis confirmed the above-reported effects on viability. *A. tubingensis* treated hyphae showed orange color as a consequence of AnV-FITC and PI staining, meaning a necrotic stage. Non-treated *A. tubingensis* and both treated and untreated *P. polonicum* were not dyed, showing no sign of apoptosis or necrosis (Fig. 7).

Discussion

Both proteomic methods used in this work revealed differences in the relative abundance of proteins after treatment of *P. polonicum* with PgAFP (Tables S1 and S2 in the Supplementary Material). Discrepancies were detected in the fold change estimated by each method. Such discrepancies can be explained by the fact that 2D-PAGE compares one

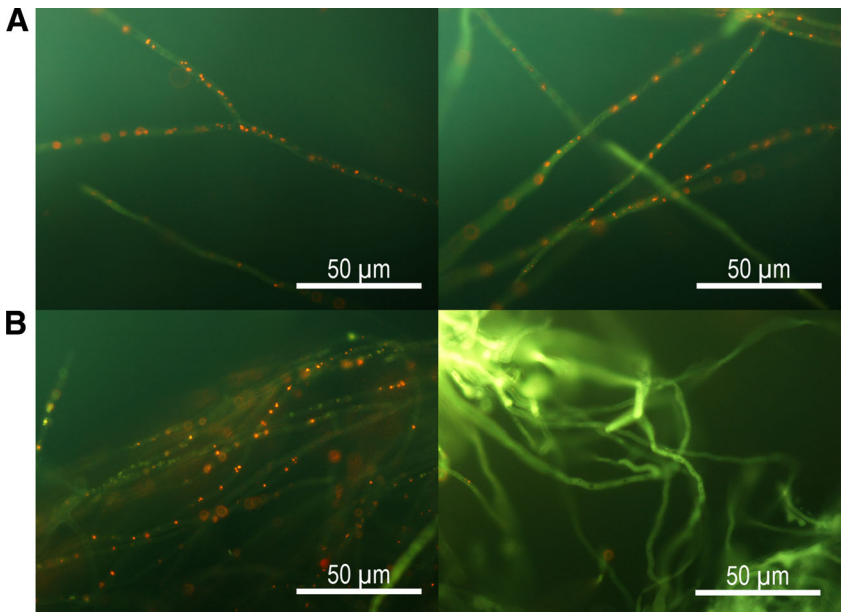

Fig. 2 Metabolic activity of *P. polonicum* (panel A) and *A. tubingensis* (panel B) tested with FUN-1 staining. Non-treated hyphae (*left*) showed intravacuolar activity as red spots. Hyphae treated with 75 µg/ml PgAFP for 24 h (*right*) showed intravacuolar activity in *P. polonicum* but very low metabolic activity in *A. tubingensis*

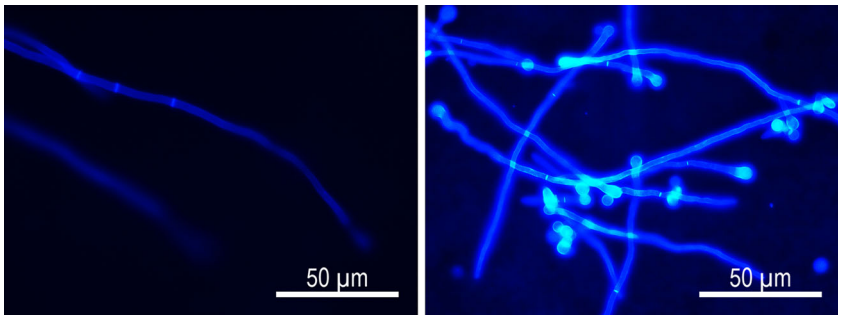

Fig. 3 Chitin distribution on *P. polonicum* stained with fluorescent brightener 28. *Left*, non-treated hyphae; *right*, hyphae treated with 75 μg/ml PgAFP for 24 h

isoform of a protein at a time, whereas label-free proteomics combines every isoform together and gives the final total abundance of that protein (Delgado et al. 2015b). Therefore, changes in the relative quantity of each isoform could be detected using 2D-PAGE, while in the label-free proteomics only a measure of total abundance of all isoforms of a given protein is carried out.

Label-free proteomics showed an increased abundance of 22 proteins related to ribosomes and spliceosomes in PgAFP-treated *P. polonicum*, according to KEGG. However, only two ribosomal proteins were found in higher amount by 2D-PAGE analysis. This fact can be explained by the narrow range of pH chosen for 2D-PAGE analysis (Görg et al. 2009). In particular, the analysis carried out is suitable for proteins with pI between 4 and 7, while proteins involved in ribosome structure or function are generally out of this range (Görg et al. 2004). Therefore, the combinatorial deployment of proteomic tools used in this study works complementarily to obtain further information about the effect of PgAFP on the proteome.

The higher relative abundance of proteins from ribosomal and spliceosomal pathways in PgAFP-treated *P. polonicum* could be regarded as a response of the mold to counteract the protein's antifungal activity. A higher relative abundance

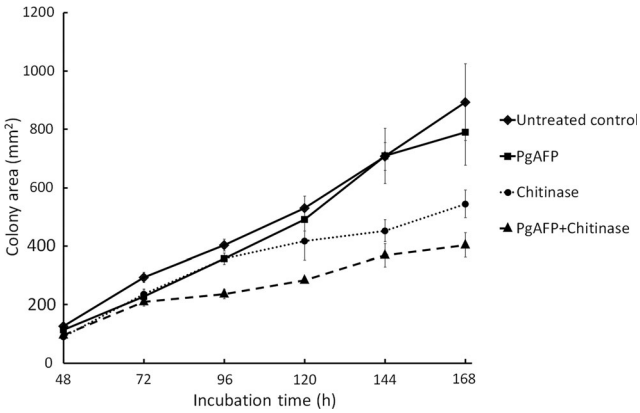

Fig. 4 Effect of PgAFP and chitinase combined treatment on *P. polonicum* growth. Untreated control: added with 2.5 ml of phosphate elution buffer and 100 μl PBS; PgAFP: added with 2.5 ml of 600 μg/ml PgAFP in phosphate elution buffer and 100 μl PBS. Chitinase: added with 2.5 ml of phosphate elution buffer and 100 μl of ≥60 units/ml chitinase from *Streptomyces griseus*; PgAFP + Chitinase: added with 2.5 ml of 600 μg/ml PgAFP in phosphate elution buffer and 100 μl PBS

of a substantial number of ribosomal and spliceosomal proteins has also been described in a recent work on the effect of PgAFP on the sensitive *A. flavus* (Delgado et al. 2015b). Twelve of the 22 proteins from this group that increased with PgAFP in *P. polonicum* also increased in *A. flavus*. Thus, the increase in proteins from ribosomal and spliceosomal pathways solely would not explain the resistance mechanism in *P. polonicum*.

The changes observed in the proteins related to metabolic pathways and biosynthesis of secondary metabolites were heterogeneous, with 8 proteins increasing and 12 decreasing in PgAFP-treated *P. polonicum* (Table 1). From these proteins, only pyruvate decarboxylase, aldehyde dehydrogenase, and phosphatidylglycerol-specific phospholipase showed similar changes in PgAFP-treated *A. flavus* (Delgado et al. 2015b). However, these enzymes are scattered among various metabolic routes, including glycolysis gluconeogenesis, purine metabolism, and aminoacyl-tRNA biosynthesis, making it unlikely that any of them explain the ability of *P. polonicum* to withstand PgAFP.

All the above changes in the abundance of the metabolic-related proteins did not entail dramatic changes in the metabolic activity, which in turn is consistent with the resistance of *P. polonicum* to PgAFP. The abundance of intracellular red spots in FUN-1 staining (Fig. 2) revealed that the metabolic activity in *P. polonicum* remained substantially unaffected by PgAFP, whereas it was greatly reduced in the sensitive *A. tubingensis* used as a control (Fig. 2), as well as in PgAFP-treated *A. flavus* (Delgado et al. 2015b).

Other effects reported for antifungal proteins, including PAF, NFAP, and PgAFP, are increased ROS levels leading to programmed cell death in sensitive molds (Leiter et al. 2005; Galgóczy et al. 2013a; Delgado et al. 2015b). Increased ROS levels have been linked to higher relative abundance of proteins involved in the glutathione pathway and heat shock proteins in PgAFP-treated *A. flavus* (Delgado et al. 2015b). The limited changes in such stress-related proteins in treated *P. polonicum* do not reveal a strong response to oxidative stress. In addition, none of the negative effects related to oxidative stress was observed in PgAFP-treated *P. polonicum*, including increased ROS levels, loss of cell membrane integrity, and necrotic signs.

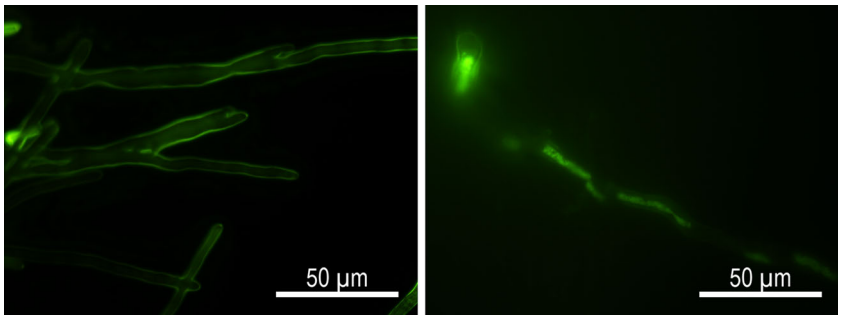

Fig. 5 PgAFP localization in *P. polonicum* (*left*) and *A. tubingensis* (*right*) treated with 20 μg/ml FITC-labeled PgAFP for 24 h. PgAFP was found solely bound to the outer layer in *P. polonicum* but mainly inside *A. tubingensis*

All the changes in the proteome discussed so far reveal that PgAFP interacts with the non-sensitive *P. polonicum*, but do not seem to explain the successful defense response. As discussed later, proteins from the cell wall integrity (CWI) pathway seem to be involved in the successful defense response.

Membrane permeabilization is a main effect described for other antifungal proteins (Thevissen et al. 1999; Hagen et al. 2007). Increased permeability also contributes to PgAFP inhibition on *A. flavus* (Delgado et al. 2015b). Similarly, the permeability of the sensitive *A. tubingensis* to SYTOX Green increased at all PgAFP concentrations tested (Fig. 1). However, membrane permeabilization in *P. polonicum* exhibited a two-step pattern: first increasing slowly at low PgAFP concentrations, then slowly declining even below the level of untreated controls with the two highest concentrations tested (Fig. 1). A similar two-step pattern in membrane permeabilization was also described for *Neurospora crassa* treated with plant defensins (Thevissen et al. 1999). The lower permeability at the highest concentrations of defensins has been explained by the apparent dependency of permeabilization on membrane polarization. The higher permeability of fungal membranes treated with defensins causes depolarization, which may ultimately decrease membrane permeability (Thevissen et al. 1996, 1999). The decline in *P. polonicum* membrane permeability at high PgAFP concentrations might be partially explained by membrane depolarization. As discussed later, other changes in membrane and cell wall can contribute to reach permeability levels well below that in untreated controls.

Growth inhibition by AFP, PAF, and PgAFP has been related to the ability to interact with specific molecules or anionic phospholipids in the cell wall and/or plasma membrane (Lacadena et al. 1998; Theis et al. 2003; Marx et al. 2008; Delgado et al. 2015b). Similarly, NFAP might bind to a G-protein-coupled receptor in a sensitive mold (Virágh et al. 2015) and AFP_{NN5353} does not bind to insensitive *Mucor circinelloides* (Binder et al. 2011). Interestingly, PgAFP was located at the outer layer in the resistant *P. polonicum* (Fig. 5). This binding may be due just to adherence to chitin or to specific receptors, but PgAFP did not bind to regenerated chitin in vitro. Given that PgAFP was not internalized by the resistant mold, no internal receptor can be detected. In addition, the proteome changes observed in PgAFP-treated *P. polonicum* can only be due to transduction signals derived from the interaction with outer layer receptors. Therefore, PgAFP may interact with specific molecules in the outer layer of *P. polonicum*, similarly to PAF (Marx et al. 2008; Batta et al. 2009). As a consequence, PgAFP resistance could be related with the ability of *P. polonicum* to produce structural changes that prevent the interaction with the specific receptors or the negatively charged phospholipids.

The fungal cell wall acts as an initial barrier in contact with hostile environments (Latgé 2007). The main components of the cell wall that may act as a barrier against antifungal proteins are polysaccharides, including glucans, glucomannans,

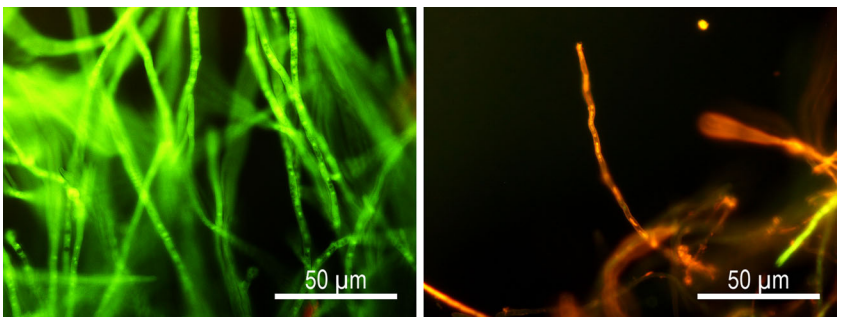

Fig. 6 Effect of 75 μg/ml PgAFP on membrane integrity of *P. polonicum* (*left*) and *A. tubingensis* (*right*) evaluated with vital acridine orange (*AO*)/ethidium bromide (*EB*) staining. *P. polonicum* hyphae showed intense green color due to only AO penetration through non-compromised membrane. *A. tubingensis* hyphae showed intense orange color due to both AO and EB penetration through compromised cell membrane

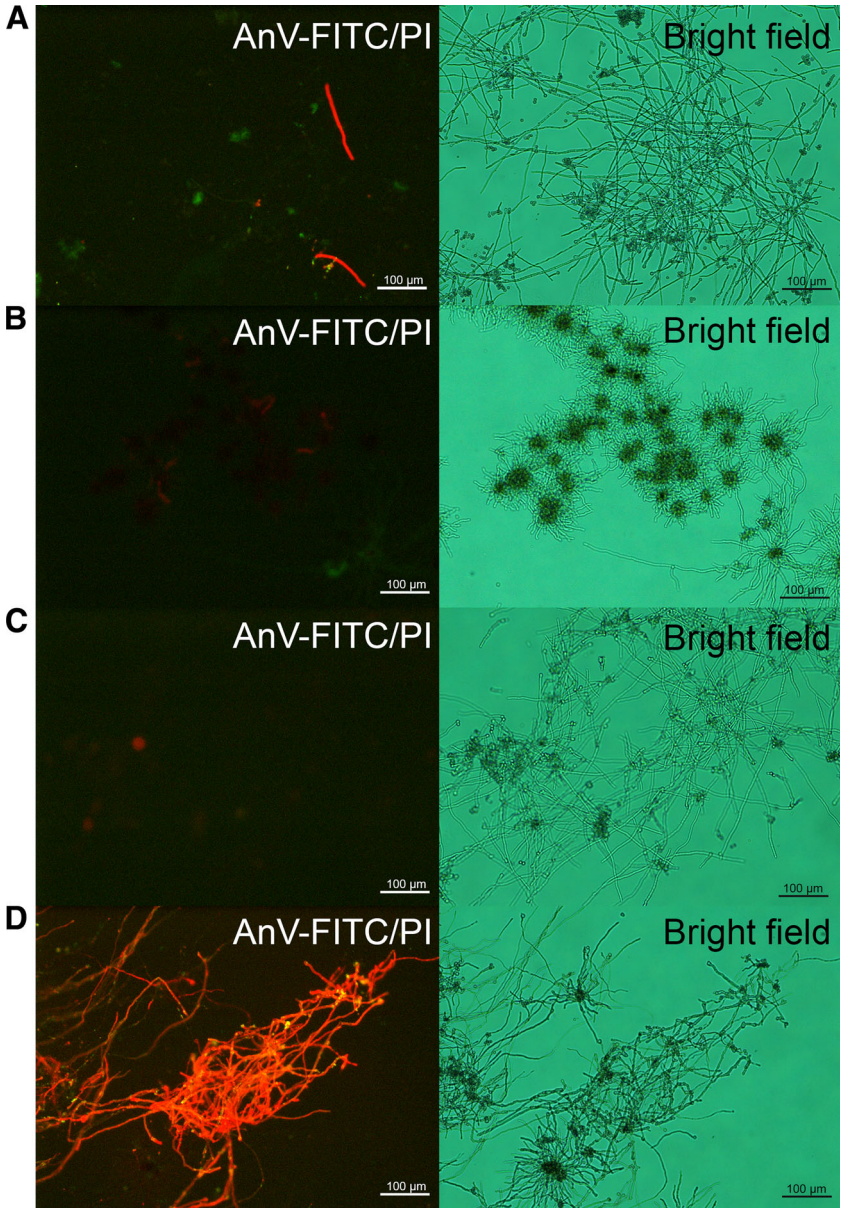

Fig. 7 Effect of 75 μg/ml PgAFP on *P. polonicum* and *A. tubingensis* hyphae viability evaluated with apoptosis detection kit at 24 h of incubation. **a** Non-treated *P. polonicum.* **b** PgAFP-treated *P. polonicum*. **c** Non-treated *A. tubingensis*. **d** PgAFP-treated *A. tubingensis*. *Left*, annexin V/FITC-propidium iodide (An/FITC-PI) staining. *Right*, the corresponding bright field view. No intense green or orange color due to apoptosis or necrosis was observed in PgAFP-treated *P. polonicum*. Only PgAFP-treated *A. tubingensis* showed intense orange color due to necrosis

and chitin. A lower chitin content in the fungal cell wall has been related to a higher permeability (Mellado et al. 2003; Rementeria et al. 2005), suggesting a barrier role of chitin. The higher amount of chitin observed in the cell wall of *P. polonicum* treated with the highest PgAFP concentration (Fig. 3) can be responsible for the lower permeability observed, being a key factor in the successful response to this antifungal protein. Chitin synthesis is also stimulated by AFP in resistant fungi (Ouedraogo et al. 2011), but not by AFP, PAF, and PgAFP in sensitive molds (Hagen et al. 2007; Binder et al. 2010; Delgado et al. 2015b). In addition, PAF and NFAP provoke delocalized chitin deposition at the hyphal tips (Binder et al. 2010; Virágh et al. 2015). Therefore, the altered chitin deposition can be related to sensitivity to antifungal proteins in contrast to our findings in *P. polonicum*.

To confirm if the increased chitin deposition itself is enough to explain the resistance to PgAFP, a joint treatment of PgAFP and chitinase was applied to *P. polonicum*. The slowest growth obtained with the combined treatment strongly infers that the increased chitin content plays a key role in the resistance of *P. polonicum* to PgAFP. Therefore, we propose that chitin cell wall reinforcement is responsible for the successful response of *P. polonicum*, due to a hampered interaction of PgAFP with specific receptors or the negatively charged phospholipids.

From the proteins involved in chitin biosynthesis, glucosamine-6-phosphate *N*-acetyltransferase was only found in treated *P. polonicum* (Table 1). The gene coding for this protein, as well as the gene encoding an α-1,3-glucan synthase, is upregulated in *A. niger* treated

with sublethal doses of caspofungin (Meyer et al. 2007). Given that an increase of glucan but not chitin synthesis results in an ineffective survival response (Hagen et al. 2007), the increase in glucosamine-6-phosphate *N*-acetyltransferase could be important for *P. polonicum* to counteract PgAFP. The increased chitin content can also be related with CWI signaling activation. The stress signals sensed by the receptor protein Wsc are transmitted to Rho1, which has been considered the master regulator of cell wall integrity signaling pathway in yeasts (Levin 2005). Then, Rho1 binds and activates Pkc (Nonaka et al. 1995; Kamada et al. 1996; Lodder et al. 1999), and the signals channeled through the Mpk signaling lead to activation of genes involved in cell wall synthesis (Igual et al. 1996; Jung and Levin 1999), resulting in an elevated chitin content (Munro et al. 2007). Rho1 and Pkc1 have been suggested as the only proteins of CWI pathway that could be involved in the survival response of AFP-resistant *Saccharomyces cerevisiae*, but its relevance has not been established (Ouedraogo et al. 2011).

In sensitive molds, chitin synthesis is not increased by antifungal proteins, as for *A. nidulans* treated with PAF (Binder et al. 2010) or *A. niger* treated with AFP (Hagen et al. 2007). The resistant *P. polonicum* showed an increased abundance of Rho1 and in chitin synthesis when treated with PgAFP (Table 1 and Fig. 3). Conversely, the sensitive *A. flavus* showed a lower relative abundance of Rho1 and a lower chitin deposition when treated with PgAFP (Delgado et al. 2015b). Therefore, it seems that the efficient response of CWI pathway activation by Rho1 could be a key role in the resistance to PgAFP, in contrast to the basal ineffective compensatory response of this pathway in sensitive molds.

In conclusion, the proteome changes and the altered permeability imply an active reaction of *P. polonicum* to PgAFP, where the increased chitin content can be related with a higher abundance of glucosamine-6-phosphate *N*-acetyltransferase and Rho1. Moreover, the combined treatment with chitinase could provide a complementary means to combat resistance to antifungal proteins.

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Compliance with ethical standards

Ethical statement This article does not contain any studies with human participants or animals performed by any of the authors.

Conflict of interest The authors declare that they have no competing interests.

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Supplementary Information

Increased chitin biosynthesis contributes to the resistance of *Penicillium polonicum* against the antifungal protein PgAFP.

Josué Delgado,[a] Rebecca A. Owens,[b] Sean Doyle,[b] Miguel A. Asensio[a] and Félix Núñez.[a]

[a] Food Hygiene and Safety, Institute of Meat Products, University of Extremadura, Cáceres, Spain.

[b] Department of Biology, Maynooth University, Maynooth, Co. Kildare, Ireland.

Corresponding author:
Miguel A. Asensio
masensio@unex.es, Tel.: +34 927 257124; Fax: +34 927 257110

Supplementary Table S1. Data on proteins whose relative abundance was affected by 10 μg/ml PgAFP in *P. polonicum* reaching over 1.5 fold change in 2D-PAGE.

Protein name	*p*- value	Fold Change	% coverage	Unique peptides	Score	tMr (Da)	Protein accesion (GI)	Gene
Hypothetical protein PDIG_30840	0.049	↑3	22	1	65	13620	255945719	Pc20g11410
40S ribosomal protein S12	0.032	↑3	29	2	138	16471	255942617	Pc18g02330
40S ribosomal protein S0	0.005	↑2.5	17	3	153	32517	255938175	Pc13g14510
Regulatory protein SUAPRGA1	0.007	↑2.1	22	3	241	32655	255944381	Pc20g04080
Hsp90 binding co-chaperone (Sba1), putative	0.011	↑2	14	2	123	23627	255953251	Pc21g03140
Histone H2B	0.040	↑1.8	18	1	78	15075	255945231	Pc20g08600
Peptidyl-prolyl cis-trans isomerase B	0.002	↑1.6	7	1	74	29893	255950084	Pc22g19060
Elongation factor 1-beta	0.001	↑1.5	19	3	173	25049	255936559	Pc13g08810
14-3-3 family protein ArtA, putative	0.041	↑1.5	16	4	204	29365	255942923	Pc18g03940
Translation elongation factor EF-2 subunit, putative	0.00003	↓4.1	20	13	621	94428	255933099	Pc12g12040
Mannitol-1-phosphate dehydrogenase	0.00003	↓3.2	14	5	264	42533	255950424	Pc22g20800
14-3-3 family protein ArtA, putative	0.004	↓2.8	42	6	492	29365	255942923	Pc18g03940
Carbamoyl-phosphate synthase, large subunit	0.006	↓2.3	5	4	215	128738	255950296	Pc22g20150
Pc15g00640	0.00091	↓2.3	22	8	446	52104	255939043	Pc15g00640
Glyceraldehyde-3-phosphate dehydrogenase	0.00051	↓2.2	4	1	137	36200	255955435	Pc21g14560
Succinate dehydrogenase subunit Sdh1, putative	0.004	↓2.1	4	2	93	71782	255944729	Pc20g06030
UDP-N-acetylglucosamine pyrophosphorylase	0.016	↓2	12	4	272	55800	255954947	Pc21g11950
Glutamine synthetase	0.015	↓2	21	6	278	41735	255947166	Pc22g03070
Glucokinase	0.003	↓2	7	3	92	54152	255950958	Pc22g23550
S-adenosylmethionine synthase	0.002	↓1.9	14	3	144	42211	255940042	Pc16g04380
Heat shock protein (Sti1), putative	0.005	↓1.9	18	10	465	62551	255955103	Pc21g12770
Aminopeptidase P, putative	0.005	↓1.9	9	6	241	65494	255949480	Pc22g15910
Acyl-CoA dehydrogenase, putative	0.003	↓1.8	14	6	256	47445	255941758	Pc16g13490
Heat shock protein	0.016	↓1.8	24	10	489	67033	255948526	Pc22g10220
Aconitate hydratase, mitochondrial	0.001	↓1.8	5	3	128	83969	255935445	Pc13g03110
Unnamed protein product	0.004	↓1.7	3	2	89	94428	255933099	Pc12g12040
Adenylylsulfate kinase AAA81521	0.00002	↓1.7	24	3	89	23642	255936451	Pc13g08270
6-phosphogluconate dehydrogenase, decarboxylating	0.003	↓1.6	32	10	606	54273	255932887	Pc12g10940
Formate dehydrogenase	0.008	↓1.6	15	5	269	50347	255931489	Pc12g04310
Sorbitol/xylulose reductase Sou1-like, putative	0.006	↓1.6	43	8	417	28712	255930855	Pc12g00830
Adenosylhomocysteinase	0.00049	↓1.6	31	12	621	49567	255940172	Pc16g05080
Hypothetical protein PDIG_65240	0.004	↓1.6	8	3	82	57162	255942351	Pc18g00980
Phosphoglucomutase PgmA	0.004	↓1.6	22	9	502	60417	255942431	Pc18g01390
Gamma-actin act-Penicillium chrysogenum	0.022	↓1.6	33	8	338	41958	255945763	Pc20g11630
Aldo/keto reductase, putative	0.003	↓1.6	20	4	217	38968	255956203	Pc21g18620
Aminopeptidase, putative	0.035	↓1.6	12	9	476	99407	255948598	Pc22g11170
UDP-glucose 4-epimerase	0.048	↓1.5	17	4	183	40587	255954639	Pc21g10370

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
25.3283	25.4701	25.4293	26.0296	25.8135	25.1901	8.55E-18	2.78E+08	2	2	23.7	13.748	25.5435	25.4092	25.6777	6	3	3	A7KAL9	A7KAL9	1	ATG8	Autophagy-related protein 8	Cvt vesicle membrane; autophagic vacuole membrane; autophagy; protein transport	Cytoplasmic vesicle › cvt vesicle membrane; Lipid-anchor. Cytoplasmic vesicle › autophagosome membrane; Lipid-anchor. Vacuole membrane; Lipid-anchor.
25.9359	25.958	25.7688	26.2537	26.4771	24.8464	2.72E-20	3.66E+08	5	5	14.7	48.681	25.8733	25.8876	25.8591	6	3	3	B6GVV5	B6GVV5	1	B6GVV5	Dipeptidase	dipeptidase activity; metal ion binding; metallopeptidase activity; proteolysis	
32.1486	32.344	32.1048	32.4583	32.8889	31.1788	0	2.91E+10	26	22	70.9	53.795	32.1872	32.1991	32.1753	6	3	3	B6GVW4; B6HST6	B6GVW4	2	B6GVW4	Pc06g00180 protein	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	
25.6197	26.1319	25.8611	25.6745	24.7594	26.4088	2.59E-26	3.3E+08	4	4	15.8	39.113	25.7425	25.8709	25.6142	6	3	3	B6GVY3	B6GVY3	1	B6GVY3	Pc06g00380 protein	dihydroorotase activity; pyrimidine nucleobase biosynthetic process	
ND*	ND	ND	23.6186	23.7295	ND	3.97E-09	1.07E+08	4	4	8.2	80.801	23.6741	ND	23.6741	2	0	2	B6GW13	B6GW13	1	B6GW13	Pc06g00700 protein	RNA binding; pseudouridine synthase activity; pseudouridine synthesis	
26.9533	27.0474	26.812	28.3298	28.2734	26.6942	4.51E-63	1.05E+09	11	11	12.2	107.93	27.3517	26.9376	27.7658	6	3	3	B6GW14	B6GW14	1	B6GW14	Pc06g00710 protein	ATP binding	
28.6422	28.9163	28.7053	29.3865	29.6388	28.6108	3.95E-214	3.04E+09	25	25	35.3	103.46	28.9833	28.7546	29.212	6	3	3	B6GW28	B6GW28	1	B6GW28	Pc06g00890 protein	ATP binding; nucleoside-triphosphatase activity	
29.5869	29.7026	29.4427	29.8201	29.9818	29.1409	1.49E-246	4.68E+09	5	5	40	14.254	29.6125	29.5774	29.6476	6	3	3	B6GW69	B6GW69	1	B6GW69	Pc06g01290 protein	nucleic acid binding; nucleotide binding	
27.7987	27.9304	27.6091	27.7059	27.7935	27.6857	5.05E-29	1.26E+09	4	4	17	24.185	27.7539	27.7794	27.7284	6	3	3	B6GWD4	B6GWD4	1	B6GWD4	Pc06g01640 protein		
28.0652	27.7069	28.1811	ND	ND	25.6953	9.80E-115	9E+08	5	5	27.3	37.381	27.4121	27.9844	25.6953	4	3	1	B6GWF0	B6GWF0	1	B6GWF0	Pc06g01800 protein	oxidoreductase activity; zinc ion binding	
27.7094	27.8295	27.5613	28.2131	28.4925	27.1509	6.00E-44	1.37E+09	5	5	25.8	14.323	27.8261	27.7001	27.9522	6	3	3	B6GWS1	B6GWS1	1	B6GWS1	Pc12g07280 protein	electron carrier activity; heme binding; iron ion binding; mitochondrion; oxidation-reduction process; respiratory chain	
27.1377	26.9309	27.1104	25.9282	26.2253	24.8245	2.78E-25	5.93E+08	5	5	46.2	17.636	26.3595	27.0597	25.6593	6	3	3	B6GWS6	B6GWS6	1	B6GWS6	Pc12g07330 protein	hydrolase activity	
32.5281	32.2987	32.464	32.0927	31.5499	31.461	0	2.73E+10	22	22	49.8	55.644	32.0657	32.4303	31.7012	6	3	3	B6GWT7	B6GWT7	1	B6GWT7	6-phosphogluconate dehydrogenase, decarboxylating	NADP binding; pentose-phosphate shunt; phosphogluconate dehydrogenase (decarboxylating) activity	
24.4966	ND	24.5435	ND	ND	23.9838	8.04E-10	79863000	2	2	10.2	30.924	24.3413	24.5201	23.9838	3	2	1	B6GWU6	B6GWU6	1	B6GWU6	Pc12g11030 protein		
ND	23.0909	23.7666	ND	23.03	25.6892	2.93E-07	85187000	3	2	11.8	28.554	23.8942	23.4287	24.3596	4	2	2	B6GWV3	B6GWV3	1	B6GWV3	Pc12g11100 protein	antioxidant activity; peroxiredoxin activity	
26.9516	27.4586	27.1494	30.0432	30.2495	28.195	9.75E-49	2.68E+09	5	5	9.3	65.3	28.3412	27.1865	29.4959	6	3	3	B6GWV7	B6GWV7	1	B6GWV7	Pc12g14680 protein	proteolysis; serine-type endopeptidase activity	
27.4879	26.1851	26.5201	ND	25.4349	27.5213	2.20E-39	5.33E+08	4	4	8.6	53.111	26.6299	26.7311	26.4781	5	3	3	B6GWX0	B6GWX0	1	B6GWX0	Pc12g14810 protein		
28.5231	28.5187	28.4229	28.4191	28.5928	26.6147	4.20E-31	2.05E+09	2	2	4.6	45.627	28.1819	28.4883	27.8755	6	3	3	B6GWX5	B6GWX5	1	B6GWX5	Extracellular acid phosphatase PhoA-Penicillium chrysogenum	hydrolase activity, acting on ester bonds	
24.085	24.375	24.1133	26.5469	25.2256	23.8382	1.80E-05	2E+08	2	2	23.9	10.867	24.6973	24.1911	25.2036	6	3	3	B6GX16	B6GX16	1	B6GX16	Pc12g07440 protein	cytochrome-c oxidase activity; mitochondrion	
26.9454	27.1968	26.9639	27.8785	27.649	28.515	2.47E-50	1.16E+09	8	8	9	137.22	27.5247	27.0353	28.0142	6	3	3	B6GX18	B6GX18	1	B6GX18	Pc12g07460 protein		
27.8646	27.9811	27.9611	26.9068	27.3833	27.5334	1.12E-60	1.21E+09	11	11	51.3	28.966	27.605	27.9356	27.2745	6	3	3	B6GX30	B6GX30	1	B6GX30	Pc12g07580 protein	ATP binding; GTPase activity; cytoplasm; metallochaperone activity; nickel cation binding	
28.7125	28.6062	28.816	28.0152	27.6159	29.3705	1.95E-115	2.35E+09	11	11	28.4	46.413	28.5227	28.7115	28.3338	6	3	3	B6GX40	B6GX40	1	B6GX40	Pc12g11190 protein	ATP binding; arginine biosynthetic process; argininosuccinate synthase activity	
28.1043	28.2698	28.0057	28.101	28.7712	27.7241	1.32E-164	1.68E+09	15	15	14.7	139.28	28.1627	28.1266	28.1988	6	3	3	B6GX48	B6GX48	1	B6GX48	Pc12g11270 protein		
25.2352	25.9211	25.3705	27.5558	27.162	27.3077	5.00E-50	5.61E+08	5	5	15.6	53.243	26.4254	25.5089	27.3419	6	3	3	B6GX54	B6GX54	1	B6GX54	FK506-binding protein	FK506 binding; histone peptidyl-prolyl isomerization; nucleolus; peptidyl-prolyl cis-trans isomerase activity; protein folding	
24.9229	24.4191	24.2252	24.0839	24.3487	26.0909	2.91E-12	1.59E+08	5	5	13.6	48.33	24.6818	24.5224	24.8412	6	3	3	B6GX70	B6GX70	1	B6GX70	Elongation factor Tu	GTP binding; GTPase activity; intracellular; translation elongation factor activity	
ND	23.3584	23.6704	24.2166	ND	26.7657	1.86E-11	1.46E+08	3	3	10.3	53.175	24.5028	23.5144	25.4912	4	2	2	B6GXF6	B6GXF6	1	B6GXF6	Pc12g11540 protein	catalytic activity; pyridoxal phosphate binding	
ND	23.9408	ND	22.3151	24.0124	ND	9.48E-05	42071000	2	2	8.1	32.67	23.4228	23.9408	23.1638	3	1	2	B6GXG1	B6GXG1	1	B6GXG1	GATA transcription factor nreB-Penicillium chrysogenum	sequence-specific DNA binding; sequence-specific DNA binding transcription factor activity; zinc ion binding	
32.7069	32.96	32.7071	32.3918	32.3617	31.4479	0	3.54E+10	16	16	30	49.864	32.4292	32.7913	32.0671	6	3	3	B6GXL6	B6GXL6	1	B6GXL6	Pc12g04310 protein	NAD binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	
26.9911	26.9187	27.1386	26.3863	25.9516	27.2732	2.32E-45	6.76E+08	4	4	10.4	48.268	26.7766	27.0161	26.5371	6	3	3	B6GXM1	B6GXM1	1	B6GXM1	Pc12g04370 protein	L-serine biosynthetic process; O-phospho-L-serine:2-oxoglutarate aminotransferase activity; pyridoxal phosphate binding	
25.8492	25.8711	25.989	26.1549	25.6158	25.8946	6.51E-10	3.51E+08	4	4	28.6	20.866	25.8958	25.9031	25.8884	6	3	3	B6GXP0	B6GXP0	1	B6GXP0	Pc12g08100 protein	acid-amino acid ligase activity	
27.3516	26.9092	ND	ND	ND	ND	2.95E-05	6.87E+08	2	2	3.2	94.834	27.1304	27.1304	ND	2	2	0	B6GXQ9	B6GXQ9	1	B6GXQ9	Pc12g11800 protein		
28.2146	28.4737	27.794	26.2885	25.746	27.088	2.16E-44	1.17E+09	5	5	35.8	15.5	27.2675	28.1608	26.3742	6	3	3	B6GXR4	B6GXR4	1	B6GXR4	Pc12g15350 protein	hemolysis by symbiont of host erythrocytes	
26.9151	26.8135	26.7768	27.5997	27.4578	26.6802	2.06E-18	7.59E+08	6	5	24.9	37.579	27.0405	26.8351	27.2459	6	3	3	B6GXW9	B6GXW9	1	B6GXW9	Pc12g04460 protein		
28.0419	28.2901	28.2491	27.5926	27.474	ND	1.40E-45	1.43E+09	6	6	24.4	31	27.9295	28.1937	27.5333	5	3	2	B6GXX2	B6GXX2	1	B6GXX2	Pc12g04490 protein	ATP binding; ATPase activity	
26.8282	26.6023	27.1187	26.4954	25.2877	26.2679	1.48E-49	5.76E+08	8	8	25.9	45.056	26.4334	26.8497	26.017	6	3	3	B6GXX8	B6GXX8	1	B6GXX8	Pc12g04550 protein	ATP binding; protein serine/threonine kinase activity	
23.0255	23.6356	23.7582	ND	ND	25.0715	1.27E-07	61471000	4	4	5.5	92.048	23.8727	23.4731	25.0715	4	3	1	B6GXX9	B6GXX9	1	B6GXX9	Pc12g04560 protein	RNA cap binding; mRNA cis splicing, via spliceosome; mRNA transport; nuclear cap binding complex	
28.4696	28.6286	28.4478	27.2728	27.8269	27.6834	5.76E-124	1.7E+09	10	10	36.4	37.08	28.0549	28.5153	27.5944	6	3	3	B6GXY7	B6GXY7	1	B6GXY7	Pc12g08170 protein	3'(2'),5'-bisphosphate nucleotidase activity; phosphatidylinositol phosphorylation; sulfur compound metabolic process	
ND	ND	ND	28.4017	27.6235	25.8281	8.40E-08	5.67E+08	3	3	26.1	10.046	27.2844	ND	27.2844	3	0	3	B6GXZ8	B6GXZ8	1	AFP	Antifungal protein	defense response to fungus; extracellular region; killing of cells of other organism	Secreted.
33.5641	33.3165	33.5017	34.1558	33.4695	33.7211	0	7.42E+10	49	49	56.6	93.881	33.6214	33.4608	33.7821	6	3	3	B6GY26;B 6HV95	B6GY26	2	B6GY26	Pc12g12040 protein	GTP binding; GTPase activity	
29.6748	30.1377	30.0776	29.8907	30.1176	29.0498	3.44E-76	5.67E+09	11	11	35.9	37.497	29.8247	29.9634	29.686	6	3	3	B6GY29	B6GY29	1	B6GY29	Pc12g15600 protein	intracellular; transporter activity	
32.4863	32.4897	32.422	31.5887	32.3553	30.77	4.45E-134	2.73E+10	9	9	44.4	28.559	32.0187	32.466	31.5713	6	3	3	B6GY55;B 6HP31	B6GY55	2	B6GY55	Pc12g00830 protein	oxidoreductase activity	
27.9671	28.2211	27.9374	27.9623	28.1855	27.3592	1.16E-122	1.51E+09	9	9	37.4	32.534	27.9388	28.0419	27.8357	6	3	3	B6GY76	B6GY76	1	B6GY76	Purine nucleoside phosphorylase	nucleoside metabolic process; purine-nucleoside phosphorylase activity	
23.5353	23.7353	23.7828	24.6761	25.1325	23.5047	1.38E-07	1.06E+08	4	4	4.7	95.179	24.0611	23.6845	24.4378	6	3	3	B6GY89	B6GY89	1	B6GY89	Pc12g08420 protein	transcription, DNA-templated; zinc ion binding	
28.9455	29.0166	28.9004	29.1895	29.3108	28.0388	1.17E-146	2.95E+09	8	8	46.3	28.409	28.9003	28.9542	28.8464	6	3	3	B6GY92	B6GY92	1	B6GY92	Proteasome subunit alpha type	cytoplasm; nucleus; proteasome core complex, alpha-subunit complex; threonine-type endopeptidase activity; ubiquitin-dependent protein catabolic process	Cytoplasm. Nucleus.
24.3173	24.3772	24.0383	23.9236	23.7191	23.0707	2.71E-10	95252000	2	2	16.5	24.861	23.9077	24.2443	23.5711	6	3	3	B6GY97	B6GY97	1	B6GY97	Pc12g08500 protein		
26.4371	26.877	26.6139	27.0421	27.0549	26.2468	3.08E-39	6.21E+08	8	8	10.9	114.64	26.712	26.6427	26.7813	6	3	3	B6GYA5	B6GYA5	1	B6GYA5	Pc12g08580 protein	oxidoreductase activity, acting on the aldehyde or oxo group of donors	
25.7655	25.5484	25.2692	25.662	26.3062	ND	9.37E-10	2.9E+08	4	4	11.3	31.164	25.7103	25.5277	25.9841	5	3	2	B6GYD4	B6GYD4	1	B6GYD4	Pc12g12300 protein	nucleic acid binding	
25.7068	25.9301	25.7043	25.8542	25.6273	24.7617	1.39E-11	2.9E+08	4	4	7.9	58.426	25.5974	25.7804	25.4144	6	3	3	B6GYE7	B6GYE7	1	B6GYE7	Pc12g15940 protein	ATP binding; cytoplasm; protein folding	
24.833	24.9735	24.9147	23.6069	26.5142	29.7519	2.64E-111	7.8E+08	13	12	35.6	51.895	25.7657	24.9071	26.6244	6	3	3	B6GYF5	B6GYF5	1	B6GYF5	Serine hydroxymethyltransferase	L-serine metabolic process; glycine hydroxymethyltransferase activity; glycine metabolic process; pyridoxal phosphate binding; tetrahydrofolate interconversion	
26.3738	26.5111	26.6284	23.2607	ND	29.0819	1.36E-77	7.2E+08	10	10	21.1	56.765	26.3712	26.5044	26.1713	5	3	2	B6GYF7	B6GYF7	1	B6GYF7	Pc12g16040 protein	cytoplasm; glucose catabolic process; manganese ion binding; phosphoglycerate mutase activity	
32.8536	31.692	32.3293	29.9633	30.1955	32.571	5.47E-215	2.37E+10	16	14	59.7	34.188	31.6008	32.2916	30.9099	6	3	3	B6GYI7	B6GYI7	1	B6GYI7	Pc12g04750 protein	L-malate dehydrogenase activity; cellular carbohydrate metabolic process; malate metabolic process	
28.0929	28.1478	27.8405	28.195	28.8959	28.5774	3.81E-68	1.79E+09	5	5	38.4	16.606	28.2916	28.027	28.5561	6	3	3	B6GYI8	B6GYI8	1	B6GYI8	Pc12g04760 protein	ribosome; structural constituent of ribosome; translation	
26.0303	26.5058	25.9027	ND	25.7162	26.5491	6.37E-18	3.7E+08	5	5	26.9	27.447	26.1408	26.1462	26.1326	5	3	2	B6GYP0	B6GYP0	1	B6GYP0	Eukaryotic translation initiation factor 3 subunit K	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; regulation of translational initiation; ribosome binding; translation initiation factor activity	Cytoplasm.
29.7605	28.8013	29.8192	28.8482	25.679	29.3718	4.74E-215	3.5E+09	17	17	44.7	58.946	28.7133	29.4603	27.9663	6	3	3	B6GYP6	B6GYP6	1	B6GYP6	Pc12g16160 protein	ATP binding; GMP biosynthetic process; GMP synthase (glutamine-hydrolyzing) activity; pyrophosphatase activity	
25.9791	26.4708	26.4376	26.2348	26.4507	25.6758	2.92E-17	4.47E+08	3	3	20.5	17.453	26.2081	26.2959	26.1204	6	3	3	B6GYQ0	B6GYQ0	1	B6GYQ0	Pc12g16200 protein	prefoldin complex; protein folding	
24.9699	24.5844	25.2074	22.0663	22.7383	29.2499	1.77E-76	5.55E+08	9	9	22.8	61.034	24.8027	24.9206	24.6848	6	3	3	B6GYQ9	B6GYQ9	1	B6GYQ9	Pc12g16290 protein	ATP binding	
27.1661	27.5407	27.2004	26.4511	27.1235	27.2765	7.16E-67	8.5E+08	7	7	22.3	73.875	27.1264	27.3024	26.9504	6	3	3	B6GYR3	B6GYR3	1	B6GYR3	Pc12g01240 protein	L-ascorbic acid binding; iron ion binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	
29.219	28.4107	29.2333	29.3266	27.8803	29.4073	1.85E-170	3.04E+09	14	14	31.5	62.306	28.9129	28.9544	28.8714	6	3	3	B6GYV7	B6GYV7	1	B6GYV7	Pc12g08900 protein	1-pyrroline-5-carboxylate dehydrogenase activity; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor; proline biosynthetic process	
29.2835	29.6439	29.328	28.7095	29.2594	27.6051	2.96E-123	3.32E+09	5	5	26.8	33.879	28.9716	29.4185	28.5247	6	3	3	B6GYW0	B6GYW0	1	B6GYW0	Pc12g08930 protein	S-methyl-5-thioadenosine phosphorylase activity; nucleoside metabolic process; phosphorylase activity	
28.073	25.1551	28.018	22.8982	ND	24.7432	1.64E-56	6.61E+08	5	5	21.9	46.421	25.7775	27.0821	23.8207	5	3	2	B6GYX0	B6GYX0	1	B6GYX0	Pc12g09030 protein	aromatic amino acid family metabolic process; fumarylacetoacetase activity	
26.7195	25.1725	26.75	ND	23.2902	ND	2.84E-17	2.97E+08	5	5	18.5	50.161	25.483	26.214	23.2902	4	3	1	B6GYX1	B6GYX1	1	B6GYX1	Pc12g09040 protein	L-phenylalanine catabolic process; homogentisate 1,2-dioxygenase activity; tyrosine metabolic process	
25.9369	24.8519	26.0183	24.3727	ND	27.6187	2.64E-56	3.17E+08	5	5	14.9	45.609	25.7597	25.6024	25.9957	5	3	2	B6GYX3	B6GYX3	1	B6GYX3	4-hydroxyphenylpyruvate dioxygenase	4-hydroxyphenylpyruvate dioxygenase activity; aromatic amino acid family metabolic process; metal ion binding	
29.4086	29.5877	29.3616	29.5136	29.2112	28.7556	3.57E-157	3.88E+09	18	18	32.8	72.589	29.3064	29.4527	29.1601	6	3	3	B6GYZ5	B6GYZ5	1	B6GYZ5	Pc12g12720 protein	ATP binding; arginine-tRNA ligase activity; arginyl-tRNA aminoacylation; cytoplasm	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
24.7808	24.8423	24.7483	26.148	ND	ND	7.21E-08	1.85E+08	3	3	4.7	100.44	25.1298	24.7904	26.148	4	3	1	B6GZ23	B6GZ23	1	B6GZ23	Coatomer subunit gamma	COPI vesicle coat; intracellular protein transport; structural molecule activity; vesicle-mediated transport	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic vesicle › COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side.
24.5632	25.561	25.7319	24.9513	24.0091	29.122	5.19E-81	5.95E+08	13	13	32.4	62.134	25.6564	25.2854	26.0274	6	3	3	B6GZ24	B6GZ24	1	B6GZ24	Pc12g16540 protein	ATP binding; aspartate–tRNA ligase activity; aspartyl-tRNA aminoacylation; cytoplasm; nucleic acid binding	
29.938	30.1047	29.8818	30.4049	30.7727	29.3255	1.54E-289	6.57E+09	20	20	45.2	65.133	30.0713	29.9749	30.1677	6	3	3	B6GZ38	B6GZ38	1	B6GZ38	Eukaryotic translation initiation factor 3 subunit D	Eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
28.0405	28.0221	28.3625	25.614	27.5409	28.4521	1.34E-149	1.4E+09	10	10	49.1	39.244	27.672	28.1417	27.2023	6	3	3	B6GZ60	B6GZ60	1	B6GZ60	Pc12g05300 protein		
27.7296	28.3389	28.4939	28.8238	28.732	28.1059	1.03E-67	2.02E+09	7	7	31.5	28.397	28.3707	28.1875	28.5539	6	3	3	B6GZ61	B6GZ61	1	B6GZ61	Pc12g05310 protein	ADP biosynthetic process; ATP binding; adenylate kinase activity	
25.8201	24.6019	25.6905	24.2249	23.9213	23.9104	2.22E-07	1.86E+08	3	3	7.3	42.524	24.6949	25.3708	24.0189	6	3	3	B6GZ62	B6GZ62	1	B6GZ62	Pc12g05320 protein	oxidoreductase activity	
26.0637	26.1665	25.866	26.5186	26.3186	25.7844	5.34E-14	4.15E+08	3	3	10.5	49.811	26.1196	26.032	26.2072	6	3	3	B6GZ66	B6GZ66	1	B6GZ66	Pc12g05380 protein	coproporphyrinogen oxidase activity; porphyrin-containing compound biosynthetic process	
24.9509	25.3304	25.1292	23.4255	22.1588	31.8341	4.29E-231	2.63E+09	18	18	38.6	51.856	25.4715	25.1368	25.8061	6	3	3	B6GZ68	B6GZ68	1	B6GZ68	Citrate synthase	cellular carbohydrate metabolic process; citrate (Si)-synthase activity; tricarboxylic acid cycle	
22.9787	21.7024	22.8759	24.811	24.2166	ND	1.81E-05	70477000	2	2	2.8	76.604	23.3169	22.519	24.5138	5	3	2	B6GZ69	B6GZ69	1	B6GZ69	Pc12g05410 protein	nucleic acid binding; nucleotide binding	
24.5581	24.0477	ND	ND	ND	27.2413	1.54E-24	1.84E+08	5	5	17	47.147	25.2824	24.3029	27.2413	3	2	1	B6GZ70	B6GZ70	1	B6GZ70	Pc12g05420 protein	cellular amino acid metabolic process; pyridoxal phosphate binding; transferase activity, transferring alkyl or aryl (other than methyl) groups	
25.932	26.9384	26.9053	24.4063	24.4006	28.5527	7.73E-41	6.46E+08	8	8	18.1	71.33	26.1892	26.5919	25.7865	6	3	3	B6GZ85	B6GZ85	1	B6GZ85	Lysine--tRNA ligase	ATP binding; cytoplasm; lysine-tRNA ligase activity; lysyl-tRNA aminoacylation; nucleic acid binding	
26.6581	26.7762	27.0714	27.4442	26.5575	27.0168	6.15E-26	7.43E+08	6	6	16	48.286	26.9207	26.8352	27.0062	6	3	3	B6GZE8	B6GZE8	1	B6GZE8	Pc12g05480 protein	catalytic activity; metal ion binding	
31.9755	32.472	32.4611	31.0594	31.4812	34.4259	0	3.81E+10	38	38	49.8	79.535	32.3125	32.3029	32.3222	6	3	3	B6GZG3	B6GZG3	1	B6GZG3	Pc12g05640 protein	ATP binding; protein folding; response to stress	
ND	25.2748	ND	25.7565	26.1318	ND	4.17E-64	2.43E+08	3	3	6.3	55.383	25.721	25.2748	25.9442	3	1	2	B6GZG5	B6GZG5	1	B6GZG5	Pc12g05660 protein	intracellular; nucleic acid binding; nucleotide binding; transport	
26.8392	27.1709	27.3519	26.9289	27.1541	26.4144	4.82E-92	7.84E+08	8	8	23.1	54.574	26.9766	27.1207	26.8324	6	3	3	B6GZH0	B6GZH0	1	B6GZH0	Pc12g09420 protein		
29.9415	30.1019	29.9143	30.3759	30.8186	29.1776	0	6.58E+09	16	16	34.8	65.115	30.055	29.9859	30.124	6	3	3	B6GZJ0	B6GZJ0	1	B6GZJ0	Coronin		
26.7813	25.8155	26.393	25.1144	24.9666	25.268	8.15E-25	3.84E+08	7	7	12.6	63.409	25.7231	26.3299	25.1163	6	3	3	B6GZP0	B6GZP0	1	B6GZP0	Pc12g05750 protein	carbohydrate metabolic process; phosphotransferase activity, alcohol group as acceptor	
29.0538	29.3896	29.1396	29.2787	29.6357	27.4829	4.92E-174	3.39E+09	13	13	62.8	31.152	28.9967	29.1943	28.7991	6	3	3	B6GZP7	B6GZP7	1	B6GZP7	Pc12g05820 protein	S-formylglutathione hydrolase activity; formaldehyde catabolic process	
27.1917	27.4058	27.0164	28.005	28.2597	27.6371	6.49E-27	1.15E+09	3	3	9.9	36.719	27.586	27.2046	27.9673	6	3	3	B6GZQ6	B6GZQ6	1	B6GZQ6	Pc12g05910 protein	nucleic acid binding; nucleotide binding	
ND	ND	ND	26.0621	ND	3.16E-21	2.14E+08	3	3	13.2	16.849	25.9444	ND	25.9444	2	0	2	B6GZQ9	B6GZQ9	1	B6GZQ9	Pc12g05940 protein	ribosome; structural constituent of ribosome; translation			
29.1432	28.4589	28.9017	28.9716	27.406	28.3003	9.83E-249	2.42E+09	16	16	32.4	85.288	28.5303	28.8346	28.226	6	3	3	B6GZU9	B6GZU9	1	B6GZU9	6-phosphofructokinase	6-phosphofructokinase activity; 6-phosphofructokinase complex; ATP binding; fructose 6-phosphate metabolic process; glycolysis	
25.7034	25.9629	25.8295	25.983	26.1363	25.5963	1.31E-38	3.46E+08	4	4	13.1	47.964	25.8686	25.8319	25.9052	6	3	3	B6GZV0	B6GZV0	1	B6GZV0	IMP-specific 5-nucleotidase 1	magnesium ion binding; nucleotide metabolic process; phosphatase activity	
21.3368	22.0634	21.4449	21.6041	22.0389	27.2517	5.33E-22	1.31E+08	5	5	15.6	46.729	22.6233	21.615	23.6316	6	3	3	B6GZX0	B6GZX0	1	B6GZX0	Pc12g05970 protein	GTP binding; cell cycle; septin complex	
25.7642	25.8924	25.6758	25.906	26.1956	25.3118	5.06E-11	3.3E+08	5	5	9.5	62.083	25.791	25.7774	25.8045	6	3	3	B6GZX1	B6GZX1	1	B6GZX1	Pc12g05980 protein	DNA binding; nucleus	
23.6805	23.843	23.7328	26.1366	24.4884	23.2291	1.99E-05	1.41E+08	2	2	7.4	30.329	24.1851	23.7521	24.618	6	3	3	B6GZY4	B6GZY4	1	B6GZY4	Pc12g06120 protein		
29.0871	29.288	29.0818	28.7463	28.6443	27.9833	6.04E-134	2.88E+09	10	10	41.6	34.961	28.8051	29.1523	28.458	6	3	3	B6GZZ1	B6GZZ1	1	B6GZZ1	Pc12g09820 protein	lactoylglutathione lyase activity; metal ion binding	
24.0064	23.998	23.8349	ND	22.961	ND	0.000827	60137000	2	2	3.1	92.523	23.7001	23.9464	22.961	4	3	1	B6GZZ4	B6GZZ4	1	B6GZZ4	Pc12g09850 protein	calcium-dependent cysteine-type endopeptidase activity; intracellular; proteolysis	
26.9095	26.8351	26.6771	26.7262	26.8545	26.0352	1.47E-108	6.25E+08	4	4	14.2	51.973	26.6729	26.8072	26.5387	6	3	3	B6H021	B6H021	1	B6H021	Pc12g13660 protein	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	
27.3734	27.2851	27.2272	27.6765	27.8182	27.1898	3.54E-20	1.02E+09	6	6	34.2	29.472	27.4284	27.2952	27.5615	6	3	3	B6H023	B6H023	1	B6H023	Pyrroline-5-carboxylate reductase	L-proline biosynthetic process; pyrroline-5-carboxylate reductase activity	
26.5896	26.7943	26.0605	ND	22.5246	26.4482	1.45E-08	3.63E+08	2	2	8.9	27.894	25.6834	26.4815	24.4864	5	3	2	B6H036	B6H036	1	B6H036	Pc12g02580 protein		
25.0077	25.5686	25.2907	ND	ND	26.2643	3.20E-43	1.94E+08	6	6	24.9	36.478	25.5328	25.289	26.2643	4	3	1	B6H051	B6H051	1	B6H051	Pc12g06180 protein	electron carrier activity; flavin adenine dinucleotide binding	
22.4889	22.8073	22.4525	ND	ND	25.5704	6.92E-06	69799000	3	3	5.7	77.628	23.3298	22.5829	25.5704	4	3	1	B6H089	B6H089	1	B6H089	Pc12g10180 protein	GTP binding; GTPase activity; translation release factor activity	
26.5703	26.505	26.8175	26.0134	25.9618	25.382	1.87E-40	4.81E+08	4	4	8.3	82.346	26.2083	26.631	25.7857	6	3	3	B6H094	B6H094	1	B6H094	Pc12g13740 protein	catalase activity; heme binding; metal ion binding; response to oxidative stress	
24.785	25.25	24.8275	25.8411	25.8527	24.8446	1.62E-07	2.29E+08	2	2	7.4	27.985	25.2335	24.9542	25.5128	6	3	3	B6H0A8	B6H0A8	1	B6H0A8	Pc12g13890 protein	sequence-specific DNA binding; sequence-specific DNA binding transcription factor activity	
25.6287	25.5569	25.6706	25.9809	26.2325	24.9335	2.83E-19	3.09E+08	3	3	26.7	21.929	25.6672	25.6187	25.7156	6	3	3	B6H0B0	B6H0B0	1	B6H0B0	Pc12g13910 protein	N-acetyltransferase activity	
26.4532	26.4082	26.6529	26.5466	26.7669	30.8229	5.76E-237	1.77E+09	22	22	26.4	117.38	27.2751	26.5048	28.0455	6	3	3	B6H0F9	B6H0F9	1	B6H0F9	Pc12g06650 protein	ATP binding; ATPase activity	
27.5367	27.3632	27.2191	27.533	27.89	26.7448	8.69E-96	1E+09	9	9	43.3	30.049	27.3811	27.373	27.3893	6	3	3	B6H0G7	B6H0G7	1	B6H0G7	Proteasome subunit beta type	cytoplasm; nucleus; proteasome core complex; proteolysis involved in cellular protein catabolic process; threonine-type endopeptidase activity	Cytoplasm. Nucleus.
27.314	27.3913	27.3782	27.6666	27.9061	27.2082	6.84E-63	1.05E+09	11	11	31.1	48.832	27.4774	27.3612	27.5936	6	3	3	B6H0H1	B6H0H1	1	B6H0H1	Pc12g10310 protein	RNA binding	
25.7625	25.9135	25.9148	26.4563	26.5726	25.1711	2.42E-16	3.9E+08	4	4	10.8	53.444	25.9651	25.8636	26.0666	6	3	3	B6H0H4	B6H0H4	1	B6H0H4	Pc12g10350 protein	carboxy-lyase activity; carboxylic acid metabolic process; pyridoxal phosphate binding	
25.6921	25.9236	25.6577	25.8664	26.0525	24.7101	1.82E-12	3.12E+08	2	2	5.6	50.521	25.6504	25.7578	25.543	6	3	3	B6H0H6	B6H0H6	1	B6H0H6	Pc12g10370 protein	peptidase activity; proteolysis	
26.0097	26.0659	25.946	27.0297	27.022	24.967	4.58E-14	4.79E+08	5	5	25.1	23.877	26.1734	26.0072	26.3396	6	3	3	B6H0I9	B6H0I9	1	B6H0I9	Pc12g14020 protein	integral component of membrane; vesicle-mediated transport	
24.1028	24.6316	24.7871	ND	ND	25.8909	2.63E-06	1.43E+08	3	3	5	66.654	24.8531	24.5072	25.8909	4	3	1	B6H0L8	B6H0L8	1	B6H0L8	Pc12g03090 protein	heme binding; succinate dehydrogenase activity	
26.14	25.9984	25.8841	26.057	26.0425	25.7743	1.88E-20	3.66E+08	6	6	16.1	53.432	25.9827	26.0075	25.9579	6	3	3	B6H0M0	B6H0M0	1	B6H0M0	Protein phosphatase PP2A regulatory subunit B	protein phosphatase type 2A complex; protein phosphatase type 2A regulator activity; signal transduction	
23.7089	23.9518	23.6006	24.7965	25.4731	23.1705	1.31E-07	1.16E+08	3	3	2.6	170.92	24.1169	23.7538	24.48	6	3	3	B6H0M1	B6H0M1	1	B6H0M1	Pc12g03120 protein	nucleus; regulation of transcription, DNA-templated	
28.2623	28.8759	28.6802	28.3139	27.187	29.2793	1.33E-51	2.19E+09	7	7	27.7	34.366	28.4331	28.6061	28.2601	6	3	3	B6H0P7	B6H0P7	1	B6H0P7	Pc12g06870 protein	ATP citrate synthase activity; cofactor binding; succinate-CoA ligase (ADP-forming) activity	
29.9769	29.6951	30.0266	30.2568	30.6666	30.6799	0	6.92E+09	22	22	38.2	73.729	30.217	29.8995	30.5344	6	3	3	B6H0S5	B6H0S5	1	B6H0S5	Pc12g10670 protein	ATP binding	
25.9456	25.9315	26.0239	25.7099	25.6678	25.7551	2.13E-24	3.44E+08	4	4	11.3	54.944	25.839	25.967	25.711	6	3	3	B6H0T7	B6H0T7	1	B6H0T7	Pc12g14280 protein	FMN binding; heme binding; metal ion binding; oxidoreductase activity	
27.9952	28.555	28.4893	27.2177	26.6845	31.2308	6.52E-167	3.13E+09	14	14	30	59.586	28.3621	28.3465	28.3777	6	3	3	B6H0W6	B6H0W6	1	B6H0W6	ATP synthase subunit alpha	ATP binding; ATP hydrolysis coupled proton transport; ATP synthesis coupled proton transport; proton-transporting ATP synthase activity, rotational mechanism; proton-transporting ATP synthase complex, catalytic core F(1); proton-transporting ATPase activity, rotational mechanism	
27.1955	27.6948	27.333	27.1198	25.8283	28.6591	7.47E-08	1.04E+09	3	3	8.3	37.076	27.3051	27.4078	27.2024	6	3	3	B6H0Y7	B6H0Y7	1	B6H0Y7	Pc12g07100 protein	oxidoreductase activity; zinc ion binding	
26.0399	26.5401	26.3188	26.9512	27.1137	26.9309	6.58E-09	5.71E+08	5	5	17.7	46.038	26.6491	26.2996	26.9986	6	3	3	B6H132	B6H132	1	B6H132	Pc12g14620 protein	heme binding; iron ion binding; oxidoreductase activity; oxygen binding; oxygen transport	
ND	ND	ND	24.4101	25.8998	ND	7.77E-06	1.42E+08	3	3	15.8	23.044	25.1549	ND	25.1549	2	0	2	B6H1A7	B6H1A7	1	B6H1A7	Pc13g01870 protein	large ribosomal subunit; structural constituent of ribosome; translation	
28.6694	28.9591	28.6653	28.9078	29.2828	27.9604	2.87E-101	2.62E+09	16	16	30.6	73.271	28.7408	28.7646	28.717	6	3	3	B6H1D5	B6H1D5	1	B6H1D5	Pc13g02680 protein	ATP binding; cytoplasm; glutamine-tRNA ligase activity; glutaminyl-tRNA aminoacylation	
24.6647	24.4202	24.5657	24.0961	23.6887	28.504	3.48E-22	3.59E+08	7	7	29.4	39.544	24.9899	24.5502	25.4296	6	3	3	B6H1D9	B6H1D9	1	B6H1D9	Pc13g02720 protein	methyltransferase activity; protein methylation	
28.2215	28.3468	28.2016	27.365	27.549	27.1806	1.14E-66	1.44E+09	10	10	28.4	58.515	27.8108	28.2567	27.3649	6	3	3	B6H1E1	B6H1E1	1	B6H1E1	Pc13g02740 protein	carbohydrate metabolic process; magnesium ion binding; phosphoacetylglucosamine mutase activity	
25.6219	25.5191	25.3224	25.4209	26.2876	ND	4.93E-14	2.71E+08	3	3	22.3	24.981	25.6344	25.4878	25.8542	5	3	2	B6H1E4	B6H1E4	1	B6H1E4	Pc13g02770 protein	oxidoreductase activity; riboflavin biosynthetic process; riboflavin synthase activity	
25.8396	25.7422	26.3322	23.7738	24.2028	26.8806	1.62E-16	3.52E+08	5	5	14.2	47.328	25.4619	25.9714	24.9524	6	3	3	B6H1F2	B6H1F2	1	B6H1F2	Pc13g02840 protein		
26.5909	26.6078	26.2519	28.7965	28.4211	29.4724	1.01E-36	1.5E+09	4	4	18.1	22.607	27.6901	26.4835	28.8966	6	3	3	B6H1F6	B6H1F6	1	B6H1F6	Pc13g02890 protein	ribosome; structural constituent of ribosome; translation	
31.9469	31.8235	31.8288	30.7172	30.6767	32.5211	7.83E-180	1.9E+10	12	12	27.2	49.758	31.5857	31.8664	31.305	6	3	3	B6H1G1	B6H1G1	1	B6H1G1	Elongation factor 1-alpha	GTP binding; GTPase activity; cytoplasm; translation elongation factor activity	
25.144	25.2127	25.4839	24.6311	25.1459	24.8456	2.09E-05	2.03E+08	3	3	19.2	19.248	25.0772	25.2802	24.8742	6	3	3	B6H1G5	B6H1G5	1	B6H1G5	Pc13g02960 protein		
28.0987	28.4312	28.341	28.7741	29.1618	27.7693	1.53E-118	2.12E+09	10	10	20.1	58.208	28.4294	28.2903	28.5684	6	3	3	B6H1H9	B6H1H9	1	B6H1H9	Pc13g02370 protein		
27.3002	26.601	27.2332	27.5593	25.7699	26.5585	1.38E-46	7.63E+08	5	5	20.9	31.597	26.837	27.0448	26.6293	6	3	3	B6H1R8	B6H1R8	1	B6H1R8	Pc13g01530 protein	oxidoreductase activity	
23.876	24.4275	24.6216	24.3359	24.4009	24.015	3.44E-07	1.19E+08	3	3	8.9	44.867	24.2795	24.3084	24.2506	6	3	3	B6H1S9	B6H1S9	1	B6H1S9	Pc13g01690 protein	intramolecular lyase activity	
28.7346	28.4427	28.541	28.7192	28.9433	27.4063	4.32E-26	2.22E+09	7	7	53.5	10.946	28.4645	28.5728	28.3563	6	3	3	B6H1T0	B6H1T0	1	B6H1T0	Pc13g01700 protein	cell redox homeostasis; electron carrier activity; protein disulfide oxidoreductase activity	
29.6745	29.7421	29.5969	31.1256	30.6112	29.7925	4.62E-36	6.91E+09	3	3	26.1	17.979	30.0905	29.6712	30.5098	6	3	3	B6H1V6	B6H1V6	1	B6H1V6	Pc13g03190 protein	ribosome; structural constituent of ribosome; translation	
27.1711	26.9807	27.3161	26.6239	25.2456	27.85	6.06E-47	7.67E+08	8	8	16.4	85.339	26.8646	27.156	26.5732	6	3	3	B6H1V7	B6H1V7	1	B6H1V7	Pc13g03200 protein	COPII vesicle coat; ER to Golgi vesicle-mediated transport; intracellular protein transport; zinc ion binding	
25.5584	23.4252	23.7283	ND	ND	23.7457	4.55E-07	87078000	4	4	4.7	98.396	24.1144	24.2373	23.7457	4	3	1	B6H1W4	B6H1W4	1	B6H1W4	Pc13g03270 protein	DNA binding; DNA topoisomerase type I activity; DNA topoisomerase type II (ATP-hydrolyzing) activity; DNA topological change; chromosome	
24.6648	24.4598	24.6776	24.9139	25.5952	24.0576	3.02E-10	1.6E+08	6	6	15.7	46.042	24.7282	24.6007	24.8556	6	3	3	B6H1X3	B6H1X3	1	B6H1X3	Pc13g03590 protein	translation initiation factor activity	
24.0075	22.7513	23.3896	ND	ND	ND	8.74E-06	40968000	3	3	7.9	53.985	23.3828	23.3828	ND	3	3	0	B6H1X4	B6H1X4	1	B6H1X4	Pc13g03600 protein	hydroxyethylthiazole kinase activity; thiamine biosynthetic process; thiamine-phosphate diphosphorylase activity	
26.8252	26.5015	26.6175	28.0366	27.5153	27.1967	1.36E-45	8.57E+08	5	5	12.5	54.104	27.1155	26.6481	27.5829	6	3	3	B6H1Z3	B6H1Z3	1	B6H1Z3	Pc13g03420 protein	cell redox homeostasis	
23.9091	ND	23.8591	24.9549	ND	ND	0.001004	1.16E+08	2	2	4.7	65.67	24.241	23.8841	24.9549	3	2	1	B6H203	B6H203	1	B6H203	Pc13g02990 protein	catalytic activity	
26.6155	27.0859	26.6435	27.2868	27.6095	26.582	2.15E-66	7.62E+08	9	9	25.1	50.579	26.9705	26.7816	27.1595	6	3	3	B6H210	B6H210	1	B6H210	Pc13g03060 protein		
23.799	23.6972	24.8192	26.016	24.3352	ND	1.57E-10	1.47E+08	3	3	14.1	35.886	24.5333	24.1051	25.1756	5	3	2	B6H231	B6H231	1	B6H231	Pc13g03800 protein	hydrolase activity; metal ion binding; nucleic acid binding	
26.0612	25.2724	26.0188	27.0264	25.7612	26.3373	5.70E-09	4.25E+08	2	2	4.8	35.459	26.0795	25.7841	26.375	6	3	3	B6H250	B6H250	1	B6H250	Pc13g04170 protein		
24.9283	25.3438	25.1046	25.6152	26.0827	25.0201	1.81E-10	2.43E+08	2	2	18	20.854	25.3491	25.1256	25.5727	6	3	3	B6H259	B6H259	1	B6H259	Pc13g04070 protein	RNA cap binding; mRNA cis splicing, via spliceosome; nuclear cap binding complex; nucleotide binding	
ND	ND	19.4823	19.1879	19.1751	28.7561	2.97E-99	2.82E+08	21	21	14.3	253.08	21.6503	19.4823	22.373	4	1	3	B6H276	B6H276	1	B6H276	Pc13g03920 protein	ATP binding; acetyl-CoA carboxylase activity; biotin carboxylase activity; fatty acid biosynthetic process; metal ion binding	
27.3019	27.5388	27.3943	29.2898	29.3203	27.5209	1.45E-92	1.85E+09	16	16	36.7	66.791	28.061	27.4117	28.7103	6	3	3	B6H2A3	B6H2A3	1	B6H2A3	Malic enzyme	NAD binding; malate dehydrogenase (decarboxylating) (NAD+) activity; malate metabolic process; metal ion binding	
28.1242	27.4668	27.826	28.2783	27.3823	27.5919	1.91E-81	1.36E+09	12	12	49.6	29.897	27.7782	27.8056	27.7508	6	3	3	B6H2A4	B6H2A4	1	B6H2A4	Orotidine 5-phosphate decarboxylase	'de novo' UMP biosynthetic process; 'de novo' pyrimidine nucleobase biosynthetic process; orotidine-5'-phosphate decarboxylase activity	
23.4482	ND	23.3936	23.9975	24.8531	ND	2.76E-38	70985000	2	2	8.5	12.108	23.9231	23.4209	24.4253	4	2	2	B6H2B7	B6H2B7	1	B6H2B7	Pc13g04630 protein	ribosome; structural constituent of ribosome; translation	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
27.7892	27.3094	27.112	28.7696	28.5997	26.7572	5.97E-38	1.43E+09	8	8	29.6	23.085	27.7229	27.4035	28.0422	6	3	3	B6H2C2	B6H2C2	1	B6H2C2	Ribosomal protein L19 (Fragment)	ribosome; structural constituent of ribosome; translation	
26.6486	27.5683	26.9312	26.2864	26.3707	30.3364	1.58E-83	1.53E+09	8	8	36	32.366	27.3569	27.0494	27.6645	6	3	3	B6H2I7	B6H2I7	1	RSSA	40S ribosomal protein S0	cytosolic small ribosomal subunit; ribosomal small subunit assembly; structural constituent of ribosome; translation	Cytoplasm.
30.5178	30.3554	30.6392	29.7839	29.1753	30.2776	2.54E-211	7.03E+09	17	17	41.1	55.928	30.1249	30.5042	29.7456	6	3	3	B6H2I3	B6H2I3	1	B6H2I3	Pc13g05320 protein	adenyl nucleotide binding; cystathionine beta-synthase activity; cysteine biosynthetic process from serine; cysteine biosynthetic process via cystathionine; cytoplasm	
29.3877	29.8822	29.5765	30.137	30.3656	29.2827	0	5.32E+09	17	17	35.3	75.854	29.7719	29.6155	29.9284	6	3	3	B6H2K4	B6H2K4	1	B6H2K4	Pc13g05400 protein	leukotriene biosynthetic process; leukotriene-A4 hydrolase activity; metallopeptidase activity; proteolysis; zinc ion binding	
25.5615	26.03	25.8387	25.6291	25.6486	27.1954	1.16E-21	3.81E+08	8	8	17.4	62.854	25.9839	25.8101	26.1577	6	3	3	B6H2L3	B6H2L3	1	B6H2L3	Pc13g14680 protein		
29.9801	30.1158	29.8087	30.0022	30.742	28.9979	1.07E-269	6.09E+09	13	13	37.6	51.2	29.9411	29.9682	29.914	6	3	3	B6H2M0	B6H2M0	1	AMPP3	Probable Xaa-Pro aminopeptidase pepP	aminopeptidase activity; manganese ion binding; metallopeptidase activity; proteolysis	
30.3878	30.4645	30.4373	30.1246	29.878	29.4611	0	7E+09	29	29	53.8	71.368	30.1255	30.4299	29.8212	6	3	3	B6H2M4	B6H2M4	1	B6H2M4	Pc13g05480 protein	calcium ion binding	
26.6479	26.5976	26.607	27.3279	27.3659	27.276	2.30E-20	7.19E+08	6	6	14.3	43.582	26.9704	26.6175	27.3232	6	3	3	B6H2M8	B6H2M8	1	B6H2M8	Pc13g05520 protein	nucleic acid binding; nucleotide binding	
26.2814	25.9621	25.7227	28.0131	28.0982	28.0431	2.54E-18	8.69E+08	3	3	19	20.609	27.0201	25.9887	28.0515	6	3	3	B6H2N0	B6H2N0	1	B6H2N0	Pc13g05540 protein	ribosome; structural constituent of ribosome; translation	
25.2129	25.3609	25.2308	25.3017	25.633	24.5893	2.56E-06	2.24E+08	2	2	5.7	34.745	25.2214	25.2682	25.1747	6	3	3	B6H2Q6	B6H2Q6	1	B6H2Q6	Pc13g15130 protein		
25.5394	25.7652	26.2095	25.6096	24.658	25.5298	4.97E-15	3.06E+08	5	5	11.8	76.89	25.5519	25.838	25.2658	6	3	3	B6H2S7	B6H2S7	1	B6H2S7	Pc13g15260 protein	vesicle docking involved in exocytosis	
26.8714	27.3836	27.2487	27.2055	27.8933	26.6729	1.30E-36	8.98E+08	4	4	15.3	22.067	27.2126	27.1679	27.2572	6	3	3	B6H2T0	B6H2T0	1	B6H2T0	Pc13g15290 protein	cytoplasm; glycolipid binding; glycolipid transporter activity	
24.185	23.7891	23.8252	27.9246	27.3768	24.163	1.03E-09	4.46E+08	3	2	18.4	22.852	25.2106	23.9331	26.4881	6	3	3	B6H2W3;B6H0T3	B6H2W3	2	B6H2W3	Pc13g05590 protein	GTP binding; protein transport; small GTPase mediated signal transduction	
26.7776	27.0298	26.4718	27.6852	27.6369	26.5949	6.45E-73	8.01E+08	7	7	19.3	61.009	27.0327	26.7597	27.3057	6	3	3	B6H2W6	B6H2W6	1	B6H2W6	Pc13g05660 protein		
24.5071	24.5214	25.0522	25.8882	25.5139	23.8603	2.34E-05	1.99E+08	3	3	8.2	48.404	24.8905	24.6936	25.0875	6	3	3	B6H305	B6H305	1	B6H305	Pc13g15710 protein	cytoplasm	
29.0581	29.0837	29.2733	29.8728	29.8281	29.6769	8.28E-209	4.17E+09	13	13	42.5	44.063	29.4655	29.1383	29.7926	6	3	3	B6H313	B6H313	1	B6H313	Pc13g15810 protein	branched-chain amino acid biosynthetic process; coenzyme binding; ketol-acid reductoisomerase activity	
25.3024	25.3749	24.9011	24.3475	24.5107	26.0057	1.24E-05	2.05E+08	2	2	8.9	24.18	25.0737	25.1928	24.9546	6	3	3	B6H349	B6H349	1	B6H349	Pc13g12610 protein	ribonucleoprotein complex; ribosome biogenesis	
ND	ND	ND	24.2207	24.9074	ND	1.66E-08	70367000	4	4	3.3	96.471	24.5641	ND	24.5641	2	0	2	B6H351	B6H351	1	B6H351	Pc13g12630 protein		
31.4781	31.7155	31.4216	32.0507	32.5102	30.7633	0	2.01E+10	19	19	29	79.192	31.6566	31.5384	31.7747	6	3	3	B6H375	B6H375	1	B6H375	Pc13g12990 protein	ATP binding	
27.6046	27.6762	27.3618	28.0627	28.3704	27.3603	1.56E-75	1.28E+09	6	6	22.8	45.243	27.7393	27.5475	27.9311	6	3	3	B6H377	B6H377	1	B6H377	Pc13g13010 protein	RNA binding; RNA processing; nucleotide binding; nucleus; ribonucleoprotein complex	
28.3694	27.8601	27.5872	29.3406	28.6917	29.2342	4.96E-69	2.25E+09	8	8	33.3	32.085	28.5139	27.9389	29.0888	6	3	3	B6H380	B6H380	1	B6H380	Pc13g05920 protein	ribosome	
26.3723	25.3725	26.0709	25.7183	25.6196	25.7502	9.61E-39	3.34E+08	8	8	10.9	96.975	25.8173	25.9385	25.696	6	3	3	B6H382	B6H382	1	B6H382	Pc13g05940 protein	oxidoreductase activity	
25.1636	25.1214	24.7195	24.458	24.6501	24.4899	6.40E-07	1.66E+08	4	4	5.1	87.859	24.7671	25.0015	24.5327	6	3	3	B6H3B8	B6H3B8	1	B6H3B8	Pc13g13260 protein	catalytic activity	
25.0572	25.6831	25.6859	25.1837	26.1077	25.6343	2.71E-17	2.68E+08	4	4	14.2	47.7	25.5586	25.4754	25.6419	6	3	3	B6H3D6	B6H3D6	1	B6H3D6	Pc13g06650 protein	ATP binding; ligase activity; metal ion binding	
28.7734	28.822	28.4467	29.4068	29.6132	30.1607	3.16E-142	3.52E+09	8	8	32	25.548	29.2038	28.6807	29.7269	6	3	3	B6H3J5	B6H3J5	1	B6H3J5	60S ribosomal protein L13	ribosome; structural constituent of ribosome; translation	
24.6297	24.8753	24.7895	23.6282	ND	26.0314	2.81E-18	1.52E+08	2	2	10	33.948	24.7908	24.7648	24.8298	5	3	2	B6H3J7	B6H3J7	1	B6H3J7	Pc13g06830 protein	3-hydroxyacyl-CoA dehydrogenase activity; NAD+ binding; fatty acid metabolic process	
28.1083	27.8753	27.7246	27.9332	28.1839	27.0333	7.78E-19	1.34E+09	4	4	30.3	10.069	27.8098	27.9028	27.7168	6	3	3	B6H3K3	B6H3K3	1	B6H3K3	Pc13g13330 protein		
26.4476	27.3096	27.2096	25.0976	25.1723	29.5671	3.75E-123	1.02E+09	10	10	30.2	50.006	26.8006	26.9889	26.6124	6	3	3	B6H3L7;CON__ENSEMBL:ENSBTAP00000025008	B6H3L7	2	B6H3L7	Pc13g13470 protein	GTP binding; GTPase activity; cytoplasm; microtubule; microtubule-based process; protein polymerization; structural constituent of cytoskeleton	Cytoplasm › cytoskeleton.
25.3543	ND	25.1753	ND	26.0583	ND	1.34E-06	1.96E+08	2	2	8.9	34.112	25.5293	25.2648	26.0583	3	2	1	B6H3M7	B6H3M7	1	B6H3M7	Pc13g06860 protein	biosynthetic process; catalytic activity	
27.4256	27.252	27.1605	26.975	27.1243	29.063	8.06E-107	1.13E+09	13	13	17.6	95.755	27.5001	27.2793	27.7208	6	3	3	B6H3P2	B6H3P2	1	B6H3P2	Eukaryotic translation initiation factor 3 subunit C	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
24.2666	ND	24.0102	24.362	24.8863	23.492	4.50E-06	98674000	3	3	11.3	34.533	24.2034	24.1384	24.2468	5	2	3	B6H3P5	B6H3P5	1	B6H3P5	Pc13g07070 protein		
24.1013	23.9393	23.9415	22.7724	ND	22.8583	2.34E-05	66795000	2	2	10.1	32.861	23.5226	23.9941	22.8154	5	3	2	B6H3Q5	B6H3Q5	1	B6H3Q5	Pc13g07470 protein		
25.5812	25.2968	25.4562	25.9621	25.2547	26.2538	5.31E-19	2.92E+08	4	4	25	21.034	25.6341	25.4447	25.8235	6	3	3	B6H3R7	B6H3R7	1	B6H3R7	Pc13g07180 protein		
25.8858	25.6	26.164	27.1953	26.8517	27.2509	7.66E-20	5.42E+08	3	3	28	19.873	26.4913	25.8833	27.0993	6	3	3	B6H3R8	B6H3R8	1	B6H3R8	Pc13g07190 protein	ribosome; structural constituent of ribosome; translation	
28.5539	28.2203	28.3943	28.2073	28.7519	28.4705	1.20E-138	1.99E+09	26	26	25.4	189.55	28.433	28.3895	28.4765	6	3	3	B6H3S1	B6H3S1	1	B6H3S1	Clathrin heavy chain	clathrin coat of coated pit; clathrin coat of trans-Golgi network vesicle; intracellular protein transport; structural molecule activity; vesicle-mediated transport	Cytoplasmic vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Membrane › coated pit; Peripheral membrane protein; Cytoplasmic side.
22.2621	22.5006	22.5007	23.1158	ND	22.0857	0.000348	34722000	2	2	8.2	28.27	22.493	22.4212	22.6007	5	3	2	B6H3U1	B6H3U1	1	B6H3U1	Pc13g07410 protein	N-acetyltransferase activity	
24.8468	25.0586	24.9146	24.9809	24.9208	24.5355	3.45E-09	1.76E+08	4	4	5	116.58	24.8762	24.94	24.8124	6	3	3	B6H3U5	B6H3U5	1	B6H3U5	Pc13g07450 protein	catalytic activity; metal ion binding; proteolysis	
29.4261	29.6155	29.4044	29.7498	30.5348	28.975	8.77E-88	4.83E+09	3	3	53.6	13.805	29.6176	29.482	29.7532	6	3	3	B6H3V3	B6H3V3	1	B6H3V3	Pc13g10440 protein	intracellular; transport	
28.767	28.4946	28.3118	29.9067	29.3441	28.7374	9.70E-39	3.04E+09	6	6	28.6	24.246	28.9269	28.5245	29.3294	6	3	3	B6H3W6	B6H3W6	1	B6H3W6	Ribosomal protein	RNA binding; large ribosomal subunit; structural constituent of ribosome; translation	
ND	ND	ND	26.1907	26.6484	ND	7.61E-11	1.83E+08	3	3	15.8	21.099	26.4196	ND	26.4196	2	0	2	B6H3X2;BGHBP3	B6H3X2	2	B6H3X2	Pc13g10970 protein	GTP binding; intracellular; signal transducer activity; small GTPase mediated signal transduction	
26.7949	26.2813	26.5756	ND	23.5518	25.4108	1.54E-13	3.43E+08	3	3	9.7	42.149	25.7229	26.5506	24.4813	5	3	2	B6H3X3	B6H3X3	1	B6H3X3	Pc13g11060 protein		
24.1551	24.4109	24.1282	24.8224	25.0889	23.9979	2.73E-06	1.29E+08	2	2	32.7	11	24.4339	24.2314	24.6364	6	3	3	B6H3Y0	B6H3Y0	1	B6H3Y0	Pc13g11030 protein		
25.9537	25.8897	25.6541	25.1361	25.6216	25.3674	4.55E-20	2.91E+08	3	3	9.1	51.022	25.6038	25.8325	25.375	6	3	3	B6H412	B6H412	1	B6H412	Pc13g10760 protein		
28.4408	28.7835	28.4778	28.6982	29.139	27.7769	3.15E-123	2.3E+09	9	9	26.8	44.534	28.5527	28.5673	28.538	6	3	3	B6H413	B6H413	1	B6H413	cAMP-dependent protein kinase regulatory subunit	cAMP binding; cAMP-dependent protein kinase complex; cAMP-dependent protein kinase regulator activity	
30.7321	30.8071	30.7256	31.1755	31.54	30.1969	9.08E-184	1.11E+10	6	3	50	17.607	30.8629	30.7549	30.9708	6	3	3	B6H433;B6HRI1	B6H433;B6HRI1	2	B6H433	Pc13g09510 protein	ribosome; structural constituent of ribosome; translation	
27.356	27.7811	27.3887	27.6487	28.072	26.4292	2.05E-32	1.1E+09	5	5	18	43.942	27.4459	27.5086	27.3833	6	3	3	B6H434	B6H434	1	B6H434	Pc13g09520 protein	carbohydrate metabolic process; chitin catabolic process; chitinase activity	
29.6973	29.8	29.6126	30.1592	30.1652	28.8971	1.16E-206	5.21E+09	13	13	55.3	27.561	29.7219	29.7033	29.7405	6	3	3	B6H436	B6H436	1	B6H436	Proteasome subunit alpha type	cytoplasm; nucleus; proteasome core complex, alpha-subunit complex; threonine-type endopeptidase activity; ubiquitin-dependent protein catabolic process	Cytoplasm. Nucleus.
27.1936	27.6738	27.8014	26.5899	26.4248	28.0512	1.66E-92	9.72E+08	9	9	41.8	37.601	27.2891	27.5563	27.022	6	3	3	B6H443	B6H443	1	GET3	ATPase get3	ATP binding; ATPase activity; endoplasmic reticulum; metal ion binding; protein insertion into ER membrane; transport	Cytoplasm. Endoplasmic reticulum.
30.7427	30.7598	30.7442	31.0001	31.187	29.8426	1.08E-187	1.03E+10	8	8	32.7	43.387	30.7127	30.7489	30.6766	6	3	3	B6H445	B6H445	1	B6H445	Pc13g09680 protein	aspartic-type endopeptidase activity; proteolysis	
23.4841	23.5624	23.57	ND	ND	27.0163	3.01E-26	1.33E+08	7	7	21.9	51.772	24.4082	23.5388	27.0163	4	3	1	B6H447	B6H447	1	B6H447	Eukaryotic translation initiation factor 3 subunit E	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
28.07	27.9424	27.8698	29.7005	29.9424	28.2626	4.09E-199	2.68E+09	12	11	28	55.769	28.6313	27.9607	29.3018	6	3	3	B6H451	B6H451	1	B6H451	Inosine-5-monophosphate dehydrogenase	GMP biosynthetic process; IMP dehydrogenase activity; adenyl nucleotide binding; metal ion binding	
28.7845	28.4416	28.6544	27.7184	25.8306	28.4103	3.15E-100	1.83E+09	14	14	37.9	56.953	27.9733	28.6268	27.3198	6	3	3	B6H453	B6H453	1	B6H453	Glycylpeptide N-tetradecanoyltransferase	N-terminal protein myristoylation; glycylpeptide N-tetradecanoyltransferase activity	
ND	ND	ND	24.5381	24.3954	24.0563	7.39E-06	70929000	2	1	10.5	24.076	24.3299	ND	24.3299	3	0	3	B6H456	B6H456	1	B6H456	Pc13g07680 protein	GTP binding; protein transport; small GTPase mediated signal transduction	
27.2814	27.6928	27.3129	28.1508	28.0011	26.6237	2.13E-72	1.16E+09	7	7	22.9	57.839	27.5104	27.429	27.5918	6	3	3	B6H474	B6H474	1	B6H474	Pc13g07790 protein	gamma-aminobutyric acid catabolic process; succinate-semialdehyde dehydrogenase [NAD(P)+] activity	
23.9781	24.6292	24.4657	24.6041	24.7149	24.7941	2.66E-07	1.34E+08	2	2	10.2	44.988	24.531	24.3577	24.7044	6	3	3	B6H478	B6H478	1	B6H478	Pc13g07870 protein	GTP binding	
29.5959	29.7258	29.6114	25.1194	26.6604	29.2736	4.23E-162	3.17E+09	8	8	61.1	23.656	28.3311	29.6444	27.0178	6	3	3	B6H4B4	B6H4B4	1	B6H4B4	Adenylyl-sulfate kinase	ATP binding; adenylylsulfate kinase activity; hydrogen sulfide biosynthetic process; sulfate assimilation	
23.9888	23.2907	25.0219	23.824	22.9195	24.1065	0.000237	95873000	2	2	5.9	43.986	23.8586	24.1004	23.6167	6	3	3	B6H4B5	B6H4B5	1	B6H4B5	Pc13g08280 protein	ATP hydrolysis coupled proton transport; hydrogen-exporting ATPase activity, phosphorylative mechanism; proton-transporting V-type ATPase, V1 domain	
25.4564	26.0117	25.6048	27.2597	27.4669	25.4203	6.80E-58	5.17E+08	5	5	16.5	46.595	26.2033	25.691	26.7157	6	3	3	B6H4D0	B6H4D0	1	B6H4D0	Pc13g08470 protein	glycerophospholipid biosynthetic process; kinase activity	
26.163	26.4326	26.196	26.0188	26.7895	25.3494	9.10E-25	4.24E+08	5	5	18.9	34.557	26.1582	26.2639	26.0526	6	3	3	B6H4D1	B6H4D1	1	B6H4D1	Pc13g08480 protein		
25.17	25.2592	25.1029	25.7363	26.5626	ND	1.92E-06	2.63E+08	2	2	8.2	34.459	25.5662	25.1774	26.1495	5	3	2	B6H4G0	B6H4G0	1	B6H4G0	Pc13g08730 protein	carbohydrate metabolic process; hydrolase activity, hydrolyzing O-glycosyl compounds	
26.9104	27.4406	27.4402	24.8488	24.0413	27.7881	2.77E-42	7E+08	12	12	15.2	151.13	26.4116	27.2638	25.5594	6	3	3	B6H4G3	B6H4G3	1	B6H4G3	Pc13g08760 protein		
31.7459	31.9912	31.7229	32.075	32.6689	31.0331	5.21E-182	2.32E+10	5	5	24.2	25.064	31.8728	31.82	31.9257	6	3	3	B6H4G8	B6H4G8	1	B6H4G8	Pc13g08810 protein	eukaryotic translation elongation factor 1 complex; translation elongation factor activity	
29.9613	29.1864	29.08	30.3669	30.161	29.7706	9.18E-111	5.16E+09	9	9	41.6	21.928	29.7544	29.4092	30.0995	6	3	3	B6H4H5	B6H4H5	1	B6H4H5	Pc13g08880 protein	ribosome; structural constituent of ribosome; translation	
27.4809	27.0344	27.4657	27.5881	27.8148	26.4192	8.81E-71	9.79E+08	5	5	21.8	41.371	27.3005	27.327	27.274	6	3	3	B6H4H6	B6H4H6	1	B6H4H6	Pc13g08890 protein	cytoplasm; nucleus	
27.8579	27.8928	27.7227	28.2675	28.5515	27.8402	8.82E-66	1.55E+09	5	5	20.7	35.373	28.0221	27.8245	28.2197	6	3	3	B6H4I2	B6H4I2	1	B6H4I2	Pc13g09710 protein	arginase activity; arginine metabolic process; metal ion binding	
29.28	29.3934	29.2587	29.5908	29.8597	28.9545	5.96E-168	4E+09	14	14	48.4	38.626	29.3895	29.3107	29.4683	6	3	3	B6H4I9	B6H4I9	1	B6H4I9	Homoserine dehydrogenase	NADP binding; homoserine dehydrogenase activity; isoleucine biosynthetic process; methionine biosynthetic process; threonine biosynthetic process	
29.088	29.2724	28.9895	29.6187	29.8241	28.5285	4.34E-56	3.64E+09	4	4	26.9	12.412	29.2202	29.1166	29.3237	6	3	3	B6H4J2	B6H4J2	1	B6H4J2	Pc13g09020 protein		
27.6017	27.8008	27.6612	27.8771	28.1812	27.1287	3.76E-79	1.24E+09	7	7	33	31.234	27.7084	27.6879	27.729	6	3	3	B6H4L8	B6H4L8	1	B6H4L8	Pc13g09260 protein	chromatin assembly or disassembly; nucleus	
32.6649	33.1776	32.6554	32.3411	32.2854	32.4619	0	3.79E+10	10	10	19.5	62.892	32.5977	32.8327	32.3628	6	3	3	B6H4M2	B6H4M2	1	B6H4M2	Pc13g09300 protein	catalytic activity; magnesium ion binding; thiamine pyrophosphate binding	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
27.0164	26.9707	27.2587	29.168	29.3605	27.2964	3.08E-40	1.66E+09	4	4	11.7	48.304	27.8451	27.0819	28.6083	6	3	3	B6H4M5	B6H4M5	1	B6H4M5	Pc13g09740 protein	oxidoreductase activity	
24.3307	22.7667	24.0948	ND	ND	23.2485	2.26E-07	57911000	2	2	8	39.642	23.6102	23.7308	23.2485	4	3	1	B6H4N2	B6H4N2	1	B6H4N2	Pc13g09810 protein	catalytic activity	
27.5204	27.8584	27.6633	27.6612	28.253	26.726	6.74E-50	1.23E+09	12	12	25.7	61.726	27.6137	27.6807	27.5467	6	3	3	B6H4P8	B6H4P8	1	B6H4P8	Pc13g09980 protein	methyltransferase activity; protein methylation	
24.5417	24.2985	24.2912	24.0229	ND	23.684	2.21E-05	1E+08	2	2	2.4	102.67	24.1677	24.3772	23.8535	5	3	2	B6H4Q5	B6H4Q5	1	B6H4Q5	Pc13g10050 protein		
23.3369	23.334	23.2744	23.3257	23.4696	22.6886	0.000549	57019000	2	2	7	37.833	23.2382	23.3151	23.1613	6	3	3	B6H4S6	B6H4S6	1	B6H4S6	Pc13g10260 protein		
26.6031	25.811	ND	23.622	ND	ND	1.18E-84	2.05E+08	2	2	17.4	7.3364	25.3454	26.2071	23.622	3	2	1	B6H4T7	B6H4T7	1	B6H4T7	Pc13g10370 protein		
29.1745	28.7342	29.186	27.8924	26.9096	29.3347	8.93E-86	2.57E+09	11	11	38.8	41.702	28.5386	29.0316	28.0456	6	3	3	B6H4U2	B6H4U2	1	B6H4U2	Pc13g11380 protein	NAD binding; isocitrate dehydrogenase (NAD+) activity; magnesium ion binding; tricarboxylic acid cycle	
ND	24.6207	ND	26.2505	25.4677	ND	8.28E-06	1.6E+08	2	2	6.1	38.178	25.4463	24.6207	25.8591	3	1	2	B6H4V7	B6H4V7	1	B6H4V7	Pc13g11500 protein		
25.1677	25.6056	25.2821	ND	ND	25.1898	1.80E-09	2.62E+08	4	4	10	56.169	25.3113	25.3518	25.1898	4	3	3	B6H4X2	B6H4X2	1	B6H4X2	Adenylyl cyclase-associated protein	actin cytoskeleton organization; cell morphogenesis	
25.6423	25.5246	25.5801	24.4711	24.3788	25.7819	6.34E-21	2.27E+08	6	6	11.5	101.64	25.2298	25.5823	24.8773	6	3	3	B6H4Z0	B6H4Z0	1	B6H4Z0	Pc13g11660 protein	carbohydrate metabolic process; glycogen phosphorylase activity; pyridoxal phosphate binding	
29.337	29.7811	29.3106	29.1632	29.4387	31.554	6.95E-187	5.65E+09	6	6	23.3	34.587	29.7641	29.4762	30.052	6	3	3	B6H4Z3	B6H4Z3	1	B6H4Z3	Pc13g11570 protein	5S rRNA binding; ribosome; structural constituent of ribosome; translation	
26.5756	26.1367	26.8209	26.4456	25.4363	27.2798	2.01E-45	5.31E+08	8	8	27.7	45.507	26.4491	26.5111	26.3872	6	3	3	B6H4Z8	B6H4Z8	1	B6H4Z8	Pc13g11970 protein	ATP binding; Arp2/3 complex-mediated actin nucleation; Arp2/3 protein complex	
25.1471	25.5911	25.5367	26.1695	26.0332	23.9838	4.52E-15	2.97E+08	6	6	14.6	46.519	25.4102	25.425	25.3955	6	3	3	B6H5U8	B6H5U8	1	B6H5U8	Pc13g11750 protein	actin filament organization; calcium ion binding; endocytosis	
24.0985	24.3589	24.1834	23.8801	24.3329	23.8926	6.31E-17	1.03E+08	2	2	12.2	20.822	24.1244	24.2136	24.0352	6	3	3	B6H548	B6H548	1	B6H548	Pc13g13540 protein	nucleus	
28.3302	28.7328	28.4013	28.3719	28.9304	27.1649	3.13E-43	2.07E+09	4	4	60.8	12.087	28.3219	28.4881	28.1557	6	3	3	B6H565	B6H565	1	B6H565	Pc13g13950 protein		
25.5314	25.925	25.6669	26.4072	26.7965	23.2737	1.14E-18	3.57E+08	2	2	10.8	31.837	25.6001	25.7078	25.4925	6	3	3	B6H581	B6H581	1	B6H581	Pc13g12090 protein	retrograde vesicle-mediated transport, Golgi to ER; structural molecule activity	
27.5295	27.3611	27.5235	28.2928	28.0622	27.9996	1.59E-114	1.23E+09	15	15	28.7	81.034	27.7948	27.4714	28.1182	6	3	3	B6H5A3	B6H5A3	1	B6H5A3	Anthranilate synthase multifunctional protein trpC-Penicillium chrysogenum	anthranilate synthase activity; indole-3-glycerol-phosphate synthase activity; phosphoribosylanthranilate isomerase activity; tryptophan metabolic process	
32.1984	32.2241	32.166	31.9246	32.3311	30.7134	0	2.48E+10	21	21	34.4	74.374	31.9263	32.1962	31.6564	6	3	3	B6H5B6	B6H5B6	1	B6H5B6	Transketolase	metal ion binding; transketolase activity	
31.5961	31.8561	31.6522	32.0337	32.3651	30.857	0	2.1E+10	13	13	64.5	33.1	31.7267	31.7015	31.7519	6	3	3	B6H5C0	B6H5C0	1	B6H5C0	Pc13g12400 protein	transferase activity	
26.2248	25.5304	25.8962	ND	ND	ND	1.55E-13	2.06E+08	5	5	12.9	46.869	25.8838	25.8838	ND	3	3	0	B6H5I7	B6H5I7	1	B6H5I7	Pc14g00170 protein	hydrolase activity, acting on ester bonds	
27.0226	26.8467	27.1204	28.4888	28.5169	27.3107	1.62E-34	1.21E+09	5	5	9.1	53.643	27.551	26.9966	28.1055	6	3	3	B6H5K5	B6H5K5	1	B6H5K5	Pc14g00350 protein	proteolysis; serine-type carboxypeptidase activity	
28.0787	27.2546	28.1455	27.342	25.5401	28.8402	4.55E-107	1.34E+09	12	12	17.7	115.08	27.5335	27.8263	27.2408	6	3	3	B6H5K9	B6H5K9	1	B6H5K9	Pc14g00390 protein	glycine catabolic process; glycine dehydrogenase (decarboxylating) activity; pyridoxal phosphate binding	
25.6096	24.9244	25.668	25.9547	24.6885	25.2593	1.31E-15	2.54E+08	4	4	15.1	44.61	25.3508	25.4007	25.3008	6	3	3	B6H5M8	B6H5M8	1	B6H5M8	Pc14g00670 protein	oxidoreductase activity; zinc ion binding	
25.7207	25.716	25.5976	25.6656	25.6572	ND	1.89E-11	2.78E+08	4	4	8.3	66.331	25.6714	25.6781	25.6614	5	3	2	B6H5P1	B6H5P1	1	B6H5P1	Pc14g00680 protein	hydrolase activity; nucleotide catabolic process	
28.2404	27.2078	28.1256	27.1191	25.8245	28.9166	5.34E-54	1.28E+09	6	6	25.2	39.088	27.5723	27.8579	27.2867	6	3	3	B6H5P2	B6H5P2	1	B6H5P2	Pc14g00690 protein	acetyl-CoA biosynthetic process from pyruvate; pyruvate dehydrogenase (acetyl-transferring) activity	
ND	17.1527	16.7005	ND	ND	31.3539	0	1.61E+09	44	44	31.5	230.96	21.7357	16.9266	31.3539	3	2	1	B6H5P7	B6H5P7	1	B6H5P7	Pc14g00740 protein	enoyl-[acyl-carrier-protein] reductase (NADH) activity; fatty acid biosynthetic process; fatty acid synthase complex	
22.2344	22.4578	22.2575	23.412	22.9219	31.4423	0	1.87E+09	43	43	29	204.01	24.121	22.3165	25.9254	6	3	3	B6H5P8	B6H5P8	1	B6H5P8	Pc14g00750 protein	fatty acid biosynthetic process; holo-[acyl-carrier-protein] synthase activity; macromolecule biosynthetic process; magnesium ion binding	
27.5165	27.6375	27.5917	27.497	27.8185	26.5671	5.23E-50	1.07E+09	4	4	15.1	31.75	27.4381	27.5819	27.2942	6	3	3	B6H5Q7	B6H5Q7	1	B6H5Q7	Pc14g00790 protein	phosphatidylinositol phosphorylation	
25.7239	25.8002	26.006	24.3218	ND	26.0129	3.59E-34	2.87E+08	4	4	16.5	40.372	25.5729	25.8434	25.1673	5	3	2	B6H5R4	B6H5R4	1	MTNA	Methylthioribose-1-phosphate isomerase	L-methionine salvage from methylthioadenosine; 5-methyl-5-thioribose-1-phosphate isomerase activity; cytoplasm; nucleus	Cytoplasm. Nucleus.
28.1269	28.3081	28.0553	28.49	28.64	27.4607	2.67E-90	1.74E+09	10	10	36.5	28.84	28.1802	28.1634	28.1969	6	3	3	B6H5U2	B6H5U2	1	B6H5U2	Pc14g01140 protein	proteasome core complex; proteolysis involved in cellular protein catabolic process; threonine-type endopeptidase activity	
24.9953	25.0133	25.7077	24.7578	25.3092	28.1069	3.13E-35	4.02E+08	10	10	34.1	41.815	25.6484	25.2388	26.058	6	3	3	B6H5U5	B6H5U5	1	B6H5U5	Pc14g01170 protein	NAD binding; isocitrate dehydrogenase (NAD+) activity; magnesium ion binding; tricarboxylic acid cycle	
28.4042	28.516	28.4672	28.7946	29.0976	27.6495	4.70E-45	2.24E+09	6	6	25.9	27.966	28.4882	28.4624	28.5139	6	3	3	B6H5V1	B6H5V1	1	B6H5V1	Pc14g01230 protein	proteasome core complex; proteolysis involved in cellular protein catabolic process; threonine-type endopeptidase activity	
27.4254	27.3674	27.4135	27.531	27.5054	26.245	9.39E-24	9.67E+08	4	4	15.8	28.685	27.248	27.4021	27.0938	6	3	3	B6H5V4	B6H5V4	1	B6H5V4	Proteasome subunit beta type	cytoplasm; nucleus; proteasome core complex; proteolysis involved in cellular protein catabolic process; threonine-type endopeptidase activity	Cytoplasm. Nucleus.
25.526	25.0611	25.5244	25.7627	25.7535	24.4863	2.97E-15	2.49E+08	3	3	11.4	30.947	25.3523	25.3705	25.3342	6	3	3	B6H5V5	B6H5V5	1	B6H5V5	Pc14g01270 protein	catalytic activity	
27.2873	26.623	27.1611	27.0593	25.8094	27.631	4.23E-61	7.37E+08	8	8	35.4	39.849	26.9285	27.0238	26.8333	6	3	3	B6H5W1	B6H5W1	1	B6H5W1	Pc14g01330 protein	cytoskeleton; regulation of actin filament polymerization	
29.1424	29.4961	29.1588	29.6007	29.8028	28.4389	2.12E-289	3.8E+09	10	10	46.6	30.338	29.2733	29.2658	29.2808	6	3	3	B6H5X1	B6H5X1	1	B6H5X1	Pc14g01430 protein	cytoplasm; mannose biosynthetic process; phosphomannomutase activity	Cytoplasm.
30.1783	30.2099	30.3175	28.5557	28.2023	29.8317	0	5.28E+09	12	10	39.1	31.186	29.5492	30.2352	28.8632	6	3	3	B6H5Z8	B6H5Z8	1	B6H5Z8	Pc14g01700 protein		
27.0867	27.2927	27.1247	ND	ND	27.2925	5.16E-75	6.83E+08	3	3	13.6	29.681	27.1992	27.1681	27.2925	4	3	1	B6H601	B6H601	1	B6H601	Eukaryotic translation initiation factor 3 subunit J	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
32.134	31.8958	31.9908	30.0958	29.4391	33.885	0	2.75E+10	17	17	46.8	47.222	31.5734	32.0069	31.14	6	3	3	B6H602	B6H602	1	B6H602	Enolase BAC82549-Penicillium chrysogenum	glycolysis; magnesium ion binding; phosphopyruvate hydratase activity; phosphopyruvate hydratase complex	
25.9498	26.1612	26.0405	26.6967	26.9152	25.9798	1.43E-47	4.68E+08	3	3	10	45.537	26.2905	26.0505	26.5306	6	3	3	B6H605	B6H605	1	B6H605	Pc14g01770 protein	L-threonine ammonia-lyase activity; metallopeptidase activity; proteolysis	
23.8543	23.4696	23.2493	26.7974	27.1425	26.1626	7.38E-35	2.96E+08	5	5	35.9	22.048	25.1126	23.5244	26.7008	6	3	3	B6H621	B6H621	1	B6H621	Pc14g01930 protein	GTP binding; intracellular; membrane; small GTPase mediated signal transduction	
28.1354	28.2166	28.0018	28.4412	28.3951	27.4523	4.30E-118	1.68E+09	9	9	25.9	43.776	28.1071	28.1179	28.0962	6	3	3	B6H629	B6H629	1	B6H629	Chorismate synthase	aromatic amino acid family biosynthetic process; chorismate biosynthetic process; chorismate synthase activity	
28.6036	29.1376	28.6689	28.6222	29.4497	28.9221	3.14E-46	2.77E+09	6	6	13.4	52.915	28.9007	28.8034	28.998	6	3	3	B6H668	B6H668	1	B6H668	Pc15g01230 protein	nucleic acid binding; nucleotide binding	
28.4381	28.5325	28.3522	28.8278	29.2982	27.7468	1.39E-126	2.27E+09	7	7	22	46.049	28.5326	28.4409	28.6243	6	3	3	B6H671	B6H671	1	B6H671	Pc15g01260 protein	Ran GTPase activator activity	
24.975	25.5454	24.8656	ND	ND	24.9495	2.22E-12	1.79E+08	6	6	7.4	108.97	25.0839	25.1287	24.9495	4	3	1	B6H6B5	B6H6B5	1	B6H6B5	Pc15g01800 protein	ATP binding; ATP biosynthetic process; hydrogen-exporting ATPase activity, phosphorylative mechanism; integral component of membrane; metal ion binding	
30.5132	29.816	30.362	20.5762	21.271	ND	1.72E-42	4.19E+09	6	6	12.6	50.552	26.5077	30.2304	20.9236	5	3	2	B6H6C3	B6H6C3	1	B6H6C3	Pc15g01880 protein	hydrolase activity, acting on ester bonds	
28.4273	28.1934	28.379	25.6333	25.8784	25.1256	1.86E-110	1.2E+09	11	11	23.1	87.152	26.9395	28.3333	25.5457	6	3	3	B6H6C5	B6H6C5	1	B6H6C5	Pc15g01900 protein	Mo-molybdopterin cofactor biosynthetic process; carbohydrate metabolic process; cation binding; cytosol; molybdopterin synthase activity; molybdopterin synthase complex	
26.1017	26.2499	26.2021	27.4126	27.5195	25.9192	1.10E-16	6E+08	2	2	7.1	48.413	26.5675	26.1846	26.9504	6	3	3	B6H6G8	B6H6G8	1	B6H6G8	Pc15g00210 protein	carbohydrate metabolic process	
29.6038	29.7761	29.5768	30.0305	30.0999	28.7854	2.64E-164	4.94E+09	12	12	59.3	26.967	29.6454	29.6523	29.6386	6	3	3	B6H6H8	B6H6H8	1	B6H6H8	Proteasome subunit alpha type	cytoplasm; nucleus; proteasome core complex, alpha-subunit complex; threonine-type endopeptidase activity; ubiquitin-dependent protein catabolic process	Cytoplasm. Nucleus.
27.6226	27.9524	27.6303	26.5773	26.7874	27.6766	1.47E-77	1.06E+09	9	9	38	33.662	27.3744	27.7351	27.0138	6	3	3	B6H6I2	B6H6I2	1	B6H6I2	Pc15g00360 protein		
25.3482	25.522	25.5345	26.2189	26.303	24.8429	2.83E-07	3.03E+08	3	3	14.9	19.11	25.6282	25.4682	25.7882	6	3	3	B6H6I9	B6H6I9	1	B6H6I9	Pc15g00430 protein		
25.2644	25.857	25.963	25.693	25.9287	ND	1.62E-49	2.95E+08	4	4	44	14.045	25.7412	25.6948	25.8108	5	3	2	B6H6J0	B6H6J0	1	B6H6J0	V-type proton ATPase subunit F	ATP hydrolysis coupled proton transport; proton-transporting ATPase activity, rotational mechanism; proton-transporting V-type ATPase, V1 domain	
28.2195	28.2893	27.9535	28.6286	29.2317	27.6017	3.64E-52	2.06E+09	8	8	48.2	26.074	28.3207	28.1541	28.4873	6	3	3	B6H6J5	B6H6J5	1	B6H6J5	Pc15g00490 protein	nucleoside metabolic process; orotate phosphoribosyltransferase activity; pyrimidine nucleotide biosynthetic process	
30.7427	31.0083	30.8863	29.8184	29.8516	30.1147	0	8.74E+09	25	25	62.9	51.908	30.4037	30.8791	29.9282	6	3	3	B6H6L0	B6H6L0	1	B6H6L0	Pc15g00640 protein	Rab GDP-dissociation inhibitor activity; protein transport	
26.4171	26.3548	26.6569	26.1444	25.524	27.5506	3.31E-45	5.2E+08	6	6	20.9	37.171	26.4413	26.4763	26.4063	6	3	3	B6H6M5	B6H6M5	1	B6H6M5	Pc15g00800 protein	cytoskeleton; regulation of actin filament polymerization	
29.0502	29.1861	29.0506	30.0115	30.1771	28.5871	1.81E-186	4.07E+09	7	7	22.9	49.227	29.3438	29.0956	29.5919	6	3	3	B6H6P7	B6H6P7	1	B6H6P7	Pc15g01030 protein	carbohydrate metabolic process	
28.9451	29.032	28.8268	29.123	29.5532	28.0624	8.20E-196	3.02E+09	9	9	14.6	83.832	28.9238	28.9347	28.9129	6	3	3	B6H721	B6H721	1	B6H721	Pc16g01190 protein	intracellular	
28.1633	28.2272	28.1493	27.8356	28.4809	27.9175	1.56E-40	6.6E+09	9	9	26.4	47.664	28.129	28.1799	28.078	6	3	3	B6H735	B6H735	1	B6H735	Pc16g02160 protein	metal ion binding; protein dephosphorylation; protein serine/threonine phosphatase activity	
25.7601	ND	25.6472	25.57	ND	ND	1.53E-60	2.59E+08	2	2	26.2	15.802	25.6591	25.7037	25.57	3	2	1	B6H747	B6H747	1	B6H747	Pc16g02610 protein	small ribosomal subunit; structural constituent of ribosome; translation	
25.375	25.3925	25.2548	25.4953	25.9019	25.1712	1.04E-07	2.52E+08	3	3	24.3	25.501	25.4318	25.3408	25.5228	6	3	3	B6H760	B6H760	1	B6H760	Pc16g01820 protein		
28.2671	28.4233	28.3799	28.5154	29.2312	27.7156	1.95E-85	2.06E+09	7	7	39.8	21.933	28.4221	28.3568	28.4874	6	3	3	B6H762	B6H762	1	B6H762	Pc16g01840 protein	guanylate kinase activity; purine nucleotide metabolic process	
27.6578	27.7498	27.4455	26.8306	26.85	29.0149	1.37E-129	1.22E+09	10	10	46	36.695	27.5914	27.6177	27.5652	6	3	3	B6H769	B6H769	1	B6H769	Eukaryotic translation initiation factor 3 subunit F	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
28.7706	29.2166	28.8015	29.5268	29.8496	28.2111	4.91E-132	3.33E+09	14	14	54.8	39.621	29.0627	28.9296	29.1958	6	3	3	B6H774	B6H774	1	B6H774	Pc16g02020 protein		
26.9642	27.1155	27.0174	28.0814	28.1528	27.0324	2.02E-134	1.05E+09	9	9	39.1	39.368	27.394	27.0324	27.7555	6	3	3	B6H777	B6H777	1	B6H777	Pc16g02050 protein		
26.997	26.9654	26.5586	26.8559	26.7166	26.3855	2.78E-19	6.54E+08	4	4	18.8	20.505	26.7465	26.8404	26.6527	6	3	3	B6H779	B6H779	1	B6H779	Pc16g02070 protein		
26.4733	26.5156	26.5612	26.344	26.2094	27.6989	1.24E-31	6.16E+08	4	4	15.4	21.709	26.6337	26.5167	26.7508	6	3	3	B6H787	B6H787	1	B6H787	Pc16g02160 protein	rRNA binding; ribosome; structural constituent of ribosome; translation	
24.2912	24.1855	24.1278	ND	ND	25.9048	1.42E-06	1.21E+08	2	2	14.1	18.008	24.6273	24.2015	25.9048	4	3	1	B6H7A6	B6H7A6	1	B6H7A6	Pc16g02000 protein		
24.3169	ND	24.4113	ND	ND	ND	2.62E-05	71101000	2	2	15	16.687	24.3641	24.3641	ND	2	2	0	B6H7B1	B6H7B1	1	B6H7B1	Pc16g02280 protein		
24.9676	24.6304	25.6201	ND	ND	23.7623	1.44E-08	1.3E+08	3	3	8	45.354	24.7451	25.0727	23.7623	4	3	1	B6H7C0	B6H7C0	1	B6H7C0	Pc16g02370 protein		
25.7019	25.8043	25.4802	24.2721	25.3918	24.8081	3.73E-15	2.43E+08	4	4	21.6	23.931	25.2431	25.6622	24.824	6	3	3	B6H7C4	B6H7C4	1	B6H7C4	Pc16g06520 protein		
24.5101	24.4715	24.3875	24.1368	24.5009	23.3888	2.38E-12	1.16E+08	2	2	8.8	35.743	24.2326	24.4564	24.0088	6	3	3	B6H7F2	B6H7F2	1	B6H7F2	Pc16g09600 protein	oxidoreductase activity	
24.5206	24.6609	24.6337	ND	23.5684	24.7711	8.52E-05	1.12E+08	2	2	8	25.844	24.4309	24.6051	24.1697	5	3	2	B6H7H7	B6H7H7	1	B6H7H7	Pc16g06600 protein	N-acetyltransferase activity	
25.8658	26.2402	26.0753	27.2417	27.0793	25.575	5.61E-41	5.31E+08	7	7	12.2	93.592	26.3462	26.0604	26.632	6	3	3	B6H7J0	B6H7J0	1	B6H7J0	E3 ubiquitin-protein ligase	ubiquitin-protein ligase activity	
26.9567	27.4113	27.2797	25.0454	25.6744	27.2013	5.54E-42	6.92E+08	4	4	24.9	41.123	26.5948	27.2159	25.9737	6	3	3	B6H7J3	B6H7J3	1	B6H7J3	Pc16g02790 protein	catalytic activity; pyridoxal phosphate binding	
26.6796	26.8353	26.4963	26.0778	26.8577	ND	3.16E-37	5.22E+08	2	2	29.2	15.378	26.5894	26.6704	26.4678	5	3	2	B6H7N4	B6H7N4	1	B6H7N4	Pc16g03290 protein	hydrolase activity	
26.6751	26.5225	26.5363	26.5912	26.9875	25.9757	7.16E-17	5.59E+08	5	5	23.7	31.271	26.548	26.5779	26.5181	6	3	3	B6H7U0	B6H7U0	1	B6H7U0	Pc16g03770 protein		
29.4315	29.0192	29.2136	27.6765	27.4805	30.8427	1.32E-72	3.62E+09	5	5	47.5	17.651	28.944	29.2214	28.6665	6	3	3	B6H7X2	B6H7X2	1	B6H7X2	Pc16g08430 protein	peptidyl-lysine modification to hypusine; positive regulation of translational elongation; positive regulation of translational termination; ribosome binding; translation elongation factor activity; translational frameshifting	
28.0748	28.4147	28.2561	28.2215	28.1332	27.465	6.20E-136	1.67E+09	7	7	27.1	51.388	28.0942	28.2485	27.9399	6	3	3	B6H805	B6H805	1	B6H805	Aminomethyltransferase	aminomethyltransferase activity; cytoplasm; glycine catabolic process; transaminase activity	
24.613	24.9378	24.9577	22.8303	22.099	23.1573	3.18E-08	1.15E+08	3	3	9.4	41.668	23.7658	24.8361	22.6955	6	3	3	B6H823	B6H823	1	B6H823	Pc16g08230 protein	oxidoreductase activity	
26.6063	26.7543	26.1241	26.6581	27.0432	24.7469	7.64E-45	5.49E+08	9	9	21.3	67.206	26.3221	26.4949	26.1494	6	3	3	B6H832	B6H832	1	B6H832	Signal recognition particle subunit SRP68	7S RNA binding; SRP-dependent cotranslational protein targeting to membrane; endoplasmic reticulum signal peptide binding; signal recognition particle binding; signal recognition particle, endoplasmic reticulum targeting	Cytoplasm.
27.5091	25.4063	27.0866	26.6161	24.8631	28.0753	9.99E-47	7E+08	11	11	14.4	115.95	26.5927	26.6673	26.5182	6	3	3	B6H835	B6H835	1	B6H835	Pc16g08350 protein	GTP binding; GTPase activity	
31.3262	31.655	31.392	31.7261	32.124	31.1272	0	1.8E+10	27	27	37.5	79.674	31.5584	31.4577	31.6591	6	3	3	B6H844	B6H844	1	B6H844	Pc16g09030 protein	RNA binding; nucleotide binding	
23.5961	24.0639	23.9074	25.6672	24.6651	ND	1.97E-17	1.15E+08	4	4	6.6	92.097	24.3799	23.8558	25.1662	5	3	2	B6H855	B6H855	1	B6H855	Pc16g10440 protein		

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
22.6915	ND	23.8208	ND	ND	24.6669	6.12E-06	46210000	2	2	1.8	142.55	23.7264	23.2562	24.6669	3	2	1	B6H868	B6H868	1	B6H868	Pc16g04070 protein	RNA binding	
28.7451	29.0143	28.4174	30.0975	30.2313	27.4159	1.85E-71	3.65E+09	6	6	32.3	14.562	28.9869	28.7256	29.2482	6	3	3	B6H873	B6H873	1	B6H873	Pc16g04120 protein	ribosome; structural constituent of ribosome; translation	
22.8965	23.3067	23.2158	24.4202	23.407	23.648	0.00147	68256000	2	2	27.7	10.259	23.4824	23.1397	23.8251	6	3	3	B6H8C8	B6H8C8	1	B6H8C8	Pc16g09330 protein	metal ion binding; mitochondrial intermembrane space protein transporter complex; protein import into mitochondrial inner membrane; protein transporter activity	
25.8015	25.6153	25.5667	25.6494	26.1397	ND	3.99E-15	2.79E+08	3	3	13	37.998	25.7545	25.6612	25.8946	5	3	2	B6H8D0	B6H8D0	1	B6H8D0	Pc16g09350 protein		
ND	22.7712	ND	23.5963	23.8775	27.0845	1.25E-10	1.18E+08	4	4	19.9	25.324	24.3324	22.7712	24.8527	4	1	3	B6H8E2	B6H8E2	1	B6H8E2	Pc16g10560 protein	ribosome; structural constituent of ribosome; translation	
25.7095	26.0223	26.0939	26.2003	26.8707	25.7759	3.96E-15	4.17E+08	2	2	18.9	22.053	26.1121	25.9419	26.2823	6	3	3	B6H8E5	B6H8E5	1	B6H8E5	Pc16g10610 protein	membrane; protein transport	
24.8064	24.5179	24.6748	ND	ND	ND	5.47E-22	87730000	2	2	7.9	39.494	24.6663	24.6663	ND	3	3	0	B6H8F4	B6H8F4	1	B6H8F4	Pc16g04220 protein		
27.5205	25.3403	26.5089	23.8921	23.2206	31.052	4.13E-166	1.79E+09	14	14	52.2	33.174	26.2558	26.4566	26.0549	6	3	3	B6H8F9	B6H8F9	1	B6H8F9	Pc16g05650 protein	oxidoreductase activity	
28.1732	28.453	28.1351	28.6518	28.7071	28.2525	1.69E-174	1.97E+09	8	8	26.8	40.673	28.3955	28.2537	28.5372	6	3	3	B6H8I0	B6H8I0	1	B6H8I0	Eukaryotic translation initiation factor 3 subunit H	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; translation initiation factor activity	Cytoplasm.
25.3993	25.8621	25.5481	25.7414	26.0464	24.9128	7.74E-12	2.95E+08	2	2	9.1	35.082	25.585	25.6031	25.5669	6	3	3	B6H8K0	B6H8K0	1	B6H8K0	Pc16g08500 protein	cytoplasm; iron ion binding; iron-sulfur cluster assembly; iron-sulfur cluster binding	
28.4027	28.6731	28.4462	28.4847	28.9393	27.9867	1.90E-135	2.16E+09	9	9	57.9	33.181	28.4888	28.5074	28.4702	6	3	3	B6H8K8	B6H8K8	1	B6H8K8	Proliferating cell nuclear antigen	DNA binding; DNA polymerase processivity factor activity; DNA replication; PCNA complex; nucleus; regulation of DNA replication	Nucleus.
28.8838	28.8941	28.5943	28.97	29.5169	28.2324	7.75E-66	2.79E+09	7	7	26.5	36.412	28.8486	28.7908	28.9064	6	3	3	B6H8M0	B6H8M0	1	B6H8M0	Pc16g05860 protein		
29.669	29.5907	29.327	28.6395	28.7663	29.9164	5.25E-70	3.86E+09	6	6	35	22.567	29.3181	29.5289	29.1074	6	3	3	B6H8N7	B6H8N7	1	B6H8N7	40S ribosomal protein S8	ribosome; structural constituent of ribosome; translation	
24.5957	25.3842	25.3683	24.1955	24.8248	31.0783	2.19E-105	1.78E+09	12	12	45.5	42.178	25.9078	25.1161	26.6995	6	3	3	B6H8Q7	B6H8Q7	1	B6H8Q7	S-adenosylmethionine synthase	ATP binding; S-adenosylmethionine biosynthetic process; metal ion binding; methionine adenosyltransferase activity; one-carbon metabolic process	
24.1422	24.1807	24.2321	24.2989	ND	24.3115	8.62E-21	99839000	4	4	11.5	53.003	24.2331	24.185	24.3052	5	3	2	B6H8R4	B6H8R4	1	B6H8R4	Pc16g04460 protein	ATP hydrolysis coupled proton transport; hydrogen-exporting ATPase activity, phosphorylative mechanism; proton-transporting ATPase activity, rotational mechanism; vacuolar proton-transporting V-type ATPase, V1 domain	
25.9372	26.922	26.7954	25.186	25.4783	26.6632	6.86E-37	4.63E+08	5	5	57.8	17.63	26.1637	26.5515	25.7758	6	3	3	B6H8T6	B6H8T6	1	B6H8T6	Pc16g06200 protein	RNA binding	
31.0106	31.0185	31.0152	31.5989	31.8041	30.4088	5.80E-268	1.38E+10	20	20	59.6	43.749	31.1427	31.0148	31.2706	6	3	3	B6H8T7	B6H8T7	1	B6H8T7	Pc16g06210 protein	GTP binding	
27.6982	27.1795	26.5279	29.2235	28.9781	28.159	3.10E-40	1.69E+09	7	7	32	24.103	27.961	27.1352	28.7868	6	3	3	B6H8U2	B6H8U2	1	B6H8U2	Ribosomal protein L15	ribosome; structural constituent of ribosome; translation	
25.7869	25.5675	25.7055	26.8478	27.2845	26.1117	9.11E-28	4.6E+08	8	8	31.6	32.147	26.2173	25.6866	26.748	6	3	3	B6H8V2	B6H8V2	1	B6H8V2	Pc16g09240 protein		
25.2864	26.1387	25.8583	ND	25.0708	25.8713	5.20E-15	2.9E+08	4	4	16.9	35.689	25.6451	25.7611	25.471	5	3	2	B6H8V3	B6H8V3	1	B6H8V3	Pc16g09250 protein	oxidoreductase activity	
28.5094	28.3219	27.8579	30.299	30.278	28.5665	8.63E-37	3.55E+09	7	7	41.3	20.917	28.9721	28.2297	29.7145	6	3	3	B6H8V4	B6H8V4	1	B6H8V4	60S ribosomal protein L20	ribosome; structural constituent of ribosome; translation	
29.9245	30.7722	30.4796	29.2079	28.9031	31.6484	1.25E-221	7.75E+09	21	21	54.7	44.077	30.156	30.3921	29.9198	6	3	3	B6H903	B6H903	1	B6H903	Phosphoglycerate kinase	ATP binding; glycolysis; phosphoglycerate kinase activity	
26.8388	26.7486	26.3895	27.1058	26.0259	26.7335	1.84E-15	6.09E+08	6	6	10.7	87.085	26.6403	26.6589	26.6217	6	3	3	B6H908	B6H908	1	B6H908	Pc16g06290 protein		
25.0545	25.1952	25.289	ND	ND	25.2409	4.67E-07	1.65E+08	4	4	9.6	40.542	25.1949	25.1796	25.2409	4	3	1	B6H917	B6H917	1	B6H917	Uroporphyrinogen decarboxylase	protoporphyrinogen IX biosynthetic process; uroporphyrinogen decarboxylase activity	
29.1598	28.6312	29.2675	29.5384	27.2495	30.3484	1.98E-35	3.59E+09	5	5	21.2	33.11	29.0325	29.0195	29.0454	6	3	3	B6H919	B6H919	1	B6H919	Pc16g10120 protein	ribosome; ribosome biogenesis; structural constituent of ribosome; translational elongation	
25.0813	25.0085	24.9335	24.9874	25.2618	24.8769	2.40E-40	1.9E+08	2	2	2.7	113.61	25.0249	25.0078	25.042	6	3	3	B6H939	B6H939	1	B6H939	Pc16g03390 protein		
ND	ND	ND	ND	24.5999	24.6624	0.00023	36460000	2	2	3	90.729	24.6312	ND	24.6312	2	0	2	B6H953	B6H953	1	B6H953	Pc16g04770 protein		
ND	23.0817	23.0233	24.4505	24.3962	26.273	1.07E-07	1.16E+08	4	4	29.1	21.442	24.2449	23.0525	25.0399	5	2	3	B6H958	B6H958	1	B6H958	Pc16g09800 protein	GTP binding; Golgi apparatus; endoplasmic reticulum; intracellular protein transport; vesicle-mediated transport	
27.2056	26.9352	27.3598	27.3567	27.0408	26.7529	1.16E-106	8.42E+08	10	10	49.1	37.172	27.1085	27.1669	27.0502	6	3	3	B6H960	B6H960	1	B6H960	Serine/threonine-protein phosphatase	hydrolase activity	
26.4252	27.0596	26.6659	28.1793	28.4764	26.3535	5.18E-52	9.96E+08	6	6	19.5	45.541	27.1933	26.7169	27.6697	6	3	3	B6H977	B6H977	1	B6H977	Pc16g10080 protein	ATP binding; metal ion binding; protein folding; response to heat	
32.9699	32.5817	33.0725	32.2532	32.1283	31.2312	0	3.58E+10	17	17	31.5	48.832	32.3728	32.8747	31.8709	6	3	3	B6H9B6	B6H9B6	1	B6H9B6	Adenosylhomocysteinase	adenosylhomocysteinase activity; one-carbon metabolic process	
25.407	25.5092	25.2224	26.4052	26.7381	25.3628	3.68E-65	3.04E+08	8	8	8.2	120.56	25.7741	25.3795	26.1687	6	3	3	B6H9E0	B6H9E0	1	B6H9E0	Eukaryotic translation initiation factor 3 subunit A	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
32.8801	32.9799	32.9559	33.6671	33.2836	32.3346	0	5.12E+10	30	30	59.2	61.795	33.0169	32.9387	33.0951	6	3	3	B6H9L7	B6H9L7	1	B6H9L7	Pc16g11070 protein	ATP binding; cytoplasm; protein refolding	
26.1358	25.7452	26.2345	26.5169	25.5644	27.6671	5.67E-18	5.06E+08	6	5	12.1	65.216	26.3107	26.0385	26.5828	6	3	3	B6H9M2	B6H9M2	1	B6H9M2	Amine oxidase	amine metabolic process; copper ion binding; primary amine oxidase activity; quinone binding	
26.4101	26.599	26.704	24.389	23.4347	25.1856	1.14E-29	3.7E+08	4	4	26.5	27.334	25.4537	26.571	24.3364	6	3	3	B6H9R2	B6H9R2	1	B6H9R2	Pc16g11920 protein	oxidoreductase activity	
28.111	28.4917	28.1652	28.2761	29.0167	27.4315	1.99E-167	1.89E+09	12	12	25.5	79.903	28.2487	28.256	28.2414	6	3	3	B6H9T9	B6H9T9	1	B6H9T9	Catalase	catalase activity; heme binding; hydrogen peroxide catabolic process; metal ion binding	
29.705	29.5852	29.5017	29.978	30.2341	29.188	4.88E-266	5.01E+09	19	19	32.3	92.521	29.6987	29.5973	29.8	6	3	3	B6H9W1	B6H9W1	1	B6H9W1	Pc16g14140 protein	NAD binding; histidine biosynthetic process; histidinol dehydrogenase activity; phosphoribosyl-AMP cyclohydrolase activity; phosphoribosyl-ATP diphosphatase activity; zinc ion binding	
27.8032	29.6147	27.4142	25.69	27.1753	29.2053	1.58E-174	1.85E+09	7	7	51	23.128	27.8171	28.2774	27.3569	6	3	3	B6H9W9	B6H9W9	1	B6H9W9	Superoxide dismutase	metal ion binding; superoxide dismutase activity; superoxide metabolic process	
24.4205	24.4697	24.6498	ND	22.8512	26.6428	1.37E-10	1.7E+08	3	3	7.3	59.263	24.6068	24.5133	24.747	5	3	2	B6HA00	B6HA00	1	B6HA00	Pc16g14540 protein	COPI vesicle coat; clathrin adaptor complex; intracellular protein transport; retrograde vesicle-mediated transport, Golgi to ER	
24.2739	25.3137	25.1786	ND	ND	23.7621	7.10E-09	1.19E+08	3	3	4	100.88	24.6321	24.9221	23.7621	4	3	1	B6HA04	B6HA04	1	B6HA04	Pc16g14580 protein		
27.7961	28.1412	27.7826	30.1738	29.3441	29.2552	2.88E-113	2.94E+09	6	6	58.5	14.709	28.7488	27.9066	29.591	6	3	3	B6HA20	B6HA20	1	B6HA20	Pc16g14740 protein	ribosome; structural constituent of ribosome; translation	
28.1028	28.5492	28.6958	28.86	29.2006	27.4352	1.86E-121	2.31E+09	15	15	23.9	95.566	28.4739	28.4493	28.4986	6	3	3	B6HA22	B6HA22	1	B6HA22	Pc16g14760 protein	intracellular protein transport; nucleocytoplasmic transport; protein transporter activity	
24.2745	24.4317	24.8123	ND	ND	26.9255	9.26E-14	1.68E+08	6	6	6.5	123.37	25.111	24.5062	26.9255	4	3	1	B6HAA3	B6HAA3	1	B6HAA3	Pc16g12120 protein	ATP binding; aminoacyl-tRNA editing activity; cytoplasm; isoleucine-tRNA ligase activity; isoleucyl-tRNA aminoacylation	
31.2563	31.3262	30.8652	28.8673	27.9172	30.4863	2.23E-113	9.31E+09	9	9	41	14.724	30.1198	31.1492	29.0903	6	3	3	B6HAB7;B6GYM8	B6HAB7;B6GYM8	2	B6HAB7	Histone H4	DNA binding; nucleosome; nucleosome assembly; nucleus	Nucleus. Chromosome.
28.8552	28.4561	28.4815	26.3977	ND	27.3782	3.46E-19	1.53E+09	3	3	16.9	15.333	27.9137	28.5976	26.8879	5	3	2	B6HAB8;REV__B6H871	B6HAB8	2	B6HAB8	Histone H3	DNA binding; nucleosome; nucleosome assembly; nucleus	
ND	ND	ND	26.4313	22.8176	23.7352	5.16E-45	3.02E+08	2	2	16.8	31.569	24.328	ND	24.328	3	0	3	B6HAE6	B6HAE6	1	B6HAE6	Pc16g12550 protein	diphthine synthase activity; peptidyl-diphthamide biosynthetic process from peptidyl-histidine	
24.4494	24.6428	24.665	24.0048	24.0631	24.9554	1.33E-10	1.29E+08	3	3	9.2	46.898	24.4634	24.5858	24.3411	6	3	3	B6HAF7	B6HAF7	1	B6HAF7	Pc16g12660 protein	ATP binding; metal ion binding; phosphoribosylglycinamide transaminase activity; pyridoxal phosphate binding	
28.9074	28.9756	28.72	29.2402	29.0934	28.8804	3.45E-154	2.91E+09	17	17	33.8	55.617	28.9695	28.8677	29.0713	6	3	3	B6HAF9	B6HAF9	1	B6HAF9	Pc16g12680 protein		
24.4533	24.5268	24.2674	23.4891	ND	25.6547	1.54E-13	1.11E+08	5	5	8.5	86.694	24.4783	24.4158	24.5719	5	3	2	B6HAG7	B6HAG7	1	B6HAG7	Pc16g12760 protein	RNA binding; tRNA (cytosine-5-)-methyltransferase activity	
26.1128	ND	26.3895	25.5023	25.3609	26.7838	8.71E-19	3.65E+08	4	4	14.4	53.073	26.0299	26.2512	25.8823	5	2	3	B6HAG9	B6HAG9	1	B6HAG9	Pc16g12780 protein	metal ion binding; metalloendopeptidase activity; proteolysis	
ND	ND	ND	ND	24.6645	26.7191	2.91E-14	1.79E+08	6	6	20.9	33.538	25.6918	ND	25.6918	2	0	2	B6HAH1	B6HAH1	1	B6HAH1	Pc16g12800 protein	RNA binding; methyltransferase activity; rRNA processing; tRNA processing	
23.9704	ND	23.9656	26.0207	23.8824	23.5907	5.73E-06	1.38E+08	2	2	13.6	13.474	24.286	23.968	24.498	5	2	3	B6HAH5	B6HAH5	1	B6HAH5	Pc16g12840 protein		
25.7722	26.0254	25.9453	25.0611	ND	24.5536	9.70E-12	2.8E+08	4	4	16.4	37.125	25.4715	25.9143	24.8074	5	3	2	B6HAH7;B6HA25	B6HAH7	2	B6HAH7	Pc16g12860 protein	catechol 1,2-dioxygenase activity; catechol-containing compound metabolic process; ferric iron binding	
25.9212	26.7077	26.011	27.542	27.697	27.3154	3.51E-18	7.06E+08	4	4	29.3	20.497	26.8657	26.2133	27.5181	6	3	3	B6HAJ0	B6HAJ0	1	B6HAJ0	Pc16g12990 protein	large ribosomal subunit; structural constituent of ribosome; translation	
27.8771	27.5889	27.7266	ND	26.824	25.5412	1.02E-24	8.84E+08	3	3	24.4	18.12	27.1115	27.7309	26.1826	5	3	2	B6HAJ7	B6HAJ7	1	B6HAJ7	Peptidyl-prolyl cis-trans isomerase	peptidyl-prolyl cis-trans isomerase activity; protein folding	
29.0304	29.0908	28.9205	29.279	29.5299	28.18	2.37E-184	3.15E+09	11	11	32.7	51.228	29.0051	29.0139	28.9963	6	3	3	B6HAL9	B6HAL9	1	B6HAL9	Pc16g13280 protein	NADP binding; cell redox homeostasis; flavin adenine dinucleotide binding; glutathione metabolic process; glutathione-disulfide reductase activity	
26.7801	24.6522	25.9218	26.6206	24.8387	25.8845	5.42E-33	3.97E+08	5	5	22.2	39.031	25.783	25.7847	25.7812	6	3	3	B6HAM6	B6HAM6	1	B6HAM6	3-isopropylmalate dehydrogenase	3-isopropylmalate dehydrogenase activity; NAD binding; cytoplasm; leucine biosynthetic process; magnesium ion binding	
25.8089	25.8505	25.8495	26.5661	26.447	25.5595	3.80E-10	3.84E+08	5	5	11.1	57.091	26.0136	25.8363	26.1909	6	3	3	B6HAN0	B6HAN0	1	AMPP2	Probable Xaa-Pro aminopeptidase Pc16g13390	aminopeptidase activity; manganese ion binding; metallopeptidase activity; proteolysis	
29.5059	29.5797	29.5303	29.4196	29.8065	28.5275	2.11E-194	4.14E+09	14	13	48.4	47.304	29.3949	29.5386	29.2512	6	3	3	B6HAP0	B6HAP0	1	B6HAP0	Pc16g13490 protein	acyl-CoA dehydrogenase activity; flavin adenine dinucleotide binding	
25.9458	25.8503	25.7727	ND	ND	25.254	4.12E-49	2.88E+08	2	2	19.4	35.65	25.7057	25.8563	25.254	4	3	1	B6HAS1	B6HAS1	1	B6HAS1	Pc16g13800 protein	transcription factor TFIIA complex; transcription initiation from RNA polymerase II promoter	
29.3224	29.1831	29.1946	28.2658	28.9976	27.3166	1.81E-139	2.84E+09	4	4	9.2	68.274	28.7133	29.2334	28.1933	6	3	3	B6HB59	B6HB59	1	B6HB59	Lysophospholipase phospholipase B plb1-Penicillium chrysogenum	phospholipase activity; phospholipid catabolic process	
26.4245	26.7847	25.8198	26.915	27.3039	25.2874	2.04E-13	5.65E+08	4	4	9.6	50.239	26.4226	26.343	26.5021	6	3	3	B6HB61	B6HB61	1	B6HB61	Pc18g02920 protein	3-deoxy-7-phosphoheptulonate synthase activity; aromatic amino acid family biosynthetic process	
28.9316	28.8676	28.8001	28.8196	29.2397	27.6609	2.63E-52	2.67E+09	6	6	26.3	34.672	28.7199	28.8664	28.5734	6	3	3	B6HB68	B6HB68	1	B6HB68	Pc18g03000 protein	carbohydrate binding; carbohydrate metabolic process; isomerase activity	
27.3903	ND	ND	27.4351	27.7171	25.4308	1.09E-09	6.43E+08	3	3	23	17.415	26.9933	27.3903	26.861	4	1	3	B6HB77	B6HB77	1	B6HB77	Pc18g03090 protein		
25.1877	25.5969	25.2934	ND	ND	25.4954	4.37E-23	1.71E+08	2	2	19.8	21.597	25.3934	25.3593	25.4954	4	3	3	B6HB93	B6HB93	1	B6HB93	Pc18g03250 protein		
26.8627	27.0667	26.856	26.8861	27.5042	25.9686	3.60E-53	7.2E+08	6	6	35.5	26.608	26.8574	26.9285	26.7863	6	3	3	B6HBA0	B6HBA0	1	B6HBA0	Pc18g03320 protein		
28.7986	28.085	28.8848	27.9702	26.9776	25.4204	8.44E-12	1.81E+09	5	5	9.1	71.156	27.6894	28.5895	26.7894	6	3	3	B6HBA3	B6HBA3	1	B6HBA3	Pc18g03360 protein	clathrin adaptor complex; intracellular protein transport; vesicle-mediated transport	
31.5061	31.7367	31.5369	31.8995	32.3517	30.5444	0	1.94E+10	36	36	50.9	98.634	31.5959	31.5932	31.5985	6	3	3	B6HBB3	B6HBB3	1	B6HBB3	Pc18g03470 protein	metallopeptidase activity; proteolysis; zinc ion binding	
28.2424	28.3138	28.1713	28.4675	28.8955	27.3262	1.44E-143	1.86E+09	7	7	33.5	35.836	28.2361	28.2425	28.2297	6	3	3	B6HBC0	B6HBC0	1	B6HBC0	Pc18g03540 protein	cell redox homeostasis; glycerol ether metabolic process; protein disulfide oxidoreductase activity	
24.9711	25.042	25.2304	25.0595	24.7081	24.3653	1.19E-12	1.86E+08	4	4	11.8	40.138	24.8961	25.0811	24.711	6	3	3	B6HBC2	B6HBC2	1	B6HBC2	Pc18g03560 protein	heme binding; peroxidase activity; response to oxidative stress	
26.1015	26.6873	26.4051	27.2767	25.7278	30.68	6.53E-124	1.69E+09	13	13	39.5	49.073	27.1464	26.398	27.8948	6	3	3	B6HBC6	B6HBC6	1	B6HBC6	Pc18g03600 protein	pyridoxal phosphate binding; transaminase activity	
27.2019	26.9306	27.3271	25.8724	26.021	27.2602	1.73E-22	7.3E+08	6	6	24	37.447	26.7689	27.1532	26.3845	6	3	3	B6HBE8	B6HBE8	1	B6HBE8	Pc18g03840 protein		
27.5584	28.0885	28.3086	26.7897	26.611	27.1137	2.30E-29	1.13E+09	2	2	25.5	10.496	27.4117	27.9852	26.8381	6	3	3	B6HBF7	B6HBF7	1	B6HBF7	Pc18g03930 protein	enzyme inhibitor activity; mitochondrion; negative regulation of nucleotide metabolic process	
32.1497	32.1382	32.2475	31.1016	31.0841	32.0187	0	2.23E+10	22	20	68.3	29.268	31.79	32.1785	31.4015	6	3	3	B6HBF8	B6HBF8	1	B6HBF8	Pc18g03940 protein		
24.4148	25.3164	25.0644	ND	22.9429	ND	8.36E-09	1.26E+08	2	2	16.3	22.013	24.4346	24.9319	22.9429	4	3	1	B6HBH2	B6HBH2	1	B6HBH2	Pc18g04080 protein	cytochrome-c oxidase activity; mitochondrial envelope	
25.0513	24.8138	24.8095	26.8854	25.932	27.9179	4.48E-07	4.3E+08	2	2	14.7	13.265	25.9017	24.8915	26.9118	6	3	3	B6HBH5	B6HBH5	1	B6HBH5	Pc18g04110 protein	ribosome; structural constituent of ribosome; translation	
24.4468	23.3396	23.3094	25.0939	23.6638	24.0218	1.08E-07	1E+08	4	4	11.1	42.003	23.9792	23.6986	24.2598	6	3	3	B6HBJ1;B6GZ20	B6HBJ1;B6GZ20	2	B6HBJ1	Pc18g00020 protein	ATP binding; protein serine/threonine kinase activity	
24.8657	24.9415	24.7438	25.4463	25.2723	24.5715	2.19E-05	1.85E+08	2	2	9.7	21.824	24.9735	24.8503	25.0967	6	3	3	B6HBK1	B6HBK1	1	B6HBK1	Pc18g04330 protein	peptide-methionine (S)-S-oxide reductase activity; protein repair; response to oxidative stress	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
26.0098	26.8291	26.2905	28.729	28.9326	27.1944	6.84E-44	1.21E+09	4	4	9.6	59.991	27.3309	26.3764	28.2853	6	3		3	B6HBR0	B6HBR0	1	B6HBR0	Pc18g04660 protein	proteolysis; serine-type carboxypeptidase activity	
24.1601	24.5462	24.4354	25.9653	26.0646	ND		5.97E-19	2.06E+08	3	3	13	31.03	25.0343	24.3805	26.0149	5	3		2	B6HBR4	B6HBR4	1	B6HBR4	Pc18g04700 protein		
27.9579	28.2172	28.0881	28.8412	28.8804	27.6365	1.72E-74	1.95E+09	10	10	30.1	39.432	28.2702	28.0877	28.4527	6	3		3	B6HBS4	B6HBS4	1	B6HBS4	Pc18g04820 protein	RNA binding	
28.5562	28.9649	28.726	29.3299	29.682	27.6619	4.49E-86	2.9E+09	5	5	27.1	27.308	28.8201	28.749	28.8913	6	3		3	B6HBU7	B6HBU7	1	B6HBU7	Pc18g00550 protein		
26.5573	26.2372	26.3677	26.3619	26.4318	26.8778	2.85E-80	5.2E+08	4	4	32.1	20.299	26.4723	26.3874	26.5572	6	3		3	B6HBV0	B6HBV0	1	B6HBV0	Actin-related protein 2/3 complex subunit 5	cytoskeleton; regulation of actin filament polymerization	
28.0473	27.8876	27.8391	28.7922	28.3591	30.5505	2.77E-80	2.71E+09	5	5	32	22.596	28.5793	27.9247	29.2339	6	3		3	B6HBV3	B6HBV3	1	B6HBV3	Pc18g00610 protein	ribosome; structural constituent of ribosome; translation	
25.8107	25.9162	25.7581	26.4343	26.9549	25.0976	2.05E-11	4.05E+08	2	2	16.7	34.266	25.9953	25.8283	26.1623	6	3		3	B6HBX1	B6HBX1	1	B6HBX1	Pc18g05010 protein	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	
26.8129	26.8379	26.8181	27.0009	27.4926	25.8863	8.51E-08	6.91E+08	2	2	16	13.87	26.8081	26.8229	26.7933	6	3		3	B6HBX3	B6HBX3	1	B6HBX3	Peptidyl-prolyl cis-trans isomerase	peptidyl-prolyl cis-trans isomerase activity; protein folding	
25.8516	25.7649	25.394	26.0483	26.9055	25.389	1.99E-08	3.78E+08	5	5	20.2	28.539	25.8922	25.6702	26.1143	6	3		3	B6HBZ5	B6HBZ5	1	B6HBZ5	Pc18g00790 protein		
30.1906	30.1737	30.2187	29.4034	29.4371	30.173	0	5.84E+09	6	6	16.2	34.563	29.9327	30.1943	29.6712	6	3		3	B6HC02	B6HC02	1	B6HC02	Pc18g00860 protein		
32.295	31.9056	32.1369	31.0511	31.039	31.5312	2.30E-288	2.07E+10	3	3	35.1	18.745	31.6598	32.1125	31.2071	6	3		3	B6HC11	B6HC11	1	B6HC11	Peptidyl-prolyl cis-trans isomerase	peptidyl-prolyl cis-trans isomerase activity; protein folding	
25.6355	25.704	25.8506	26.2526	26.1683	25.4815	3.81E-08	3.26E+08	4	4	7.6	55.1	25.8488	25.7301	25.9675	6	3		3	B6HC19	B6HC19	1	B6HC19	Pc18g05270 protein		
30.3926	30.6258	30.3297	31.3472	31.7893	30.1173	0	1.1E+10	20	19	45.2	57.739	30.767	30.4494	31.0846	6	3		3	B6HC24	B6HC24	1	B6HC24	Inosine-5-monophosphate dehydrogenase	GMP biosynthetic process; IMP dehydrogenase activity; adenyl nucleotide binding; metal ion binding	
28.5769	28.6698	28.5068	27.3681	27.9763	29.0544	1.30E-38	2.01E+09	2	2	6.3	49.512	28.3587	28.5845	28.133	6	3		3	B6HC25	B6HC25	1	B6HC25	Pc18g05330 protein	hydrolase activity; ribosome; structural constituent of ribosome; translation	
ND		25.3697	25.1937	27.0297	26.4899	25.1318	1.97E-43	3.32E+08	6	6	16.2	57.654	25.843	25.2817	26.2171	5	2		3	B6HC26	B6HC26	1	B6HC26	Pc18g05340 protein	ATP binding; cytoplasm; phenylalanine-tRNA ligase activity; phenylalanyl-tRNA aminoacylation; tRNA binding	
31.7766	31.9938	31.7907	32.0843	32.3643	30.7813	0	2.23E+10	24	24	58.5	56.856	31.7985	31.8537	31.7433	6	3		3	B6HC43	B6HC43	1	B6HC43	Pc18g00980 protein		
ND		25.1389	ND	23.9614	24.2142	ND	8.57E-05	92599000	2	2	4.5	55.419	24.4382	25.1389	24.0878	3	1		2	B6HC73	B6HC73	1	B6HC73	Pc18g05530 protein	UDP-N-acetylmuramate dehydrogenase activity; flavin adenine dinucleotide binding	
26.766	27.1434	26.8336	26.7877	27.4608	25.9786	7.92E-27	7.05E+08	4	4	27.1	22.575	26.8283	26.9143	26.7423	6	3		3	B6HC78	B6HC78	1	B6HC78	Pc18g05580 protein		
25.731	26.2847	25.599	27.0436	27.3001	25.6785	3.19E-17	4.9E+08	3	3	17.1	33.573	26.2728	25.8716	26.6741	6	3		3	B6HC86	B6HC86	1	B6HC86	Pc18g05660 protein	metal ion binding; superoxide dismutase activity; superoxide metabolic process	
26.2565	26.9046	26.5184	24.9121	ND	25.161	4.94E-09	3.97E+08	3	3	28.3	17.316	25.9505	26.5598	25.0365	5	3		2	B6HC90	B6HC90	1	B6HC90	Pc18g01180 protein	acid-amino acid ligase activity	
30.6872	31.1297	31.3759	30.5848	30.0906	31.6825	5.48E-149	1.21E+10	10	10	22.5	39.396	30.9251	31.0643	30.7859	6	3		3	B6HC93	B6HC93	1	B6HC93	Pc18g01220 protein	fructose-bisphosphate aldolase activity; glycolysis; zinc ion binding	
27.8056	27.2491	27.8747	24.9234	25.7848	28.7449	3.52E-116	1.05E+09	13	13	48.5	40.792	27.0637	27.6431	26.4844	6	3		3	B6HC95	B6HC95	1	B6HC95	Saccharopine dehydrogenase [NAD(+), L-lysine-forming]	lysine biosynthetic process via aminoadipic acid; saccharopine dehydrogenase (NAD+, L-lysine-forming) activity	
28.1315	28.2826	28.0158	28.2919	28.6356	27.4927	3.08E-122	1.74E+09	6	6	11.4	91.156	28.1417	28.1433	28.1401	6	3		3	B6HC98	B6HC98	1	B6HC98	Pc18g01270 protein		
27.757	27.9277	27.7769	27.8932	28.3057	26.9216	4.67E-56	1.32E+09	9	9	28.7	45.724	27.7637	27.8205	27.7068	6	3		3	B6HC99	B6HC99	1	B6HC99	Pc18g01280 protein		
29.8639	29.8685	30.0164	28.7253	27.7303	31.0593	5.39E-198	5.27E+09	18	18	41.6	60.344	29.544	29.9163	29.1716	6	3		3	B6HCB0	B6HCB0	1	B6HCB0	Pc18g01390 protein	carbohydrate metabolic process; intramolecular transferase activity, phosphotransferases; magnesium ion binding	
ND		25.0825	ND	25.5221	25.6707	ND	3.31E-06	1.73E+08	2	2	8	47.229	25.4251	25.0825	25.5964	3	1		2	B6HCB8	B6HCB8	1	B6HCB8	Pc18g05720 protein	biosynthetic process; catalytic activity; pyridoxal phosphate binding	
24.5167	24.3831	24.1951	24.7307	24.5017	25.078	4.84E-08	1.35E+08	3	3	9	41.666	24.5675	24.3649	24.7701	6	3		3	B6HCC3	B6HCC3	1	B6HCC3	Methionine aminopeptidase	aminopeptidase activity; metal ion binding; metalloexopeptidase activity; proteolysis	
28.7386	28.4955	29.1129	29.4412	28.4661	28.2624	7.64E-94	2.72E+09	12	12	41.2	38.427	28.7528	28.7823	28.7233	6	3		3	B6HCD5	B6HCD5	1	B6HCD5	Pc18g05890 protein	NAD binding; magnesium ion binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	
27.1906	27.4407	27.4236	25.6523	27.1911	29.3965	1.42E-123	1.13E+09	9	9	30.6	50.518	27.3825	27.3516	27.4133	6	3		3	B6HCE6	B6HCE6	1	B6HCE6	Pc18g01450 protein	hydroxymethylglutaryl-CoA synthase activity; isoprenoid biosynthetic process	
27.9348	28.1703	28.0266	29.004	29.6908	28.4737	3.90E-264	2.33E+09	11	11	34.9	63.356	28.55	28.0439	29.0562	6	3		3	B6HCE9	B6HCE9	1	B6HCE9	Pc18g01490 protein	catalytic activity; magnesium ion binding; thiamine pyrophosphate binding	
24.961	24.9716	25.245	25.2233	26.1224	24.4762	1.73E-07	2.34E+08	4	4	7.8	91.877	25.1666	25.0592	25.274	6	3		3	B6HCF7	B6HCF7	1	B6HCF7	Pc18g01570 protein	metalloendopeptidase activity; proteolysis	
28.9758	29.2997	28.9665	29.2801	29.3204	30.1567	7.06E-42	3.74E+09	5	5	51.6	14.091	29.3332	29.0807	29.5857	6	3		3	B6HCH5	B6HCH5	1	B6HCH5	Pc18g01750 protein	ribosome; structural constituent of ribosome; translation	
29.1734	28.665	29.3057	26.5921	26.2323	30.6905	0	3.07E+09	19	19	37.5	58.459	28.4432	29.048	27.8383	6	3		3	B6HCH7;REV__B6H1L1	B6HCH7	2	B6HCH7	Pyruvate kinase	glycolysis; magnesium ion binding; potassium ion binding; pyruvate kinase activity	
25.616	25.7332	25.4852	25.7572	26.3034	25.1865	4.08E-09	2.98E+08	3	3	15.9	20.727	25.6802	25.6115	25.749	6	3		3	B6HCI9	B6HCI9	1	B6HCI9	Glutathione peroxidase	glutathione peroxidase activity; response to oxidative stress	
26.9155	26.4108	26.2314	27.1788	26.5767	25.6526	3.65E-30	5.64E+08	7	7	36.9	18.458	26.4943	26.5192	26.4694	6	3		3	B6HCL7	B6HCL7	1	B6HCL7	Pc18g06210 protein	ribosome; structural constituent of ribosome; translation	
24.9563	25.2824	25.2983	24.9773	24.7665	23.9055	7.35E-17	1.87E+08	2	2	12.3	39.98	24.8644	25.179	24.5498	6	3		3	B6HCN5	B6HCN5	1	B6HCN5	Pc18g06390 protein		
27.6534	27.9423	27.5784	27.2236	27.4385	29.4915	7.43E-251	1.45E+09	15	15	63.6	28.974	27.8879	27.7247	28.0512	6	3		3	B6HCQ6	B6HCQ6	1	B6HCQ6	Pc18g02110 protein	RNA binding; small ribosomal subunit; structural constituent of ribosome; translation	
23.1699	23.7167	23.3712	ND	ND	25.3728	4.25E-07	67534000	3	3	5.2	69.039	23.9076	23.4193	25.3728	4	3		1	B6HCR1	B6HCR1	1	B6HCR1	Pc18g02160 protein		
24.4918	24.84	24.8127	25.7662	25.7045	26.691	1.25E-15	2.52E+08	7	7	11.8	66.862	25.3844	24.7148	26.0539	6	3		3	B6HCR2	B6HCR2	1	B6HCR2	Pc18g02170 protein	ATP binding; RNA binding; cytoplasm; magnesium ion binding; phenylalanine-tRNA ligase activity; phenylalanyl-tRNA aminoacylation	
30.4831	30.2648	30.533	31.0296	29.8251	31.0379	2.36E-145	8.97E+09	11	11	58.8	16.139	30.5289	30.427	30.6309	6	3		3	B6HCV7	B6HCV7	1	B6HCV7	40S ribosomal protein S12	ribosome; structural constituent of ribosome; translation	
28.3715	27.9359	27.9761	25.7299	25.7812	29.5466	1.16E-61	1.52E+09	7	7	44.3	16.492	27.5569	28.0945	27.0192	6	3		3	B6HCX3	B6HCX3	1	B6HCX3	Pc18g02490 protein	ribosome; structural constituent of ribosome; translation	
ND		24.9114	24.1877	25.5479	24.6892	ND	7.14E-10	1.58E+08	2	2	7.1	32.479	24.834	24.5496	25.1185	4	2		2	B6HCY7	B6HCY7	1	B6HCY7	Pc18g02660 protein	heme binding; iron ion binding; oxygen binding; oxygen transport	
28.1077	28.3628	28.0744	28.3465	28.3886	28.4815	5.71E-85	1.83E+09	10	10	26.9	54.134	28.2936	28.1817	28.4055	6	3		3	B6HCZ7	B6HCZ7	1	B6HCZ7	Pc18g02760 protein	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	
30.3757	29.9372	30.0474	28.9642	29.2009	30.0563	3.90E-107	5.43E+09	7	6	34.4	24.727	29.7636	30.1201	29.4071	6	3		3	B6HCZ9	B6HCZ9	1	B6HCZ9	Pc18g02780 protein	antioxidant activity; peroxiredoxin activity	
26.0665	26.2677	25.9776	26.5197	26.8318	25.3882	1.74E-27	4.39E+08	3	3	19.6	19.543	26.1753	26.1039	26.2466	6	3		3	B6HD68	B6HD68	1	B6HD68	Pc20g01310 protein	carbon-nitrogen ligase activity, with glutamine as amido-N-donor	
26.1737	26.2543	26.16	27.6826	27.5339	26.2716	2.73E-24	6.45E+08	5	5	41.7	15.886	26.6793	26.196	27.1627	6	3		3	B6HD74	B6HD74	1	B6HD74	Pc20g01370 protein	calcium ion binding	
29.0924	29.4995	29.4732	26.9602	27.3378	28.7732	1.91E-199	2.77E+09	19	19	33.7	81.356	28.5227	29.355	27.6904	6	3		3	B6HD76	B6HD76	1	B6HD76	Pc20g01390 protein	metal ion binding; metalloendopeptidase activity; proteolysis	
29.039	29.0029	28.9143	29.2188	29.3843	28.2502	8.33E-111	3.04E+09	10	10	51.4	29.963	28.9683	28.9854	28.9511	6	3		3	B6HD84	B6HD84	1	B6HD84	Proteasome subunit alpha type	cytoplasm; nucleus; proteasome core complex, alpha-subunit complex; threonine-type endopeptidase activity; ubiquitin-dependent protein catabolic process	Cytoplasm. Nucleus.
28.8714	28.9824	28.8399	28.0645	28.0739	28.5667	2.61E-151	2.33E+09	11	11	27.4	59.4	28.5665	28.8979	28.235	6	3		3	B6HD87	B6HD87	1	B6HD87	Pc20g04020 protein	cellular amino acid metabolic process; pyridoxal phosphate binding; threonine synthase activity	
27.8806	27.9038	27.7755	28.2676	28.6514	27.2085	1.04E-53	1.51E+09	4	4	15.4	32.198	27.9479	27.8533	28.0425	6	3		3	B6HD93	B6HD93	1	B6HD93	Pc20g04080 protein	mitochondrial matrix	
28.9753	29.3282	29.2486	24.9948	24.5231	28.1096	1.25E-128	2.18E+09	10	10	29.1	52.789	27.53	29.184	25.8759	6	3		3	B6HDB9	B6HDB9	1	B6HDB9	Pc20g06940 protein	aminopeptidase activity; metallopeptidase activity; proteolysis; zinc ion binding	
27.2075	26.8764	27.2034	25.9237	25.6281	26.9001	1.61E-40	6.36E+08	5	5	26.6	30.396	26.6232	27.0958	26.1506	6	3		3	B6HDC2	B6HDC2	1	B6HDC2	Pc20g06970 protein	transferase activity, transferring acyl groups	
27.6461	27.4562	27.4706	27.9434	28.3084	26.7627	2.81E-56	1.19E+09	7	7	29.4	33.714	27.5979	27.5243	27.6715	6	3		3	B6HDD5	B6HDD5	1	B6HDD5	Pc20g07100 protein		
26.9285	27.141	27.109	27.6564	27.1268	26.9646	3.33E-18	8.51E+08	7	7	25.3	33.29	27.1544	27.0595	27.2492	6	3		3	B6HDE6	B6HDE6	1	B6HDE6	Pc20g07400 protein	'de novo' IMP biosynthetic process; ATP binding; phosphoribosylaminoimidazolesuccinocarboxamide synthase activity	
27.7204	27.3438	27.187	27.4503	24.7256	27.1491	1.09E-32	8.95E+08	4	4	18.5	17.81	26.9294	27.4171	26.4417	6	3		3	B6HDF3	B6HDF3	1	B6HDF3	Pc20g07470 protein	translation initiation factor activity	
32.8192	33.0215	32.7458	33.3848	33.4053	32.3246	0	4.81E+10	14	12	47.4	35.728	32.9502	32.8622	33.0382	6	3		3	B6HDG8	B6HDG8	1	B6HDG8	Malate dehydrogenase	L-malate dehydrogenase activity; cellular carbohydrate metabolic process; malate metabolic process; tricarboxylic acid cycle	
30.1516	29.6883	30.0444	28.9451	28.3853	29.788	3.14E-193	4.75E+09	9	9	20.7	70.775	29.5004	29.9614	29.0395	6	3		3	B6HDH0	B6HDH0	1	B6HDH0	acetyl-CoA biosynthetic process from pyruvate; dihydrolipoyllysine-residue acetyltransferase activity; mitochondrial pyruvate dehydrogenase complex		
ND	ND		ND	28.0548	27.5518	26.4306	8.69E-33	4.78E+08	3	3	45.7	11.836	27.3457	ND		27.3457	3	0	3	B6HDH1	B6HDH1	1	B6HDH1	Pc20g04220 protein (Fragment)		
31.829	31.5473	31.7205	31.6542	31.8298	31.1212	7.13E-269	1.88E+10	17	17	52.4	32.647	31.617	31.699	31.5351	6	3		3	B6HDJ3	B6HDJ3	1	B6HDJ3	Pc20g07230 protein	cytoplasm; inorganic diphosphatase activity; magnesium ion binding; phosphate-containing compound metabolic process	
26.6729	26.8121	26.4543	26.4884	26.8679	26.0246	3.17E-11	5.67E+08	4	4	17.3	20.042	26.5534	26.6464	26.4603	6	3		3	B6HDJ7	B6HDJ7	1	B6HDJ7	Pc20g07270 protein	adenyl nucleotide binding	
26.3661	25.5458	25.5864	ND	ND	ND	9.25E-26	2.3E+08	3	3	28.9	17.111	25.8328	25.8328	ND	3	3		0	B6HDJ9	B6HDJ9	1	B6HDJ9	Pc20g07290 protein		
24.993	ND		25.0853	25.7657	26.2362	ND	4.14E-14	2.7E+08	3	3	8.8	53.806	25.5201	25.0391	26.001	4	2		2	B6HDK3	B6HDK3	1	B6HDK3	Pc20g11910 protein		
27.6554	27.6407	27.6084	27.3264	27.6811	26.1723	5.94E-37	1.04E+09	6	6	37.7	20.204	27.3474	27.6349	27.0599	6	3		3	B6HDM8	B6HDM8	1	B6HDM8	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	L-methionine salvage from methylthioadenosine; acireductone dioxygenase [iron(II)-requiring] activity; cytoplasm; iron ion binding; nucleus	Cytoplasm. Nucleus.
25.1175	25.6757	25.9184	21.7684	22.0387	26.9123	4.64E-21	2.57E+08	5	5	5.7	108.36	24.5718	25.5705	23.5731	6	3		3	B6HDM9	B6HDM9	1	B6HDM9	Pc20g12430 protein	intracellular protein transport; nucleus	
27.0047	27.2033	27.1513	27.7199	27.9364	26.6544	1.93E-65	9.4E+08	14	14	23.9	96.475	27.2783	27.1198	27.4369	6	3		3	B6HDQ3	B6HDQ3	1	B6HDQ3	Pc20g01680 protein	catalytic activity	
28.8283	28.327	28.6954	28.619	27.6605	28.9625	3.09E-27	2.21E+09	4	4	24.1	13.093	28.5155	28.6169	28.414	6	3		3	B6HDR5	B6HDR5	1	B6HDR5	Pc20g04380 protein	RNA binding; small ribosomal subunit; structural constituent of ribosome; translation	
ND		27.0162	26.8494	26.2031	26.5259	26.4682	3.22E-43	5.62E+08	2	2	13.3	23.767	26.6125	26.9328	26.3991	5	2		3	B6HDS9	B6HDS9	1	B6HDS9	Pc20g14720 protein	ATP synthesis coupled proton transport; membrane; proton-transporting ATP synthase activity, rotational mechanism	
28.62	28.6531	28.6316	28.7961	28.915	27.3156	1.57E-74	2.29E+09	10	10	23.2	72.529	28.4886	28.6349	28.3422	6	3		3	B6HDV7	B6HDV7	1	B6HDV7	Pc20g15010 protein	transferase activity, transferring acyl groups	
28.1467	27.4807	28.0096	27.9101	26.3748	28.2599	5.27E-88	1.38E+09	12	12	25	72.867	27.697	27.879	27.5149	6	3		3	B6HDY3	B6HDY3	1	B6HDY3	Pc20g15270 protein		
27.5851	28.2633	28.7867	22.5703	24.4192	28.1703	2.28E-123	1.25E+09	17	17	24	121.5	26.6325	28.2117	25.0532	6	3		3	B6HDY7	B6HDY7	1	B6HDY7	Pc20g15310 protein	intracellular protein transport; nucleus	
27.1698	25.3196	27.1437	25.4394	24.64	26.255	1.17E-23	5.01E+08	5	5	31.1	29.929	25.9946	26.5443	25.4448	6	3		3	B6HDZ7	B6HDZ7	1	B6HDZ7	Pc20g15430 protein	F-actin capping protein complex; WASH complex; actin cytoskeleton organization	
30.2638	30.0422	30.3612	29.7821	28.6491	30.2098	1.26E-135	6.07E+09	13	13	32.2	54.338	29.8847	30.2224	29.547	6	3		3	B6HE42	B6HE42	1	B6HE42	Dihydrolipoyl dehydrogenase	cell redox homeostasis; dihydrolipoyl dehydrogenase activity; flavin adenine dinucleotide binding	
28.8432	28.2477	28.6098	27.9333	28.5302	26.4462	2.79E-157	1.89E+09	6	6	17.6	37.239	28.1017	28.5669	27.6366	6	3		3	B6HE47	B6HE47	1	B6HE47	Pc20g15580 protein	oxidoreductase activity	
27.5933	27.9878	27.7199	28.2855	28.7219	27.3484	6.48E-173	1.51E+09	5	5	27.5	31.679	27.9428	27.767	28.1186	6	3		3	B6HE70	B6HE70	1	B6HE70	Pc20g01960 protein	'de novo' IMP biosynthetic process; amino acid binding; formyltetrahydrofolate deformylase activity; hydroxymethyl-, formyl- and related transferase activity	
31.0563	31.3111	31.043	31.4552	31.8829	30.245	0	1.42E+10	10	10	41.7	41.163	31.1656	31.1368	31.1944	6	3		3	B6HE89	B6HE89	1	B6HE89	Pc20g04810 protein	peptidyl-prolyl cis-trans isomerase activity; protein folding	
26.4027	26.3384	26.4002	28.0407	28.2256	26.0329	3.05E-39	8.41E+08	7	7	28.4	45.271	26.9067	26.3804	27.4331	6	3		3	B6HE90	B6HE90	1	B6HE90	Pc20g04820 protein	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	
24.3498	24.4793	24.3826	24.5596	25.4747	23.9953	3.61E-05	1.43E+08	2	2	13.4	19.289	24.5402	24.4039	24.6765	6	3		3	B6HEC9	B6HEC9	1	B6HEC9	Pc20g05050 protein	acid phosphatase activity; cytoplasm; non-membrane spanning protein tyrosine phosphatase activity	
24.5706	24.5485	24.5473	26.6466	26.4733	24.3658	2.54E-10	2.65E+08	3	3	6.2	63.672	25.192	24.5555	25.8286	6	3		3	B6HEH9	B6HEH9	1	B6HEH9	Pc20g02630 protein	metallocarboxypeptidase activity; proteolysis	
25.6522	25.7556	25.8674	25.8924	26.4838	25.2678	1.17E-27	3.49E+08	5	5	16	69.098	25.8199	25.7584	25.8814	6	3		3	B6HEI2	B6HEI2	1	B6HEI2	Pc20g07500 protein	intracellular; signal transduction	
26.9402	27.1533	26.8014	27.0696	27.3175	26.2144	1.17E-62	7.28E+08	3	3	22.7	15.916	26.9161	26.965	26.8672	6	3		3	B6HEJ6	B6HEJ6	1	B6HEJ6	Pc20g07640 protein	DNA binding	
23.0378	22.7215	23.3022	25.4938	24.4142	27.5177	6.84E-25	2.12E+08	7	7	16.9	63.959	24.4145	23.0205	25.8086	6	3		3	B6HEK3	B6HEK3	1	B6HEK3	Sulfate adenylyltransferase	ATP binding; adenylylsulfate kinase activity; cysteine biosynthetic process; cytoplasm; hydrogen sulfide biosynthetic process; methionine biosynthetic process; sulfate adenylyltransferase (ATP) activity; sulfate assimilation	Cytoplasm.
24.414	25.2336	24.5092	27.1642	26.6913	26.9375	6.39E-45	3.99E+08	12	12	17.2	118.41	25.825	24.7189	26.931	6	3		3	B6HEL3	B6HEL3	1	B6HEL3	Pc20g07810 protein	phospholipid binding	
28.1999	28.9594	28.9119	29.3462	29.8698	27.8141	2.66E-69	3.01E+09	4	4	42.9	16.492	28.8502	28.6904	29.01	6	3		3	B6HEM5	B6HEM5	1	B6HEM5	Pc20g07930 protein	acid-amino acid ligase activity	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
24.1028	24.554	24.5312	24.8875	24.4562	24.2349	1.57E-07	1.33E+08	3	3	14.3	28.884	24.4611	24.396	24.5262	6	3	3	B6HEM8	B6HEM8	1	B6HEM8	Pc20g07960 protein	methyltransferase activity	
27.9671	28.1293	28.0042	28.8927	28.7297	27.7786	1.79E-104	1.85E+09	9	9	19.4	70.451	28.2503	28.0335	28.467	6	3	3	B6HEN3	B6HEN3	1	B6HEN3	Pc20g08010 protein	translation initiation factor activity	
24.8281	24.6482	24.3224	24.5912	24.434	24.4009	1.11E-11	1.45E+08	5	5	4.3	161.55	24.5375	24.5996	24.4753	6	3	3	B6HEP0	B6HEP0	1	B6HEP0	Pc20g08080 protein	DNA binding; hydrolase activity, acting on ester bonds; nucleobase-containing compound metabolic process; regulation of DNA-templated transcription, elongation; regulation of transcription from RNA polymerase II promoter	
23.1349	23.2237	ND	ND	ND	26.8252	2.09E-16	1.06E+08	5	5	23.3	34.089	24.3946	23.1793	26.8252	3	2	1	B6HER9	B6HER9	1	B6HER9	Pc20g00110 protein		
25.3277	25.3463	25.0766	25.4326	25.241	26.4629	2.71E-07	2.65E+08	3	3	12.8	16.624	25.4812	25.2502	25.7122	6	3	3	B6HEV9	B6HEV9	1	B6HEV9	Pc20g08290 protein	ribosome; structural constituent of ribosome; translation	
29.6761	29.6458	29.79	28.0204	28.6097	29.5472	8.38E-146	3.83E+09	15	15	46.4	52.748	29.2148	29.7039	28.7257	6	3	3	B6HEW2	B6HEW2	1	B6HEW2	Pc20g08320 protein	dipeptidase activity; tripeptidase activity	
26.7622	26.4854	26.7159	26.0745	26.0407	25.1192	7.65E-57	4.82E+08	3	3	14.8	36.044	26.1997	26.6545	25.7448	6	3	3	B6HEX1	B6HEX1	1	B6HEX1	Pc20g08410 protein	carbohydrate binding; hexose metabolic process; isomerase activity	
28.5648	28.4328	28.3174	28.4101	27.5737	27.9682	2.07E-249	1.86E+09	7	7	17.6	49.828	28.2112	28.4383	27.984	6	3	3	B6HEY7	B6HEY7	1	B6HEY7	Pc20g08570 protein	dihydrolipoyllysine-residue succinyltransferase activity; oxoglutarate dehydrogenase complex; tricarboxylic acid cycle	
31.2105	31.1026	30.9039	30.4788	28.976	30.4902	7.41E-72	1.02E+10	3	2	29.5	13.979	30.527	31.0724	29.9817	6	3	3	B6HEY9	B6HEY9	1	B6HEY9	Histone H2A	DNA binding; nucleosome; nucleosome assembly; nucleus	Nucleus. Chromosome.
31.0941	30.9043	30.7014	30.2019	29.0852	30.2918	4.30E-132	8.96E+09	5	5	31.9	15.084	30.3798	30.8999	29.8596	6	3	3	B6HEZ0	B6HEZ0	1	B6HEZ0	Histone H2B	DNA binding; nucleosome; nucleosome assembly; nucleus	Nucleus. Nucleus. Chromosome.
27.5382	27.5	27.6115	27.4162	27.5786	26.9914	8.38E-77	1.04E+09	9	9	31.1	49.747	27.4393	27.5499	27.3287	6	3	3	B6HF38	B6HF38	1	B6HF38	Pc20g00270 protein	biosynthetic process; catalytic activity	
29.0748	28.4882	28.6095	30.1595	29.3894	29.688	4.04E-90	3.69E+09	12	12	45.8	29.303	29.2349	28.7242	29.7456	6	3	3	B6HF51	B6HF51	1	B6HF51	Pc20g02900 protein	RNA binding; ribosome; structural constituent of ribosome; translation	
28.4668	28.1393	28.3825	27.9404	27.0408	27.8014	1.05E-200	1.61E+09	10	10	45.1	39.284	27.9619	28.3296	27.5942	6	3	3	B6HF52	B6HF52	1	B6HF52	Pc20g02910 protein	N-acetyl-gamma-glutamyl-phosphate reductase activity; NAD binding; NADP binding; aspartate metabolic process; aspartate-semialdehyde dehydrogenase activity; cytoplasm; isoleucine biosynthetic process; lysine biosynthetic process via diaminopimelate; methionine biosynthetic process; threonine biosynthetic process	
28.1164	28.2408	28.1685	26.3405	23.5463	27.4084	6.69E-48	1.17E+09	9	9	25.1	49.28	26.9702	28.1753	25.7651	6	3	3	B6HF62	B6HF62	1	B6HF62	Pc20g05510 protein	ATP binding; cytoplasm; tryptophan-tRNA ligase activity; tryptophanyl-tRNA aminoacylation	
25.0235	24.9839	25.1532	25.2174	25.694	24.2644	1.15E-20	1.96E+08	4	4	5.7	121.04	25.0561	25.0535	25.0586	6	3	3	B6HF80	B6HF80	1	B6HF80	Pc20g09210 protein		
27.7761	27.7292	27.3252	28.016	27.9644	26.7652	2.67E-35	1.2E+09	6	6	14.5	63.704	27.596	27.6102	27.5819	6	3	3	B6HF85	B6HF85	1	B6HF85	Pc20g09260 protein		
26.83	27.2434	27.0785	27.7539	27.8386	26.5993	9.84E-89	9.24E+08	4	4	9.2	78.652	27.2239	27.0506	27.3973	6	3	3	B6HF99	B6HF99	1	B6HF99	Pc20g09400 protein	proteolysis; serine-type peptidase activity	
23.929	24.2195	23.9372	26.1319	26.2948	23.7424	4.34E-10	2E+08	3	3	2.3	248.61	24.7091	24.0286	25.3897	6	3	3	B6HFA0	B6HFA0	1	B6HFA0	Pc20g09410 protein	ATP binding; ATP-dependent helicase activity; nucleic acid binding	
26.7381	27.1292	26.699	27.0984	27.1004	27.5243	5.64E-52	7.6E+08	7	7	28.1	39.261	27.0482	26.8554	27.241	6	3	3	B6HFA6	B6HFA6	1	B6HFA6	Pc20g09470 protein	ATP binding; protein serine/threonine kinase activity	
26.1567	25.9865	26.6377	26.8283	ND	28.2481	4.38E-41	6.45E+08	9	9	14.3	119.58	26.7715	26.2603	27.5382	5	3	2	B6HFA7	B6HFA7	1	B6HFA7	Pc20g09480 protein	ATP binding; aminoacyl-tRNA editing activity; valine-tRNA ligase activity; valyl-tRNA aminoacylation	
27.4243	26.8895	26.9553	27.7925	27.5475	27.5132	6.39E-68	9.57E+08	8	8	32.8	29.197	27.3537	27.0897	27.6178	6	3	3	B6HFE0	B6HFE0	1	RS3A	40S ribosomal protein S1	cytosolic small ribosomal subunit; structural constituent of ribosome; translation	Cytoplasm.
27.4986	27.6351	27.5152	28.3843	28.7005	27.3778	1.47E-77	1.41E+09	7	7	35.4	27.349	27.8519	27.5496	28.1542	6	3	3	B6HFE2	B6HFE2	1	B6HFE2	Pc20g00460 protein		
25.7789	24.9032	25.3356	ND	24.3817	25.5152	4.26E-06	2.03E+08	3	3	37.8	8.9385	25.1829	25.3392	24.9485	5	3	2	B6HFF4	B6HFF4	1	B6HFF4	40S ribosomal protein S27	metal ion binding; ribosome; structural constituent of ribosome; translation	
25.1357	25.1141	25.6583	25.7293	25.742	27.5925	8.24E-19	3.63E+08	6	6	17.3	50.005	25.8287	25.3027	26.3546	6	3	3	B6HFH1	B6HFH1	1	B6HFH1	Pc20g05890 protein	GTP cyclohydrolase II activity; riboflavin biosynthetic process	
27.166	26.6195	27.9816	27.0205	24.8637	26.4134	8.28E-62	7.86E+08	11	11	30.1	53.379	26.6774	27.2557	26.0992	6	3	3	B6HFH3	B6HFH3	1	B6HFH3	Pc20g05910 protein	ATP binding; ATP-dependent helicase activity; nucleic acid binding	
30.1001	30.1148	30.1133	30.2519	30.4949	29.4489	1.55E-226	6.57E+09	18	18	43.8	53.426	30.0873	30.1094	30.0652	6	3	3	B6HFN8	B6HFN8	1	B6HFN8	Pc20g00490 protein	ATP binding; cytoplasm; serine-tRNA ligase activity; seryl-tRNA aminoacylation	
29.569	29.79	29.5578	30.2739	30.4972	29.0385	8.05E-218	5.56E+09	14	14	35.4	50.486	29.7877	29.639	29.9365	6	3	3	B6HFP1	B6HFP1	1	B6HFP1	Pc20g00530 protein	NAD binding; amino acid binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	
29.8879	30.2695	29.9837	29.8391	30.266	30.0221	3.14E-192	6.24E+09	16	16	42.4	46.432	30.0447	30.0471	30.0424	6	3	3	B6HFP4	B6HFP4	1	B6HFP4	Pc20g00560 protein	nucleosome assembly; nucleus	
27.7817	27.9297	28.0694	27.1557	27.6357	27.9874	1.62E-98	1.3E+09	8	8	20.2	56.375	27.7599	27.9269	27.5929	6	3	3	B6HFP6	B6HFP6	1	B6HFP6	Pc20g03150 protein		
23.9968	24.6895	24.4461	ND	ND	23.7682	1.59E-06	86152000	2	2	6	51.745	24.2251	24.3775	23.7682	4	1	1	B6HFQ2	B6HFQ2	1	B6HFQ2	Pc20g03210 protein	L-serine biosynthetic process; phosphoserine phosphatase activity	
ND		26.3969	25.5883	25.2856	25.5214	24.9668	6.88E-25	2.77E+08	2	2	14.9	24.454	25.5518	25.9926	25.2579	5	2	3	B6HFR0	B6HFR0	1	B6HFR0	Pc20g03290 protein		
28.9039	29.2718	29.0413	29.3064	29.2546	28.5871	1.47E-107	3.25E+09	10	10	29.4	52.48	29.0609	29.0723	29.0494	6	3	3	B6HFS2	B6HFS2	1	B6HFS2	Pc20g06010 protein	arginine biosynthetic process via ornithine; argininosuccinate lyase activity	
26.1245	26.5912	26.2387	25.3188	25.2565	27.9508	4.15E-63	5.11E+08	11	11	24.6	71.127	26.2467	26.3181	26.1754	6	3	3	B6HFS4	B6HFS4	1	B6HFS4	Pc20g06030 protein	electron transport chain; flavin adenine dinucleotide binding; oxidoreductase activity, acting on the CH-CH group of donors; tricarboxylic acid cycle	
23.3164	24.5339	24.2092	24.4024	23.3112	26.9415	1.41E-24	1.81E+08	7	7	16.6	57.658	24.4524	24.0198	24.885	6	3	3	B6HFS6	B6HFS6	1	B6HFS6	T-complex protein 1 subunit delta	ATP binding; cytoplasm; protein folding	
ND	ND		ND	25.506	25.9237	25.2952	1.37E-07	2.6E+08	2	2	23.9	9.9776	25.5749	ND	25.5749	3	0	3	B6HFU3	B6HFU3	1	B6HFU3	Pc20g10480 protein		
24.3549	22.6601	24.5793	21.883	ND	ND		0.000104	64995000	2	2	4.7	49.987	23.3693	23.8648	21.883	4	3	1	B6HFW0	B6HFW0	1	B6HFW0	Pc20g10670 protein	ATP binding; protein kinase activity	
26.5051	26.7028	26.611	26.8574	27.2966	25.9275	6.07E-32	6.09E+08	5	5	32.3	20.8	26.6501	26.6063	26.6938	6	3	3	B6HG06	B6HG06	1	B6HG06	Inosine triphosphate pyrophosphatase	cytoplasm; deoxyribonucleoside triphosphate catabolic process; metal ion binding; nucleoside-triphosphate diphosphatase activity; nucleotide binding; nucleotide metabolic process; nucleus	Cytoplasm. Nucleus.
24.6977	ND	24.3234	ND	ND	24.3937	1.30E-08	73547000	3	3	9.7	56.813	24.4716	24.5106	24.3937	3	2	1	B6HG11	B6HG11	1	B6HG11	Aspartokinase	amino acid binding; aspartate kinase activity; lysine biosynthetic process via diaminopimelate; threonine biosynthetic process	
27.8867	28.2258	27.9378	28.9134	28.8403	27.5856	1.23E-84	1.87E+09	4	4	53.8	10.234	28.2316	28.0168	28.4464	6	3	3	B6HG14	B6HG14	1	B6HG14	Pc20g00670 protein	metal ion binding; mitochondrion; protein transport	
27.0441	27.9568	27.2985	31.1551	30.523	31.0634	3.62E-50	5.55E+09	7	7	40.9	16.435	29.1735	27.4331	30.9139	6	3	3	B6HG15	B6HG15	1	B6HG15	Pc20g00680 protein	nucleotide binding; ribosome; structural constituent of ribosome; translation	
23.5599	22.3733	23.5231	ND	ND	26.9912	2.14E-19	1.21E+08	5	5	12.7	55.038	24.1119	23.1521	26.9912	4	3	1	B6HG18	B6HG18	1	B6HG18	Pc20g00710 protein	cytoplasm; translation release factor activity, codon specific	
31.208	31.3447	31.2043	31.2871	31.4441	30.1528	0	1.37E+10	25	25	55.6	58.305	31.1068	31.2523	30.9613	6	3	3	B6HG21	B6HG21	1	B6HG21	Glucose-6-phosphate 1-dehydrogenase	NADP binding; glucose-6-phosphate dehydrogenase activity; pentose-phosphate shunt	
23.2035	22.9713	22.9408	24.2557	23.9451	24.309	0.000589	68071000	2	2	18.3	12.317	23.6042	23.0386	24.1699	6	3	3	B6HG22	B6HG22	1	B6HG22	Pc20g03340 protein	ribosome; structural constituent of ribosome; translation	
26.4995	26.1383	26.5125	26.1276	26.328	24.7507	1.15E-16	4.37E+08	6	6	15.7	55.828	26.0594	26.3835	25.7354	6	3	3	B6HG86	B6HG86	1	B6HG86	Pc20g11520 protein	methylmalonate-semialdehyde dehydrogenase (acylating) activity	
ND	ND		ND	25.3506	25.8948	ND	1.02E-34	99575000	3	3	15.2	25.944	25.6227	ND	25.6227	2	0	2	B6HG91	B6HG91	1	B6HG91	Pc20g11570 protein		
28.4931	28.6022	28.4202	28.8943	28.8049	27.5884	4.50E-136	2.19E+09	9	9	39.3	28.168	28.4672	28.5052	28.4292	6	3	3	B6HG92	B6HG92	1	B6HG92	Proteasome subunit alpha type	cytoplasm; nucleus; proteasome core complex, alpha-subunit complex; threonine-type endopeptidase activity; ubiquitin-dependent protein catabolic process	Cytoplasm. Nucleus.
24.0256	23.8987	23.845	23.2778	22.6251	23.6685	6.11E-05	75611000	2	2	8.4	23.224	23.5568	23.9231	23.1905	6	3	3	B6HG96	B6HG96	1	B6HG96	Pc20g11620 protein		
26.021	26.1445	25.8303	24.2158	24.7953	30.3007	5.93E-169	1.06E+09	16	16	65.1	41.756	26.2179	25.9986	26.4373	6	3	3	B6HG97;CON__P60712	B6HG97	2	B6HG97	Gamma-actin act-Penicillium chrysogenum	ATP binding; cytoplasm; cytoskeleton	
28.3991	28.0346	28.4727	29.1591	27.2469	28.1258	4.23E-230	2.02E+09	15	15	24.9	84.596	28.2397	28.3022	28.1772	6	3	3	B6HG99	B6HG99	1	B6HG99	Pc20g11650 protein	'de novo' IMP biosynthetic process; ATP binding; cytoplasm; metal ion binding; phosphoribosylamine-glycine ligase activity; phosphoribosylformylglycinamidine cyclo-ligase activity; purine nucleobase biosynthetic process	
31.9736	32.2599	31.9665	32.4644	33.0564	31.2755	0	2.86E+10	12	12	24.9	45.58	32.166	32.0667	32.2654	6	3	3	B6HGB9	B6HGB9	1	B6HGB9	Pc20g11850 protein	eukaryotic translation elongation factor 1 complex; translation elongation factor activity	
22.3658	22.4683	22.5575	22.5414	22.1782	27.2448	2.61E-62	1.35E+08	4	4	8.9	52.808	23.226	22.4639	23.9882	6	3	3	B6HGC6	B6HGC6	1	B6HGC6	Pc20g00750 protein	RNA binding; RNA processing; pseudouridine synthase activity; pseudouridine synthesis	
27.7613	27.7081	27.2863	ND	27.217	26.8648	3.73E-22	1.08E+09	3	3	20.8	16.828	27.3675	27.5852	27.0409	5	3	2	B6HGF6	B6HGF6	1	B6HGF6	Pc20g03580 protein	sequence-specific DNA binding	
27.7923	27.8376	27.578	29.2165	29.388	27.7494	1.13E-140	2.01E+09	9	9	35.1	37.081	28.2603	27.736	28.7846	6	3	3	B6HGF7	B6HGF7	1	B6HGF7	Eukaryotic translation initiation factor 3 subunit I	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
25.3825	25.3519	25.3302	25.8058	25.9625	24.9789	2.36E-13	2.69E+08	4	4	31.8	16.808	25.4686	25.3549	25.5824	6	3	3	B6HGH7	B6HGH7	1	B6HGH7	Pc20g06450 protein	DNA-directed RNA polymerase activity; nucleotide binding; transcription, DNA-templated	
23.5234	24.4048	23.8836	25.1627	25.0481	ND	5.99E-07	1.23E+08	2	2	4.2	51.596	24.4045	23.9373	25.1054	5	3	2	B6HGI2	B6HGI2	1	B6HGI2	Pc20g12210 protein		
26.1443	26.5564	26.3245	27.0954	27.0598	25.9484	9.47E-25	1.64E+08	10	10	17.6	92.832	26.5215	26.3417	26.7012	6	3	3	B6HGL1	B6HGL1	1	B6HGL1	Pc20g12700 protein	mannosyl-oligosaccharide glucosidase activity; oligosaccharide metabolic process	
24.8798	25.9708	25.781	24.4145	24.4165	27.8747	9.81E-58	3.67E+08	9	9	9	146.83	25.5562	25.5439	25.5686	6	3	3	B6HGR5	B6HGR5	1	B6HGR5	Pc20g01010 protein	ATP binding; cytoplasm; glycine-tRNA ligase activity; glycyl-tRNA aminoacylation	
26.3458	26.5661	26.2492	27.3459	27.2277	25.5687	9.04E-45	6.03E+08	8	8	36.4	30.164	26.5506	26.387	26.7141	6	3	3	B6HGR9	B6HGR9	1	B6HGR9	Pc20g01050 protein	cytoplasm	
24.6403	25.3547	25.3395	26.2347	26.2649	23.9681	7.61E-19	2.69E+08	3	3	5.8	89.784	25.3003	25.1115	25.4892	6	3	3	B6HGU2	B6HGU2	1	B6HGU2	Pc20g03790 protein		
23.5479	24.9035	24.0711	26.4247	26.4417	27.6422	4.70E-42	3.6E+08	4	4	33.8	16.782	25.5052	24.1742	26.8362	6	3	3	B6HGW5	B6HGW5	1	B6HGW5	Pc20g13260 protein	ribosome; structural constituent of ribosome; translation	
30.6026	29.774	30.5578	30.8086	31.1604	30.4833	4.71E-185	8.72E+09	5	5	43.8	21.964	30.5645	30.3115	30.8174	6	3	3	B6HGW6	B6HGW6	1	B6HGW6	Pc20g13270 protein		
24.3705	24.6817	24.7777	ND	ND	27.1028	3.05E-23	1.75E+08	4	4	12.6	60.95	25.2332	24.61	27.1028	4	3	1	B6HGX4	B6HGX4	1	B6HGX4	Pc20g13350 protein	2 iron, 2 sulfur cluster binding; 2-methylcitrate dehydratase activity; propionate catabolic process, 2-methylcitrate cycle	
27.0852	27.868	27.5681	28.2562	28.4698	26.6527	7.15E-77	1.29E+09	5	5	14	60.152	27.65	27.5071	27.7929	6	3	3	B6HGY3	B6HGY3	1	B6HGY3	Pc20g13440 protein	UDP-N-acetylmuramate dehydrogenase activity; flavin adenine dinucleotide binding	
24.7855	24.9384	27.005	ND	ND	26.8847	2.81E-25	3.26E+08	6	6	18.1	50.942	25.9034	25.5763	26.8847	4	3	1	B6HGY9	B6HGY9	1	B6HGY9	Citrate synthase	cellular carbohydrate metabolic process; transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer; tricarboxylic acid cycle	
24.8052	25.5703	24.552	ND	25.3697	26.2386	2.89E-09	2.24E+08	4	4	18.5	29.882	25.3072	24.9758	25.8042	5	3	2	B6HGZ5;B6H6H7U4	B6HGZ5;B6H7U4	2	B6HGZ5	Pc20g13570 protein	oxidoreductase activity	
26.4349	26.0633	26.3818	25.372	25.8613	24.3387	4.83E-35	3.73E+08	3	3	25.3	16.463	25.742	26.2933	25.1907	6	3	3	B6HH06	B6HH06	1	B6HH06	Pc20g13690 protein	cofactor binding	
23.9301	ND	24.6212	ND	ND	23.1358	0.000514	72951000	2	2	2.8	111.2	23.8957	24.2757	23.1358	3	2	1	B6HH22	B6HH22	1	B6HH22	Pc20g13850 protein		
24.7229	24.9296	25.0442	25.2726	25.5173	24.8345	1.13E-08	1.96E+08	2	2	14.7	19.88	25.0535	24.8989	25.2081	6	3	3	B6HH27	B6HH27	1	B6HH27	Pc20g13900 protein		
28.1987	28.2027	28.4674	28.6846	27.5694	28.136	3.75E-222	1.83E+09	6	6	42.5	26.362	28.2098	28.2896	28.13	6	3	3	B6HH38	B6HH38	1	B6HH38	Pc20g01120 protein	mature ribosome assembly; ribosome binding	
28.4402	27.9428	28.225	26.934	26.1398	27.4439	1.50E-38	1.32E+09	5	5	11.8	40.068	27.521	28.2027	26.8392	6	3	3	B6HH40	B6HH40	1	B6HH40	Pc20g01150 protein	damaged DNA binding; nucleotide-excision repair; nucleus; proteasome-mediated ubiquitin-dependent protein catabolic process	
25.631	25.2455	25.2569	24.6747	26.4867	24.5842	3.17E-16	2.53E+08	7	7	11.6	47.757	25.3131	25.3778	25.2485	6	3	3	B6HH51	B6HH51	1	B6HH51	Pc20g01270 protein	aspartic-type endopeptidase activity; proteolysis	
26.8794	27.1705	27.0924	27.0307	26.923	26.7173	2.28E-62	7.46E+08	7	7	29.5	31.183	26.9689	27.0474	26.8903	6	3	3	B6HH62	B6HH62	1	B6HH62	Pc20g03920 protein	proteasome regulatory particle; proteolysis	
24.5214	24.8549	24.6312	23.4321	24.9857	24.0613	1.70E-08	1.36E+08	4	4	12.5	43.41	24.4144	24.6691	24.1597	6	3	3	B6HH64	B6HH64	1	B6HH64	Pc20g03940 protein	post-chaperonin tubulin folding pathway	
28.3336	28.5514	28.2992	29.2437	29.5992	27.0472	3.33E-208	2.46E+09	9	9	9.2	135.33	28.5124	28.3947	28.63	6	3	3	B6HH67	B6HH67	1	B6HH67	Pc20g03970 protein	COPI vesicle coat; intracellular protein transport; structural molecule activity; vesicle-mediated transport	
27.0758	27.3423	26.9439	27.4631	27.703	25.9187	1.67E-17	8.73E+08	4	4	19	25.696	27.0745	27.1207	27.0283	6	3	3	B6HH78	B6HH78	1	B6HH78	Pc20g06720 protein	catalytic activity	
24.8106	25.2325	25.2938	23.1956	23.7309	30.4111	3.52E-178	1.16E+09	14	14	42.4	44.455	25.4458	25.1123	25.7792	6	3	3	B6HH80	B6HH80	1	B6HH80	Pc20g06740 protein	ATP binding; ATP-dependent helicase activity; nucleic acid binding	
24.184	23.7519	24.2468	23.0696	23.3621	22.8858	3.89E-07	79652000	3	3	2.9	122.75	23.5834	24.0609	23.1058	6	3	3	B6HH84	B6HH84	1	B6HH84	Pc20g06780 protein	alpha-mannosidase activity; carbohydrate binding; mannose metabolic process; zinc ion binding	
29.5833	28.5584	28.4415	28.6604	28.4464	28.5423	7.07E-76	2.58E+09	11	11	36.5	44.328	28.7054	28.8611	28.5497	6	3	3	B6HHA4	B6HHA4	1	B6HHA4	Pc20g14180 protein	ribosome; structural constituent of ribosome; translation	
29.5451	28.6714	29.5197	29.1991	28.594	29.2034	2.43E-139	3.4E+09	15	15	41	54.025	29.1221	29.2454	28.9988	6	3	3	B6HHB0	B6HHB0	1	B6HHB0	Pc20g14240 protein	N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity; purine ribonucleotide biosynthetic process	
25.1407	25.5346	25.4437	25.8838	26.2222	24.9164	3.98E-09	2.82E+08	3	3	31.4	13.272	25.5236	25.373	25.6741	6	3	3	B6HHB6	B6HHB6	1	B6HHB6	Pc20g14300 protein		
26.0644	26.0033	25.8158	25.662	25.9858	24.8972	9.09E-25	3.29E+08	7	7	18.9	44.629	25.7381	25.9612	25.515	6	3	3	B6HHD2	B6HHD2	1	B6HHD2	Pc20g14470 protein	ATP binding; protein serine/threonine kinase activity	
27.0382	27.2074	26.9724	28.1438	28.1138	26.6528	2.36E-37	1.03E+09	5	5	54.2	12.51	27.3547	27.0727	27.6368	6	3	3	B6HHD3	B6HHD3	1	B6HHD3	Pc20g14480 protein	metal ion binding; mitochondrion; protein transport	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
28.0244	27.627	27.8671	27.573	26.5835	29.5477	2.26E-132	1.54E+09	9	9	52.5	42.27	27.8704	27.8395	27.9014	6	3	3	B6HHI9	B6HHI9	1	B6HHI9	Pc21g05430 protein	catalytic activity; pyridoxal phosphate binding	
25.994	25.1858	25.6786	26.5021	26.3531	25.7618	6.32E-14	3.63E+08	2	2	6.7	49.942	25.9126	25.6195	26.2057	6	3	3	B6HHL3	B6HHL3	1	B6HHL3	Pc21g09780 protein	oxidoreductase activity	
27.5073	27.9507	27.545	28.9648	28.689	27.7993	3.78E-40	1.68E+09	8	8	13.4	62.56	28.076	27.6676	28.4844	6	3	3	B6HHM1	B6HHM1	1	B6HHM1	Pc21g09860 protein	carbon-nitrogen ligase activity, with glutamine as amido-N-donor	
24.3492	24.8385	24.8173	23.42	23.0989	26.2145	1.07E-14	1.63E+08	4	4	16.6	31.085	24.4564	24.6683	24.2445	6	3	3	B6HHM5	B6HHM5	1	B6HHM5	Pc21g09900 protein	2 iron, 2 sulfur cluster binding; electron carrier activity; oxidoreductase activity; tricarboxylic acid cycle	
28.2999	28.7192	28.4072	28.8402	29.1083	27.7941	1.84E-96	2.26E+09	10	10	37.3	40.396	28.5281	28.4754	28.5808	6	3	3	B6HHR8	B6HHR8	1	B6HHR8	Pc21g18480 protein		
28.6812	28.3067	28.7514	29.4811	29.6856	27.9629	2.55E-157	2.84E+09	7	7	29.2	37.918	28.8115	28.5798	29.0432	6	3	3	B6HHT2	B6HHT2	1	B6HHT2	Pc21g18620 protein		
26.0066	25.7384	25.8908	24.4939	ND	26.9347	3.49E-13	3.29E+08	3	3	29.6	11.778	25.8129	25.8786	25.7143	5	3	2	B6HHU9	B6HHU9	1	B6HHU9	Pc21g22970 protein		
22.4981	23.2321	22.7657	24.8723	24.2799	27.0304	4.93E-09	1.61E+08	2	2	5.3	63.682	24.1131	22.832	25.3942	6	3	3	B6HHV2	B6HHV2	1	B6HHV2	Pc21g23000 protein		
26.6039	25.8165	26.9942	27.3927	25.5356	27.2666	1.59E-37	6.3E+08	9	8	29.6	46.672	26.6016	26.4715	26.7316	6	3	3	B6HHX8	B6HHX8	1	B6HHX8	Pc21g01100 protein	acyl-CoA dehydrogenase activity; flavin adenine dinucleotide binding	
27.3555	27.2456	27.4302	26.8813	26.5666	26.5928	4.77E-62	8.33E+08	10	10	19.1	62.276	27.012	27.3438	26.6802	6	3	3	B6HHX9	B6HHX9	1	B6HHX9	Pc21g01110 protein	ligase activity	
31.3415	31.2257	31.4124	30.9293	29.9355	32.2519	0	1.46E+10	20	20	57.5	55.213	31.1827	31.3265	31.0389	6	3	3	B6HI25	B6HI25	1	B6HI25	ATP synthase subunit beta	ATP binding; ATP hydrolysis coupled proton transport; ATP synthesis coupled proton transport; proton-transporting ATP synthase activity, rotational mechanism; proton-transporting ATP synthase complex, catalytic core F(1)	
28.5035	28.7598	28.8878	28.7942	29.4856	27.9977	4.40E-103	2.62E+09	5	5	35.1	16.571	28.7381	28.717	28.7592	6	3	3	B6HJ27	B6HJ27	1	B6HJ27	Pc21g10090 protein	actin cytoskeleton; actin filament depolymerization	
26.981	26.7693	26.8164	26.8243	26.8282	25.6854	1.70E-43	6.57E+08	4	4	13.1	26.065	26.6508	26.8556	26.446	6	3	3	B6HJ28	B6HJ28	1	B6HJ28	Pc21g10100 protein		
26.791	26.8675	26.7679	26.8964	27.2176	26.1961	1.13E-25	6.64E+08	4	4	21.9	21.111	26.7894	26.8088	26.7701	6	3	3	B6HJ47	B6HJ47	1	B6HJ47	Pc21g14440 protein	Arp2/3 complex-mediated actin nucleation; Arp2/3 protein complex	
23.9464	22.9706	ND	22.6035	ND	ND	1.01E-31	42424000	3	2	20.1	14.828	23.1735	23.4585	22.6035	3	2	1	B6HI57	B6HI57	1	B6HI57	Pc21g11570 protein	DNA binding; nucleosome; nucleosome assembly; nucleus	Nucleus. Nucleus. Chromosome.
30.4692	30.7611	30.399	32.2303	31.441	34.4322	0	2.69E+10	15	15	52.5	36	31.6221	30.5431	32.7011	6	3	3	B6HI59	B6HI59	1	B6HI59	Glyceraldehyde-3-phosphate dehydrogenase	NAD binding; NADP binding; glucose metabolic process; glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity	
28.4748	28.5325	28.6311	27.8025	26.9007	28.4688	9.37E-85	1.87E+09	20	20	23.8	130.36	28.1351	28.5461	27.724	6	3	3	B6HI62	B6HI62	1	B6HI62	Pc21g14590 protein	hydrolase activity; metal ion binding	
25.5967	25.8892	25.5194	26.881	26.9175	24.8157	1.62E-21	4.08E+08	4	4	21.2	31.636	25.9366	25.6684	26.2047	6	3	3	B6HI63	B6HI63	1	B6HI63	Pc21g14600 protein	mRNA binding; mRNA cleavage factor complex; mRNA polyadenylation	
27.1849	27.385	27.626	26.7015	26.9393	26.0674	5.25E-39	8.27E+08	6	6	17	63.677	26.984	27.3986	26.5694	6	3	3	B6HI67	B6HI67	1	B6HI67	Serine/threonine-protein phosphatase	hydrolase activity	
21.7129	21.6536	21.8783	ND		20.7357	27.0604	5.45E-12	1.09E+08	3	3	20	19.091	22.6082	21.7482	23.8981	5	3	2	B6HI69	B6HI69	1	B6HI69	Pc21g18690 protein		
26.6508	25.2308	26.7886	26.2447	24.828	26.7797	7.67E-29	4.59E+08	5	5	13.7	43.317	26.0871	26.2234	25.9508	6	3	3	B6HI86	B6HI86	1	B6HI86	Pc21g18870 protein	ATP binding; cytoplasm; tyrosine-tRNA ligase activity; tyrosyl-tRNA aminoacylation	
25.5343	23.1318	25.3755	22.8671	ND	27.9471	7.77E-41	2.92E+08	11	11	12.6	147.6	24.9712	24.6806	25.4071	5	3	2	B6HI87	B6HI87	1	B6HI87	Pc21g18880 protein	'de novo' IMP biosynthetic process; phosphoribosylformylglycinamidine synthase activity	
28.0217	28.3606	28.1465	28.813	29.2779	27.9947	1.37E-152	2.11E+09	14	14	28.7	70.284	28.4358	28.1763	28.6952	6	3	3	B6HIA0	B6HIA0	1	B6HIA0	Pc21g23240 protein	2-isopropylmalate synthase activity; leucine biosynthetic process	
25.982	26.3638	26.6853	26.2011	26.2066	28.4978	2.61E-23	6.72E+08	6	6	30.3	23.483	26.6561	26.3437	26.9685	6	3	3	B6HIA3	B6HIA3	1	B6HIA3	Pc21g23270 protein	RNA binding; small ribosomal subunit; structural constituent of ribosome; translation	
24.6514	24.8982	24.6616	25.7631	25.5625	24.1184	5.47E-16	1.86E+08	6	6	5.4	128.12	24.9425	24.737	25.148	6	3	3	B6HIC8	B6HIC8	1	B6HIC8	Pc21g01360 protein	catalytic activity	
26.9173	26.5808	27.0156	26.7491	28.1111	27.1377	1.63E-16	8.36E+08	4	4	8.1	53.491	27.0853	26.8379	27.3326	6	3	3	B6HIE1	B6HIE1	1	B6HIE1	Pc21g01490 protein	nucleic acid binding; nucleotide binding	
28.1472	28.1395	28.1789	28.294	28.6875	27.0954	5.60E-133	1.69E+09	5	5	31.5	28.956	28.0904	28.1552	28.0256	6	3	3	B6HIE7	B6HIE7	1	B6HIE7	Pc21g05900 protein	oxidoreductase activity	
25.2723	26.0605	26.0795	25.7193	25.9473	24.8628	4.94E-05	3.15E+08	2	2	11.3	32.294	25.6569	25.8041	25.5098	6	3	3	B6HIF2	B6HIF2	1	B6HIF2	Pc21g05950 protein	Mo-molybdopterin cofactor biosynthetic process	
25.6006	ND		26.5978	26.1201	25.7943	24.886	1.58E-15	3.25E+08	4	4	39	16.201	25.8448	25.5992	26.0085	5	2	2	B6HIF3	B6HIF3	1	B6HIF3	Pc21g05960 protein	intracellular	
24.9873	25.0511	24.7485	25.2132	25.5683	23.9622	7.57E-13	1.88E+08	2	2	10.6	35.757	24.9218	24.929	24.9146	6	3	3	B6HIG4	B6HIG4	1	B6HIG4	Pc21g06070 protein	hydrolase activity	
26.0357	25.9617	25.9762	26.3569	26.0087	23.8057	1.96E-46	3.55E+08	4	4	17.4	38.967	25.6908	25.9912	25.3904	6	3	3	B6HIH2	B6HIH2	1	B6HIH2	Pc21g10250 protein	FMN binding; pyridoxamine-phosphate oxidase activity; pyridoxine biosynthetic process	
24.8472	25.7141	25.3297	24.5264	24.618	24.5667	4.86E-09	1.99E+08	3	3	5	90.774	24.9337	25.297	24.5703	6	3	3	B6HII3	B6HII3	1	B6HII3	Pc21g10360 protein		
25.583	26.12	25.3154	24.6417	25.0346	28.6669	8.09E-24	5.38E+08	8	8	28.3	40.44	25.8936	25.6728	26.1144	6	3	3	B6HII4	B6HII4	1	B6HII4	Pc21g10370 protein	UDP-glucose 4-epimerase activity; cellular metabolic process; coenzyme binding; galactose metabolic process	
21.7767	21.8386	21.7858	ND		21.3455	27.7629	1.04E-18	1.63E+08	3	3	15.1	20.777	22.9019	21.8004	24.5542	5	3	2	B6HIR2	B6HIR2	1	B6HIR2	Pc21g23500 protein		
28.0099	27.6725	28.0163	28.6892	28.9678	27.5215	1.27E-36	1.76E+09	6	6	21.7	36.417	28.1462	27.8995	28.3928	6	3	3	B6HIT0	B6HIT0	1	B6HIT0	Pc21g01510 protein	oxidoreductase activity	
28.1823	28.0409	28.0531	25.9164	25.8484	27.7283	9.23E-93	1.17E+09	2	2	17.6	14.9	27.2949	28.0921	26.4977	6	3	3	B6HIT1	B6HIT1	1	B6HIT1	Pc21g01520 protein	ribosome; structural constituent of ribosome; translation	
30.3151	30.5408	30.232	30.5676	30.8141	29.4457	1.02E-208	7.85E+09	8	8	46	22.346	30.3192	30.3626	30.2758	6	3	3	B6HIW5	B6HIW5	1	B6HIW5	Pc21g06220 protein	Rho GDP-dissociation inhibitor activity; cytoplasm	
25.4837	24.11	24.6903	22.9081	ND	24.4863	2.44E-05	1.21E+08	2	2	7.9	35.447	24.3197	24.7613	23.6972	5	3	2	B6HIX3	B6HIX3	1	B6HIX3	Pc21g06300 protein	oxidoreductase activity; zinc ion binding	
24.3318	25.1984	24.5512	25.0728	25.2362	24.0593	8.81E-21	1.6E+08	3	3	9.3	59.339	24.7416	24.6938	24.7894	6	3	3	B6HIY5	B6HIY5	1	B6HIY5	Pc21g06420 protein	S-adenosylmethionine-dependent tRNA (m5U54) methyltransferase activity	
24.2451	24.1145	24.344	ND	ND	26.4372	2.42E-29	1.2E+08	5	5	20.8	47.46	24.7852	24.2345	26.4372	4	3	1	B6HIY6	B6HIY6	1	B6HIY6	Pc21g06430 protein	ATP binding; Arp2/3 complex-mediated actin nucleation; Arp2/3 protein complex	
29.7661	29.6943	29.7071	29.8332	30.0984	28.0956	1.62E-167	4.84E+09	6	6	51.5	25.776	29.5324	29.7225	29.3424	6	3	3	B6HIZ4	B6HIZ4	1	B6HIZ4	Carbonic anhydrase	carbon utilization; carbonate dehydratase activity; zinc ion binding	
26.8192	27.0518	26.8631	26.8043	27.2619	26.0997	1.49E-32	6.96E+08	7	7	29	34.894	26.8167	26.9114	26.722	6	3	3	B6HJ13	B6HJ13	1	B6HJ13	Pc21g14980 protein	dTDP-4-dehydrorhamnose reductase activity; extracellular polysaccharide biosynthetic process	
24.8495	24.5432	26.6842	24.4941	ND	25.2815	5.10E-58	2.3E+08	8	8	16	77.399	25.1705	25.3589	24.8878	5	3	2	B6HJ22;B6H720	B6HJ22	2	B6HJ22	Pc21g15090 protein	GTP binding; GTPase activity	
25.1528	25.1646	25.9102	24.4618	ND	27.2171	1.89E-30	2.56E+08	10	10	20	66.251	25.5813	25.4092	25.8394	5	3	2	B6HJ23	B6HJ23	1	B6HJ23	Pc21g15100 protein	ATP binding; ATP hydrolysis coupled proton transport; hydrogen-exporting ATPase activity, phosphorylative mechanism; proton-transporting ATPase activity, rotational mechanism; proton-transporting V-type ATPase, V1 domain	
26.4225	26.4231	26.0187	26.8904	26.7238	30.2212	8.34E-201	1.29E+09	11	11	33.8	43.899	27.1166	26.2881	27.9451	6	3	3	B6HJ33	B6HJ33	1	B6HJ33	Pc21g19210 protein	cytoplasm; hydrolase activity	
32.0188	31.4509	31.9963	28.4213	27.8727	31.1117	0	1.42E+10	41	41	63.7	90.387	30.4786	31.822	29.1352	6	3	3	B6HJ39	B6HJ39	1	B6HJ39	Pc21g19270 protein	ATP binding; nucleoside-triphosphatase activity	
24.1628	24.2309	24.0507	24.5374	24.9468	23.1867	7.29E-06	1.14E+08	2	2	6.7	30.951	24.1859	24.1481	24.2236	6	3	3	B6HJ43	B6HJ43	1	B6HJ43	Defective in cullin neddylation protein		
28.7675	29.0462	28.7536	29.3076	29.8519	27.6264	1.61E-81	3.06E+09	4	4	18.1	24.518	28.8922	28.8558	28.9286	6	3	3	B6HJ59	B6HJ59	1	B6HJ59	Pc21g23710 protein		
27.9984	27.7879	28.0113	28.2261	28.1492	27.0852	4.11E-69	1.45E+09	5	5	33.6	24.817	27.8763	27.9325	27.8202	6	3	3	B6HJ77	B6HJ77	1	B6HJ77	Pc21g01810 protein		
29.8833	30.2827	30.0845	30.8764	31.3248	29.3962	0	8.15E+09	18	18	40.4	60.504	30.308	30.0835	30.5324	6	3	3	B6HJ92	B6HJ92	1	B6HJ92	Importin subunit alpha	cytoplasm; nucleus; protein import into nucleus; protein transporter activity	
28.8887	28.7953	28.9478	27.2075	27.2207	29.3544	8.64E-96	2.31E+09	13	13	30.4	69.079	28.4024	28.8773	27.9275	6	3	3	B6HJA0	B6HJA0	1	B6HJA0	Pc21g02050 protein	ATP binding; cytoplasm; proline-tRNA ligase activity; prolyl-tRNA aminoacylation	
29.8539	30.0262	29.7844	30.1601	30.4991	28.7774	1.61E-82	5.8E+09	8	8	21	39.916	29.8502	29.8882	29.8122	6	3	3	B6HJG5	B6HJG5	1	B6HJG5	Pc21g15240 protein	isoprenoid biosynthetic process; transferase activity	
27.5805	27.8194	27.6139	27.311	28.3615	26.8372	2.06E-51	1.25E+09	9	9	30	42.17	27.6765	27.6713	27.6817	6	3	3	B6HJG8	B6HJG8	1	B6HJG8	Pc21g15270 protein		
25.9116	25.4267	25.9846	25.0788	ND	25.5222	2.87E-17	2.57E+08	5	5	17.3	37.314	25.5848	25.7743	25.3005	5	3	2	B6HJI8	B6HJI8	1	B6HJI8	Pc21g19480 protein	intracellular; negative regulation of actin filament polymerization	
25.5792	25.6258	25.4601	27.7997	28.2032	25.3092	1.46E-07	6.43E+08	3	3	18.5	10.129	26.3295	25.555	27.104	6	3	3	B6HJJ3	B6HJJ3	1	B6HJJ3	Pc21g19530 protein	ribosome; structural constituent of ribosome; translation	
29.1763	29.393	29.1281	30.0926	30.4149	29.2922	9.56E-207	4.68E+09	14	14	42.8	47.576	29.5828	29.2325	29.9332	6	3	3	B6HJN0	B6HJN0	1	B6HJN0	Pc21g02360 protein	tRNA binding	
ND	ND		ND	24.3933	ND	23.3198	0.001253	61527000	2	2	6.2	39.757	23.8565	ND		23.8565	2	0	2	B6HJN7	B6HJN7	1	B6HJN7	Pc21g02430 protein		
29.9254	30.0074	30.0793	29.9403	29.6216	29.3417	2.53E-262	5.51E+09	24	24	37.7	114.74	29.8193	30.004	29.6345	6	3	3	B6HJN8	B6HJN8	1	B6HJN8	Pc21g02440 protein	ATP binding; cellular protein modification process; ligase activity; small protein activating enzyme activity	
ND	22.525	22.5966	ND	ND	25.4694	1.02E-07	58713000	3	3	4.5	100.27	23.5303	22.5608	25.4694	3	2	1	B6HJP8	B6HJP8	1	B6HJP8	Pc21g06810 protein	enzyme regulator activity; proteasome complex; regulation of protein catabolic process	
27.7696	27.7948	27.5552	27.8874	28.5472	26.8784	5.24E-65	1.32E+09	8	8	23.9	36.639	27.7388	27.7065	27.771	6	3	3	B6HJQ4	B6HJQ4	1	B6HJQ4	Pc21g06870 protein	hydroxymethylbilane synthase activity; peptidyl-pyrromethane cofactor linkage; tetrapyrrole biosynthetic process	
28.3248	28.5807	28.3872	28.2094	28.2659	27.5754	1.63E-48	1.83E+09	6	6	21.2	41.538	28.2239	28.4309	28.0169	6	3	3	B6HJQ8	B6HJQ8	1	B6HJQ8	Pc21g06910 protein	response to oxidative stress	
26.215	26.6431	26.1085	26.3561	26.7056	26.1718	8.41E-110	4.91E+08	4	4	23.1	27.936	26.3667	26.3222	26.4112	6	3	3	B6HJS4	B6HJS4	1	B6HJS4	Pc21g11050 protein		
24.8402	23.6262	25.5934	24.139	22.793	23.8506	1.30E-09	1.45E+08	4	4	23.8	32.415	24.0074	24.6866	23.3282	6	3	3	B6HJW8	B6HJW8	1	B6HJW8	Pc21g19720 protein	thiamine biosynthetic process	
25.9282	26.0077	25.8154	26.7459	27.1829	25.5741	4.77E-20	4.53E+08	6	6	21.1	54.88	26.209	25.9171	26.501	6	3	3	B6HJY1	B6HJY1	1	B6HJY1	Pc21g19830 protein	nucleus	
25.2073	25.1275	24.4847	24.8625	23.7774	24.1178	4.06E-11	1.55E+08	3	3	7.7	68.415	24.5962	24.9399	24.2525	6	3	3	B6HK05	B6HK05	1	B6HK05	Pc21g02550 protein	ATP binding; glycolysis; kinase activity; phosphotransferase activity, alcohol group as acceptor	
25.3964	25.311	25.2769	25.9895	26.2821	25.0402	6.67E-20	2.79E+08	4	4	42.3	12.538	25.5494	25.3281	25.7706	6	3	3	B6HK07	B6HK07	1	B6HK07	Transcription initiation factor IIA subunit 2	regulation of transcription, DNA-templated; transcription factor TFIIA complex; transcription initiation from RNA polymerase II promoter	Nucleus.
25.2776	25.4518	25.0541	25.948	26.2522	25.0563	2.72E-59	2.85E+08	3	3	20.5	27.196	25.5067	25.2612	25.7522	6	3	3	B6HK28	B6HK28	1	B6HK28	Pc21g07040 protein	mRNA splicing, via spliceosome; nucleotide binding; snRNA binding	
31.0895	31.1002	31.1778	32.1012	32.1109	30.9702	0	1.69E+10	20	20	48.5	56.245	31.425	31.1225	31.7274	6	3	3	B6HK48	B6HK48	1	B6HK48	Pc21g11280 protein	cell redox homeostasis; endoplasmic reticulum; glycerol ether metabolic process; isomerase activity; protein disulfide oxidoreductase activity	
25.4044	24.9392	25.3824	26.1299	24.7681	24.7189	2.39E-61	2.48E+08	4	4	9.9	67.814	25.2238	25.242	25.2056	6	3	3	B6HK64	B6HK64	1	B6HK64	Pc21g11440 protein	DNA binding; DNA replication; nucleus	
24.0073	23.996	24.139	24.6154	23.8083	26.2933	1.01E-09	1.45E+08	4	4	10.8	38.065	24.4766	24.0474	24.9057	6	3	3	B6HK67	B6HK67	1	B6HK67	Pc21g15700 protein	thiamine biosynthetic process	
24.3446	24.6549	24.2529	27.1977	27.257	29.7095	6.16E-162	9.37E+08	17	17	36.7	80.772	26.2361	24.4175	28.0547	6	3	3	B6HK72	B6HK72	1	B6HK72	Pc21g15760 protein	ATP binding; cytoplasm; glutamate-tRNA ligase activity; glutamyl-tRNA aminoacylation	
27.2914	27.6187	27.4335	27.5373	27.9299	26.1468	2.40E-34	1.02E+09	5	5	23.6	35.445	27.3263	27.4479	27.2047	6	3	3	B6HK77	B6HK77	1	B6HK77	Pc21g15810 protein		
33.0426	33.373	33.0929	33.3515	33.0817	32.5618	0	5.3E+10	6	6	49	16.647	33.0839	33.1695	32.9983	6	3	3	B6HK84	B6HK84	1	B6HK84	Nucleoside diphosphate kinase	ATP binding; CTP biosynthetic process; GTP biosynthetic process; UTP biosynthetic process; nucleoside diphosphate kinase activity	
25.2363	25.4943	25.2654	25.85	26.0841	24.9961	3.97E-16	2.78E+08	5	5	8.5	76.996	25.4877	25.332	25.6434	6	3	3	B6HK87	B6HK87	1	B6HK87	Methylenetetrahydrofolate reductase	methionine metabolic process; methylenetetrahydrofolate reductase (NAD(P)H) activity; tetrahydrofolate interconversion	
26.0235	24.5287	26.3131	23.8257	ND	24.8582	1.54E-18	2.21E+08	7	7	7.5	132.11	25.1098	25.6218	24.3419	5	3	2	B6HKA3	B6HKA3	1	B6HKA3	Pc21g20090 protein		
26.8422	27.1565	27.0145	27.6846	27.9714	27.7432	7.81E-112	9.89E+08	10	10	32.6	52.602	27.4021	27.0044	27.7997	6	3	3	B6HKA8	B6HKA8	1	B6HKA8	Pc21g20140 protein	zinc ion binding	
28.1344	28.4309	28.1551	28.5265	28.4649	27.8056	1.43E-115	1.83E+09	20	20	17.4	170.28	28.2529	28.2401	28.2657	6	3	3	B6HKD5	B6HKD5	1	B6HKD5	Pc21g02880 protein	FMN binding; heme binding; iron ion binding; iron-sulfur cluster binding; oxidoreductase activity	
28.9225	28.6283	28.7186	24.8982	25.1506	28.9094	1.03E-138	1.83E+09	7	7	38.5	27.976	27.5379	28.7565	26.3194	6	3	3	B6HKG0	B6HKG0	1	B6HKG0	Pc21g07340 protein	intracellular transport	
27.1693	27.477	27.2599	28.1348	28.4434	26.8998	3.72E-89	1.17E+09	5	5	28.6	26.379	27.564	27.3021	27.826	6	3	3	B6HKG1	B6HKG1	1	B6HKG1	Pc21g07350 protein	nucleus; regulation of transcription, DNA-templated	
25.7063	26.2302	26.1932	23.8837	23.0898	25.6199	8.75E-37	2.8E+08	4	4	7.4	88.787	25.1205	26.0432	24.1978	6	3	3	B6HKH0;B6HJL5	B6HKH0	2	B6HKH0	Pc21g11520 protein		
ND	ND		ND	25.1825	24.8931	ND	1.68E-34	78109000	3	3	3.5	138.79	25.0378	ND		25.0378	2	0	2	B6HKH7	B6HKH7	1	B6HKH7	Pc21g11590 protein		
31.0679	31.1691	31.0579	31.3155	31.796	30.0376	3.71E-146	1.34E+10	7	7	69.7	12.911	31.074	31.0983	31.0497	6	3	3	B6HKJ1	B6HKJ1	1	B6HKJ1	Pc21g11730 protein	deaminase activity	
29.4913	29.7731	29.5747	29.9927	30.3515	28.8782	1.34E-75	5.05E+09	6	6	36.1	21.634	29.6769	29.613	29.7408	6	3	3	B6HKJ3	B6HKJ3	1	B6HKJ3	Pc21g11750 protein	adenine phosphoribosyltransferase activity; adenine salvage; cytoplasm; nucleoside metabolic process	
ND	23.4561	23.5967	ND	ND	ND	0.001074	57953000	2	2	4.1	51.385	23.5264	23.5264	ND	2	2	0	B6HKJ8	B6HKJ8	1	B6HKJ8	Pc21g15970 protein	cytoplasm; pyrophosphatase activity	
27.0065	26.8625	26.8257	26.7814	27.6369	26.2195	1.77E-25	7.29E+08	11	11	13.9	127.1	26.8887	26.8982	26.8793	6	3	3	B6HKL7	B6HKL7	1	B6HKL7	Ubiquitin carboxyl-terminal hydrolase	cysteine-type peptidase activity; ubiquitin-dependent protein catabolic process	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
26.1241	25.945	25.867	25.9314	26.6414	25.0483	2.53E-08	3.73E+08	3	3	10.3	28.848	25.9262	25.9787	25.8737	6	3	3	B6HKN6	B6HKN6	1	B6HKN6	pentose-phosphate shunt, non-oxidative branch; ribose-5-phosphate isomerase activity		
26.0174	26.2676	26.2264	26.5259	26.7496	25.4307	1.12E-37	4.79E+08	6	6	16.4	39.304	26.2029	26.1705	26.2354	6	3	3	B6HKN7	B6HKN7	1	B6HKN7	Pc21g20450 protein		
21.5794	21.9739	22.1715	19.6222	21.1648	29.4816	1.96E-87	5.01E+08	16	16	34.5	71.511	22.6656	21.9083	23.4229	6	3	3	B6HKP0	B6HKP0	1	B6HKP0	Pc21g20480 protein	ATP citrate synthase activity; cellular carbohydrate metabolic process; cofactor binding; succinate-CoA ligase (ADP-forming) activity	
29.7122	29.1735	29.6072	27.5405	28.7494	30.7656	1.89E-167	4.12E+09	15	15	37.3	52.608	29.2581	29.4976	29.0185	6	3	3	B6HKP1	B6HKP1	1	B6HKP1	Pc21g20490 protein	ATP binding	
26.7643	26.906	26.7025	26.947	27.066	25.9943	4.72E-17	6.5E+08	5	5	35.8	18.183	26.73	26.7909	26.6691	6	3	3	B6HKP6	B6HKP6	1	B6HKP6	Pc21g02980 protein		
29.8627	30.0849	29.793	30.4935	30.933	29.2516	7.16E-46	6.64E+09	5	5	19.4	22.059	30.0698	29.9135	30.2261	6	3	3	B6HKR2	B6HKR2	1	B6HKR2	Pc21g03140 protein		
27.0039	26.8024	26.453	27.1801	26.6425	26.9745	3.78E-34	6.81E+08	4	4	18.7	26.405	26.8427	26.7531	26.9324	6	3	3	B6HKR4	B6HKR4	1	B6HKR4	Pc21g03160 protein	nucleic acid binding; nucleotide binding	
27.0359	27.0297	27.3309	26.0581	24.9822	26.1171	5.31E-79	6.11E+08	6	6	35.5	36.086	26.4257	27.1322	25.7191	6	3	3	B6HKR7	B6HKR7	1	B6HKR7	Pc21g03190 protein	NAD binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	
26.4163	26.7323	26.4731	26.5479	24.3917	25.9328	6.06E-103	4.87E+08	6	6	12.6	81.283	26.0823	26.5406	25.6241	6	3	3	B6HKS5	B6HKS5	1	B6HKS5	Pc21g07420 protein	DNA repair; nuclease activity	
28.2348	28.2743	28.1382	29.4267	29.542	28.195	9.58E-88	2.47E+09	8	8	28.2	39.55	28.6352	28.2158	29.0546	6	3	3	B6HKS6	B6HKS6	1	B6HKS6	Pc21g07430 protein	cell redox homeostasis; endoplasmic reticulum; glycerol ether metabolic process; isomerase activity; protein disulfide oxidoreductase activity	
24.2426	24.3137	24.0853	24.8143	24.4449	24.1727	1.27E-05	1.2E+08	2	2	7.6	40.599	24.3456	24.2139	24.4773	6	3	3	B6HKV3	B6HKV3	1	B6HKV3	Pc21g11820 protein		
30.1848	30.5393	30.2913	30.9638	31.1137	29.6134	2.67E-263	8.68E+09	13	13	48.3	43.807	30.451	30.3385	30.5636	6	3	3	B6HKW0	B6HKW0	1	B6HKW0	Pc21g11890 protein	nucleic acid binding; nucleotide binding	
29.9088	29.2256	29.8228	28.481	27.2392	28.9676	1.41E-168	3.64E+09	16	16	40.3	55.414	28.9408	29.6524	28.2293	6	3	3	B6HKW6	B6HKW6	1	B6HKW6	Pc21g11950 protein	nucleotidyltransferase activity	
25.6661	25.7421	25.6419	26.4817	26.3862	27.1038	5.22E-11	4.21E+08	4	4	21.1	15.248	26.1703	25.6834	26.6572	6	3	3	B6HKX2	B6HKX2	1	B6HKX2	40S ribosomal protein S24	nucleotide binding; ribosome; structural constituent of ribosome; translation	
25.2356	25.5637	25.1203	24.8217	25.2144	24.8872	7.22E-22	2.08E+08	4	4	15	37.975	25.1405	25.3065	24.9744	6	3	3	B6HKY8	B6HKY8	1	B6HKY8	Pc21g16300 protein	GTP cyclohydrolase I activity; cytoplasm; tetrahydrofolate biosynthetic process	
25.0574	25.5626	25.5258	24.5967	24.5246	25.1126	6.22E-07	2.09E+08	4	4	12.6	49.667	25.0633	25.3819	24.7446	6	3	3	B6HKY9	B6HKY9	1	B6HKY9	Pc21g16310 protein	nucleus	
26.3049	26.6619	26.4234	26.6264	27.2333	25.7649	3.36E-39	5.45E+08	9	9	11	156.82	26.5025	26.4634	26.5416	6	3	3	B6HKZ0	B6HKZ0	1	B6HKZ0	Pc21g16320 protein	5'-3' exonuclease activity; intracellular; nuclear-transcribed mRNA catabolic process; nucleic acid binding	
30.9163	31.2059	30.9631	31.8039	31.9991	30.4447	8.98E-141	1.49E+10	7	7	62.1	11.217	31.2222	31.0285	31.4159	6	3	3	B6HL06	B6HL06	1	B6HL06	Pc21g20560 protein	ATP binding; cytoplasm; protein folding	
ND		24.5382	24.374	22.1962	22.1746	25.4223	1.34E-07	93620000	2	2	8.6	37.216	23.7411	24.4561	23.2644	5	2	3	B6HL19	B6HL19	1	B6HL19	Serine/threonine-protein phosphatase	hydrolase activity	
23.4923		23.4595	23.5216	23.9231	23.8796	23.2006	0.000289	70594000	2	2	9.1	26.309	23.5794	23.4911	23.6678	6	3	3	B6HL40	B6HL40	1	B6HL40	Pc21g03310 protein	RNA binding; exosome (RNase complex)	
ND		23.9474	23.9678	23.8869	23.6894	24.0396	6.43E-06	81783000	2	2	4.4	49.568	23.9062	23.9576	23.872	5	2	3	B6HL43	B6HL43	1	B6HL43	Pc21g03340 protein	ubiquitin ligase complex; ubiquitin-protein ligase activity	
ND		24.1987	23.552	25.2768	25.8105	24.4969	3.44E-06	1.34E+08	2	2	11.4	27.704	24.667	23.8753	25.1948	5	2	3	B6HL47	B6HL47	1	B6HL47	Pc21g03380 protein	ribosome; ribosome biogenesis	
31.8694	32.0762	31.8233	31.8092	32.2733	31.021	0	2.2E+10	8	8	45	27.105	31.8121	31.923	31.7012	6	3	3	B6HL49	B6HL49	1	B6HL49	Triosephosphate isomerase	gluconeogenesis; glycolysis; triose-phosphate isomerase activity	
26.6235	26.5949	26.7389	26.0991	25.4045	25.531	2.26E-83	4.88E+08	3	3	15.7	41.912	26.1653	26.6525	25.6782	6	3	3	B6HL63	B6HL63	1	B6HL63	Pc21g07690 protein	catalytic activity	
26.3527	26.2822	26.2833	26.448	26.8332	26.0975	4.51E-47	4.88E+08	2	2	25.4	12.922	26.3828	26.306	26.4596	6	3	3	B6HL98	B6HL98	1	B6HL98	Pc21g12120 protein	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances; proton transport; vacuolar proton-transporting V-type ATPase complex	
23.8256	ND		24.2236	23.3935	23.7886	27.9125	6.73E-18	2.2E+08	7	7	16.6	56.213	24.6287	24.0246	25.0315	5	2	3	B6HLA9	B6HLA9	1	B6HLA9	Pc21g12230 protein	heme binding	
25.3151	25.542	24.9101	25.0693	26.4701	25.0849	1.63E-05	2.6E+08	3	3	10.9	30.296	25.3986	25.2557	25.5414	6	3	3	B6HLB7	B6HLB7	1	B6HLB7	Uncharacterized protein		
25.7396	25.7424	25.5798	27.2467	27.246	28.3886	1.15E-110	6.77E+08	6	6	23.8	39.973	26.6572	25.6872	27.6271	6	3	3	B6HLC8	B6HLC8	1	B6HLC8	Pc21g16520 protein	ribosome; structural constituent of ribosome; translation	
27.8689	28.4868	28.1174	28.6861	29.0187	27.5898	3.26E-41	1.94E+09	7	7	16.6	40.468	28.2946	28.1577	28.4315	6	3	3	B6HLD8	B6HLD8	1	B6HLD8	Pc21g16630 protein	nucleosome assembly; nucleus	
25.6258	25.9614	25.6319	26.1636	26.6228	24.9771	2.04E-51	5.56E+08	5	5	16.9	37.331	25.8368	25.7397	25.9339	6	3	3	B6HLF0	B6HLF0	1	B6HLF0	Pc21g20930 protein	catalytic activity	
27.146	27.3329	27.2773	27.3456	27.2355	26.3201	9.16E-26	8.47E+08	7	7	36.1	30.249	27.1096	27.252	26.9671	6	3	3	B6HLL8	B6HLL8	1	B6HLL8	Pc21g08250 protein	aromatic amino acid family biosynthetic process; chorismate metabolic process; chorismate mutase activity	
26.2828	26.3678	26.1319	26.6206	26.7521	25.2109	2.43E-10	4.69E+08	4	4	22.3	22.277	26.2277	26.2608	26.1945	6	3	3	B6HLN7	B6HLN7	1	B6HLN7	Uncharacterized protein		
ND	ND		23.0443	21.7872	ND		27.4032	3.65E-17	1.46E+08	3	3	12.4	28.244	24.0782	23.0443	24.5952	3	1	2	B6HLP6	B6HLP6	1	B6HLP6	Pc21g12600 protein	oxidoreductase activity	
22.4582	21.3955	22.1431	ND		ND		26.8385	2.20E-08	87819000	3	3	21.1	12.498	23.2088	21.9989	26.8385	4	3	3	B6HLQ4	B6HLQ4	1	B6HLQ4	Pc21g16780 protein		
26.6072	27.0527	26.7837	28.8	29.2071	28.74	1.82E-160	1.58E+09	17	17	22.4	97.459	27.8651	26.8145	28.9157	6	3	3	B6HLR9	B6HLR9	1	B6HLR9	Pc21g16930 protein	RISC complex; gene silencing by RNA; hydrolase activity, acting on ester bonds; nucleic acid binding	
29.6427	26.7162	30.2243	30.3899	26.5497	26.3938	2.38E-88	3.99E+09	5	5	42.9	15.846	28.3194	28.8611	27.7778	6	3	3	B6HLS0	B6HLS0	1	B6HLS0	Superoxide dismutase [Cu-Zn]	metal ion binding; superoxide dismutase activity; superoxide metabolic process	
33.5526	33.6388	33.4608	33.3497	33.9936	32.501	4.38E-207	6.77E+10	15	15	48.5	35.44	33.4161	33.5507	33.2814	6	3	3	B6HLS1	B6HLS1	1	B6HLS1	Transaldolase	cytoplasm; pentose-phosphate shunt; sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity	
29.2208	28.8273	28.8358	29.665	29.6869	28.3286	7.97E-108	3.34E+09	9	9	19.6	52.308	29.0941	28.9613	29.2268	6	3	3	B6HLS3	B6HLS3	1	B6HLS3	Vacuolar serine proteinase AAG44693-Penicillium chrysogenum	negative regulation of catalytic activity; proteolysis; serine-type endopeptidase activity	
25.2163	24.2588	25.1422	ND		ND		25.8972	6.57E-27	1.56E+08	3	3	10.4	52.936	25.1286	24.8724	25.8972	4	3	1	B6HLY2	B6HLY2	1	B6HLY2	Pc21g08400 protein	catalytic activity	
25.2496	25.3264	25.1671	ND		25.0598	ND		3.86E-07	1.81E+08	2	2	9	30.674	25.2007	25.2477	25.0598	4	3	1	B6HM01	B6HM01	1	B6HM01	Pc21g08590 protein	glutathione biosynthetic process; hydroxyacylglutathione hydrolase activity; zinc ion binding	
31.3298	31.5327	31.3287	32.0121	32.3596	30.546	0	1.86E+10	20	20	41.2	62.487	31.5182	31.3971	31.6392	6	3	3	B6HM17	B6HM17	1	B6HM17	Pc21g12770 protein		
25.2183	25.7324	25.3568	27.0756	27.1534	24.8465	2.26E-19	4.13E+08	3	3	2.4	167.01	25.8972	25.4358	26.3585	6	3	3	B6HM18	B6HM18	1	B6HM18	Pc21g12780 protein		
27.9123	28.2474	27.9974	26.3382	26.4535	31.0407	0	2.42E+09	21	21	54.1	57.522	27.9983	28.0524	27.9442	6	3	3	B6HM19	B6HM19	1	B6HM19	Pc21g12790 protein	nucleotidyltransferase activity	
25.1604	25.0414	25.1817	25.3303	25.7402	ND		4.07E-12	1.79E+08	4	4	12.8	31.999	25.2908	25.1278	25.5353	5	3	2	B6HM60	B6HM60	1	B6HM60	Pc21g17290 protein		
27.3597	27.6092	27.4773	26.4616	26.7069	26.9745	2.59E-28	8.53E+08	7	7	38.1	30.568	27.0982	27.4821	26.7143	6	3	3	B6HM81	B6HM81	1	B6HM81	Pc21g11730 protein	hydrolase activity; isopentenyl-diphosphate delta-isomerase activity; isoprenoid biosynthetic process	
24.3303	24.5978	24.8259	24.5733	24.6543	23.726	0.000278	1.35E+08	2	2	18.2	26.233	24.4513	24.5847	24.3178	6	3	3	B6HM89	B6HM89	1	B6HM89	Pc21g04160 protein	methyltransferase activity	
25.0871	25.3163	25.315	25.5512	26.0299	25.1984	8.35E-35	2.5E+08	2	2	44.8	10.79	25.4163	25.2395	25.5931	6	3	3	B6HMA0	B6HMA0	1	B6HMA0	Pc21g04270 protein		
24.1472	24.9014	25.0359	24.0036	25.7368	23.6623	1.01E-22	1.65E+08	5	5	12.6	56.364	24.5812	24.6948	24.4676	6	3	3	B6HMA7	B6HMA7	1	B6HMA7	Pc21g04340 protein		
25.32	25.2819	25.7835	26.1947	25.2273	24.7248	2.48E-25	2.88E+08	3	3	39.8	13.993	25.422	25.4618	25.3823	6	3	3	B6HMC4	B6HMC4	1	B6HMC4	Pc21g08660 protein	RNA splicing; small nuclear ribonucleoprotein complex	
28.8755	28.9938	28.8575	29.1893	28.6892	29.3053	3.57E-63	2.97E+09	3	3	36.8	7.7109	28.9851	28.909	29.0613	6	3	3	B6HME1	B6HME1	1	B6HME1	Pc21g08830 protein	ribosome; structural constituent of ribosome; translation	
27.6749	27.6602	27.2617	27.7146	27.2908	29.42	5.66E-39	1.47E+09	4	4	24	27.417	27.837	27.5323	28.1418	6	3	3	B6HMI5	B6HMI5	1	B6HMI5	Pc21g17430 protein	ribosome; structural constituent of ribosome; translation	
30.3197	30.2571	30.2588	30.2352	29.8439	28.9375	6.23E-173	6.45E+09	8	8	29.5	37.957	29.9754	30.2785	29.6722	6	3	3	B6HMI8	B6HMI8	1	B6HMI8	Pc21g17460 protein	adenosine kinase activity; purine ribonucleoside salvage	
24.3214	24.3352	23.9961	24.561	24.0701	25.5939	9.21E-09	1.34E+08	4	4	29.1	15.043	24.4796	24.2176	24.7417	6	3	3	B6HMK2	B6HMK2	1	B6HMK2	Pc21g21880 protein	large ribosomal subunit; structural constituent of ribosome; translation	
ND	ND		ND		23.7533	ND		27.1065	5.90E-18	1.04E+08	8	8	5.1	246.69	25.4299	ND		25.4299	2	0	2	B6HMK8	B6HMK8	1	B6HMK8	Pc21g21940 protein	'de novo' pyrimidine nucleobase biosynthetic process; ATP binding; amino acid binding; aspartate carbamoyltransferase activity; carbamoyl phosphate biosynthetic process; glutamine catabolic process; metal ion binding	
26.7525	27.2367	27.3045	28.2533	28.3761	26.7436	1.46E-11	1.1E+09	4	4	10	51.229	27.4445	27.0979	27.791	6	3	3	B6HML4	B6HML4	1	B6HML4	Pc21g22000 protein	carbohydrate metabolic process	
30.9675	31.0331	30.8866	31.169	31.6373	29.979	0	1.22E+10	10	10	62.7	18.654	30.9454	30.9624	30.9284	6	3	3	B6HMN3	B6HMN3	1	B6HMN3	Pc21g04520 protein		
24.874	24.9937	24.9546	26.3704	25.2116	25.9803	1.13E-13	2.56E+08	6	5	12.7	77.15	25.3974	24.9408	25.8541	6	3	3	B6HMN7	B6HMN7	1	B6HMN7	Amine oxidase	amine metabolic process; copper ion binding; primary amine oxidase activity; quinone binding	
24.4401	24.9346	24.578	ND		24.8887	24.5111	1.15E-11	1.28E+08	3	3	8.1	51.454	24.6705	24.6509	24.6999	5	3	2	B6HMP2	B6HMP2	1	B6HMP2	Pc21g04610 protein		
30.2728	30.0014	30.0515	28.0122	28.2815	29.2024	1.26E-199	4.58E+09	12	12	42.9	39.983	29.3036	30.1086	28.4987	6	3	3	B6HMQ2	B6HMQ2	1	B6HMQ2	Phospho-2-dehydro-3-deoxyheptonate aldolase	3-deoxy-7-phosphoheptulonate synthase activity; aromatic amino acid family biosynthetic process; chorismate biosynthetic process	
28.1514	28.1188	28.0127	28.4397	28.5894	27.6236	2.40E-71	1.7E+09	8	8	47.2	21.304	28.1559	28.0943	28.2176	6	3	3	B6HMS7	B6HMS7	1	B6HMS7	Proteasome subunit beta type	cytoplasm; nucleus; proteasome core complex; proteolysis involved in cellular protein catabolic process; threonine-type endopeptidase activity	Cytoplasm. Nucleus.
26.3003	26.4415	26.4617	27.0542	26.9115	26.0935	1.11E-24	5.75E+08	8	8	26	48.869	26.5438	26.4012	26.6864	6	3	3	B6HMW7	B6HMW7	1	B6HMW7	Pc21g17590 protein	acyl-CoA dehydrogenase activity; flavin adenine dinucleotide binding	
25.391	24.8989	26.2423	26.2349	23.9099	25.1887	2.52E-34	2.82E+08	4	4	13.2	56.479	25.311	25.5108	25.1112	6	3	3	B6HMY6	B6HMY6	1	B6HMY6	Pc21g17790 protein	ATP binding; glutathione synthase activity	
28.3887	28.6942	28.5325	28.6524	29.2915	27.7076	6.85E-65	2.31E+09	6	6	32.1	22.914	28.5445	28.5385	28.5505	6	3	3	B6HN57	B6HN57	1	B6HN57	Pc21g04870 protein	ATP binding; nucleotide kinase activity; phosphotransferase activity, phosphate group as acceptor	
26.2923	26.3185	26.1643	25.4602	25.5474	27.1874	4.69E-42	4.34E+08	4	4	14.3	48.919	26.1617	26.2584	26.065	6	3	3	B6HNS8	B6HNS8	1	B6HNS8	Eukaryotic translation initiation factor 3 subunit M	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
24.3659	24.3471	24.4158	25.0299	24.6921	ND		3.26E-12	1.25E+08	2	2	15.2	36.766	24.5702	24.3763	24.861	5	3	2	B6HNA6	B6HNA6	1	B6HNA6	Pc21g13560 protein	membrane; vesicle-mediated transport	
27.181	27.7876	27.6919	28.0751	28.3955	26.9552	1.74E-65	1.26E+09	5	5	26.1	26.707	27.681	27.5535	27.8086	6	3	3	B6HNB0	B6HNB0	1	B6HNB0	Pc21g13600 protein	cytoplasm; translation initiation factor activity	
26.0458	25.3869	25.5905	25.3114	25.2528	29.1505	5.97E-80	6.99E+08	6	6	31.9	28.315	26.123	25.6744	26.5716	6	3	3	B6HNB2	B6HNB2	1	B6HNB2	Pc21g13620 protein	RNA binding; small ribosomal subunit; structural constituent of ribosome; translation	
26.9196	27.4413	27.2318	25.2646	24.6012	28.6403	1.15E-100	8.24E+08	10	10	29.7	55.091	26.6831	27.1976	26.1687	6	3	3	B6HND0	B6HND0	1	B6HND0	Pc21g17880 protein	4-aminobutyrate transaminase activity; gamma-aminobutyric acid metabolic process; pyridoxal phosphate binding	
27.4325	27.3784	27.3256	27.5641	27.6659	27.251	2.10E-50	1.03E+09	9	9	24.3	53.94	27.4362	27.3788	27.4936	6	3	3	B6HND2	B6HND2	1	B6HND2	Serine/threonine-protein phosphatase	cytoplasm; metal ion binding; nucleus; phosphoprotein phosphatase activity; protein dephosphorylation	
27.368	27.494	27.3699	26.5884	27.0217	26.0756	4.09E-38	8.21E+08	9	9	17.9	53.713	26.9863	27.4107	26.5619	6	3	3	B6HND3	B6HND3	1	B6HND3	Pc21g17910 protein		
26.2226	25.6873	25.4984	26.0151	26.4161	25.1233	9.24E-16	3.48E+08	5	5	3.5	156.77	25.8271	25.8028	25.8515	6	3	3	B6HNK7	B6HNK7	1	B6HNK7	Pc21g05120 protein	actin cortical patch; calcium ion binding; endocytosis	
25.2179	25.688	25.3434	26.6713	26.8096	24.0989	4.20E-46	3.48E+08	3	3	7.6	54.66	25.6382	25.4164	25.8599	6	3	3	B6HNR7	B6HNR7	1	B6HNR7	Pc21g13920 protein		
24.5356	24.9823	24.6812	ND		ND		25.8889	7.54E-16	1.35E+08	2	2	10	28.022	25.022	24.7331	25.8889	4	3	1	B6HNT9	B6HNT9	1	B6HNT9	Pc21g18110 protein	electron carrier activity	
28.1145	27.891	27.6756	29.5604	28.7454	29.3631	5.70E-131	2.35E+09	6	6	56.6	11.392	28.5583	27.8937	29.223	6	3	3	B6HNU7	B6HNU7	1	B6HNU7	Pc21g18200 protein	ribosome; structural constituent of ribosome; translation	
26.5288	26.6182	26.6132	26.7524	27.3815	24.9223	1.08E-67	5.86E+08	3	3	19.1	36.811	26.4694	26.5867	26.3521	6	3	3	B6HNV3	B6HNV3	1	B6HNV3	Pc21g18260 protein	NAD binding; oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	
30.0092	29.9361	29.9906	29.3592	29.6952	29.6548	4.22E-86	5.24E+09	7	7	19.6	39.85	29.7742	29.9786	29.5697	6	3	3	B6HNV8	B6HNV8	1	B6HNV8	Pc21g18310 protein	nucleic acid binding; nucleotide binding	
27.9808	25.6575	28.3822	24.128	23.9257	ND		1.18E-93	7.55E+08	14	10	33.9	53.694	26.0148	27.3402	24.0269	5	3	2	B6HNY3	B6HNY3	1	B6HNY3	Pc21g22810 protein	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	
24.9277	ND	25.163	26.361	26.1465	25.9336	5.51E-61	3E+08	2	2	4.7	61.761	25.7064	25.0454	26.1471	5	2	3	B6HNY5	B6HNY5	1	B6HNY5	Pc22g02800 protein	calcium ion binding; endoplasmic reticulum; protein folding	
28.1426	28.0964	28.1602	26.3406	26.7786	27.2659	8.00E-190	1.21E+09	13	13	23.8	62.713	27.464	28.133	26.795	6	3	3	B6HNY6	B6HNY6	1	B6HNY6	Pc22g02810 protein	methylmalonate-semialdehyde dehydrogenase (acylating) activity	
27.2122	27.2249	27.1317	27.1499	27.2035	26.1954	3.30E-58	8.01E+08	5	5	30.9	27.182	27.0196	27.1896	26.8496	6	3	3	B6HNY8	B6HNY8	1	MTNB	Methylthioribulose-1-phosphate dehydratase	L-methionine biosynthetic process from S-adenosylmethionine; L-methionine salvage from methylthioadenosine; cytoplasm; methylthioribulose 1-phosphate dehydratase activity; zinc ion binding	Cytoplasm.
27.5785	27.4567	27.6397	27.3061	26.9744	27.915	3.08E-112	1.07E+09	10	10	15.7	100.43	27.4784	27.5583	27.3985	6	3	3	B6HP13	B6HP13	1	B6HP13	Pc22g01690 protein	COPII vesicle coat; ER to Golgi vesicle-mediated transport; intracellular protein transport; zinc ion binding	
24.2799	23.9032	24.1006	24.2879	24.6905	23.4593	1.41E-05	1.06E+08	2	2	9.1	24.821	24.1202	24.0946	24.1459	6	3	3	B6HP21	B6HP21	1	B6HP21	Pc22g01250 protein		
24.1832	24.8381	24.4413	27.11	27.6421	28.2076	4.03E-16	5.78E+08	5	5	26.2	24.262	26.0704	24.4875	27.6532	6	3	3	B6HP22	B6HP22	1	B6HP22	Pc22g01260 protein	GTP binding; GTPase activity; intracellular protein transport; nucleocytoplasmic transport; small GTPase mediated signal transduction	
25.726	25.4362	25.6956	ND		ND	ND		1.41E-06	1.78E+08	2	2	15.2	15.429	25.6193	25.6193	ND		3	0	B6HP26	B6HP26	1	B6HP26	Pc22g01300 protein	sterol binding	
26.8096	27.0583	26.9101	27.4417	27.5444	26.0669	1.26E-89	7.8E+08	6	6	30.4	31.943	26.9718	26.926	27.0176	6	3	3	B6HP43	B6HP43	1	B6HP43	Pc22g01470 protein	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; nitrogen compound metabolic process	
27.982	27.5813	27.6266	25.0707	24.5768	27.3023	1.66E-11	8.58E+08	4	4	23.3	13.693	26.6899	27.73	25.6499	6	3	3	B6HP44	B6HP44	1	B6HP44	Pc22g01480 protein	ribosome; structural constituent of ribosome; translation	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
32.2089	31.8394	32.1499	31.5162	29.9396	31.4365	0	2.02E+10	25	25	40.1	85.352	31.5151	32.0661	30.9641	6	3	3	B6HP52	B6HP52	1	B6HP52	Pc22g02000 protein	4 iron, 4 sulfur cluster binding; aconitate hydratase activity; tricarboxylic acid cycle	
24.0664	23.6432	24.0799	23.6567	24.0861	25.6513	5.79E-06	1.06E+08	3	3	5.3	56.739	24.1972	23.9298	24.4647	6	3	3	B6HP54	B6HP54	1	B6HP54	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity; trehalose biosynthetic process	
28.9815	28.4938	28.0633	30.5378	29.929	30.9436	6.91E-105	4.91E+09	11	11	40.8	29.46	29.4915	28.5129	30.4702	6	3	3	B6HP58	B6HP58	1	B6HP58	ribonucleoprotein complex; ribosome biogenesis	
27.3784	27.4139	27.3002	27.4237	ND	27.0995	3.09E-05	7.35E+08	3	3	1.6	225.95	27.3231	27.3641	27.2616	5	3	2	B6HP95	B6HP95	1	B6HP95	Pc22g02290 protein	nuclear pore; protein import into nucleus	
26.9051	27.2602	27.0331	27.5931	27.8544	26.2721	5.10E-42	8.95E+08	5	5	28.6	24.986	27.153	27.0661	27.2399	6	3	3	B6HP97	B6HP97	1	B6HP97	3,4-dihydroxy-2-butanone 4-phosphate synthase	3,4-dihydroxy-2-butanone-4-phosphate synthase activity; metal ion binding; riboflavin biosynthetic process	
26.3243	26.2208	26.2677	26.1768	26.2986	25.2473	3.68E-40	4.2E+08	4	4	8.9	65.475	26.0892	26.2709	25.9076	6	3	3	B6HPA6	B6HPA6	1	B6HPA6	Pc22g02400 protein	deaminase activity	
23.9085	24.9797	24.6075	ND	ND	29.2138	3.25E-48	5.07E+08	16	16	18.3	126.34	25.6774	24.4986	29.2138	4	3	1	B6HPC5	B6HPC5	1	B6HPC5	Pc22g02510 protein	ATP binding; aminoacyl-tRNA editing activity; cytoplasm; leucine-tRNA ligase activity; leucyl-tRNA aminoacylation	
27.4616	27.7935	27.6738	28.7256	27.6462	29.9002	2.65E-23	2.09E+09	3	3	31.6	18.099	28.2002	27.643	28.7573	6	3	3	B6HPD8	B6HPD8	1	B6HPD8	Pc22g02470 protein		
27.6884	27.5216	27.6978	26.5	27.503	26.1064	3.64E-136	9.72E+08	9	9	27	45.6	27.1695	27.6359	26.7031	6	3	3	B6HPF6	B6HPF6	1	B6HPF6	Pc22g00420 protein	transferase activity, transferring acyl groups other than amino-acyl groups	
24.7957	24.5446	24.4464	24.8636	24.9203	24.0486	2.88E-06	1.45E+08	2	2	4.4	47.41	24.6032	24.5956	24.6109	6	3	3	B6HPJ7	B6HPJ7	1	B6HPJ7	Pc22g00830 protein		
24.651	24.8349	ND	25.824	26.1518	26.6072	1.56E-09	2.45E+08	4	4	25.8	17.854	25.6138	24.743	26.1943	5	2	3	B6HPK2	B6HPK2	1	B6HPK2	Pc22g00880 protein	RNA binding; ribosome; structural constituent of ribosome; translation	
27.0083	27.1181	27.1118	26.3776	26.8428	27.0155	5.82E-46	7.07E+08	7	7	26.1	43.233	26.9123	27.0794	26.7453	6	3	3	B6HPK3	B6HPK3	1	B6HPK3	Pc22g01490 protein		
27.7465	27.5943	27.8105	27.4045	28.1466	26.6295	2.68E-51	1.17E+09	4	4	13.5	26.643	27.5553	27.7171	27.3935	6	3	3	B6HPK7	B6HPK7	1	B6HPK7	Pc22g01530 protein	hydrolase activity	
23.7418	23.8286	23.8006	25.0591	25.496	23.6634	1.38E-10	1.27E+08	5	5	10.8	52.097	24.2649	23.7904	24.7395	6	3	3	B6HPL1	B6HPL1	1	B6HPL1	Pc22g01590 protein		
26.7852	26.9906	26.7699	25.2378	25.2648	24.148	1.25E-08	4.68E+08	3	3	25.9	14.925	25.8661	26.8486	24.8836	6	3	3	B6HPL2	B6HPL2	1	B6HPL2	Pc22g01600 protein	catalytic activity	
25.214	25.1718	24.9245	25.7873	24.9267	26.4526	1.14E-18	2.59E+08	3	3	33.9	6.7207	25.4128	25.1034	25.7222	6	3	3	B6HPL5	B6HPL5	1	B6HPL5	Pc22g01560 protein	ribosome; structural constituent of ribosome; translation	
27.1174	25.4906	27.5588	23.8237	ND	26.7193	1.49E-66	5.02E+08	9	9	36.4	40.792	26.142	26.7223	25.2715	5	3	2	B6HPM1	B6HPM1	1	B6HPM1	Pc22g01670 protein	ATP binding; MAP kinase activity	
27.4425	27.4443	27.5514	27.3756	27.9584	26.4442	7.60E-98	1.06E+09	4	4	28.4	28.73	27.3694	27.4794	27.2594	6	3	3	B6HPN0	B6HPN0	1	B6HPN0	Pc22g02600 protein	phosphatase activity	
25.711	26.0544	25.4728	26.1413	26.6728	24.9019	1.22E-11	3.69E+08	4	4	8.6	47.768	25.8257	25.7461	25.9053	6	3	3	B6HPP1	B6HPP1	1	B6HPP1	Pc22g01060 protein		
29.5596	29.2535	29.537	29.9432	30.2357	28.5867	2.27E-71	4.53E+09	11	11	24.5	61.427	29.5193	29.45	29.5885	6	3	3	B6HPP6	B6HPP6	1	CBPYA	Carboxypeptidase Y homolog A	proteolysis; serine-type carboxypeptidase activity; vacuole	Vacuole.
25.9426	25.5685	25.4648	26.1307	26.2124	24.4908	5.65E-32	3.25E+08	5	5	15.4	36.74	25.635	25.6586	25.6113	6	3	3	B6HPP7	B6HPP7	1	B6HPP7	Pc22g00900 protein	ribosome biogenesis	
25.8116	26.4345	26.2474	26.4779	26.3053	28.9664	1.19E-38	7.57E+08	8	8	18	58.545	26.7072	26.1645	27.2499	6	3	3	B6HPQ4	B6HPQ4	1	B6HPQ4	Pc22g00970 protein	glutamate decarboxylase activity; glutamate metabolic process; pyridoxal phosphate binding	
29.0976	29.3323	28.8862	28.519	28.5433	29.5796	2.46E-127	3.08E+09	9	9	29.5	41.476	28.993	29.1054	28.8806	6	3	3	B6HPR0	B6HPR0	1	B6HPR0	Pc22g00970 protein	ATP binding; glutamate-ammonia ligase activity; glutamine biosynthetic process	
28.9781	29.1683	28.8681	29.8018	30.0563	28.5199	1.29E-248	3.73E+09	7	7	37.4	35.727	29.2321	29.0048	29.4593	6	3	3	B6HPS1	B6HPS1	1	B6HPS1	Thioredoxin reductase	cytoplasm; flavin adenine dinucleotide binding; removal of superoxide radicals; thioredoxin-disulfide reductase activity	
25.8541	26.0619	25.9559	27.2433	27.3283	25.5958	1.44E-20	5.23E+08	7	7	3.6	208.77	26.3399	25.9573	26.7224	6	3	3	B6HPW0	B6HPW0	1	B6HPW0	Pc22g06700 protein	nuclear pore; transport	
31.9935	32.3517	32.169	34.1126	34.4518	32.7604	0	5.63E+10	30	30	37.2	99.113	32.9732	32.1714	33.7749	6	3	3	B6HPX5	B6HPX5	1	B6HPX5	Pc22g11170 protein	metallopeptidase activity; proteolysis; zinc ion binding	
32.0969	31.3072	32.0751	30.6195	29.3038	34.1789	0	2.84E+10	27	27	44.1	69.562	31.5969	31.8264	31.3674	6	3	3	B6HPY0	B6HPY0	1	B6HPY0	Pc22g11240 protein	ATP binding	
31.7943	32.0323	31.8642	29.8504	29.3821	31.0458	0	1.57E+10	20	20	47.9	61.293	30.9949	31.8969	30.0928	6	3	3	B6HQ15	B6HQ15	1	B6HQ15	Glucose-6-phosphate isomerase	gluconeogenesis; glucose-6-phosphate isomerase activity; glycolysis	
27.896	28.1116	27.9146	29.1545	29.369	27.5587	9.56E-234	2.08E+09	11	11	35.2	31.849	28.3341	27.9741	28.6941	6	3	3	B6HQ31	B6HQ31	1	B6HQ31	Eukaryotic translation initiation factor 3 subunit G	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; nucleotide binding; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
27.404	28.2698	27.9194	28.0997	27.8719	27.0952	5.16E-83	1.37E+09	7	7	21.5	49.907	27.7767	27.8644	27.6889	6	3	3	B6HQ47	B6HQ47	1	B6HQ47	Pc22g24000 protein	ATP binding; ATP-dependent helicase activity; nucleic acid binding	
27.0352	26.6706	26.6585	26.9036	26.4867	24.6642	1.13E-17	5.85E+08	4	4	13.9	27.055	26.4031	26.7881	26.0181	6	3	3	B6HQ79	B6HQ79	1	B6HQ79	40S ribosomal protein S6	ribosome; structural constituent of ribosome; translation	
23.3828	23.5359	23.6206	ND	ND	23.268	2.05E-06	47448000	3	3	1	449.93	23.4518	23.5131	23.268	4	3	1	B6HQ81	B6HQ81	1	B6HQ81	Pc22g06970 protein	ubiquitin-protein ligase activity	
27.3994	27.5226	27.6241	25.8399	ND	28.3176	8.07E-150	8.79E+08	22	22	15	233.58	27.3407	27.5154	27.0787	5	3	2	B6HQ85	B6HQ85	1	B6HQ85	Pc22g11310 protein	FMN binding; flavin adenine dinucleotide binding; glutamate biosynthetic process; glutamate synthase (NADH) activity; iron ion binding; iron-sulfur cluster binding	
26.1469	25.9917	26.1549	27.0668	27.3217	25.7038	1.67E-18	5.27E+08	5	5	12.6	46.079	26.3976	26.0978	26.6975	6	3	3	B6HQ94	B6HQ94	1	B6HQ94	Pc22g11400 protein		
25.164	26.0494	25.5518	26.861	26.7986	24.9189	1.12E-34	3.89E+08	6	6	10.4	90.067	25.8906	25.5884	26.1928	6	3	3	B6HQ97	B6HQ97	1	B6HQ97	Pc22g11430 protein		
26.5272	26.8282	26.5078	26.4474	26.8242	25.7597	3.00E-15	5.41E+08	3	3	14	32.402	26.4824	26.6211	26.3438	6	3	3	B6HQA9	B6HQA9	1	B6HQA9	Pc22g11550 protein	hydrolase activity	
23.9753	24.2897	24.0825	24.4543	24.1806	24.0946	6.36E-06	1.07E+08	2	2	10.3	32.022	24.1795	24.1158	24.2432	6	3	3	B6HQC5	B6HQC5	1	B6HQC5	Pc22g15870 protein		
29.4223	29.7489	29.6342	30.3121	30.5382	29.3043	6.54E-197	5.52E+09	13	13	32.1	67.743	29.8267	29.6018	30.0515	6	3	3	B6HQC9	B6HQC9	1	AMPP1	Probable Xaa-Pro aminopeptidase P	aminopeptidase activity; metal ion binding; metallopeptidase activity; proteolysis	
31.1539	31.3158	31.0562	31.8198	32.1963	30.9153	0	1.64E+10	14	14	53.8	32.296	31.4095	31.1753	31.6438	6	3	3	B6HQD1	B6HQD1	1	B6HQD1	Pc22g15930 protein	catalytic activity; pyridoxal phosphate biosynthetic process	
24.5055	24.3888	24.5614	23.9502	ND	ND	4.23E-09	1.15E+08	3	3	5.5	76.143	24.3515	24.4852	23.9502	4	3	1	B6HQD7	B6HQD7	1	B6HQD7	Pc22g19950 protein	catalytic activity	
31.3694	31.1412	31.5617	32.2349	31.1907	31.4003	0	1.78E+10	22	22	35.3	72.646	31.483	31.3575	31.6086	6	3	3	B6HQE1	B6HQE1	1	B6HQE1	Pc22g19990 protein	ATP binding; protein folding	
24.4423	25.3492	25.2336	ND	ND	23.9398	4.08E-37	1.33E+08	4	4	4	119.03	24.7412	25.0084	23.9398	4	3	1	B6HQE7	B6HQE7	1	B6HQE7	Pc22g20050 protein	intracellular protein transport; nucleus	
28.1134	28.2838	28.2664	28.3622	28.6502	26.7448	4.03E-177	1.73E+09	5	5	21.8	28.312	28.0701	28.2212	27.9191	6	3	3	B6HQE9	B6HQE9	1	B6HQE9	Pc22g20070 protein	nucleic acid binding; nucleotide binding	
29.2293	28.3443	28.9841	28.7828	27.1576	29.8846	8.16E-147	2.87E+09	16	16	18.7	128.19	28.7305	28.8526	28.6083	6	3	3	B6HQF5	B6HQF5	1	B6HQF5	Pc22g20150 protein	ATP binding; catalytic activity; metal ion binding; nitrogen compound metabolic process	
27.9231	28.2994	28.0945	28.4851	28.735	27.9212	3.16E-162	1.8E+09	7	7	31.2	26.192	28.2431	28.1057	28.3805	6	3	3	B6HQI1	B6HQI1	1	B6HQI1	Pc22g24360 protein	ATP hydrolysis coupled proton transport; hydrogen-exporting ATPase activity, phosphorylative mechanism; proton-transporting ATPase activity, rotational mechanism; proton-transporting two-sector ATPase complex, catalytic domain	
27.1363	27.2099	26.9337	29.3222	29.5643	27.8057	5.71E-63	1.87E+09	11	11	33.1	38.152	27.9954	27.0933	28.8974	6	3	3	B6HQI9	B6HQI9	1	B6HQI9	Pc22g07020 protein	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; nitrogen compound metabolic process	
23.9961	23.4695	23.917	25.6327	25.52	22.3365	3.83E-12	1.37E+08	4	4	20.1	25.646	24.1453	23.7942	24.4964	6	3	3	B6HQJ3	B6HQJ3	1	B6HQJ3	Pc22g07060 protein	intracellular protein transport; membrane; vesicle-mediated transport	
ND		26.9123	25.9853	26.7017	26.8703	25.6941	2.26E-27	5.56E+08	3	3	19.7	23.619	26.4328	26.4488	26.4221	5	2	3	B6HQL0	B6HQL0	1	B6HQL0	Pc22g07230 protein	ferric iron binding; ferroxidase activity; iron-sulfur cluster assembly; mitochondrion	
26.4974	26.9611	26.5565	25.5068	24.9882	29.374	1.82E-89	8.89E+08	7	7	22	45.239	26.6473	26.6717	26.623	6	3	3	B6HQM6; B6GZG1	B6HQM6	2	B6HQM6	Pc22g11710 protein	glycolysis; intracellular membrane-bounded organelle; pyruvate dehydrogenase (acetyl-transferring) activity	
ND	26.3492	ND		26.6747	26.603	ND		1.96E-06	4.49E+08	2	2	11.5	20.12	26.5423	26.3492	26.6388	3	1	2	B6HQN2	B6HQN2	1	B6HQN2	Pc22g11770 protein	ribosome; structural constituent of ribosome; translation	
25.3472	23.181	ND		25.3863	ND	ND	0.000216	1.13E+08	3	3	24.2	23.012	24.6382	24.2641	25.3863	3	2	1	B6HQQ6	B6HQQ6	1	B6HQQ6	Pc22g16110 protein	hydrolase activity	
30.6286	30.6125	30.705	30.4033	31.08	29.2972	1.66E-238	8.94E+09	11	11	39.5	27.895	30.4616	30.6487	30.2745	6	3	3	B6HQQ7	B6HQQ7	1	B6HQQ7	Pc22g16120 protein	hydrolase activity	
26.9622	27.1335	26.9482	27.1281	27.5868	26.1856	2.87E-103	7.87E+08	7	7	31.4	31.238	26.9907	27.0146	26.9668	6	3	3	B6HQR0	B6HQR0	1	B6HQR0	Pc22g16150 protein	oxidoreductase activity	
ND	25.6131	ND		25.2401	25.3295	24.6074	5.28E-09	2.13E+08	3	3	11.4	39.426	25.1975	25.6131	25.059	4	1	3	B6HQS6	B6HQS6	1	B6HQS6	Pc22g20230 protein		
29.5482	29.3645	29.0779	28.7396	28.8428	29.9349	6.82E-170	3.62E+09	6	6	58.8	17.658	29.2513	29.3302	29.1725	6	3	3	B6HQS9	B6HQS9	1	B6HQS9	Pc22g20260 protein	RNA binding; small ribosomal subunit; structural constituent of ribosome; translation	
25.7313	25.8652	25.7981	25.5113	26.1903	ND		3.10E-19	3E+08	4	4	19.5	29.368	25.8192	25.7982	25.8508	5	3	2	B6HQT1	B6HQT1	1	B6HQT1	Pc22g20280 protein		
25.438	25.2733	25.247	ND	23.4234	ND		7.83E-07	1.61E+08	3	3	11.2	34.23	24.8454	25.3194	23.4234	4	3	1	B6HQT7	B6HQT7	1	B6HQT7	Pc22g20340 protein	oxidoreductase activity	
25.4884	25.2591	25.4857	25.0789	ND	ND		4.75E-22	2.07E+08	3	3	22.6	30.241	25.328	25.4111	25.0789	4	3	1	B6HQU9	B6HQU9	1	B6HQU9	Pc22g24400 protein	FMN binding; oxidoreductase activity	
27.5352	27.4249	27.68	27.3904	26.7438	25.7685	8.14E-25	9.05E+08	3	3	14.7	27.754	27.0905	27.5467	26.6342	6	3	3	B6HQW2	B6HQW2	1	B6HQW2	Pc22g24530 protein	hydrolase activity	
30.1905	30.2543	30.1661	30.3103	30.754	29.4888	1.97E-29	7.09E+09	5	5	36.7	18.257	30.194	30.2036	30.1844	6	3	3	B6HQX3	B6HQX3	1	B6HQX3	Pc22g24640 protein	oxidoreductase activity	
22.7334	23.2064	22.971	22.822	22.9577	30.7591	4.62E-260	1.19E+09	16	16	60.8	34.968	24.2416	22.9703	25.5129	6	3	3	B6HQX5	B6HQX5	1	B6HQX5	Pc22g03140 protein		
24.7317	26.8392	25.9001	23.7994	25.7389	27.3059	1.13E-33	3.88E+08	6	6	13.1	51.247	25.7192	25.8237	25.6147	6	3	3	B6HR04	B6HR04	1	B6HR04	Kynureninase	L-kynurenine catabolic process; NAD biosynthetic process; cytoplasm; kynureninase activity; pyridoxal phosphate binding; tryptophan catabolic process	Cytoplasm.
28.388	28.8496	28.5645	29.1609	29.5815	27.7654	8.24E-101	2.64E+09	12	12	27.6	53.443	28.7183	28.6007	28.8359	6	3	3	B6HR30	B6HR30	1	B6HR30	Pc22g12130 protein		
27.0528	27.0902	26.8132	24.793	24.7972	27.1767	2.72E-48	5.66E+08	4	4	24.1	25.986	26.2872	26.9854	25.589	6	3	3	B6HR31	B6HR31	1	B6HR31	Pc22g12140 protein	clathrin coat of coated pit; clathrin coat of trans-Golgi network vesicle; intracellular protein transport; structural molecule activity; vesicle-mediated transport	
26.6859	26.1947	27.1691	27.5735	25.6075	26.8928	2.27E-71	6.77E+08	6	6	9.9	83.943	26.6873	26.6832	26.6913	6	3	3	B6HR36	B6HR36	1	B6HR36	Pc22g16290 protein		
22.5591	22.6488	22.3985	23.3886	21.8274	27.3829	1.07E-27	1.59E+08	7	7	20.1	43.251	23.3676	22.5355	24.1997	6	3	3	B6HR53	B6HR53	1	B6HR53	Pc22g16470 protein	GTP binding; cell cycle; septin complex	
26.1723	26.6903	26.2292	25.705	26.4477	27.1617	2.67E-43	4.94E+08	3	3	26.2	16.294	26.4011	26.364	26.4381	6	3	3	B6HR56	B6HR56	1	B6HR56	Pc22g20470 protein	ribosome; structural constituent of ribosome; translation	
25.6681	25.6509	26.2557	25.2563	24.7493	25.1676	7.87E-25	2.94E+08	3	3	8.1	37.152	25.458	25.8583	25.0578	6	3	3	B6HR58	B6HR58	1	B6HR58	Pc22g20490 protein	catalytic activity; cellular metabolic process; coenzyme binding	
29.304	29.5874	29.437	30.0806	29.9735	29.3903	9.33E-65	4.75E+09	14	14	39.9	43.911	29.6288	29.4428	29.8148	6	3	3	B6HR72	B6HR72	1	B6HR72	Branched-chain-amino-acid aminotransferase	L-isoleucine transaminase activity; L-valine transaminase activity; branched-chain amino acid biosynthetic process	
26.029	25.0275	26.125	25.4506	25.9046	26.968	5.54E-48	3.45E+08	5	5	50.3	15.871	25.9174	25.7272	26.1077	6	3	3	B6HR74	B6HR74	1	B6HR74	Pc22g20650 protein	ribosome; structural constituent of ribosome; translation	
ND		26.7786	27.8305	ND	ND	ND	0.000113	6.32E+08	2	2	4	52.756	27.3045	27.3045	ND	2	2	0	B6HRA1	B6HRA1	1	B6HRA1	Pc22g24860 protein	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	
26.3133	26.1447	26.1887	26.5583	26.4859	25.6977	6.01E-55	4.67E+08	5	5	10.8	51.175	26.2314	26.2155	26.2473	6	3	3	B6HRF7	B6HRF7	1	B6HRF7	Pc22g07840 protein		
30.4679	30.5699	30.4663	30.4404	31.1378	29.4392	0	8.51E+09	9	9	44.9	17.96	30.4202	30.5014	30.3391	6	3	3	B6HRG1	B6HRG1	1	B6HRG1	Pc22g12180 protein	calcium ion binding	
26.8979	26.564	26.6807	23.2801	24.9085	27.1749	1.22E-19	4.83E+08	3	3	9	42.444	25.9177	26.7142	25.1212	6	3	3	B6HRL5	B6HRL5	1	MTLD	Mannitol-1-phosphate 5-dehydrogenase	coenzyme binding; mannitol metabolic process; mannitol-1-phosphate 5-dehydrogenase activity	
25.8919	25.7585	25.5212	25.4772	24.2994	25.0928	1.46E-11	2.56E+08	5	5	9.3	71.322	25.3402	25.7239	24.9565	6	3	3	B6HRL8	B6HRL8	1	B6HRL8	Pc22g20830 protein	ATP binding; protein serine/threonine kinase activity	
22.5654	22.6476	22.5982	22.4849	22.306	25.0209	0.000226	55017000	2	2	2.3	96.441	22.9372	22.6037	23.2706	6	3	3	B6HRL9	B6HRL9	1	B6HRL9	Pc22g20840 protein	intracellular protein transport; membrane coat; structural molecule activity; vesicle-mediated transport	
31.0094	31.2791	30.9809	31.9194	32.0664	30.8345	2.08E-215	1.6E+10	17	17	36	58.546	31.3483	31.0898	31.6068	6	3	3	B6HRP4	B6HRP4	1	B6HRP4	Pc22g25050 protein	inositol biosynthetic process; inositol-3-phosphate synthase activity; phospholipid biosynthetic process	
25.9706	26.8997	26.1856	24.6021	25.0781	27.7624	1.42E-50	4.84E+08	6	6	30.9	39.821	26.0831	26.3519	25.8142	6	3	3	B6HRP6	B6HRP6	1	B6HRP6	Pc22g25070 protein	S-(hydroxymethyl)glutathione dehydrogenase activity; ethanol oxidation; zinc ion binding	
25.9126	26.3456	26.1359	25.9212	26.8321	25.1047	3.46E-10	4.04E+08	5	5	11.5	45.348	26.042	26.1314	25.9527	6	3	3	B6HRR4	B6HRR4	1	B6HRR4	Pc22g03580 protein	aspartic-type endopeptidase activity; proteolysis	
24.101	23.779	23.9792	ND	ND	25.0411	6.55E-06	77957000	2	2	4.3	64.432	24.2251	23.9531	25.0411	4	3	1	B6HRT0	B6HRT0	1	B6HRT0	Pc22g03740 protein	gamma-glutamyltransferase activity; glutathione metabolic process	
28.5846	28.8514	28.7421	29.0653	28.844	27.7701	1.99E-89	2.53E+09	9	9	50	32.766	28.6429	28.7261	28.5598	6	3	3	B6HRT5	B6HRT5	1	B6HRT5	Proteasome subunit beta type	cytoplasm; nucleus; proteasome core complex; proteolysis involved in cellular protein catabolic process; threonine-type endopeptidase activity	Cytoplasm. Nucleus.
26.5053	26.7116	26.5377	27.4182	27.6905	26.3817	4.95E-120	7.2E+08	8	8	22.6	49.988	26.8742	26.5849	27.1635	6	3	3	B6HRU6	B6HRU6	1	B6HRU6	Pc22g08010 protein	nucleic acid binding; nucleotide binding	
28.4654	28.2059	28.4545	28.3998	27.6668	27.5508	1.30E-122	1.77E+09	13	13	25	64.926	28.1239	28.3753	27.8724	6	3	3	B6HRV3	B6HRV3	1	B6HRV3	Pc22g08080 protein		
26.2701	25.7937	25.7016	26.5023	25.5911	25.5266	9.63E-15	3.64E+08	3	3	27.4	12.938	25.8976	25.9218	25.8734	6	3	3	B6HRX7	B6HRX7	1	B6HRX7	Pc22g12590 protein		
30.6737	30.8056	30.6688	31.7949	32.1241	30.2824	0	1.36E+10	23	23	36.5	78.489	31.0583	30.7161	31.4005	6	3	3	B6HRY6	B6HRY6	1	B6HRY6	Pc22g16760 protein	cytoplasm; dipeptidyl-peptidase activity; proteolysis	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
28.5259	28.0148	28.6019	28.7235	27.7689	28.6894	1.30E-133	2.03E+09	11	11	45.1	45.799	28.3874	28.3809	28.3939	6	3	3	B6HRY8	B6HRY8	1	B6HRY8	Branched-chain-amino-acid aminotransferase	L-isoleucine transaminase activity; L-leucine transaminase activity; L-valine transaminase activity; branched-chain amino acid biosynthetic process	
28.3206	28.2442	28.4242	28.3036	28.7843	27.074	1.96E-23	1.86E+09	4	4	42.5	14.081	28.1918	28.3297	28.054	6	3	3	B6HRZ8	B6HRZ8	1	B6HRZ8	Pc22g16880 protein	heme binding	
28.1776	28.2395	28.0434	27.6957	27.9284	28.087	9.93E-67	1.54E+09	8	8	33.4	33.531	28.0286	28.1535	27.9037	6	3	3	B6HS12	B6HS12	1	B6HS12	Uricase	peroxisome; purine nucleobase metabolic process; urate catabolic process; urate oxidase activity	Peroxisome.
23.6755	23.5693	23.2177	24.263	23.9493	26.5405	5.06E-10	1.35E+08	3	3	25.9	15.881	24.2026	23.4875	24.9176	6	3	3	B6HS14	B6HS14	1	B6HS14	Pc22g20980 protein	ribosome; structural constituent of ribosome; translation	
26.1661	26.3588	26.2687	26.1999	26.8076	25.421	1.34E-28	4.52E+08	5	5	24.7	24.478	26.2037	26.2645	26.1428	6	3	3	B6HS32	B6HS32	1	B6HS32	Pc22g21160 protein	'de novo' IMP biosynthetic process; phosphoribosylglycinamide formyltransferase activity	
30.6139	30.6855	30.4068	30.3224	30.7734	28.7332	5.49E-194	8.03E+09	6	6	56.7	21.32	30.2559	30.5688	29.943	6	6	3	B6HS43	B6HS43	1	B6HS43	Pc22g25220 protein	FMN binding; negative regulation of transcription, DNA-templated; oxidoreductase activity	
27.3189	26.3837	27.2572	26.0773	24.9031	26.8863	1.42E-53	6.03E+08	7	7	41	30.06	26.4711	26.9866	25.9556	6	6	3	B6HS52	B6HS52	1	B6HS52	Pc22g25320 protein	F-actin capping protein complex; WASH complex; actin cytoskeleton organization	
28.3515	26.932	28.5332	27.6546	24.6219	27.0527	9.05E-168	1.24E+09	10	9	36	48.164	27.191	27.9389	26.4431	6	6	3	B6HS72;B6H360;B6H467;B6GW60	B6HS72	4	B6HS72	Pc22g03870 protein	ATP binding; MAP kinase activity	
25.224	ND	24.7179	ND	ND		23.3218	4.66E-10	85543000	3	3	6.9	55.413	24.4212	24.9709	23.3218	3	2	1	B6HS79	B6HS79	1	B6HS79	Succinyl-CoA:3-ketoacid-coenzyme A transferase	3-oxoacid CoA-transferase activity; ketone body catabolic process; mitochondrion	
26.2078	25.7408	26.0044	24.8578	25.395	24.1931	1.72E-26	2.96E+08	2	2	18.5	17.583	25.3998	25.9843	24.8153	6	3	3	B6HS85	B6HS85	1	B6HS85	Pc22g08180 protein		
23.9355	23.7447	ND	25.0247	25.2641	ND	1.84E-08	1.1E+08	2	2	24.8	13.213	24.4923	23.8401	25.1444	4	2	2	B6HSA1	B6HSA1	1	B6HSA1	Pc22g08360 protein	nucleic acid binding; nucleotide binding	
27.9554	27.1438	28.1941	28.089	26.4537	26.5453	6.78E-59	1.17E+09	5	5	14.9	65.6	27.3969	27.7644	27.0293	6	6	3	B6HSB4	B6HSB4	1	B6HSB4	Pc22g12740 protein		
25.3334	25.139	24.9937	25.3517	25.8679	24.9686	1.82E-15	2.25E+08	6	6	9.5	70.115	25.2757	25.1554	25.396	6	6	3	B6HSB9	B6HSB9	1	B6HSB9	Signal recognition particle subunit SRP72	7S RNA binding; SRP-dependent cotranslational protein targeting to membrane; signal recognition particle, endoplasmic reticulum targeting	Cytoplasm.
25.1017	24.3314	24.2307	ND	ND	24.4825	4.49E-05	98866000	2	2	5.6	50.831	24.5366	24.5546	24.4825	4	3	1	B6HSC6	B6HSC6	1	B6HSC6	Pc22g17020 protein	nucleic acid binding; nucleotide binding	
25.9576	25.885	26.1988	22.9743	22.775	25.709	4.07E-29	2.67E+08	3	3	17.6	35.91	24.9166	26.0138	23.8194	6	3	3	B6HSE9	B6HSE9	1	B6HSE9	Pc22g17250 protein	cofactor binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	
26.5023	27.0053	26.7801	26.2984	25.9384	26.4093	1.47E-36	5.39E+08	5	5	20.2	57.081	26.489	26.7625	26.2154	6	3	3	B6HSG0	B6HSG0	1	B6HSG0	Catalase	catalase activity; heme binding; hydrogen peroxide catabolic process; metal ion binding	
27.8322	27.811	27.8456	27.4432	27.7927	26.7964	3.80E-33	1.19E+09	7	7	26.6	31.294	27.5868	27.8296	27.3441	6	3	3	B6HSG3	B6HSG3	1	B6HSG3	Pc22g21270 protein	catalytic activity	
30.4301	30.3925	30.2947	30.2119	30.7257	29.1646	3.19E-140	7.33E+09	9	9	35.4	16.139	30.2032	30.3725	30.034	6	6	3	B6HSI1	B6HSI1	1	B6HSI1	Pc22g21460 protein	fatty-acyl-CoA binding	
28.8293	28.9753	28.7022	29.1331	29.4234	27.7147	1.15E-56	2.79E+09	5	5	27.4	28.909	28.7963	28.8356	28.7571	6	6	3	B6HSI5	B6HSI5	1	B6HSI5	Pc22g25470 protein	6-phosphogluconolactonase activity; pentose-phosphate shunt	
25.5557	25.7448	25.5824	25.7986	25.8498	25.2043	1.05E-09	2.9E+08	4	4	13.6	40.093	25.6226	25.6277	25.6176	6	6	3	B6HSJ3	B6HSJ3	1	B6HSJ3	Pc22g25550 protein	pyridoxal 5'-phosphate salvage; pyridoxal kinase activity	
27.7326	27.9254	27.7581	27.8795	27.8524	27.2703	2.40E-68	1.3E+09	7	7	36.7	19.653	27.7364	27.8054	27.6674	6	6	3	B6HSJ4	B6HSJ4	1	B6HSJ4	Pc22g25560 protein	dUTP diphosphatase activity; dUTP metabolic process	
26.7015	26.6686	26.6682	ND		25.5744	28.7378	4.24E-53	8.4E+08	2	2	17.3	16.66	26.8701	26.6794	27.1561	5	3	2	B6HSK3	B6HSK3	1	B6HSK3	Pc22g25650 protein	ATP synthesis coupled proton transport; proton-transporting ATP synthase activity, rotational mechanism; proton-transporting ATP synthase complex, catalytic core F(1); proton-transporting ATPase activity, rotational mechanism	
26.7818	27.0551	26.8691	28.9366	28.7372	27.914	9.44E-87	1.42E+09	11	11	24.8	53.696	27.7156	26.902	28.5293	6	6	3	B6HSL3	B6HSL3	1	B6HSL3	Pc22g03990 protein	nucleic acid binding; nucleotide binding	
31.3182	31.0866	31.2414	31.5076	31.8093	30.5431	0	1.48E+10	21	21	52.9	54.222	31.251	31.2154	31.2867	6	6	3	B6HSP3	B6HSP3	1	B6HSP3	Pc22g08480 protein	ATP binding; glycolysis; hexokinase activity	
27.1068	27.6493	26.9075	24.4704	24.8933	30.7455	2.04E-256	1.76E+09	13	13	40.1	46.736	26.9621	27.2212	26.703	6	6	3	B6HSS5;B6HP80	B6HSS5	2	B6HSS5	Aspartate aminotransferase	L-aspartate:2-oxoglutarate aminotransferase activity; L-phenylalanine:2-oxoglutarate aminotransferase activity; biosynthetic process; cellular amino acid metabolic process; pyridoxal phosphate binding	
32.499	32.4823	32.4715	32.6876	31.6351	32.4514	0	3.25E+10	22	22	57.7	49.832	32.3711	32.4843	32.258	6	6	3	B6HSV9	B6HSV9	1	B6HSV9	Glutamate dehydrogenase	cellular amino acid metabolic process; oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor	
28.3645	28.183	28.3871	26.9854	27.0821	27.577	2.72E-116	1.44E+09	10	10	36.3	39.5	27.7632	28.3115	27.2149	6	6	3	B6HSW1;B6H847	B6HSW1	2	B6HSW1	Pc22g21480 protein	NAD binding; magnesium ion binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	
24.7779	26.2863	25.2895	25.4619	25.2143	30.0628	3.83E-99	9.68E+08	14	14	43.8	50.283	26.1821	25.4513	26.913	6	6	3	B6HSX8;B6GWY6;B6HA43;CON__ENSEMBL:ENSBTAP00000016242	B6HSX8	4	B6HSX8	Pc22g21650 protein	GTP binding; GTPase activity; microtubule; microtubule-based process; protein polymerization; structural constituent of cytoskeleton	
27.2668	27.6195	27.5531	27.7967	28.2912	26.9154	6.53E-62	1.17E+09	13	13	13.3	137.12	27.5738	27.4798	27.6678	6	6	3	B6HSY0	B6HSY0	1	B6HSY0	Pc22g21670 protein	calcium ion binding	
28.3479	28.2852	28.2107	27.3276	27.4082	28.0925	4.65E-76	1.53E+09	12	12	28.1	55.762	27.9453	28.2812	27.6094	6	6	3	B6HT18	B6HT18	1	B6HT18	Pc22g04380 protein	biosynthetic process; oxo-acid-lyase activity	
25.3642	25.4784	25.4068	ND		26.0195	25.2099	9.71E-29	2.46E+08	3	3	6	63.306	25.4958	25.4165	25.6147	5	3	2	B6HT20	B6HT20	1	B6HT20	Pc22g04400 protein		
25.3231	25.5992	25.239	ND		23.5278	26.2406	7.80E-14	1.83E+08	3	3	24.9	19.31	25.1859	25.3871	24.8842	5	3	2	B6HT23	B6HT23	1	B6HT23	Pc22g04430 protein	oxidoreductase activity	
24.663	25.147	24.8156	25.0016	25.2024	24.0383	3.24E-09	1.72E+08	5	5	17.7	38.105	24.8113	24.8752	24.7474	6	6	3	B6HT31	B6HT31	1	B6HT31	Pc22g08720 protein	deadenylation-dependent decapping of nuclear-transcribed mRNA; hydrolase activity	
25.6177	25.993	25.8854	24.7149	24.9961	25.0404	1.19E-23	2.65E+08	3	3	19.3	26.933	25.3746	25.8321	24.9171	6	6	3	B6HT33	B6HT33	1	B6HT33	Pc22g08740 protein	intracellular; ubiquitin-dependent protein catabolic process; ubiquitin-specific protease activity	
25.7989	25.5818	26.323	25.7585	27.2454	26.3692	5.49E-45	4.37E+08	9	9	21.8	65.524	26.1795	25.9013	26.4577	6	6	3	B6HT46	B6HT46	1	B6HT46	Pc22g08870 protein	ATP binding; asparagine-tRNA ligase activity; asparaginyl-tRNA aminoacylation; cytoplasm; nucleic acid binding	
25.4543	26.2181	25.8346	26.8629	26.2654	25.7988	7.74E-43	4.1E+08	5	5	11.2	87.809	26.0723	25.8356	26.309	6	6	3	B6HT47	B6HT47	1	B6HT47	Pc22g08880 protein	nucleic acid binding; nucleotide binding	
25.8302	26.0372	25.8034	26.2288	26.0261	24.7845	2.07E-22	3.42E+08	5	5	4.5	158.39	25.785	25.8903	25.6798	6	6	3	B6HT65	B6HT65	1	B6HT65	Pc22g13370 protein		
28.0771	28.0994	28.6392	29.5141	29.7882	27.7155	3.47E-182	2.7E+09	15	15	30.6	77.686	28.6389	28.2719	29.006	6	6	3	B6HT75;B6HLH5	B6HT75	2	B6HT75	Pc22g13470 protein	tryptophan synthase activity	
23.4784	23.5213	23.6068	22.821	22.5257	25.8962	1.89E-11	99017000	2	2	6.2	56.054	23.6416	23.5355	23.7477	6	6	3	B6HT76	B6HT76	1	B6HT76	Pc22g13480 protein	ATP binding; ATP hydrolysis coupled proton transport; hydrogen-exporting ATPase activity, phosphorylative mechanism; proton-transporting V-type ATPase, V1 domain	
24.341	24.7408	24.7168	24.9898	25.5002	24.1455	9.82E-09	1.66E+08	3	3	9.6	42.639	24.739	24.5995	24.8785	6	6	3	B6HTA7	B6HTA7	1	B6HTA7	Pc22g21810 protein	ubiquitin-dependent protein catabolic process	
22.4333	ND	22.5204	ND	ND	27.8301	1.22E-53	1.74E+08	3	3	23.2	24.682	24.2613	22.4769	27.8301	3	2	1	B6HTH1	B6HTH1	1	B6HTH1	Superoxide dismutase	metal ion binding; superoxide dismutase activity; superoxide metabolic process	
22.3925	22.6029	22.4425	22.8094	22.0843	28.4119	1.24E-64	2.67E+08	11	11	14.1	118.8	23.4572	22.4793	24.4352	6	6	3	B6HTI0	B6HTI0	1	B6HTI0	Pc22g04770 protein	oxoglutarate dehydrogenase (succinyl-transferring) activity; thiamine pyrophosphate binding; tricarboxylic acid cycle	
25.7634	25.8027	25.7585	25.8987	26.3638	25.2096	3.71E-26	3.42E+08	7	7	35.5	36.097	25.7995	25.7749	25.824	6	6	3	B6HTJ9	B6HTJ9	1	B6HTJ9	Deoxyhypusine hydroxylase	cytoplasm; deoxyhypusine monooxygenase activity; metal ion binding; nucleus; peptidyl-lysine modification to hypusine	Cytoplasm. Nucleus.
26.1931	26.1056	25.696	25.189	25.5847	25.2216	6.60E-12	3.13E+08	5	5	11.6	69.328	25.665	25.9982	25.3318	6	6	3	B6HTL2	B6HTL2	1	B6HTL2	Pc22g13590 protein	catalytic activity	
27.7427	27.3541	27.5607	26.9995	27.959	ND	4.97E-46	9.77E+08	2	2	29.7	17.873	27.5232	27.5525	27.4793	5	3	2	B6HTN4	B6HTN4	1	B6HTN4	Pc22g17810 protein		
29.7772	29.8839	29.6219	30.319	30.7186	28.986	1.15E-109	5.91E+09	6	6	16.6	40.966	29.8844	29.761	30.0079	6	6	3	B6HTP0	B6HTP0	1	B6HTP0	Pc22g17870 protein		
ND		24.4016	ND	24.8852	24.5406	ND	2.84E-08	86897000	3	3	22.9	18.157	24.6091	24.4016	24.7129	3	1	2	B6HTP6	B6HTP6	1	B6HTP6	Pc22g17930 protein	SUMO ligase activity	
ND	ND	ND	ND		24.7648	26.8762	0.000963	2.75E+08	2	2	5.3	64.208	25.8205	ND	25.8205	2	0	2	B6HTP7	B6HTP7	1	B6HTP7	Asparagine synthetase	ATP binding; L-asparagine biosynthetic process; asparagine synthase (glutamine-hydrolyzing) activity	
27.5774	27.7846	27.5978	28.0603	27.7679	27.3848	1.22E-63	1.25E+09	10	10	35.8	48.102	27.6954	27.6533	27.7376	6	6	3	B6HTQ4	B6HTQ4	1	MAP22	Methionine aminopeptidase 2-2	cytoplasm; metal ion binding; metalloaminopeptidase activity; protein initiator methionine removal; proteolysis	Cytoplasm.
24.6849	24.6209	25.0832	27.616	27.3783	24.5901	1.17E-10	4.74E+08	4	4	18.5	29.694	25.6622	24.7963	26.5282	6	6	3	B6HTQ6	B6HTQ6	1	B6HTQ6	Pc22g18030 protein	structural molecule activity	
ND		20.9509	ND	21.2453	21.1683	24.4611	3.02E-05	24408000	2	2	7.2	40.112	21.9564	20.9509	22.2916	4	1	3	B6HTQ8	B6HTQ8	1	B6HTQ8	Pc22g22040 protein		
23.8358	23.9399	23.9952	24.5696	24.6605	25.3663	6.84E-12	1.23E+08	3	3	19.1	23.472	24.3945	23.9236	24.8655	6	6	3	B6HTR0	B6HTR0	1	B6HTR0	Pc22g22060 protein	GTP binding; protein transport; small GTPase mediated signal transduction	
25.3668	25.1759	25.4931	25.8551	24.6242	ND	0.001401	3.22E+08	2	2	1.5	172.51	25.303	25.3453	25.2396	5	3	2	B6HTR6	B6HTR6	1	B6HTR6	Pc22g22120 protein	4-alpha-glucanotransferase activity; amylo-alpha-1,6-glucosidase activity; glycogen biosynthetic process; glycogen catabolic process	
27.4961	27.3195	27.4171	28.1071	27.6831	27.7514	7.24E-86	1.16E+09	6	6	27.2	40.565	27.6291	27.4109	27.8472	6	6	3	B6HTS2	B6HTS2	1	B6HTS2	Phospho-2-dehydro-3-deoxyheptonate aldolase	3-deoxy-7-phosphoheptulonate synthase activity; aromatic amino acid family biosynthetic process; chorismate biosynthetic process	
29.3211	29.3503	29.1958	30.4019	30.619	29.1714	1.06E-266	5.04E+09	26	26	49.2	84.532	29.6766	29.2891	30.0641	6	6	3	B6HTS8	B6HTS8	1	B6HTS8	Eukaryotic translation initiation factor 3 subunit B	eukaryotic 43S preinitiation complex; eukaryotic 48S preinitiation complex; eukaryotic translation initiation factor 3 complex; formation of translation preinitiation complex; nucleotide binding; regulation of translational initiation; translation initiation factor activity	Cytoplasm.
29.9446	29.6402	29.8722	30.3538	29.1345	29.9185	0	5.54E+09	17	17	52.4	53.195	29.8106	29.819	29.8023	6	6	3	B6HTW7	B6HTW7	1	B6HTW7	Pc22g04840 protein		
30.0108	30.2609	30.0654	29.9627	30.4315	28.7046	0	6.09E+09	9	9	36.9	36.479	29.906	30.1124	29.6996	6	6	3	B6HTW8	B6HTW8	1	B6HTW8	Pc22g04850 protein	oxidoreductase activity	
ND		24.0408	24.2318	ND	ND	24.5511	6.58E-07	71217000	3	3	6.9	73.087	24.2745	24.1363	24.5511	3	2	1	B6HTY2	B6HTY2	1	B6HTY2	Pc22g04990 protein	ATP binding; protein serine/threonine kinase activity	
26.5066	26.9311	26.6413	25.9376	26.4434	26.7019	6.75E-21	5.59E+08	8	8	11.5	94.791	26.527	26.693	26.361	6	6	3	B6HTY7	B6HTY7	1	B6HTY7	Pc22g05050 protein		
23.6736	24.8807	24.5071	24.8009	25.2668	23.6862	6.82E-09	1.43E+08	2	2	3.2	81.324	24.4692	24.3538	24.5847	6	6	3	B6HTZ2	B6HTZ2	1	B6HTZ2	Pc22g09190 protein	nucleus	
28.0329	28.1127	27.8429	28.1635	28.4822	26.8728	5.12E-41	1.52E+09	4	4	11	56.954	27.9178	27.9962	27.8395	6	6	3	B6HU11	B6HU11	1	B6HU11	Pc22g09380 protein	carbohydrate metabolic process	
28.4683	28.6245	28.5568	29.5919	29.7078	28.0985	3.84E-81	2.91E+09	11	11	22.2	56.002	28.8413	28.5498	29.1328	6	6	3	B6HU25	B6HU25	1	B6HU25	Pc22g13950 protein	aminopeptidase activity; metallopeptidase activity; proteolysis; zinc ion binding	
26.0748	26.3704	26.1628	26.8014	26.9467	25.2407	4.41E-32	4.71E+08	4	4	14.6	34.559	26.2661	26.2027	26.3296	6	6	3	B6HU43	B6HU43	1	B6HU43	Pc22g18040 protein	metal ion binding	
29.0672	27.3633	29.0544	28.9663	25.6952	28.4144	3.27E-181	2.23E+09	11	11	45.3	43.368	28.0935	28.4949	27.692	6	6	3	B6HU67	B6HU67	1	B6HU67	Pc22g18320 protein	ATP binding; diphosphomevalonate decarboxylase activity; isoprenoid biosynthetic process	
26.3771	26.8312	26.8238	26.7153	26.1611	27.3318	2.36E-38	6.37E+08	8	8	21.5	56.907	26.7067	26.6774	26.7361	6	6	3	B6HU83	B6HU83	1	B6HU83	Pc22g22460 protein	ATP binding; cytoplasm; protein folding	
24.6131	22.4154	24.594	ND	ND	ND	0.000196	1.01E+08	2	2	5.4	50.931	23.8742	23.8742	ND	3	3	0	B6HUB4	B6HUB4	1	B6HUB4	Pc22g22470 protein	carbohydrate catabolic process; mannan endo-1,6-alpha-mannosidase activity	
23.9506	24.5301	24.0153	25.0393	25.1318	ND	1.58E-08	1.3E+08	3	3	13	37.984	24.5334	24.1653	25.0856	5	3	2	B6HUC7	B6HUC7	1	B6HUC7	Pc22g05140 protein		
28.4832	28.5669	28.5278	28.069	28.3111	27.2708	3.46E-200	1.87E+09	6	6	66.2	15.595	28.2048	28.5259	27.8836	6	6	3	B6HUD5	B6HUD5	1	B6HUD5	Pc22g05220 protein	acid-amino acid ligase activity	
26.1343	26.1503	26.374	25.9944	25.9381	ND	1.01E-07	3.77E+08	2	2	4.1	59.058	26.1182	26.2195	25.9663	5	3	2	B6HUF2	B6HUF2	1	B6HUF2	Pc22g09390 protein	coenzyme binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	
25.505	26.1244	25.654	23.7362	24.5888	27.3629	2.00E-34	3.15E+08	3	3	7.3	65.508	25.4952	25.7611	25.2293	6	6	3	B6HUF3	B6HUF3	1	B6HUF3	Pc22g09400 protein	alcohol metabolic process; choline dehydrogenase activity; flavin adenine dinucleotide binding	
25.586	26.0612	25.971	ND	ND	ND	3.49E-12	2.65E+08	2	2	14.7	23.846	25.8727	25.8727	ND	3	3	0	B6HUJ8	B6HUJ8	1	B6HUJ8	Pc22g14330 protein		
26.424	26.6565	26.357	27.0935	26.973	26.94	5.17E-41	6.26E+08	6	6	26.4	35.198	26.7407	26.4792	27.0022	6	6	3	B6HUL3	B6HUL3	1	B6HUL3	Pc22g18410 protein	acetolactate synthase activity; amino acid binding; branched-chain amino acid biosynthetic process	
25.8417	25.8392	25.5982	25.6176	25.4802	25.7892	3.45E-27	3E+08	4	4	9.8	52.831	25.6943	25.7597	25.629	6	6	3	B6HUL4	B6HUL4	1	B6HUL4	Pc22g18420 protein	RNA binding	
27.7607	28.2124	27.8758	28.1518	27.892	27.6935	5.96E-84	1.47E+09	3	3	25.5	15.499	27.9311	27.9496	27.9125	6	6	3	B6HUM0	B6HUM0	1	B6HUM0	Pc22g18480 protein	actin cytoskeleton; actin filament depolymerization	
26.1861	26.7653	25.9727	26.2936	26.6495	26.343	1.80E-14	4.91E+08	4	4	4.6	120.44	26.3684	26.3081	26.4287	6	6	3	B6HUM5	B6HUM5	1	B6HUM5	Pc22g18530 protein	ubiquitin ligase complex; ubiquitin-dependent protein catabolic process; ubiquitin-ubiquitin ligase activity	
27.5648	27.8912	27.6226	28.5042	28.7846	27.0253	2.53E-106	1.48E+09	10	10	25.2	64.814	27.8988	27.6929	28.1047	6	6	3	B6HUP3	B6HUP3	1	B6HUP3	Pc22g22710 protein	branched-chain amino acid biosynthetic process; dihydroxy-acid dehydratase activity	

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.

A. Total data

Log2 LFQ intensity *P. polonicum* Control 1	Log2 LFQ intensity *P. polonicum* Control 2	Log2 LFQ intensity *P. polonicum* Control 3	Log2 LFQ intensity *P. polonicum* Treated 1	Log2 LFQ intensity *P. polonicum* Treated 2	Log2 LFQ intensity *P. polonicum* Treated 3	PEP	Intensity	Peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Log2 (Mean)	Log2 (Mean *P. polonicum* Control)	Log2 (Mean *P. polonicum* Treated)	Valid values	Valid values *P. polonicum* Control	Valid values *P. polonicum* Treated	Protein IDs	Majority protein IDs	Proteins	Gene ID	Protein Name	Gene ontology (GO)	Subcellular location
25.3099	25.2879	24.9506	25.0516	25.6209	24.5818	5.27E-09	2.18E+08	4	4	13	40.529	25.1338	25.1828	25.0847	6	3	3	B6HUS7	B6HUS7	1	B6HUS7	tRNA (guanine-N(7)-)-methyltransferase	nucleus; tRNA (guanine-N7-)-methyltransferase activity; tRNA binding	Nucleus.
25.0425	25.3901	25.3521	24.9987	24.9458	24.6259	6.20E-06	1.99E+08	2	2	18.2	13.74	25.0592	25.2615	24.8568	6	3	3	B6HUU4	B6HUU4	1	B6HUU4	Pc22g05600 protein	prefoldin complex; protein folding	
25.0459	25.0343	24.983	25.1241	25.254	ND	7.35E-06	1.78E+08	2	2	7.5	29.24	25.0882	25.0211	25.189	5	3	2	B6HUW6	B6HUW6	1	B6HUW6	Pc22g09850 protein	proteolysis	
26.7236	27.0894	26.7646	27.1767	27.5231	ND	6.49E-06	7.1E+08	2	2	17.8	11.684	27.0555	26.8592	27.3499	5	3	2	B6HVD0	B6HVD0	1	B6HVD0	Thioredoxin	cell redox homeostasis; glycerol ether metabolic process; protein disulfide oxidoreductase activity	
25.2479	25.4004	25.3001	25.0245	24.9335	29.8475	1.80E-148	8.28E+08	16	16	27.8	87.308	25.959	25.3162	26.6018	6	3	3	B6HV10	B6HV10	1	B6HV10	Pc22g18630 protein	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity; methionine biosynthetic process; zinc ion binding	
25.3107	24.8499	25.3507	25.2063	ND	24.7271	5.31E-05	2.21E+08	3	3	6.9	64.115	25.0889	25.1704	24.9667	5	3	2	B6HV21	B6HV21	1	B6HV21	Pc22g18750 protein	DNA repair; NuA4 histone acetyltransferase complex; chromatin binding; chromatin remodeling; histone H2A acetylation; histone H4 acetylation	
27.9002	28.0403	27.9236	28.3572	28.5136	27.2312	2.55E-48	1.56E+09	5	5	44.7	22.533	27.9944	27.9547	28.034	6	3	3	B6HV27	B6HV27	1	B6HV27	Proteasome subunit beta type	cytoplasm; nucleus; proteasome core complex; proteolysis involved in cellular protein catabolic process; threonine-type endopeptidase activity	Cytoplasm. Nucleus.
24.8066	25.2932	25.172	25.2391	25.5143	23.9816	1.33E-21	2.07E+08	6	6	12.8	63.936	25.0011	25.0906	24.9117	6	3	3	B6HV28	B6HV28	1	B6HV28	Pc22g18830 protein		
25.012	25.2659	25.173	24.8835	24.9929	24.4483	1.19E-13	1.89E+08	3	3	5.1	107.4	24.9626	25.1503	24.7749	6	3	3	B6HV30	B6HV30	1	B6HV30	Pc22g18850 protein		
26.9092	27.2805	27.1335	27.3073	27.4067	ND	3.31E-39	7.94E+08	2	2	18.3	16.887	27.2074	27.1077	27.357	5	3	2	B6HV52	B6HV52	1	B6HV52	Pc22g23060 protein	mitochondrion; oxidoreductase activity	
30.4146	30.7713	30.3745	30.6337	31.1439	30.1938	4.11E-121	9.28E+09	13	13	26.4	60.432	30.5886	30.5201	30.6572	6	3	3	B6HV58	B6HV58	1	B6HV58	Pc22g05690 protein		
28.0117	28.0745	28.0099	28.0206	28.0592	26.75	3.38E-97	1.44E+09	7	7	32.6	38.339	27.821	28.0321	27.6099	6	3	3	B6HV64	B6HV64	1	B6HV64	Pc22g05750 protein	carbohydrate metabolic process; fructose 1,6-bisphosphate 1-phosphatase activity	
29.7932	30.3044	30.4576	31.0908	30.7306	29.2517	1.47E-194	8.07E+09	9	9	31.3	35.992	30.2714	30.1851	30.3577	6	3	3	B6HV68	B6HV68	1	B6HV68	Pc22g05790 protein	ATPase activator activity; response to stress	
29.0942	29.2498	29.1389	28.8937	28.8677	28.8379	1.74E-86	3.08E+09	14	14	41.4	48.799	29.0137	29.161	28.8664	6	3	3	B6HV69	B6HV69	1	B6HV69	Saccharopine reductase Lys7-Penicillium chrysogenum	oxidoreductase activity	
25.9708	25.7503	25.5597	25.6681	26.8811	25.648	1.55E-11	3.61E+08	2	2	14.2	19.025	25.913	25.7603	26.0657	6	3	3	B6HV73	B6HV73	1	B6HV73	Pc22g05840 protein	mitochondrial electron transport, ubiquinol to cytochrome c; ubiquinol-cytochrome-c reductase activity	
28.166	27.7592	28.1025	26.7538	26.9148	29.0442	2.52E-66	1.44E+09	11	11	27.9	59.824	27.7901	28.0092	27.5709	6	3	3	B6HV83;B6H557	B6HV83	2	B6HV83	Pc22g10020 protein	alcohol metabolic process; choline dehydrogenase activity; flavin adenine dinucleotide binding	
22.9437	22.7608	ND	23.4234	ND	25.4644	0.000102	66684000	2	2	5.2	53.379	23.6481	22.8523	24.4439	4	2	2	B6HV84	B6HV84	1	B6HV84	Pc22g10030 protein	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	
26.3533	26.7416	26.6898	ND	ND	29.2822	4.76E-79	7.65E+08	9	9	41.2	40.858	27.2667	26.5949	29.2822	4	3	1	B6HV94	B6HV94	1	B6HV94	Pc22g10140 protein	transferase activity, transferring acyl groups other than amino-acyl groups	
33.3424	33.4305	33.3169	34.0821	34.3824	33.3166	0	7.67E+10	35	35	62.1	66.842	33.6452	33.3633	33.927	6	3	3	B6HVA2	B6HVA2	1	B6HVA2	Pc22g10220 protein	ATP binding	
25.423	25.9139	25.7595	26.2132	26.4807	25.0604	3.70E-18	3.39E+08	4	4	26.7	25.786	25.8084	25.6988	25.9181	6	3	3	B6HVB2	B6HVB2	1	B6HVB2	Pc22g14750 protein	acid-amino acid ligase activity	
23.5554	23.5206	23.7706	ND	23.0498	28.1215	5.64E-44	2.62E+08	6	6	18.1	40.008	24.4036	23.6156	25.5857	5	3	2	B6HVB8	B6HVB8	1	B6HVB8	Pc22g14810 protein	oxidoreductase activity	
26.5392	26.6435	26.5432	27.045	27.0241	25.824	4.22E-09	5.98E+08	3	3	12.8	22.408	26.6032	26.5753	26.631	6	3	3	B6HVD3	B6HVD3	1	B6HVD3	Proteasome subunit beta type	cytoplasm; nucleus; proteasome core complex; proteolysis involved in cellular protein catabolic process; threonine-type endopeptidase activity	Cytoplasm. Nucleus.
27.6903	27.7136	28.1953	26.2537	25.2069	29.6209	9.99E-85	1.49E+09	15	15	41.2	56.101	27.4468	27.8664	27.0272	6	3	3	B6HVE2	B6HVE2	1	B6HVE2	Pc22g18980 protein	GTP binding; GTPase activity	
26.8523	26.8938	26.9067	25.8732	25.7261	26.3676	5.77E-44	5.56E+08	7	7	11.4	117.76	26.4366	26.8843	25.989	6	3	3	B6HVE6	B6HVE6	1	B6HVE6	Pc22g19020 protein	catalytic activity; metal ion binding	
29.6884	29.6992	29.558	30.4235	30.7536	29.1483	4.97E-82	5.85E+09	8	8	30.2	29.399	29.8785	29.6485	30.1085	6	3	3	B6HVF0	B6HVF0	1	B6HVF0	Peptidyl-prolyl cis-trans isomerase	peptidyl-prolyl cis-trans isomerase activity; protein folding	
26.2346	25.7333	26.364	28.1905	25.3435	29.426	9.37E-89	1.09E+09	15	14	25.5	72.531	26.882	26.1107	27.6533	6	3	3	B6HVF1	B6HVF1	1	B6HVF1	Pc22g19070 protein	ATP binding; ATP-dependent helicase activity; nucleic acid binding	
28.646	25.6849	28.1985	27.0096	25.1169	29.4523	1.41E-172	1.47E+09	14	14	33	64.964	27.3514	27.5098	27.1929	6	3	3	B6HVF4	B6HVF4	1	B6HVF4	Pc22g19100 protein	IMP cyclohydrolase activity; phosphoribosylaminoimidazolecarboxamide formyltransferase activity; purine nucleotide biosynthetic process	
28.1638	28.7823	28.2245	29.9832	30.4511	28.8712	1.37E-70	3.57E+09	2	2	5.5	72.532	29.0794	28.3902	29.7685	6	3	3	B6HVF5	B6HVF5	1	B6HVF5	Pc22g19110 protein	proteolysis; serine-type endopeptidase activity	
ND	23.5221	23.5275	22.9749	22.9877	26.2897	2.38E-12	1.08E+08	3	3	5.3	97.209	23.8604	23.5248	24.0841	5	2	3	B6HVH0	B6HVH0	1	B6HVH0	Pc22g23250 protein	N-acetyl-gamma-glutamyl-phosphate reductase activity; NAD binding; acetylglutamate kinase activity; arginine biosynthetic process; mitochondrion	
31.0944	31.5463	31.1163	31.6714	31.8012	30.9104	0	1.57E+10	11	11	53.3	16.913	31.3567	31.2523	31.461	6	3	3	B6HVH5	B6HVH5	1	B6HVH5	Pc22g23300 protein		
24.3144	ND	24.4783	24.2705	ND	23.5879	9.15E-05	1.09E+08	2	2	8	41.455	24.1628	24.3963	23.9292	4	2	2	B6HVI9	B6HVI9	1	B6HVI9	Pc22g06010 protein		
ND	ND	ND	23.9019	ND	24.19	0.000948	73176000	2	2	5.1	64.999	24.0459	ND	24.0459	2	0	2	B6HVJ5	B6HVJ5	1	B6HVJ5	Pc22g06070 protein	carbohydrate metabolic process; glycerol kinase activity; glycerol-3-phosphate metabolic process	
24.0313	24.6244	24.1628	24.1962	24.2862	23.8342	1.16E-36	1.11E+08	4	4	2.6	221.94	24.1892	24.2728	24.1055	6	3	3	B6HVK0	B6HVK0	1	B6HVK0	Pc22g06130 protein		
26.2847	26.6937	26.5377	22.9118	ND	25.5591	1.17E-13	3.43E+08	3	3	26.3	13.85	25.5974	26.5053	24.2355	5	3	2	B6HVK8	B6HVK8	1	B6HVK8	Cyclin-dependent kinases regulatory subunit	cell cycle; cell division; cyclin-dependent protein serine/threonine kinase regulator activity	
24.0216	23.9412	24.4564	23.6001	23.7157	ND	1.53E-05	90123000	2	2	7.5	37.586	23.947	24.1397	23.6579	5	3	2	B6HVM8	B6HVM8	1	B6HVM8	Pc22g15090 protein	homocysteine S-methyltransferase activity	
27.1009	27.9877	27.711	28.3328	29.0461	27.5422	1.77E-53	1.55E+09	15	15	13.5	137.85	27.9535	27.5999	28.307	6	3	3	B6HVP9	B6HVP9	1	B6HVP9	Pc22g19160 protein	RNA binding	
23.4761	23.426	23.4675	23.9576	ND	23.5874	0.000624	64807000	2	2	8	42.123	23.5829	23.4565	23.7725	5	3	3	B6HVT2	B6HVT2	1	B6HVT2	Pc22g23450 protein		
28.7391	28.8346	28.6005	28.6063	29.2566	27.8654	4.13E-94	2.42E+09	9	9	24.9	54.163	28.6504	28.7248	28.5761	6	3	3	B6HVU2	B6HVU2	1	B6HVU2	Pc22g23550 protein	ATP binding; glycolysis; hexokinase activity	
28.1637	27.8615	27.8208	27.9159	28.3356	27.2527	5.24E-136	1.46E+09	10	10	22.5	64.644	27.8917	27.9487	27.8348	6	3	3	B6HVU7	B6HVU7	1	B6HVU7	Ubiquitin carboxyl-terminal hydrolase	cysteine-type peptidase activity; ubiquitin-dependent protein catabolic process	
25.6798	25.7077	25.867	24.5722	ND	27.0979	1.93E-19	2.97E+08	8	8	8.4	154.84	25.7849	25.7515	25.8351	5	3	2	B6HVW2	B6HVW2	1	B6HVW2	L-aminoadipate-semialdehyde dehydrogenase	L-aminoadipate-semialdehyde dehydrogenase activity; lysine biosynthetic process via aminoadipic acid; phosphopantetheine binding	
25.9187	25.5481	25.7953	26.8252	26.6587	25.8365	2.97E-21	4.23E+08	5	5	12.4	52.117	26.0971	25.754	26.4401	6	3	3	B6HVW7	B6HVW7	1	B6HVW7	Pc22g06360 protein	biosynthetic process; catalytic activity; pyridoxal phosphate binding	
28.6906	28.5028	28.5688	27.1945	26.7033	27.7496	1.47E-159	1.69E+09	8	8	26.4	47.768	27.9016	28.5874	27.2158	6	3	3	B6HW12	B6HW12	1	B6HW12	Pc22g19440 protein	biosynthetic process; cellular amino acid metabolic process; pyridoxal phosphate binding; transaminase activity	
31.951	32.2171	32.0201	32.546	33.1683	31.7555	3.87E-114	2.87E+10	5	5	34.7	18.595	32.2763	32.0627	32.4899	6	3	3	B6HW45	B6HW45	1	B6HW45	Pc22g23760 protein	oxidoreductase activity	
26.6914	26.958	27.2066	ND	ND	27.114	2.00E-41	5.13E+08	4	4	40.9	16.932	26.9925	26.952	27.114	4	3	1	B6HW47	B6HW47	1	B6HW47	Pc22g23780 protein	acid-amino acid ligase activity	
25.5373	25.7013	24.8204	25.4892	25.7819	26.138	4.47E-28	2.74E+08	2	2	10.1	17.747	25.578	25.353	25.8031	6	3	3	B6HW48	B6HW48	1	B6HW48	Pc22g23790 protein		
ND	ND	ND	ND	26.15	24.3884	5.10E-25	1.85E+08	3	3	17.1	21.589	25.2692	ND	25.2692	2	0	2	B6HW49	B6HW49	1	B6HW49	Pc22g23800 protein	N-acetyltransferase activity	
30.4207	30.5531	30.4411	30.6642	30.7151	29.6967	0	8.22E+09	13	13	39.6	57.933	30.4152	30.4716	30.3587	6	3	3	B6HW50	B6HW50	1	B6HW50	Pc22g23810 protein	fumarate hydratase activity; fumarate metabolic process; tricarboxylic acid cycle; tricarboxylic acid cycle enzyme complex	
25.2815	25.6671	25.5206	25.208	25.627	26.5515	2.26E-52	2.95E+08	7	7	19.7	46.586	25.6426	25.4897	25.7955	6	3	3	B6HW52	B6HW52	1	B6HW52	Aspartate aminotransferase	L-aspartate:2-oxoglutarate aminotransferase activity; L-phenylalanine:2-oxoglutarate aminotransferase activity; biosynthetic process; cellular amino acid metabolic process; pyridoxal phosphate binding	
27.8204	27.99	27.7392	28.2699	28.7174	27.8345	1.54E-27	1.58E+09	7	7	42.3	17.162	28.0619	27.8499	28.2739	6	3	3	B6HW55	B6HW55	1	B6HW55	Pc22g23860 protein	translation initiation factor activity	
28.2201	28.5615	28.4865	28.7272	28.6168	28.3128	7.47E-112	2.1E+09	11	11	38.6	51.985	28.4875	28.4227	28.5523	6	3	3	O94225	O94225	1	HOSM	Homocitrate synthase, mitochondrial	homocitrate synthase activity; lysine biosynthetic process via aminoadipic acid; mitochondrion	Mitochondrion.

*ND: Not Detected

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.
B. Quantitative and qualitative results

Majority protein IDs	PEP	Peptides	Sequence coverage [%]	Mol. weight [kDa]	*Log2 (Mean PP52 Control)	*Log2 (Mean PP52 Treated)	Valid values PP52 Control	Valid values PP52 Treated	t-test p value	Fold Change PP52 Treated v Control	Gene ID	Protein Name	Gene ontology (GO)	Sequence Description from Blast2GO analysis
B6HCE9	3.90E-264	11	34.9	63.356	28.0439	29.0562	3	3	0.047812	2.017096352	B6HCE9	Pc18g01490 protein	catalytic activity; magnesium ion binding; thiamine pyrophosphate binding	pyruvate decarboxylase
B6HF51	4.04E-90	12	45.8	29.303	28.7242	29.7456	3	3	0.023538	2.029972242	B6HF51	Pc20g02900 protein	RNA binding; ribosome; structural constituent of ribosome; translation	40s ribosomal protein s4
B6H3J5	3.16E-142	8	32	25.548	28.6807	29.7269	3	3	0.014614	2.065083332	B6H3J5	60S ribosomal protein L13	ribosome; structural constituent of ribosome; translation	60s ribosomal protein l13
B6H8V2	9.11E-28	8	31.6	32.147	25.6866	26.748	3	3	0.038089	2.086912337	B6H8V2	Pc16g09240 protein		hmg box
B6HNY5	5.51E-61	2	4.7	61.761	25.0454	26.1471	2	3	0.009021	2.146029637	B6HNY5	Pc22g02800 protein	calcium ion binding; endoplasmic reticulum; protein folding	calnexin
B6HG22	0.000589	2	18.3	12.317	23.0386	24.1699	3	3	0.001293	2.190651513	B6HG22	Pc20g03340 protein	ribosome; structural constituent of ribosome; translation	60s ribosomal protein l33
B6H380	4.96E-69	8	33.3	32.085	27.9389	29.0888	3	3	0.019561	2.219015892	B6H380	Pc13g05920 protein	ribosome	60s ribosomal protein l7
B6HGI2	5.99E-07	2	4.2	51.596	23.9373	25.1054	3	2	0.039277	2.24724902	B6HGI2	Pc20g12210 protein		camp independent regulatory protein
B6H3R8	7.66E-20	3	28	19.873	25.8833	27.0993	3	3	0.00406	2.323081872	B6H3R8	Pc13g07190 protein	ribosome; structural constituent of ribosome; translation	60s ribosomal protein l11
B6HSA1	1.84E-08	2	24.8	13.213	23.8401	25.1444	2	2	0.013496	2.469638707	B6HSA1	Pc22g08360 protein	nucleic acid binding; nucleotide binding	pre-mrna branch site protein p14
B6HAJ0	3.51E-18	4	29.3	20.497	26.2133	27.5181	3	3	0.00868	2.47054614	B6HAJ0	Pc16g12990 protein	large ribosomal subunit; structural constituent of ribosome; translation	60s ribosomal protein l17
B6HNU7	5.70E-131	6	56.6	11.392	27.8937	29.223	3	3	0.008575	2.512772397	B6HNU7	Pc21g18200 protein	ribosome; structural constituent of ribosome; translation	60s ribosomal protein
B6HCR2	1.25E-15	7	11.8	66.862	24.7148	26.0539	3	3	0.016668	2.52981169	B6HCR2	Pc18g02170 protein	ATP binding; RNA binding; cytoplasm; magnesium ion binding; phenylalanine-tRNA ligase activity; phenylalanyl-tRNA aminoacylation	phenylalanyl-trna beta subunit
B6HPK2	1.56E-09	4	25.8	17.854	24.743	26.1943	2	3	0.017014	2.734638251	B6HPK2	Pc22g00880 protein	RNA binding; ribosome; structural constituent of ribosome; translation	40s ribosomal protein s18
B6HPX5	0	30	37.2	99.113	32.1714	33.7749	3	3	0.038274	3.038901682	B6HPX5	Pc22g11170 protein	metallopeptidase activity; proteolysis; zinc ion binding	puromycin-sensitive aminopeptidase
B6HSL3	9.44E-87	11	24.8	53.696	26.902	28.5293	3	3	0.007306	3.089300049	B6HSL3	Pc22g03990 protein	nucleic acid binding; nucleotide binding	rnp domain protein
B6HBR4	5.97E-19	3	13	31.03	24.3805	26.0149	3	2	0.001744	3.104605591	B6HBR4	Pc18g04700 protein		alpha beta hydrolase
B6H8U2	3.10E-40	7	32	24.103	27.1352	28.7868	3	3	0.024105	3.14190596	B6H8U2	Ribosomal protein L15	ribosome; structural constituent of ribosome; translation	60s ribosomal protein l15
B6HA20	2.88E-113	6	58.5	14.709	27.9066	29.591	3	3	0.005907	3.214111549	B6HA20	Pc16g14740 protein	ribosome; structural constituent of ribosome; translation	40s ribosomal protein s22
B6HQJ9	5.71E-63	11	33.1	38.152	27.0933	28.8974	3	3	0.03161	3.492112411	B6HQJ9	Pc22g07020 protein	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; nitrogen compound metabolic process	nitrilase
B6GX54	5.00E-50	5	15.6	53.243	25.5089	27.3419	3	3	0.001558	3.562648128	B6GX54	FK506-binding protein	FK506 binding; histone peptidyl-prolyl isomerization; nucleolus; peptidyl-prolyl cis-trans isomerase activity; protein folding	fkbp-type peptidyl-prolyl
B6HBR0	6.84E-44	4	9.6	59.991	26.3764	28.2853	3	3	0.033312	3.755278747	B6HBR0	Pc18g04660 protein	proteolysis; serine-type carboxypeptidase activity	pheromone processing carboxypeptidase
B6HLC8	1.15E-110	6	23.8	39.973	25.6872	27.6271	3	3	0.007258	3.836684145	B6HLC8	Pc21g16520 protein	ribosome; structural constituent of ribosome; translation	60s ribosomal protein l4
B6HP58	6.91E-105	11	40.8	29.46	28.5129	30.4702	3	3	0.007843	3.88329148	B6HP58	Pc22g02060 protein	ribonucleoprotein complex; ribosome biogenesis	60s ribosomal protein l8
B6GZ69	1.81E-05	2	2.8	76.604	22.519	24.5138	3	2	0.040024	3.98560849	B6GZ69	Pc12g05410 protein	nucleic acid binding; nucleotide binding	rna binding protein
B6HBH5	4.48E-07	2	14.7	13.265	24.8915	26.9118	3	3	0.025135	4.056484568	B6HBH5	Pc18g04110 protein	ribosome; structural constituent of ribosome; translation	60s ribosomal protein l34
B6H2N0	2.54E-18	3	19	20.609	25.9887	28.0515	3	3	0.000229	4.177847986	B6H2N0	Pc13g05540 protein	ribosome; structural constituent of ribosome; translation	60s ribosomal protein l18
B6HLR9	1.82E-160	17	22.4	97.459	26.8145	28.9157	3	3	0.000427	4.290572017	B6HLR9	Pc21g16930 protein	RISC complex; gene silencing by RNA; hydrolase activity, acting on ester bonds; nucleic acid binding	transcription factor (snd1 p100)
B6HEL3	6.39E-45	12	17.2	118.41	24.7189	26.931	3	3	0.001642	4.633428149	B6HEL3	Pc20g07810 protein	phospholipid binding	cytoskeleton assembly control protein
B6GWV7	9.75E-49	5	9.3	65.3	27.1865	29.4959	3	3	0.026083	4.956803267	B6GWV7	Pc12g14680 protein	proteolysis; serine-type endopeptidase activity	tripeptidyl-peptidase sed2
B6H1F6	1.01E-36	4	18.1	22.607	26.4835	28.8966	3	3	0.001833	5.326212541	B6H1F6	Pc13g02890 protein	ribosome; structural constituent of ribosome; translation	60s ribosomal protein l27
B6HHV2	4.93E-09	2	5.3	63.682	22.832	25.3942	3	3	0.041169	5.906199137	B6HHV2	Pc21g23000 protein		domain protein
B6HGW5	4.70E-42	4	33.8	16.782	24.1742	26.8362	3	3	0.00918	6.32914228	B6HGW5	Pc20g13260 protein	ribosome; structural constituent of ribosome; translation	ribosomal protein l14
B6HEK3	6.84E-25	7	16.9	63.959	23.0205	25.8086	3	3	0.039385	6.907003717	B6HEK3	Sulfate adenylyltransferase	ATP binding; adenylylsulfate kinase activity; cysteine biosynthetic process; cytoplasm; hydrogen sulfide biosynthetic process; methionine biosynthetic process; sulfate adenylyltransferase (ATP) activity; sulfate assimilation	atp sulphurylase
B6HP22	4.03E-16	5	26.2	24.262	24.4875	27.6532	3	3	0.001022	8.973743827	B6HP22	Pc22g01260 protein	GTP binding; GTPase activity; intracellular protein transport; nucleocytoplasmic transport; small GTPase mediated signal transduction	gtp-binding nuclear protein gsp1 ran
B6H621	7.38E-35	5	35.9	22.048	23.5244	26.7008	3	3	0.000707	9.040609252	B6H621	Pc14g01930 protein	GTP binding; intracellular; membrane; small GTPase mediated signal transduction	rho gtpase rho1
B6HG15	3.62E-50	7	40.9	16.435	27.4331	30.9139	3	3	0.00049	11.16375141	B6HG15	Pc20g00680 protein	nucleotide binding; ribosome; structural constituent of ribosome; translation	60s ribosomal protein l23
B6HK72	6.16E-162	17	36.7	80.772	24.4175	28.0547	3	3	0.012172	12.44289258	B6HK72	Pc21g15760 protein	ATP binding; cytoplasm; glutamate-tRNA ligase activity; glutamyl-tRNA aminoacylation	glutamyl-trna synthetase
B6GXZ8	8.40E-08	3	26.1	10.046	ND*	27.2844	0	3	N/A	Detected in Treated Only	AFP	Antifungal protein	defense response to fungus; extracellular region; killing of cells of other organism	antifungal protein
B6GW13	3.97E-09	4	8.2	80.801	ND	23.6741	0	2	N/A	Detected in Treated Only	B6GW13	Pc06g00700 protein	RNA binding; pseudouridine synthase activity; pseudouridine synthesis	pseudouridine synthase
B6GZQ9	3.16E-21	3	13.2	16.849	ND	25.9444	0	2	N/A	Detected in Treated Only	B6GZQ9	Pc12g05940 protein	ribosome; structural constituent of ribosome; translation	40s ribosomal protein s13
B6H1A7	7.77E-06	3	15.8	23.044	ND	25.1549	0	2	N/A	Detected in Treated Only	B6H1A7	Pc13g01870 protein	large ribosomal subunit; structural constituent of ribosome; translation	60s ribosomal protein l16
B6H351	1.66E-08	4	3.3	96.471	ND	24.5641	0	2	N/A	Detected in Treated Only	B6H351	Pc13g12630 protein		fes cip4 homology domain protein
B6H3X2	7.61E-11	3	15.8	21.099	ND	26.4196	0	2	N/A	Detected in Treated Only	B6H3X2	Pc13g10970 protein	GTP binding; intracellular; signal transducer activity; small GTPase mediated signal transduction	adp-ribosylation factor
B6H456	7.39E-06	2	10.5	24.076	ND	24.3299	0	3	N/A	Detected in Treated Only	B6H456	Pc13g07680 protein	GTP binding; protein transport; small GTPase mediated signal transduction	gtp-binding protein ypt5
B6H953	0.00023	2	3	90.729	ND	24.6312	0	2	N/A	Detected in Treated Only	B6H953	Pc16g04770 protein		formin binding protein
B6HAE6	5.16E-45	2	16.8	31.569	ND	24.328	0	3	N/A	Detected in Treated Only	B6HAE6	Pc16g12550 protein	diphthine synthase activity; peptidyl-diphthamide biosynthetic process from peptidyl-histidine	diphthine synthase
B6HAH1	2.91E-14	6	20.9	33.538	ND	25.6918	0	2	N/A	Detected in Treated Only	B6HAH1	Pc16g12800 protein	RNA binding; methyltransferase activity; rRNA processing; tRNA processing	rrna 2 -o-methyltransferase fibrillarin
B6HDH1	8.69E-33	3	45.7	11.836	ND	27.3457	0	3	N/A	Detected in Treated Only	B6HDH1	Pc20g04220 protein		Pc20g04220, partial
B6HFU3	1.37E-07	2	23.9	9.9776	ND	25.5749	0	3	N/A	Detected in Treated Only	B6HFU3	Pc20g10480 protein		small nuclear ribonucleoprotein
B6HG91	1.02E-34	3	15.2	25.944	ND	25.6227	0	2	N/A	Detected in Treated Only	B6HG91	Pc20g11570 protein		lysine decarboxylase-like protein
B6HJN7	0.001253	2	6.2	39.757	ND	23.8565	0	2	N/A	Detected in Treated Only	B6HJN7	Pc21g02430 protein		cell wall biogenesis protein glutathione transferase
B6HKH7	1.68E-34	3	3.5	138.79	ND	25.0378	0	2	N/A	Detected in Treated Only	B6HKH7	Pc21g11590 protein		oxysterol binding protein
B6HMK8	5.90E-18	8	5.1	246.69	ND	25.4299	0	2	N/A	Detected in Treated Only	B6HMK8	Pc21g21940 protein	'de novo' pyrimidine nucleobase biosynthetic process; ATP binding; amino acid binding; aspartate carbamoyltransferase activity; carbamoyl phosphate biosynthetic process; glutamine catabolic process; metal ion binding	bifunctional pyrimidine biosynthesis protein
B6HTP7	0.000963	2	5.3	64.208	ND	25.8205	0	2	N/A	Detected in Treated Only	B6HTP7	Asparagine synthetase	ATP binding; L-asparagine biosynthetic process; asparagine synthase (glutamine-hydrolyzing) activity	asparagine synthetase
B6HVJ5	0.000948	2	5.1	64.999	ND	24.0459	0	2	N/A	Detected in Treated Only	B6HVJ5	Pc22g06070 protein	carbohydrate metabolic process; glycerol kinase activity; glycerol-3-phosphate metabolic process	glycerol kinase
B6HW49	5.10E-25	3	17.1	21.589	ND	25.2692	0	2	N/A	Detected in Treated Only	B6HW49	Pc22g23800 protein	N-acetyltransferase activity	glucosamine 6-phosphate
B6H9B6	0	17	31.5	48.832	32.8747	31.8709	3	3	0.047415	-2.005288762	B6H9B6	Adenosylhomocysteinase	adenosylhomocysteinase activity; one-carbon metabolic process	adenosylhomocysteinase
B6HSW1	2.72E-116	10	36.3	39.5	28.3115	27.2149	3	3	0.004849	-2.138634586	B6HSW1	Pc22g21480 protein	NAD binding; magnesium ion binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	tartrate
B6HAH7	9.70E-12	4	16.4	37.125	25.9143	24.8074	3	2	0.013725	-2.153868244	B6HAH7	Pc16g12860 protein	catechol 1,2-dioxygenase activity; catechol-containing compound metabolic process; ferric iron binding	catechol
B6HBF7	2.30E-29	2	25.5	10.496	27.9852	26.8381	3	3	0.01266	-2.214621271	B6HBF7	Pc18g03930 protein	enzyme inhibitor activity; mitochondrion; negative regulation of nucleotide metabolic process	mitochondrial atpase
B6HS85	1.72E-26	2	18.5	17.583	25.9843	24.8153	3	3	0.035032	-2.248620192	B6HS85	Pc22g08180 protein		arginine deiminase type-3
B6H3Q5	2.34E-05	2	10.1	32.861	23.9941	22.8154	3	2	0.000589	-2.263695645	B6H3Q5	Pc13g07470 protein		methyltransferase domain-containing protein
B6GZP0	8.15E-25	7	12.6	63.409	26.3299	25.1163	3	3	0.014481	-2.319156213	B6GZP0	Pc12g05750 protein	carbohydrate metabolic process; phosphotransferase activity, alcohol group as acceptor	d-xylulose kinase
B6HNY6	8.00E-190	13	23.8	62.713	28.133	26.795	3	3	0.007521	-2.528076289	B6HNY6	Pc22g02810 protein	methylmalonate-semialdehyde dehydrogenase (acylating) activity	methylmalonate-semialdehyde dehydrogenase

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *P. polonicum* treated with 10 µg/ml PgAFP and untreated control.
B. Quantitative and qualitative results

Majority protein IDs	PEP	Peptides	Sequence coverage [%]	Mol. weight [kDa]	*Log2 (Mean PP52 Control)	*Log2 (Mean PP52 Treated)	Valid values PP52 Control	Valid values PP52 Treated	t-test p value	Fold Change PP52 Treated v Control	Gene ID	Protein Name	Gene ontology (GO)	Sequence Description from Blast2GO analysis
B6GZ62	2.22E-07	3	7.3	42.524	25.3708	24.0189	3	3	0.027743	-2.552586764	B6GZ62	Pc12g05320 protein	oxidoreductase activity	dimeric dihydrodiol
B6HH40	1.50E-38	5	11.8	40.068	28.2027	26.8392	3	3	0.028319	-2.573033071	B6HH40	Pc20g01150 protein	damaged DNA binding; nucleotide-excision repair; nucleus; proteasome-mediated ubiquitin-dependent protein catabolic process	uv excision repair protein rad23
B6HW12	1.47E-159	8	26.4	47.768	28.5874	27.2158	3	3	0.011116	-2.587573782	B6HW12	Pc22g19440 protein	biosynthetic process; cellular amino acid metabolic process; pyridoxal phosphate binding; transaminase activity	aspartate aminotransferase
B6GWS6	2.78E-25	5	46.2	17.636	27.0597	25.6593	3	3	0.031413	-2.639601239	B6GWS6	Pc12g07330 protein	hydrolase activity	nudix family protein
B6HKR7	5.31E-79	6	35.5	36.086	27.1322	25.7191	3	3	0.020853	-2.662958601	B6HKR7	Pc21g03190 protein	NAD binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	glycerate dehydrogenase
B6HC90	4.94E-09	3	28.3	17.316	26.5598	25.0365	3	2	0.009928	-2.874458098	B6HC90	Pc18g01180 protein	acid-amino acid ligase activity	ubiquitin conjugating enzyme
B6HMQ2	1.26E-199	12	42.9	39.983	30.1086	28.4987	3	3	0.01213	-3.052264527	B6HMQ2	Phospho-2-dehydro-3-deoxyheptonate aldolase	3-deoxy-7-phosphoheptulonate synthase activity; aromatic amino acid family biosynthetic process; chorismate biosynthetic process	phospho-2-dehydro-3-deoxyheptonate aldolase
B6HD76	1.91E-199	19	33.7	81.356	29.355	27.6904	3	3	0.042724	-3.170213494	B6HD76	Pc20g01390 protein	metal ion binding; metalloendopeptidase activity; proteolysis	metallopeptidase
B6HAB8	3.46E-19	3	16.9	15.333	28.5976	26.8879	3	2	0.023759	-3.270769291	B6HAB8	Histone H3	DNA binding; nucleosome; nucleosome assembly; nucleus	histone h3
B6GXR4	2.16E-44	5	35.8	15.5	28.1608	26.3742	3	3	0.01502	-3.4500087	B6GXR4	Pc12g15350 protein	hemolysis by symbiont of host erythrocytes	terl_asptn ame: full=terrelysin ame:
B6HQ15	0	20	47.9	61.293	31.8969	30.0928	3	3	0.02264	-3.492281853	B6HQ15	Glucose-6-phosphate isomerase	gluconeogenesis; glucose-6-phosphate isomerase activity; glycolysis	glucose-6-phosphate isomerase
B6HPL2	1.25E-08	3	25.9	14.925	26.8486	24.8836	3	3	0.006321	-3.904154105	B6HPL2	Pc22g01600 protein	catalytic activity	hit domain protein
B6H823	3.18E-08	3	9.4	41.668	24.8361	22.6955	3	3	0.002985	-4.409515051	B6H823	Pc16g08230 protein	oxidoreductase activity	myo-inositol 2-dehydrogenase
B6H9R2	1.14E-29	4	26.5	27.334	26.571	24.3364	3	3	0.012132	-4.706387142	B6H9R2	Pc16g11920 protein	oxidoreductase activity	short-chain dehydrogenase
B6H6C5	1.86E-110	11	23.1	87.152	28.3333	25.5457	3	3	0.000279	-6.904466771	B6H6C5	Pc15g01900 protein	Mo-molybdopterin cofactor biosynthetic process; carbohydrate metabolic process; cation binding; cytosol; molybdopterin synthase activity; molybdopterin synthase complex	oligo- -glucosidase
B6HDB9	1.25E-128	10	29.1	52.789	29.184	25.8759	3	3	0.042942	-9.905158081	B6HDB9	Pc20g06940 protein	aminopeptidase activity; metallopeptidase activity; proteolysis; zinc ion binding	aspartyl aminopeptidase
B6H6C3	1.72E-42	6	12.6	50.552	30.2304	20.9236	3	2	0.000145	-633.3284155	B6H6C3	Pc15g01880 protein	hydrolase activity, acting on ester bonds	phosphatidylglycerol specific phospholipase
B6GXQ9	2.95E-05	2	3.2	94.834	27.1304	ND	2	0	N/A	Detected in Control Only	B6GXQ9	Pc12g11800 protein		Pc12g11800
B6H1X4	8.74E-06	3	7.9	53.985	23.3828	ND	3	0	N/A	Detected in Control Only	B6H1X4	Pc13g03600 protein	hydroxyethylthiazole kinase activity; thiamine biosynthetic process; thiamine-phosphate diphosphorylase activity	thiamine biosynthetic bifunctional
B6H5I7	1.55E-13	5	12.9	46.869	25.8838	ND	3	0	N/A	Detected in Control Only	B6H5I7	Pc14g00170 protein	hydrolase activity, acting on ester bonds	phosphatidylglycerol specific
B6H7B1	2.62E-05	2	15	16.687	24.3641	ND	2	0	N/A	Detected in Control Only	B6H7B1	Pc16g02280 protein		Pc16g02280
B6H8F4	5.47E-22	2	7.9	39.494	24.6663	ND	3	0	N/A	Detected in Control Only	B6H8F4	Pc16g04220 protein		gpi anchored
B6HDJ9	9.25E-26	3	28.9	17.111	25.8328	ND	3	0	N/A	Detected in Control Only	B6HDJ9	Pc20g07290 protein		Pc20g07290
B6HKJ8	0.001074	2	4.1	51.385	23.5264	ND	2	0	N/A	Detected in Control Only	B6HKJ8	Pc21g15970 protein	cytoplasm; pyrophosphatase activity	exopolyphosphatase
B6HP26	1.41E-06	2	15.2	15.429	25.6193	ND	3	0	N/A	Detected in Control Only	B6HP26	Pc22g01300 protein	sterol binding	lipid transfer
B6HRA1	0.000113	2	4	52.756	27.3045	ND	2	0	N/A	Detected in Control Only	B6HRA1	Pc22g24860 protein	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	aldehyde dehydrogenase
B6HU84	0.000196	2	5.4	50.931	23.8742	ND	3	0	N/A	Detected in Control Only	B6HU84	Pc22g22470 protein	carbohydrate catabolic process; mannan endo-1,6-alpha-mannosidase activity	glycosyl
B6HUJ8	3.49E-12	2	14.7	23.846	25.8727	ND	3	0	N/A	Detected in Control Only	B6HUJ8	Pc22g14330 protein		ankyrin repeat protein

*ND: Not detected in sample by LC-MS/MS

IV.5. Efecto del calcio sobre la actividad de PgAFP y el metabolismo en mohos sensibles en medio de cultivo y queso

Proteome changes explain calcium-mediated ineffectiveness of the antifungal protein PgAFP against* Aspergillus flavus *in cheese

Proteome changes explain calcium-mediated ineffectiveness of the antifungal protein PgAFP against *Aspergillus flavus* in cheese

Josué Delgado[a], Rebecca A. Owens[b], Sean Doyle[b], Félix Núñez[a], Miguel A. Asensio[a*]

[a] Food Hygiene and Safety, Institute of Meat Products, University of Extremadura, Cáceres, Spain

[b] Department of Biology, Maynooth University, Maynooth, Co. Kildare, Ireland

*Corresponding author

Miguel A. Asensio

Phone: 34-927-257124, Fax: 34-927-257110

E-mail address: masensio@unex.es

Abstract

Aspergillus flavus ability to produce aflatoxins in dairy products possesses a hazard potential. The antifungal protein PgAFP from *Penicillium chrysogenum* inhibits various foodborne toxigenic fungi, including *Aspergillus flavus*. However, PgAFP was not capable of inhibiting *A. flavus* growth in cheese, which was related to cations content. $CaCl_2$prevented *A. flavus* inhibition in potato dextrose broth (PDB), increasing *A. flavus* permeability, but no further increase was obtained with PgAFP addition. PgAFP did not alter metabolic capability, chitin deposition, intracellular ROS levels, and hyphae viability of *A. flavus* grown with $CaCl_2$. Comparative proteomic analysis revealed changes in protein abundance after PgAFP treatment of *A. flavus* in a calcium-enriched PDB leading to higher amounts of 125 proteins, related to numerous metabolic pathways, including oxidative stress. Additionally, 70 proteins were found in lower abundance, most of them involved in metabolic pathways and biosynthesis of secondary metabolites. These changes would rule out the blockage of potential PgAFP receptors in *A. flavus* by calcium. *A. flavus* resistance to PgAFP in 0.1 M $CaCl_2$ seems to be mediated by calcineurin, G-protein, and γ-glutamyltranspeptidase that combat oxidative stress and impede apoptosis. These findings could serve to design new strategies to improve PgAFP activity against aflatoxigenic molds in dairy products.

Keywords: antifungal protein; cheese; proteomics; calcium; calcineurin

1. Introduction

Some moulds are able to produce mycotoxins in foods, which causes serious problems throughout the world. *A. flavus* is one of the most concerning moulds, due essentially to aflatoxin production in cereals and nuts. Additionally, *A. flavus* is able to grow and produce aflatoxins and cyclopiazonic acid on intermediate moisture foods, including ripened cheese (Kokkonen et al., 2005; Lie and Marth, 1967; López-Díaz et al., 1996). The strategies to prevent mycotoxin accumulation on ripened foods include taking advantage of antifungal proteins produced by moulds that prevent growth of mycotoxigenic fungi.

The antifungal protein PgAFP is produced by *Penicillium chrysogenum* CECT 20922 (formerly RP42C), that was isolated from dry-cured ham (Rodríguez-Martín et al.,

2010). PgAFP belongs to a group of small, basic and cysteine-rich proteins, which also includes PAF and Pc-Arctin from *P. chrysogenum* (Chen et al., 2013; Marx et al., 1995), AFP and its variant AFP_{NN5353} from *Aspergillus giganteus* (Binder et al., 2011; Nakaya et al., 1990), AcAFP and AcAMP from *Aspergillus clavatus* (Hajji et al., 2010; Skouri-Gargouri and Gargouri, 2008), NFAP from *Neosartorya fischeri* (Kovács et al., 2011), and FPAP from *Fusarium polyphialidicum* (Galgóczy et al., 2013b). PgAFP can efficiently inhibit various toxigenic moulds in culture medium, even *A. flavus* on a ripened meat product, but not *Penicillium polonicum* (Delgado et al., 2015a). *A. flavus* inhibition coincides with increased permeability to SYTOX Green, depressed metabolic capability, compromised cell membrane, apoptosis, and necrosis. The proposed mechanism of action for PgAFP is based on the lower relative abundance of Rho GTPase Rho1 and G protein subunit β CpcB leading to alteration of both cell wall integrity and response to oxidative stress (Delgado et al., 2015b). Conversely, higher levels of Rho GTPase Rho1 are involved in the resistance of *P. polonicum* leading to increased chitin biosynthesis (Delgado et al., 2015c).

The presence of cations in the media has been shown to decrease the antifungal capability of these proteins (Galgóczy et al., 2013a; Kaiserer et al., 2003; Theis et al., 2003; Thevissen et al., 1999, 1996). High levels of extracellular divalent or monovalent cations seem to reduce the antifungal protein's capability of provoking permeabilization or altered calcium influx, as has been described for PAF (Binder et al., 2010), AFP (Theis et al., 2003), and NFAP (Galgóczy et al., 2013a). However, the ultimate mechanism responsible for this effect has not been elucidated. High external calcium levels transiently increase cytosolic calcium levels in *A. nidulans* (Nelson et al., 2004). Intracellular Ca^{2+} is a secondary messenger regulating various responses to stress signals in fungi, including antifungal proteins (Binder et al., 2011, 2010). Given that divalent cations are present in several foods, particularly calcium in cheeses, the effect of high levels of this cation on PgAFP antifungal activity against sensitive moulds should be studied.

Comparative proteomic analysis has been described as a powerful tool to study the unknown effect of substances on moulds and yeasts. It has been used to study the effect of H_2O_2 on moulds (Lessing et al., 2007) and to identify the mechanism of action of antifungal compounds (Cagas et al., 2011; Delgado et al., 2015b; Gautam et al., 2008). Comparative 2D-PAGE is able to notice changes in protein expression level, isoforms

or post-translational modifications (Görg et al., 2004). However, this technique does not reveal the whole proteome, as it depends on the range of pH chosen (Görg et al., 2009), and it is not able to effectively analyse membrane and hydrophobic proteins (Rabilloud et al., 2009; Zhu et al., 2010). Label-free mass spectrometry-based proteomic analysis is able to identify proteins typically underrepresented in 2D-PAGE studies (Owens et al., 2014), providing deeper proteome coverage. Thus, these two techniques seem to provide complementary information to study the PgAFP mechanism of action in moulds.

Results obtained from proteomic analysis guides the use of specific assays to elucidate the mechanisms of action. The relative abundance of *A. flavus* proteins can also give information about the differential response of this mould against PgAFP when grown in a calcium-enriched medium.

The objective of the present work was to test the inhibitory activity of PgAFP against *A. flavus* growth in cheese, and to study the effect of cations, mainly calcium, on PgAFP antifungal potential. The changes induced by high calcium levels, in the proteome profile and in selected metabolic and structural characteristics of *A. flavus* with and without PgAFP were studied.

2. Materials and methods

2.1 Strains

The PgAFP producer *Penicillium chrysogenum* RP42C (Spanish Type Culture Collection, CECT 20922) and *Aspergillus flavus* CECT 2687 were used to carry out the tests. The latter produced aflatoxin in an intermediate moisture food (Bernáldez et al., 2014)

2.2 PgAFP Purification

P. chrysogenum CECT 20922 was grown in potato dextrose broth (PDB, Scharlab, Barcelona, Spain) pH 4.5, at 25 °C for 21 days without shaking. Mycelium was removed, the culture medium was filtered to get cell-free medium and PgAFP was obtained by fast protein liquid chromatography as previously described (Acosta et al., 2009; Rodríguez-Martín et al. 2010). Briefly, the cell-free medium was chromatographed on cationic and gel filtration columns, and the extracts containing purified PgAFP were pooled from several batches. The protein concentration was quantified by the Lowry method (Lowry et al., 1951) and the stock solution was diluted

in the elution buffer to the desired active concentration range (1.17-75 µg/mL) for the various assays.

2.3 Proteomics

2.3.1 Protein extraction.

A. flavus CECT 2687 was cultured in triplicates in 50 mL PDB supplemented with 0.1 M of $CaCl_2$, at 25 °C for 24 h with shaking at 200 rpm in either presence (10 µg/mL) or absence of PgAFP, similarly as previously described to compare the effect of the same PgAFP concentration in *A. flavus* with no calcium added (Delgado et al., 2015b). Mycelium was harvested, filtered, washed, and lysed as described by Carberry et al. (2006). The lysed mycelia were centrifuged (10,000g; 30 min), the supernatant was precipitated with trichloroacetic acid/acetone (Carpentier et al., 2005), and analysed by the two following methods as previously described by (Delgado et al., 2015b).

2.3.2 Two-dimensional PAGE.

Resuspended extracts containing 250 µg of protein were loaded onto Immobiline Dry strips (IPG strip; Amersham Biosciences, Uppsala, Sweden) in the pH range 4–7, followed by electrofocusing, and electrophoresis using the ProteanXi-II Cell (Bio-Rad Laboratories) as described by Carberry et al. (2006). Resulting gels (n=5) were stained with colloidal Coomassie Blue (Sigma-Aldrich, St. Louis, MO, USA), scanned, normalized and analysed using Progenesis^{TM} SameSpot software (TotalLab, Newcastle, UK).

Protein spots showing differences ($p \leq 0.05$, fold change ≥ 1.5) were excised, distained, sonicated, dehydrated, and trypsin in-gel digested according to Shevchenko et al. (2006). Then, the digested supernatant was dried using a DNA Speed Vac Concentrator (Thermo Fischer Scientific, Austin, TX, USA), resuspended in 0.1% formic acid (20 µL), and filtered through 0.22 µm cellulose spin-filters (Agilent Technologies, Ireland). The samples were analysed by a 6340 Model Ion Trap LC-Mass Spectrometer (Agilent Technologies, Ireland) using electrospray ionisation on a Zorbax 300 SB C-18 Nano-HPLC Chip (150 mm x 75 µm). The eluted peptides were ionized and analysed by mass spectrometry. MS^n analysis was carried out on the three most abundant peptide precursor ions at each time point, as selected automatically by the mass spectrometer. MASCOT MS/MS Ion search, NCBI (National Centre for Biotechnology Information) database, FungiFun (Priebe et al., 2011) and KEGG (Kyoto Encyclopedia of Genes and Genome, *www.genome.jp/**kegg**/*) were used for protein identification and functional characterisation.

2.3.3 Label-free comparative quantitative proteomic analysis.

The protein precipitated lysates were resuspended in 8 M urea, reduced with dithiothreitol and alkylated with iodoacetic acid (Owens et al., 2014). Samples digested with trypsin combined with ProteaseMax surfactant were desalted prior to analysis using C18 ZipTips® (Millipore, Darmstadt, Germany). One μg of every peptide mixture was analysed via a Thermo Scientific Q-Exactive mass spectrometer coupled to a Dionex RSLCnano. LC gradients ran from 4-35% B (A: 0.1% formic acid, B: 80% acetonitrile, 0.1% formic acid) over 2 h, and data was collected using a Top15 method for MS/MS scans (Dolan et al., 2014; O'Keeffe et al., 2014; Owens et al., 2015). Comparative proteome abundance and data analysis was performed using MaxQuant software (Version 1.3.0.5) (Cox and Mann, 2008), with Andromeda used for database searching and Perseus (Version 1.4.1.3) used to organise the data. Carbamidomethylation of cysteines was set as a fixed modification, while oxidation of methionines and acetylation of N-terminals were set as variable modifications. The maximum peptide/protein false discovery rates were set to 1%. The LFQ algorithm was used to generate normalised spectral intensities and infer relative protein abundance (Luber et al., 2010). Proteins that matched to a contaminants database or the reverse database were removed and proteins were only retained in final analysis if detected in at least two replicates from at least one treatment group. Quantitative analysis was performed using a *t*-test to compare pairs of samples, and proteins with significant change in abundance (p value ≤ 0.05; fold change ≥ 2) were included in the quantitative results. Qualitative analysis was also performed, to detect proteins that were found in at least 2 replicates of a particular treatment, but undetectable in the comparison sample group.

2.4 Effect of cations on PgAFP activity

The growth of PgAFP-treated *A. flavus* was evaluated on microtiter plates (DeltaLab, Rubí, Spain), containing 200 μL of PDB supplemented with 0.1M and 0.01M $CaCl_2$ and 10^5 conidia per well incubated at 25 °C without shaking. An additional plate containing only PDB was set as a control. Seven different two-fold dilutions of PgAFP, from 75 to 1.17 μg/mL, and a non-treated control were assayed. Optical density was measured at 550 nm every 24 h during 96 h in a microplate reader (TECAN Infinite M2000, Männendorf, Switzerland). Additionally, to test the effect of the monovalent KCl and the divalent $MgCl_2$, two different plates were evaluated following the same procedure

described in this paragraph, and containing 0.01 and 0.1 M of KCl or $MgCl_2$. These cation concentrations were chosen as those present in cheeses (Chekri et al., 2012).

Given that 0.1 M $CaCl_2$ was the concentration that abolished PgAFP antifungal ability and this concentration is well within in the cheese composition, the following assays were carried out using this concentration. Additionally, all the following tests were also carried out with *A. flavus* grown in PDB with no calcium added as controls. All the micrographs from the same assay were taken with the same exposure.

2.5 Metabolic tests

To study the effect of $CaCl_2$ on the metabolism of PgAFP-treated *A. flavus*, the following tests were carried out according to Delgado et al. (2015b). *A. flavus* was cultured in PDB supplemented with 0.1 M $CaCl_2$ in either presence (75 µg/mL, to maximise the potential effect of this antifungal protein) or absence of PgAFP at 25 ºC for 24 h without shaking. Additionally, to test the effect on membrane permeability on a whole range of PgAFP and calcium concentrations, the seven PgAFP two-fold dilutions from 75 to 1.17 µg/mL as well as 0.1 M and 0.01 M $CaCl_2$ were assayed.

To assess membrane permeability, *A. flavus* grown in microtiter plates with different $CaCl_2$ and PgAFP concentrations were supplemented with 0.2 µM SYTOX Green (Molecular Probes, Eugene, OR, USA). The emitted fluorescence was measured at 10, 30, and 210 min.

To study the metabolic capability through viability staining, mycelia were washed with 10 mM HEPES (pH 7.5) before staining with 100 µL FUN-1 (Molecular Probes) for 30 min at 25 ºC according to Kaiserer et al. (2003). Stained hyphae were examined and photographed by fluorescence microscopy.

Induction of ROS production was evaluated by incubating the grown hyphae with 20 µM 2', 7' dichlorofluorescein diacetate (Molecular Probes) for 2 h at 25 ºC, and observed by fluorescence microscopy.

Membrane integrity was assessed with acridine orange/ethidium bromide (AO/EB) double staining (Sigma-Aldrich). *A. flavus* cultures were stained with 4 µg/mL of AO/EB, incubated 30 min and washed twice with PBS to be observed by fluorescence microscopy.

To detect apoptotic events, grown mycelia were stained with Apoptosis Detection Kit (Sigma-Aladrich) composed by Annexin V-fluorescein isothiocyanate/propidium iodide (AnV-FITC/PI), according to manufacturer´s instructions.

2.6 Chitin staining

Conidia of *A. flavus* were inoculated in 10 mL PDB in a Petri dish containing a coverglass (Harris et al., 1994) and incubated at 25 °C for 24 h in the presence (75 µg/mL) and absence of PgAFP. Mycelia were washed, fixed and stained with fluorescent brightener 28 (Sigma-Aldrich) to visualize chitin in a fluorescence microscopy as previously described (Delgado et al., 2015b). Additional batches with no $CaCl_2$ added were also run as controls.

2.7 Localization of FITC-labelled PgAFP

PgAFP was labelled by DareBio S.L. (Elche, Spain), as previously described (Delgado et al., 2015b). *A. flavus* was grown in PDB in presence of 20 µg/mL PgAFP-FITC for 24 h at 25 °C. Hyphae were washed twice with PBS and visualized by fluorescence microscopy.

2.8 Effect of PgAFP on *A. flavus* in cheese

One cm thick wedges of commercial Gouda type cheese of 10 cm^2 were dipped in ethanol and dried in a laminar flow cabinet (Bio Flow II, Telstar, Tarrasa, Spain). The wedges were separately placed in pre-sterilized containers after vapour-liquid equilibrium with a saturated KCl solution, to reach a_w values of 0.84 similar to those at the final stage of cheese ripening. Next, PgAFP was added in 200 µL PBS to treated samples at two concentrations (18 and 35 µg/cm^2) and left to dry in a flow cabinet. The non-treated batch received the same volume of PBS but with no PgAFP. Then, a volume of 100 µL of a suspension of *A. flavus* spores was spread onto the upper surface of cheese wedges to reach *c.a.* 10^5 conidia/cm^2. The containers were incubated for 96 h and growth of the resulting mycelia was assessed.

2.9 Statistical analysis.

Statistical analyses were performed with IBM SPSS v.22 (www-03.ibm.com/software/products/es/spss-stats-standard). Growth inhibition and membrane permeability data were tested for normality (Kolmogorov–Smirnov with Lilliefors correction) and homoscedasticity (Levene's test). These data were non-normally distributed, then mean values were compared using non-parametric Kruskal–Wallis test. To compare treatments in pairs, Mann–Whitney U test was applied ($p \leq 0.05$).

3. Results

3.1 Antifungal activity of PgAFP on cheese

To study the potential application of PgAFP against *A. flavus* in the dairy industry, the antifungal activity of 18 and 35 μg/cm^2 PgAFP was tested on cheese wedges incubated simulating common ripening conditions. Growth of *A. flavus* on cheese treated with any of the two PgAFP concentrations was exuberant (Fig. 1). Then, PgAFP did not affect *A. flavus* growth in cheese.

3.2 Effect of cations on PgAFP antifungal activity

The effect of calcium, magnesium, and potassium on PgAFP antifungal ability against *A. flavus* was studied in PDB cultures (Fig. 2). The maximum O.D. reached at 96 h in cultures without PgAFP was affected by KCl and $CaCl_2$, being lower with KCl ($p \leq 0.05$) but higher with $CaCl_2$ ($p \leq 0.05$). Control cultures, with no cations added, confirmed that 18.75 μg/mL PgAFP reduced *A. flavus* growth over 50% at 96 h. With either 0.01M (data not shown) or 0.1 M KCl, PgAFP antifungal activity was essentially unaffected. Similarly, 0.01 M $MgCl_2$ did not have a deep impact on PgAFP antifungal activity, whereas 0.1 M $MgCl_2$ lowered PgAFP effect, so that 50% growth inhibition was not reached at 96 h incubation even at the highest PgAFP concentration tested ($p > 0.05$). The strongest effect was obtained with $CaCl_2$; with 0.01 M $CaCl_2$, 37.5 μg/mL PgAFP was required to reach 50% *A. flavus* growth inhibition at 96 h, but with 0.1 M $CaCl_2$ no growth inhibition was obtained even with 75 μg/mL PgAFP ($p > 0.05$).

3.3 PgAFP localization and membrane permeability

Given that 0.1 M $CaCl_2$ abolished PgAFP antifungal activity, and this concentration is well within the range of calcium levels in ripened cheese (Chekri et al., 2012), only $CaCl_2$ was tested for the remaining assays. To know whether calcium influences PgAFP localization, *A. flavus* grown in PDB supplemented with 0.1 M $CaCl_2$ was treated with FITC-labelled PgAFP. The FITC-labelled PgAFP was visualized bound to the outer layer of *A. flavus* hyphae, but it was not able to penetrate into the cytoplasm (Fig. 3). The antifungal activity of FITC-labelled PgAFP was checked against *A. flavus* in $CaCl_2$-free PDB, showing similar levels to those of non FITC-labelled PgAFP (data not shown).

To assess the influence of $CaCl_2$ on *A. flavus* permeabilization by PgAFP, the SYTOX Green uptake test was used. With no calcium added, fluorescence values increased as PgAFP concentration increased from 0 to 4.69 μg/mL ($p \leq 0.05$) and then progressively decreased from 9.38 to 75 μg/mL (Fig. 4), similarly to previous results (Delgado et al.,

294 2015b). With 0.01 M $CaCl_2$, a slightly higher PgAFP concentration (18.75 µg/mL) was
295 required to reach the highest fluorescence values reached at 4.69-9.38 µg/mL PgAFP in
296 the control batch without $CaCl_2$. In addition, the decrease of fluorescence obtained at
297 the highest PgAFP concentrations (37.5-75 µg/mL) with 0.01 M $CaCl_2$ was even more
298 pronounced than that obtained with 0 or 0.1 M $CaCl_2$. Therefore, *A. flavus* permeability
299 was strongly increased by either PgAFP or 0.1 M $CaCl_2$. However, PgAFP at any
300 concentration barely increased *A. flavus* permeability in 0.1 M $CaCl_2$ PDB (Fig. 4).

301 **3.4 Effect of PgAFP in presence of calcium on protein profile**

302 No differences ($p > 0.05$) in *A. flavus* mycelia weigh were noticed between PgAFP-
303 treated and untreated samples grown in PDB supplemented with 0.1 M $CaCl_2$. , 2D-
304 PAGE comparative proteomic analysis revealed 19 unique proteins from 24 spots,
305 whose relative abundance was altered in treated samples (Supplementary material Table
306 S1). In the PgAFP-treated batch, the relative abundance was from 1.5 to 1.6 fold higher
307 for 7 proteins including G-protein complex β subunit CpcB, whilst 12 proteins,
308 identified from 17 spots were found between 1.6 and 2.5 fold lower. Among proteins
309 found in reduced quantities, three isoforms of elongation factor 3, and two isoforms
310 each of aminopeptidase putative, glycogen branching enzyme GbeA putative, and
311 aldehyde dehydrogenase AldA putative were identified. The two spots found from the
312 last protein have different molecular masses and charges, possibly due to breakdown
313 and side-chain deamination.

314 The label-free quantitative analysis in PDB supplemented with 0.1 M $CaCl_2$ revealed a
315 total of 1651 proteins, 195 of them showed altered relative abundance due to PgAFP-
316 treatment (Supplementary material Table S2). A total of 125 proteins were detected in
317 higher amount in PgAFP-treated *A. flavus*. Among them, 90 proteins were found in a
318 higher concentration, from 2 to 53 fold, and 35 proteins were exclusively detected in the
319 treated batch. In addition, 70 proteins were detected in lower amount in PgAFP-treated
320 samples, 32 of them were found in lower abundance, from 2.1 to 703 fold, and the 38
321 remaining were not detected in the treated batch.

322 According to KEGG, 13 out of the 70 proteins found in lower amount following PgAFP
323 treatment were involved in metabolic pathways and biosynthesis of secondary
324 metabolites. In contrast, among the proteins whose abundance was higher in PgAFP-
325 treated *A. flavus*, 23 of them were related with ribosome and 11 with spliceosome. From
326 the proteins of the oxidative stress-related glutathione metabolism, glutathione S
327 transferase GliG-like and γ-glutamyltranspeptidase (γGT) showed higher relative

abundance in PgAFP-treated samples (Supplementary material Table S2). In addition, G-protein complex β subunit CpcB recently described as related to the mechanism of action of antifungal proteins (Delgado et al., 2015b), was also increased in PgAFP treated samples (Supplementary material Table S1).

All 19 proteins showing relative abundance altered in 2D-PAGE were found in the label-free proteomic assay, but showing different fold change in both methods.

3.5 Effect on metabolic capability and chitin deposition

The metabolic capability of *A. flavus* grown with 0.1 M of $CaCl_2$ was not influenced by PgAFP, as shown by FUN-1 staining. Intravacuolar red spots were present in both PgAFP-treated and non-treated batches, revealing a normal metabolic capability (Fig. 5).

Chitin deposition has been described as a successful response against PgAFP in resistant *P. polonicum* (Delgado et al., 2015c). Staining with fluorescent brightener 28 showed that 0.1 M $CaCl_2$ made no difference to chitin deposition in non PgAFP-treated *A. flavus* (Fig. 6). However, 0.1 M $CaCl_2$ prevented the decreased chitin deposition provoked by PgAFP, keeping a similar level to that observed in the non PgAFP-treated control. As expected, PgAFP-treated controls with no calcium added displayed alterations (Fig. 5 and 6), but non-treated *A. flavus* remaining unaltered.

3.6 Effect on oxidative status and viability

Given that oxidative stress is commonly induced by antifungal proteins in sensitive species, the influence of calcium on ROS generation in *A. flavus* by PgAFP was explored by 2', 7' dichlorofluorescein diacetate staining. Both PgAFP-treated and non-treated hyphae showed a very weak green halo, indicating a low level of intracellular ROS (data not shown).

Hyphae viability and apoptotic or necrotic processes of *A. flavus* grown in 0.1 M $CaCl_2$ PDB were studied with AO/EB double staining and AnV-FITC/PI staining, respectively. The AO/EB double staining showed a predominant green colour both in PgAFP-treated and untreated samples due to AO but not EB staining (Fig. 7). This implies that 0.1 M $CaCl_2$ made it possible that PgAFP-treated *A. flavus* remained viable. Moreover, both treated and non-treated batches were not stained by AnV-FITC/PI (Fig. 8), implying that PgAFP did not induce apoptosis or necrosis in cultures containing 0.1 M $CaCl_2$. As expected, PgAFP-treated controls with no calcium added displayed alterations (Fig. 7 and 8), whilst non-treated *A. flavus* remained unaltered.

4. Discussion

The efficacy of just 5 µg/cm^2 PgAFP to reduce *A. flavus* counts was demonstrated on dry-fermented sausage (Delgado et al., 2015a). Such effect would also be useful in ripened cheese, but the high calcium levels might interfere with PgAFP activity. The treatment with PgAFP was not effective in reducing *A. flavus* growth on cheese (Fig. 1). Both dry-fermented sausage and cheese assays were run under identical environmental conditions of 25 °C and keeping constant relative humidity by means of a saturated KCl solution (Delgado et al., 2015a). Environmental factors such as pH or NaCl concentration may affect PgAFP antifungal activity. However this activity appears not to be affected by monovalent cations, and withstands a broad range of pH values (Delgado et al., 2015a). Given that the PgAFP concentrations tested on cheese were up to 7-fold higher than that effective on the sausage, the lack of PgAFP activity has to be related to cheese composition. Other researchers have proved that over 20-100 mM mono- and divalent cations suppress the inhibitory activity of other antifungal proteins in culture media (Galgóczy et al., 2013a; Kaiserer et al., 2003; Theis et al., 2003; Thevissen et al., 1999, 1996). Average calcium, magnesium, and potassium concentrations in cheese are *c.a.* 0.14, 0.013, and 0.03 M, respectively (Chekri et al., 2012). Given that these concentrations are higher than those suppressing the activity of other antifungal proteins, the effect of each of these minerals on PgAFP activity against *A. flavus* was investigated.

The antifungal capability of all concentrations of PgAFP tested against *A. flavus* in PDB was strongly reduced with 0.1 M $CaCl_2$ or $MgCl_2$ (Fig. 2), whereas only the effect of low PgAFP concentrations was prevented with 0.01 M concentrations of these divalent cations. For the monovalent potassium salt, 0.01 and 0.1 M only slightly reduced PgAFP antifungal activity. These results support that the lack of activity of PgAFP on *A. flavus* observed in cheese could be explained solely by the calcium content.

Similar results have been reported for AFP, PAF, NFAP, and plant defensins, where the antifungal activity was significantly counteracted in presence of high concentrations of monovalent cations or $MgCl_2$ (Galgóczy et al., 2013a; Kaiserer et al., 2003; Theis et al., 2003; Thevissen et al., 1999). This loss of antifungal activity has been explained by a saturation of the cellular target of antifungal proteins with cations, making the target site no longer accessible for the antifungal protein (Theis et al., 2003). Small, basic, and cysteine-rich antifungal proteins from moulds have positive net charge, and cations

could interfere by competing for putative binding sites at the fungal cell surface (Martín-Urdiroz et al., 2009; Marx, 2004).

FITC-labelled PgAFP was located both bound to outer layer and intracellularly in *A. flavus* grown in PDB with no $CaCl_2$ added (Delgado et al., 2015b). However, when *A. flavus* was grown in 0.1 M $CaCl_2$ PDB, FITC-labelled PgAFP was only found at the outer layer but not internalized (Fig. 3), implying that membrane permeability was not compromised. When grown in 0.1 M $CaCl_2$ PDB, *A. flavus* permeability to SYTOX Green increased to the maximum level provoked by PgAFP with no calcium added (Fig. 4), similarly to the pattern obtained in *A. niger* with 1 M $CaCl_2$ (Gomaa et al., 2013). When *A. flavus* was grown with both PgAFP and 0.1 M $CaCl_2$, no further increase in permeability was observed. Thus, all the above results support that calcium ions did not prevent PgAFP from binding the outer layer. Moreover, no other detrimental effect was observed in *A. flavus* at any PgAFP concentration through ROS levels and metabolic capability or viability, as evaluated by FUN-1, AO/EB, and AnV-FITC/PI staining. Therefore, calcium might have rendered the putative membrane targets non-accessible to PgAFP. Nonetheless, comparative proteomics disclosed remarkable changes in fungal metabolism triggered by PgAFP when grown in 0.1 M $CaCl_2$ PDB.

A total of 19 and 195 proteins showed altered relative abundances by $CaCl_2$ according to 2D-PAGE and label-free proteomics, respectively. The discrepancies between the number of proteins obtained by these two methods have been explained as a consequence of 2D-PAGE being able to separate isoforms and post translational modifications but only within a limited pH range, whereby the whole proteome is not represented (Görg et al., 2009, 2004). In contrast, label-free proteomics is not able to separate isoforms and compares the total quantity of the protein, but has a higher coverage with regard to pH and molecular mass range. Hence, the discrepancies observed in relation to the fold change for any given protein seem to be related to the involvement of isoforms or post-translational modifications, as well as the different threshold used by both methods (Delgado et al., 2015b, 2015c).

The comparative proteomic assays for *A. flavus* in presence of $CaCl_2$ revealed a large number of proteins affected by PgAFP exposure. According to KEGG, proteins related with ribosome and spliceosome accounted for the 27% of the proteins with altered relative amount. The relative quantities for most proteins of these two groups were higher in PgAFP-treated samples. Similar results were obtained for ribosomal and spliceosomal proteins when PgAFP was applied to cultures grown in absence of $CaCl_2$

of both *A. flavus* (Delgado et al., 2015b) and the PgAFP-resistant *P. polonicum* (Delgado et al., 2015c). Given that the increase of these two groups of proteins is a common response to PgAFP in both sensitive and resistant moulds, it does not seem to be crucial to discriminate when inhibition is overcome.

The mechanism of action of antifungal proteins has been described through different interrelated metabolic pathways, including oxidative stress, cell wall integrity (CWI) pathway, and chitin synthesis (Delgado et al., 2015b; Hagen et al., 2007; Marx et al., 2008). Some proteins involved in these pathways showed higher relative abundance in response to PgAFP in *A. flavus* grown in 0.1 M $CaCl_2$ PDB, including G-protein complex β subunit CpcB, and proteins of the oxidative stress-related glutathione pathway, namely glutathione S-transferase GliG-like and γ-glutamyltranspeptidase (γGT). These proteome changes would rule out the blockage of PgAFP receptors in *A. flavus* when grown in presence of $CaCl_2$, suggesting a survival reaction of *A. flavus* to the antifungal protein as discussed below.

No significant differences were found in the protein Rho GTPase Rho1 between PgAFP-treated and untreated *A. flavus* grown with 0.1M $CaCl_2$ (Supplementary material Table S2). Lower Rho1 levels have been identified among the main factors involved in the inhibition of *A. flavus* by PgAFP in PDB with no $CaCl_2$ added (Delgado et al., 2015b), whereas higher levels of Rho1 play a key role increasing chitin deposition in PgAFP-treated *P. polonicum*, likely activating Pkc/Mpk pathway (Delgado et al., 2015c). The unaltered chitin deposition in PgAFP-treated *A. flavus* grown with $CaCl_2$ (Fig. 6) can be related by the substantially unaffected quantity of Rho1 and any other protein related to the CWI pathway. This relationship has been demonstrated for PgAFP-treated moulds, with a decreased chitin deposition attributed to the lower relative amount of Rho1 in *A. flavus* (Delgado et al., 2015b), and an increased chitin deposition related to a higher relative amount of Rho1 in *P. polonicum* (Delgado et al., 2015c). High calcium levels *per se* did not increase chitin deposition in cultures without PgAFP (Fig. 6) Extracellular calcium can act as a stress signal in moulds that increases the intracellular Ca^{2+} concentration and leads to the activation of calmodulin, which in turn can activate calcineurin (Thewes, 2014). Calcineurin is a heterodimer comprised of subunits A and B. Calcineurin Ca^{2+}-binding regulatory subunit CnaB is essential for activation of the calcineurin A (calmodulin-binding catalytic subunit CnaA) that is important in stress adaptation (Juvvadi et al., 2003). Calcineurin regulates the transcription factor CRZ1A, that induces transcription of chitin synthases chsA and

463 chsC in filamentous fungi, but can also control chitin synthases themselves (Fortwendel
464 et al., 2010) or interact genetically with the endogenous calcineurin regulators,
465 calcipressins (Soriani et al., 2008) Activation of calmodulin-calcineurin signalling by
466 high cytosolic Ca^{2+} concentration leads to *A. fumigatus* growth in presence of antifungal
467 drugs (Juvvadi et al., 2015) The 0.1 M $CaCl_2$ level led to the higher relative abundance
468 of CnaB in both PgAFP-treated and untreated *A. flavus* (Supplementary material Table
469 S1) than with no calcium added (Delgado et al., 2015b). Thus, the protective effect of
470 high calcium levels in *A. flavus* can be mediated by increased CnaB.
471 G protein CpcB may also play a central role in vegetative growth and development, as
472 its deficiency severely impaired cellular growth in aspergilli (Kong et al., 2013). The
473 lower quantity of CpcB has been related to apoptosis signalling in PgAFP-treated *A.*
474 *flavus* (Delgado et al., 2015b). In the present work, the higher relative abundance of
475 CpcB subunit was accompanied by neither apoptotic nor necrotic signals in PgAFP-
476 treated *A. flavus* grown in 0.1 M $CaCl_2$. Therefore, CpcB can be considered a key factor
477 in promoting or arresting apoptotic events by PgAFP, leading to sensitivity or
478 resistance, respectively. The protective mechanism mediated by CpcB in *A. flavus*
479 grown with calcium seems to be based on the modulation of glutathione and ROS
480 levels.
481 From the proteins related with the oxidative stress, the most outstanding change derived
482 from PgAFP treatment in the present study was a higher relative abundance of GST
483 GliG-like and γGT. The former does not seem to be involved in the resistance of *A.*
484 *flavus* to PgAFP in presence of high calcium levels, since GST GliG-like also increased
485 when the treatment was applied with no calcium added (Delgado et al., 2015b).
486 However, a lower relative amount of γGT was observed in non-enriched calcium
487 medium, parallel to high ROS levels in *A. flavus* treated with PgAFP. γGT has been
488 shown to be important in the maintenance of the redox status upon oxidative stress in
489 fungi (Kang et al., 2005; Park et al., 2005, 2004; Springael and Penninckx, 2003)Thus,
490 the higher γGT relative abundance could be related to the successful response of *A.*
491 *flavus* to PgAFP in the calcium-enriched culture medium. No direct link between
492 increased calcium levels and γGT induction can be stablished at present. However, it is
493 plausible that a primary adaptive response mediated by CnaB or CpcB allow the time
494 for *A. flavus* to develop an effective response to oxidative stress, leading to increased
495 γGT levels.To overcome the protective role of divalent cations against antifungal

proteins, PgAFP treatment could be combined with other preservatives showing complementary mechanisms of action. New studies with extended incubation time would also help to assess the effect of PgAFP on mould growth and mycotoxin production in ripened cheese.

5. Conclusion

This work gives the basis to rule out the hypothesis that divalent cations block specific receptors for PgAFP. The obtained results demonstrate that *A. flavus* resistance to PgAFP in 0.1 M $CaCl_2$ is mainly mediated by an increased CnaB, CpcB and γGT, enhancing the response to oxidative stress and impeding apoptosis. Understanding the mechanism of resistance against PgAFP can be useful to design strategies aiming to prevent growth of mycotoxigenic moulds in foods with high levels of divalent cations.

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Figure captions

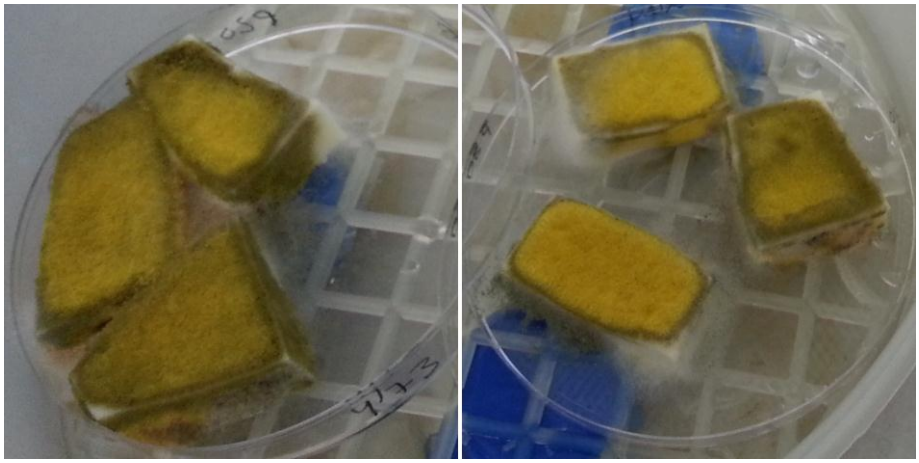

Figure 1. Exuberant growth of *A. flavus* in cheese wedges treated with 18 µg/cm^2 (left) and 35 µg/cm^2 PgAFP (right).

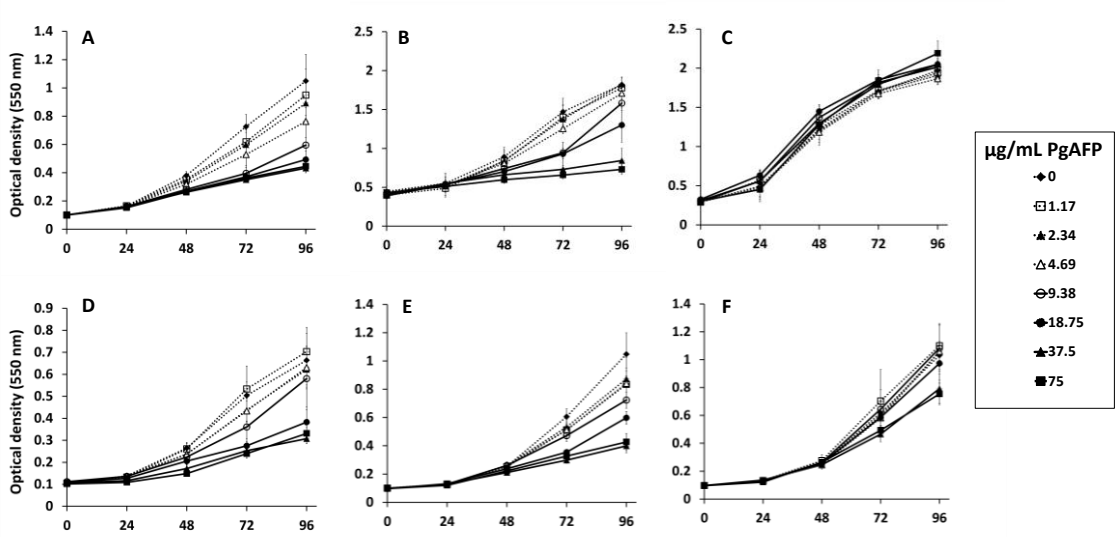

Figure 2. Effect of selected cations on the antifungal activity of different PgAFP concentrations against *A. flavus*. Growth development in potato dextrose broth for 96 h supplemented with (A) no cations, (B) 0.01 M $CaCl_2$, (C) 0.1 M $CaCl_2$, (D) 0.1 M KCl, (E) 0.01M $MgCl_2$ and (F) 0.1 M $MgCl_2$. Vertical represent standard deviation of the mean.

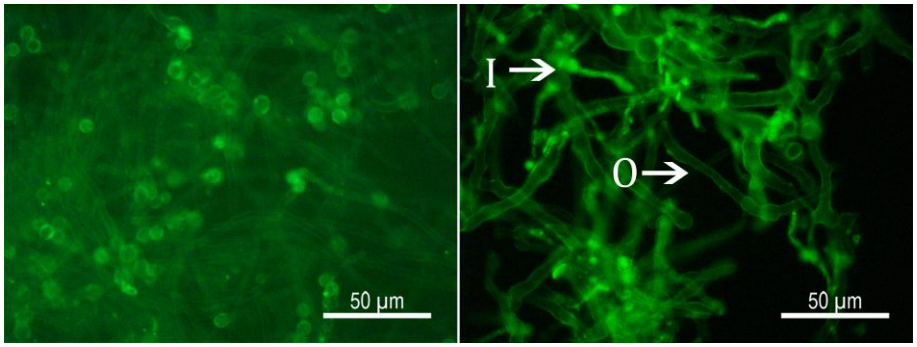

Figure 3. FITC-labelled PgAFP localization in *A. flavus* grown in presence of 0.1 M $CaCl_2$ (left). PgAFP was only visualized bound to the outer layer of *A. flavus* hyphae, but not in the cytoplasm. FITC-labelled PgAFP localization in *A. flavus* without $CaCl_2$ (right). PgAFP was visualized both in the cytoplasm (I) and bound to the outer layer (O) of *A. flavus* hyphae.

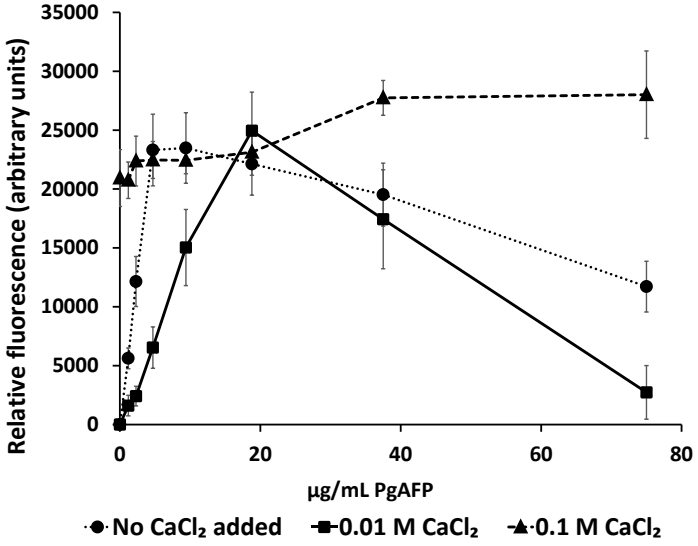

Figure 4. Effect of two different concentrations of $CaCl_2$ on membrane permeability of *A. flavus* treated with PgAFP (0-75 µg/mL) at 210 min after SYTOX Green addition. Vertical represent standard deviation of the mean.

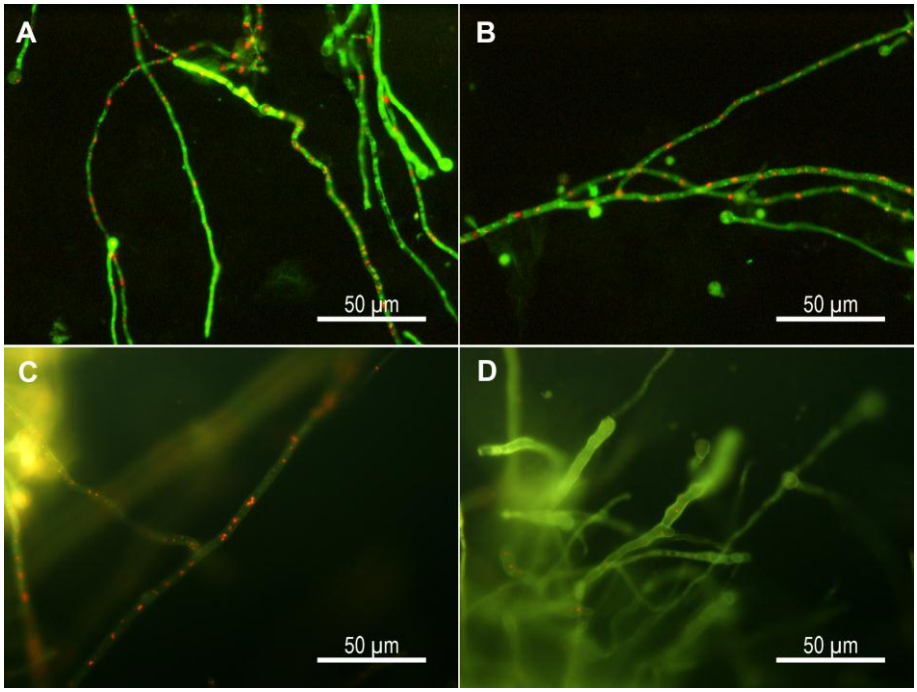

Figure 5. Metabolic capability of *A. flavus* grown with 0.1 M $CaCl_2$ (A and B) or without calcium (C and D) revealed by FUN-1 staining. Non-treated control (A) and hyphae treated with 75 µg/mL PgAFP (B) showed intravacuolar red spots, indicating unaltered metabolic capability with $CaCl_2$. Vertical represent standard deviation of the mean). With no calcium added, non-treated control also displayed intravacuolar red spots (C), whereas *A. flavus* grown with 75 µg/mL PgAFP scarcely showed red spots (D).

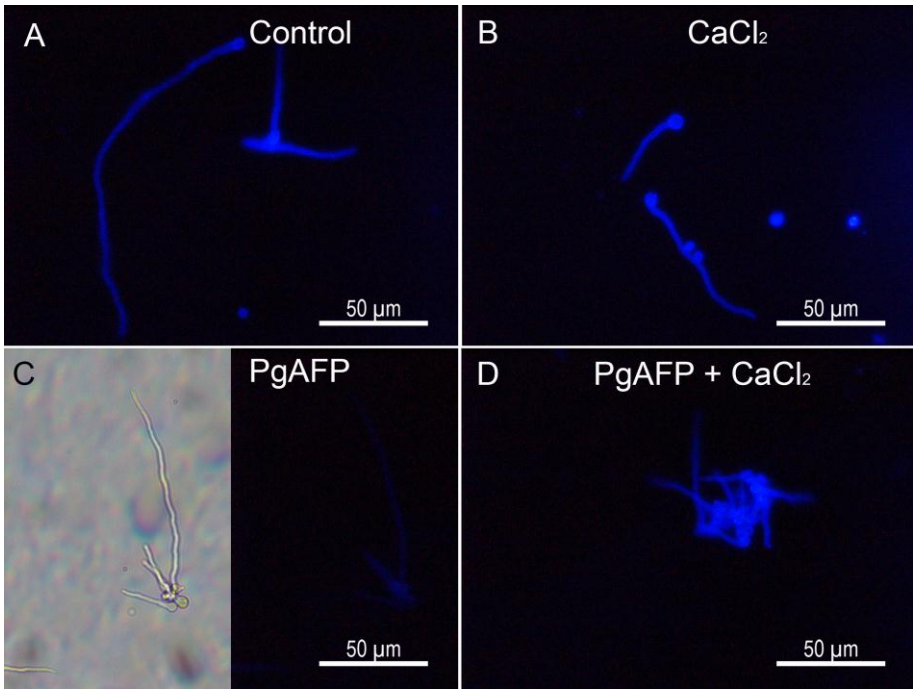

Figure 6. Effect of calcium on chitin deposition PgAFP-treated *A. flavus* grown in potato dextrose broth and stained with fluorescent brightener 28. A: non-PgAFP treated

with no $CaCl_2$ added; B: non-PgAFP treated supplemented with 0.1M $CaCl_2$; C: PgAFP treated (75 µg/mL) with no $CaCl_2$ added, bright field (left) and fluorescence observation (right); D: PgAFP treated (75 µg/mL) supplemented with 0.1M $CaCl_2$. $CaCl_2$ did not increase chitin deposition *per se* in non-PgAFP treated samples (panels A-B) but prevented lower chitin content in PgAFP-treated samples (panels C-D).

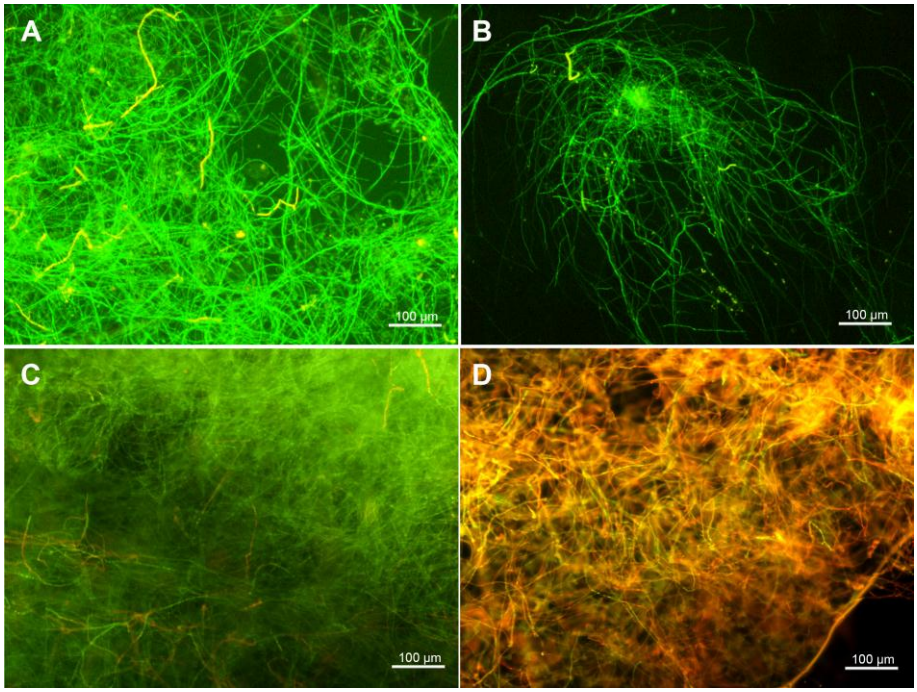

Figure 7. Effect of PgAFP on hyphae viability revealed by acridine orange/ethidium bromide (AO/EB) double staining of *A. flavus* grown in potato dextrose broth supplemented with 0.1 M $CaCl_2$ (A and B) and without added $CaCl_2$ (C and D). Merged pictures of green (AO) and red colour (EB) from samples non-treated (A and C) and treated with 75 µg/mL PgAFP (B) showing scarce orange colour due to the lack of EB penetration, meaning that remained viable. *A. flavus* treated with 75 µg/mL PgAFP grown with no added calcium (D) showed intense orange colour due to compromised membrane.

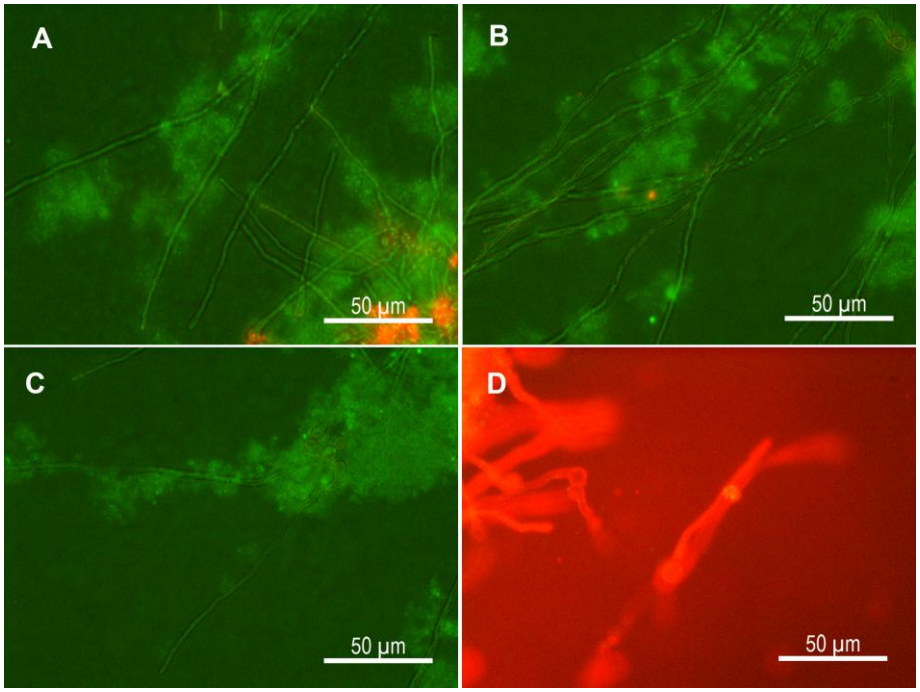

Figure 8. Induction of apoptosis or necrosis by PgAFP on *A. flavus* grown in potato dextrose broth supplemented with 0.1 M $CaCl_2$ (A and B) and with no calcium added (C and D), evaluated with Annexin V-fluorescein isothiocyanate/propidium iodide (AnV-FITC/PI). Merged pictures of green (AnV-FITC) and red colour (PI) from non-treated hyphae (A and C) or treated with 75 µg/mL PgAFP (B) showing no green or red intense fluorescence due to no apoptotic or necrotic event. *A. flavus* grown in PDB with no calcium added and treated with 75 µg/mL PgAFP (D) displayed intense red colour due to AnV-FITC and PI penetration as a consequence of necrotic events.

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Supplementary Information

Proteome changes explain calcium-mediated inefficacy of the antifungal protein PgAFP against *Aspergillus flavus* in cheese.

Josué Delgado[a], Rebecca A. Owens[b], Sean Doyle[b], Félix Núñez[a], and Miguel A. Asensio[a]

[a] Food Hygiene and Safety, Institute of Meat Products, University of Extremadura, Cáceres, Spain.

[b] Department of Biology, Maynooth University, Maynooth, Co. Kildare, Ireland.

Corresponding author:
Miguel A. Asensio
masensio@unex.es, Tel.: +34 927 257124; Fax: +34 927 257110

Supplementary Table S1. Data on proteins whose relative abundance was affected by 10 μg/mL PgAFP in *Aspergillus flavus* grown in 0.1 M $CaCl_2$ PDB, reaching over 1.5 fold change in 2D-PAGE.

Protein name	*p*- value	Fold Change	% coverage	Unique peptides	Score	tMr (Da)	Protein accesion (GI)	Gene
thiazole biosynthesis enzyme Sti35	5,65E-04	↑1.6	48	9	489	35315	238487974	AFLA_037160
metallopeptidase MepB	0,016	↑1.6	4	2	99	81812	238482735	AFLA_076890
phosphoglucomutase PgmA	0,008	↑1.6	40	14	835	60491	238486686	AFLA_030710
aspartic endopeptidase Pep2	0,002	↑1.6	34	7	448	43394	238486794	AFLA_031250
glyceraldehyde 3-phosphate dehydrogenase GpdA	0,008	↑1.5	53	9	621	36378	238485566	AFLA_025100
G-protein complex beta subunit CpcB	0,008	↑1.5	50	9	543	35395	238504184	AFLA_051980
Coatomer subunit epsilon, putative	0,001	↑1.5	41	7	515	31556	238489197	AFLA_018160
translation elongation factor EF-2 subunit, putative	0,011	↓2.5	20	11	616	94681	238496883	AFLA_136640
glycogen branching enzyme GbeA, putative	0,011	↓2.4	18	9	474	78872	238506945	AFLA_119670
glycogen branching enzyme GbeA, putative	0,002	↓2.1	14	7	326	78872	238506945	AFLA_119670
translation elongation factor eEF-3, putative	0,002	↓1.9	11	7	401	118573	238482677	AFLA_076600
aminopeptidase , putative	0,015	↓1.8	37	22	1270	99216	238503357	AFLA_007140
molecular chaperone and allergen Mod-E/Hsp90/Hsp1	0,001	↓1.8	11	5	203	79640	238503321	AFLA_006960
conserved hypothetical protein	0,002	↓1.8	14	6	315	81507	238499825	AFLA_093270
aminopeptidase, putative	0,009	↓1.7	20	10	581	99216	238503357	AFLA_007140
phosphoglucomutase, putative	0,012	↓1.7	7	3	177	64611	238493075	AFLA_043120
peptidyl-prolyl cis-trans isomerase Cpr7, putative	0,007	↓1.7	29	8	382	41268	238493059	AFLA_043040
UDP-N-acetylglucosamine pyrophosphorylase	0,008	↓1.6	50	17	919	56416	238498918	AFLA_071350
ATP citrate lyase subunit (Acl), putatibe	0,037	↓1.6	44	12	663	52846	238490538	AFLA_106350
pyruvate dehydrogenase E1 component alpha subunit, putat	0,016	↓1.6	36	11	550	45578	238489957	AFLA_021960
aldehyde dehydrogenase AldA, putative	0,013	↓1.6	11	4	242	54290	238491024	AFLA_108790
aldehyde dehydrogenase AldA, putative	0,008	↓1.6	17	6	335	54290	238491024	AFLA_071350
translation elongation factor eEF-3, putative	0,004	↓1.6	5	3	152	118573	238482677	AFLA_076600
translation elongation factor eEF-3, putative	0,013	↓1.6	15	8	466	118573	238482677	AFLA_076600

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
32,0735	31,5171	31,1105	30,71	30,6453	30,9018	+	0	2,64E+10	18	18	18	48,3	63,572	31,1597	31,567	30,7524	6	3	3	0,048136	0,814662	B8NPM2	B8NPM2	1	AFLA_000860	Tripeptidyl peptidase A
24,0678	24,6431	NaN	NaN	24,6052	NaN		2,51E-28	3,35E+08	5	5	5	14,5	45,487	24,4387	24,3554	24,6052	3	2	1	-0,249826	B8NPN7	B8NPN7	1	AFLA_001010	Benzoate 4-monooxygenase cytochrome P450, putative
24,3051	24,3078	24,8275	24,0966	24,1309	23,5585		4,99E-13	2,26E+08	4	4	4	9,4	60,765	24,2044	24,4801	23,9287	6	3	3	0,095693	0,551464	B8NPT7	B8NPT7	1	AFLA_001510	Glutamyl-tRNA(Gln) amidotransferase subunit A, putative
27,4449	27,0871	25,5714	25,9636	25,6272	25,8664		4,26E-66	5,93E+08	7	7	7	36,6	38,004	26,2601	26,7011	25,8191	6	3	3	0,204758	0,88206	B8NQM7	B8NQM7	1	AFLA_001710	Aldo-keto reductase, putative
25,8516	24,5015	NaN	NaN	24,1264	24,229		9,02E-17	1,18E+08	2	2	2	28,7	17,86	24,6771	25,1766	24,1777	4	2	2	0,278051	0,998899	B8NQP1	B8NQP1	1	AFLA_001850	Uncharacterized protein
28,0329	28,0245	28,0251	27,8729	27,4412	27,3416	+	3,69E-42	2,16E+09	7	7	7	24,1	35,104	27,7897	28,0275	27,5519	6	3	3	0,043409	0,475606	B8NQQ2	B8NQQ2	1	AFLA_001960	Aldehyde dehydrogenase, putative
29,305	28,6706	28,4263	28,1419	28,4807	28,6314		4,41E-154	4,35E+09	10	10	10	23,2	63,769	28,6093	28,8006	28,418	6	3	3	0,270098	0,382648	B8NQR5	B8NQR5	1	AFLA_002090	Extracellular serine carboxypeptidase, putative
31,213	31,3179	31,6476	31,7722	31,9076	31,5883		0	2,79E+10	44	44	44	65,2	90,553	31,5744	31,3928	31,756	6	3	3	0,086156	-0,36322	B8NQU3	B8NQU3	1	AFLA_002370	Cell division control protein Cdc48
27,631	27,3376	26,8503	27,1315	27,2838	27,3358		9,82E-96	1,73E+09	10	10	10	44,4	30,601	27,2617	27,273	27,2504	6	3	3	0,928191	0,0226186	B8NQU8	B8NQU8	1	AFLA_002420	Defective in cullin neddylation protein
26,1612	25,7272	25,5607	25,6725	25,9203	26,0531		1,33E-43	6,18E+08	3	3	3	45,2	14,756	25,8492	25,8164	25,882	6	3	3	0,771195	-0,065635	B8NQV0	B8NQV0	1	AFLA_002440	Uncharacterized protein
29,4073	28,44	28,9205	29,3134	28,8754	29,0824		0	4,68E+09	10	10	10	47,4	37,661	29,0065	28,9226	29,0904	6	3	3	0,613254	-0,167785	B8NQV7	B8NQV7	1	AFLA_002510	Actin monomer binding protein, putative
NaN	24,4392	27,154	25,9214	24,7349	NaN		1,88E-28	6,22E+08	3	3	3	29,3	10,128	25,5624	25,7966	25,3282	4	2	2	0,781772	0,468475	B8NPV3	B8NPV3	1	AFLA_002560	60S ribosomal protein L37a
28,054	29,263	30,6036	30,0802	29,0931	28,5092		3,47E-296	1,1E+10	20	20	20	56,5	43,9	29,2672	29,3069	29,2275	6	3	3	0,931457	0,0794106	B8NPW4	B8NPW4	1	AFLA_002670	Curved DNA-binding protein (42 kDa protein)
24,2456	23,9461	23,9251	23,929	24,1668	24,4084		6,42E-14	1,76E+08	4	4	4	5,8	78,653	24,1035	24,0389	24,1681	6	3	3	0,496435	-0,129142	B8NPX8	B8NPX8	1	AFLA_002810	tRNA nucleotidyltransferase
25,45	26,1788	25,3217	25,9767	25,2487	25,0795		1,44E-34	5,42E+08	3	3	3	33,8	18,242	25,5426	25,6502	25,435	6	3	3	0,604601	0,215167	B8NPY8	B8NPY8	1	AFLA_002910	Uncharacterized protein
28,8895	28,8123	28,8528	29,0467	28,6346	28,5603		9,32E-245	5,37E+09	12	12	12	51	43,132	28,7994	28,8515	28,7472	6	3	3	0,532517	0,104325	B8NPZ5	B8NPZ5	1	AFLA_002980	N,N-dimethylglycine oxidase
27,876	27,1573	27,4468	27,5028	27,7038	27,9661		3,17E-103	1,91E+09	6	6	6	48,1	17,749	27,6088	27,4934	27,7242	6	3	3	0,404827	-0,230869	B8NQ08	B8NQ08	1	AFLA_003110	Cyanate hydratase (Cyanase) (EC 4.2.1.104) (Cyanate hydrolase) (Cyanate lyase)
27,7894	26,9469	25,5887	25,3851	27,0086	27,3322		1,53E-197	2,95E+09	20	20	20	23,9	145,25	26,6751	26,775	26,5753	6	3	3	0,831532	0,199713	B8NQ19	B8NQ19	1	AFLA_003220	Phospholipase D (PLD), putative
NaN	NaN	24,9342	25,3021	25,257	24,8017		1,46E-11	3,08E+08	6	6	6	11	76,159	25,0737	24,9342	25,1203	4	1	3	1	-0,186026	B8NQ20	B8NQ20	1	AFLA_003230	Uncharacterized protein
28,8303	28,7327	28,7107	29,069	28,8037	28,7582		1,54E-160	4,59E+09	10	10	10	30,4	53,426	28,8174	28,7579	28,877	6	3	3	0,31478	-0,119049	B8NQW0	B8NQW0	1	AFLA_003440	Translation initiation factor 4B
24,7784	24,6044	24,628	25,0364	24,7852	NaN		4,07E-14	2,54E+08	6	6	6	29,6	36,932	24,7665	24,6703	24,9108	5	3	2	0,132256	-0,240543	B8NQW3	B8NQW3	1	AFLA_003470	Oxidoreductase family, NAD-binding Rossmann fold protein
NaN	25,1891	29,344	27,5469	24,4478	NaN		1,47E-72	1E+09	5	5	5	34,4	14,925	26,632	27,2666	25,9974	4	2	2	0,672783	1,26918	B8NQW4	B8NQW4	1	AFLA_003480	60S ribosomal protein L32
30,1166	30,0054	29,7777	28,9446	29,5757	29,5781		0	7,45E+09	13	13	13	71,9	24,841	29,6664	29,9666	29,3661	6	3	3	0,061632	0,600444	B8NQY1	B8NQY1	1	AFLA_003650	Uracil phosphoribosyltransferase
28,0155	27,6032	26,8272	27,2719	27,5284	27,6195		1,24E-60	1,85E+09	16	16	16	48,6	55,467	27,4776	27,482	27,4733	6	3	3	0,982061	0,0086969	B8NQY6	B8NQY6	1	AFLA_003700	Mitochondrial cytochrome b2, putative
NaN	NaN	NaN	NaN	23,5699	23,5492		3,31E-26	2,66E+08	4	4	4	17,4	47,811	23,5595	NaN	23,5595	2	0	2	1	NaN	B8NQZ7	B8NQZ7	1	AFLA_003810	Endonuclease/exonuclease/phosphatase family protein
29,8539	29,4853	29,2128	29,546	29,7026	29,7115		6,76E-242	8,19E+09	13	13	13	68,2	29,218	29,5853	29,5173	29,6533	6	3	3	0,520597	-0,136023	B8NR05	B8NR05	1	AFLA_003890	Proteasome subunit alpha type (EC 3.4.25.1)
27,9617	28,117	27,8017	28,1147	28,1472	28,0886		4,30E-194	2,94E+09	11	11	11	48,2	39,926	28,0385	27,9602	28,1168	6	3	3	0,165863	-0,156666	B8NR08	B8NR08	1	AFLA_003920	Cysteine synthase (O-acetylserine (Thiol)-lyase) (Csase)
27,224	27,2806	26,9439	27,0498	26,8968	26,9679		2,71E-26	1,4E+09	3	3	3	5,3	74,929	27,0605	27,1495	26,9715	6	3	3	0,19053	0,178015	B8NR18	B8NR18	1	AFLA_004020	Uncharacterized protein
26,5554	26,4674	26,5632	26,9564	26,2414	26,3765		4,03E-24	1,09E+09	4	4	4	66,2	7,7117	26,5267	26,5287	26,5248	6	3	3	0,986797	0,0038986	B8NR19	B8NR19	1	AFLA_004030	Uncharacterized protein
24,9215	25,5144	25,8126	26,0771	25,9349	25,2404		1,73E-86	9,91E+08	15	15	15	46	59,97	25,5835	25,4162	25,7508	6	3	3	0,414561	-0,334623	B8NR20	B8NR20	1	AFLA_004040	Actin interacting protein 2
27,8377	27,2837	28,0752	28,2784	27,7665	28,0988		1,37E-101	2,07E+09	4	4	4	48,6	11,543	27,8901	27,7322	28,0479	6	3	3	0,320069	-0,315692	B8NR25	B8NR25	1	AFLA_004090	Uncharacterized protein
24,7894	23,8782	23,1912	NaN	NaN	NaN		3,65E-09	1,16E+08	3	3	3	9,7	45,489	23,9529	23,9529	NaN	3	3	0	1	NaN	B8NR26	B8NR26	1	AFLA_004100	Transesterase (LovD), putative
27,7087	28,066	28,3664	28,0188	28,2336	28,4512		7,66E-183	2,3E+09	17	17	16	34,3	77,514	28,1408	28,047	28,2345	6	3	3	0,455919	-0,187527	B8NQ64	B8NQ64	1	AFLA_004550	Vacuolar dynamin-like GTPase VpsA, putative
28,3535	27,6579	27,85	27,2048	28,0342	27,7643		5,18E-236	3,45E+09	23	23	23	43,6	76,132	27,8108	27,9538	27,6678	6	3	3	0,422537	0,286002	B8NQ65	B8NQ65	1	AFLA_004560	Vacuolar ATP synthase catalytic subunit A, putative
25,397	25,1721	25,7024	25,3183	25,3457	24,6603		2,32E-32	1,03E+09	11	10	10	32,8	45,502	25,266	25,4238	25,1081	6	3	3	0,309782	0,315729	B8NQ69	B8NQ69	1	AFLA_004600	Eukaryotic translation initiation factor eIF-4A subunit, putative
30,4934	30,1925	29,8827	29,9779	30,053	30,213		5,21E-274	1,18E+10	14	14	14	46,8	39,497	30,1354	30,1895	30,0813	6	3	3	0,598349	0,108242	B8NQ72	B8NQ72	1	AFLA_004630	Farnesyl-pyrophosphate synthetase
31,7492	32,1488	31,8322	32,0902	31,6559	31,3933		0	2,23E+10	20	20	20	69,9	38,243	31,8116	31,9101	31,7131	6	3	3	0,452534	0,196937	B8NQ74	B8NQ74	1	AFLA_004650	Thiamine biosynthesis protein (Nmt1), putative
27,1048	27,0589	26,9552	27,2195	27,0569	26,9942		1,43E-66	1,39E+09	8	8	8	37	39,99	27,0649	27,0396	27,0902	6	3	3	0,563367	-0,0505867	B8NQ82	B8NQ82	1	AFLA_004730	Ribokinase
29,1315	29,0991	29,4057	29,4816	29,5441	29,3631		0	9E+09	36	36	36	48,7	147,49	29,3375	29,2121	29,463	6	3	3	0,086261	-0,250857	B8NQA1	B8NQA1	1	AFLA_004920	Phosphoribosylformylglycinamidine synthase
NaN	25,496	25,2161	NaN	NaN	NaN		1,19E-26	4,18E+08	4	4	4	30,4	17,901	25,3561	25,3561	NaN	2	2	0	1	NaN	B8NQA4	B8NQA4	1	AFLA_004950	Cytochrome c oxidase subunit Va, putative
30,3758	30,0181	29,5886	29,956	30,0727	30,2281		4,30E-133	8,81E+09	8	8	8	82,4	12,091	30,0399	29,9941	30,0856	6	3	3	0,723414	-0,0914567	B8NQA5	B8NQA5	1	AFLA_004960	Antibiotic biosynthesis monooxygenase family protein
23,9111	22,9263	NaN	NaN	NaN	NaN		3,40E-05	36316000	2	2	2	3,5	62,125	23,4187	23,4187	NaN	2	2	0	1	NaN	B8NR85	B8NR85	1	AFLA_005600	SNARE domain protein
28,7918	28,6723	28,3325	28,2444	28,1581	28,3564		2,43E-194	3,69E+09	12	12	12	40,2	39,9	28,4259	28,5989	28,253	6	3	3	0,081124	0,345879	B8NR86	B8NR86	1	AFLA_005610	NAP family protein
25,2682	24,0655	23,3112	NaN	NaN	NaN		1,61E-09	1,65E+09	5	5	5	13,5	65,179	24,215	24,215	NaN	3	3	0	1	NaN	B8NR95	B8NR95	1	AFLA_005700	Aromatic amino acid aminotransferase, putative
31,5775	32,1415	32,8978	29,1156	27,988	28,5129	+	0	2,31E+10	24	24	24	71	40,245	30,3722	32,2056	28,5388	6	3	3	0,001874	3,6668	B8NR98	B8NR98	1	AFLA_005730	60S ribosomal protein L4, putative
27,6931	26,1539	27,1631	25,6613	26,6022	25,0738		6,06E-213	2,25E+09	11	11	10	40,6	44,435	26,3912	27,0034	25,7791	6	3	3	0,125654	1,22428	B8NRA6	B8NRA6	1	AFLA_005810	Septin
28,8752	28,5795	28,3688	28,2924	28,5149	28,6474		5,15E-126	3,66E+09	26	26	26	24,8	158,99	28,5464	28,6078	28,4849	6	3	3	0,531638	0,122906	B8NRB0	B8NRB0	1	AFLA_005850	5'-3' exoribonuclease 1 (EC 3.1.13.-)
27,8767	27,5179	27,0562	27,2508	27,7761	27,5276		1,27E-48	2,03E+09	7	7	7	26,1	48,983	27,5009	27,4836	27,5182	6	3	3	0,908285	-0,0345669	B8NRB1	B8NRB1	1	AFLA_005860	Chromatin assembly factor 1 subunit C, putative
NaN	23,4966	23,7626	24,4281	23,4685	22,7958		3,38E-16	1,77E+08	3	3	3	7,6	36,687	23,5903	23,6296	23,5641	5	2	3	0,922509	0,0654586	B8NRB2	B8NRB2	1	AFLA_005870	GTP cyclohydrolase I, putative
28,3478	28,4498	28,0477	28,1308	28,3061	28,4848		2,69E-126	3,66E+09	30	30	30	36,6	128,71	28,2945	28,2818	28,3072	6	3	3	0,87987	-0,0254656	B8NRC2	B8NRC2	1	AFLA_005970	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)
26,664	27,8085	25,601	26,5961	26,2521	26,506		1,49E-19	1,97E+09	7	7	7	22,9	50,88	26,5713	26,6911	26,4514	6	3	3	0,729211	0,239759	B8NQD0	B8NQD0	1	AFLA_006100	HypA-like protein, putative
25,1952	25,2112	25,6478	25,3631	26,1106	26,452		6,18E-39	7,76E+08	9	9	9	18,5	74,533	25,6633	25,3514	25,9752	6	3	3	0,152911	-0,623807	B8NQD2	B8NQD2	1	AFLA_006120	Glutamine dependent NAD+ synthetase, putative
26,5767	26,0724	25,9382	26,1342	26,2874	26,4574		4,42E-39	7,78E+08	9	9	9	25,5	46,12	26,2444	26,1958	26,293	6	3	3	0,675476	-0,0972036	B8NQD3	B8NQD3	1	AFLA_006130	NADH pyrophosphatase, putative
25,9222	26,4159	25,8831	25,7749	25,7543	25,5468		2,42E-15	6,65E+08	7	7	7	16,9	51,283	25,8829	26,0737	25,692	6	3	3	0,109772	0,381734	B8NQE2	B8NQE2	1	AFLA_006220	Exopolyphosphatase, putative
26,9834	26,8338	26,4989	26,7351	26,7357	26,6664		6,34E-60	1,26E+09	13	13	13	23,8	82,675	26,7422	26,772	26,7124	6	3	3	0,702109	0,0596244	B8NQE8	B8NQE8	1	AFLA_006280	Methylenetetrahydrofolate reductase (EC 1.5.1.20)
33,6746	33,4854	33,317	32,2475	31,9621	32,1464	+	0	1,02E+11	11	11	11	73,9	17,009	32,8055	33,4924	32,1187	6	3	3	0,000493	1,37371	B8NQF0	B8NQF0	1	AFLA_006300	Nucleoside diphosphate kinase (EC 2.7.4.6)
25,5841	25,8731	24,9718	24,8682	25,3024	25,6777		3,41E-24	6,19E+08	9	9	9	12,9	110,1	25,3796	25,4764	25,2827	6	3	3	0,613483	0,193625	B8NQF1	B8NQF1	1	AFLA_006310	Alpha glucosidase II, alpha subunit, putative
28,724	28,5022	28,5165	28,9887	29,0073	28,9971	+	2,23E-145	5,2E+09	11	11	11	45,7	35,279	28,7893	28,5809	28,9977	6	3	3	0,004399	-0,416796	B8NQF3	B8NQF3	1	AFLA_006330	Uncharacterized protein
28,0818	27,4502	27,4839	27,7133	28,1716	28,2421		1,16E-174	3,74E+09	11	11	11	31,8	42,409	27,8571	27,6719	28,0424	6	3	3	0,232885	-0,370415	B8NQF5	B8NQF5	1	AFLA_006350	Thioredoxin reductase, putative
28,432	29,1136	29,5248	29,995	29,4696	29,3843		0	1,16E+10	32	32	32	55,6	83,973	29,3199	29,0235	29,6163	6	3	3	0,185756	-0,592824	B8NQF7	B8NQF7	1	AFLA_006370	Glutamyl-tRNA synthetase
27,9179	27,8581	27,7022	27,9436	28,2194	28,1745		5,66E-97	2,67E+09	8	8	8	26,9	42,264	27,9693	27,8261	28,1125	6	3	3	0,055266	-0,286449	B8NQG2	B8NQG2	1	AFLA_006420	Cdc48-dependent protein degradation adaptor protein (Shp1), putative
27,3649	27,858	27,8163	28,1491	27,8802	27,925		2,66E-142	2,3E+09	10	10	10	34,5	49,46	27,8323	27,6798	27,9848	6	3	3	0,162577	-0,305001	B8NQH0	B8NQH0	1	AFLA_006520	CRAL/TRIO domain protein
26,8012	27,5033	27,7352	28,2571	28,0365	28,529	+	2,98E-201	2,77E+09	6	6	6	43,2	28,276	27,8104	27,3466	28,2742	6	3	3	0,042131	-0,92759	B8NQH6	B8NQH6	1	AFLA_006580	WW domain protein
29,8154	29,1228	28,9246	28,5475	29,247	29,3592		9,00E-153	4,46E+09	14	14	14	69,1	37,226	29,1694	29,2876	29,0512	6	3	3	0,558353	0,236391	B8NQH9	B8NQH9	1	AFLA_006610	Lipase, putative
26,6748	26,5036	26	26,0313	26,2503	26,0674		5,48E-18	7,96E+08	6	6	6	18,9	56,385	26,2546	26,3928	26,1163	6	3	3	0,265134	0,276461	B8NQI0	B8NQI0	1	AFLA_006620	Ferrooxidoreductase Fet3, putative
30,4109	29,9117	29,4931	29,4834	29,915	29,9342		0	9,28E+09	14	14	14	39,8	55,485	29,8581	29,9386	29,7775	6	3	3	0,623686	0,161032	B8NQJ3	B8NQJ3	1	AFLA_006750	Vacuolar aspartyl aminopeptidase Lap4, putative
NaN	24,4437	NaN	25,1789	24,9359	24,6207		3,04E-10	1,72E+08	4	4	4	9,3	50,661	24,7948	24,4437	24,9118	4	1	3	1	-0,468161	B8NQK5	B8NQK5	1	AFLA_006870	SGT1 and CS domain protein
28,0847	28,1756	28,1962	27,944	28,1026	28,1299		1,03E-178	3,19E+09	11	11	11	30,2	57,131	28,1055	28,1522	28,0589	6	3	3	0,23797	0,0933094	B8NQL3	B8NQL3	1	AFLA_006950	NTF2 and RRM domain protein
32,3951	32,7439	32,8661	32,833	32,8406	32,7781		0	1,01E+11	50	50	50	62,8	79,631	32,7428	32,6684	32,8172	6	3	3	0,35505	-0,148867	B8NQL4	B8NQL4	1	AFLA_006960	Molecular chaperone and allergen Mod-E/Hsp90/Hsp1
26,3082	27,1074	27,5419	27,7844	26,9658	26,4403		2,61E-94	1,88E+09	8	8	8	45,6	32,883	27,0246	26,9858	27,0635	6	3	3	0,891126	-0,0776323	B8NQL8	B8NQL8	1	AFLA_007000	Ubiquinol-cytochrome C reductase complex core protein 2, putative
31,6213	31,4932	31,7758	31,8868	31,8092	31,7255		0	4,38E+10	20	20	20	50,6	52,027	31,7186	31,6301	31,8072	6	3	3	0,132886	-0,177029	B8NRD5	B8NRD5	1	AFLA_007020	Citrate synthase
27,3348	27,111	26,9306	26,8394	27,09	27,1103		2,95E-48	1,32E+09	8	8	8	13,8	82,063	27,0694	27,1255	27,0132	6	3	3	0,484472	0,112214	B8NRD6	B8NRD6	1	AFLA_007030	RNA binding protein Nrd1, putative
24,1887	26,4795	27,9233	28,1939	26,6803	26,6283		7,49E-147	2,5E+09	15	15	15	49,7	46,991	26,6823	26,1972	27,1675	6	3	3	0,464933	-0,970298	B8NRD7	B8NRD7	1	AFLA_007040	Homocysteine synthase CysD
NaN	NaN	26,2523	26,2586	NaN	26,7889		7,03E-06	8,06E+08	4	4	4	18,1	30,177	26,4333	26,2523	26,5238	3	1	2	1	-0,271427	B8NRE2	B8NRE2	1	AFLA_007090	WW domain protein, putative
29,3255	28,5627	28,115	27,2305	28,2861	28,5966		1,74E-85	2,95E+09	8	8	7	39,3	22,303	28,3527	28,6677	28,0377	6	3	3	0,3112	0,629966	B8NRE5;B8	B8NRE5	3	AFLA_007120	Secretion related GTPase SrgB/Ypt1
32,2428	31,8807	31,5008	31,6988	31,8304	31,9437		0	3,85E+10	41	41	41	55,5	99,049	31,8495	31,8748	31,8243	6	3	3	0,833776	0,0505219	B8NRE7	B8NRE7	1	AFLA_007140	Aminopeptidase, putative
27,3925	26,3414	25,8625	25,4508	25,8197	26,085		2,38E-24	5,37E+08	6	6	6	31,5	26,192	26,1587	26,5321	25,7852	6	3	3	0,20046	0,746976	B8NXD5	B8NXD5	1	AFLA_007540	Glutathione S-transferase, putative
30,6132	30,0639	30,291	29,24	29,5566	29,8233	+	0	5,83E+09	13	13	13	63,5	23,657	29,9313	30,3227	29,54	6	3	3	0,027938	0,782756	B8NXF1	B8NXF1	1	AFLA_007700	Uncharacterized protein
28,796	29,0945	29,6672	28,9629	28,8176	28,3886		0	7,3E+09	36	36	34	42,9	138,64	28,9545	29,1859	28,723	6	3	3	0,207697	0,462873	B8NXH1;B8	B8NXH1	2	AFLA_007900	5-oxo-L-prolinase, putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
25,1003	24,7012	24,1308	23,2829	23,5267	24,5395		2,24E-10	1,71E+08	5	5	5	5,8	102,45	24,2136	24,6441	23,7831	6	3	3	0,145135	0,861034	B8NXL0	B8NXL0	1	AFLA_008290	Kinesin-like protein
26,8243	26,7248	26,4097	26,5098	26,715	26,7176		9,88E-21	1,16E+09	3	3	3	53	17,169	26,6502	26,6529	26,6475	6	3	3	0,971383	0,0054461	B8NXL1	B8NXL1	1	AFLA_008300	Ubiquitin conjugating enzyme (UbcB), putative
26,271	28,2351	28,1239	28,9199	28,7492	28,6706		1,21E-147	3,93E+09	15	15	15	53,5	45,738	28,1616	27,5433	28,7799	6	3	3	0,12603	-1,23656	B8NXL2	B8NXL2	1	AFLA_008310	Acetyl-CoA-acetyltransferase, putative
25,8273	23,9418	24,6027	24,4603	24,9209	25,8554		6,50E-26	4,25E+08	10	8	8	19,5	77,093	24,9347	24,7906	25,0788	6	3	3	0,69683	-0,288234	B8NXN6	B8NXN6	1	AFLA_008560	Alpha-1,2-mannosidase, putative subfamily
33,1083	32,9815	30,4271	31,982	32,0373	32,267		0	5,19E+10	25	25	24	63,4	58,659	32,1339	32,1723	32,0954	6	3	3	0,934418	0,0768712	B8NXR9	B8NXR9	1	AFLA_008890	Glutamate decarboxylase (EC 4.1.1.15)
22,588	24,8237	26,2695	28,7058	24,4512	24,3072		8,81E-275	2,53E+09	17	17	17	39,6	64,187	25,1909	24,5604	25,8214	6	3	3	0,521492	-1,26099	B8NXS1	B8NXS1	1	AFLA_008910	Uncharacterized protein
NaN	NaN	NaN	26,2119	26,2701	26,5487		3,45E-43	8,27E+08	6	6	6	17,5	57,585	26,3436	NaN	26,3436	3	0	3	1	NaN	B8NXS3	B8NXS3	1	AFLA_008930	Purple acid phosphatase (EC 3.1.3.2)
31,4563	30,9611	30,3612	30,4518	30,8777	30,9745		0	1,71E+10	19	19	19	40	60,878	30,8471	30,9262	30,768	6	3	3	0,67894	0,158186	B8NXS9	B8NXS9	1	AFLA_008990	Carboxypeptidase Y homolog A (EC 3.4.16.5)
27,1562	27,7956	29,8709	28,1926	28,0242	27,8922		4,64E-103	5,75E+09	10	10	10	53,5	17,943	28,1553	28,2742	28,0363	6	3	3	0,787134	0,237904	B8NXT0	B8NXT0	1	AFLA_009000	Ribosomal protein S13p/S18e
25,0051	24,7307	24,5684	24,7559	24,4326	24,5595		2,27E-11	2,92E+08	6	6	6	14,5	47,521	24,6754	24,7681	24,5826	6	3	3	0,306694	0,185435	B8NXT5	B8NXT5	1	AFLA_009050	TPR repeat protein
25,5541	25,0788	24,7048	24,1309	24,9723	24,7866		5,62E-20	4,49E+08	7	7	7	9,3	127,59	24,8713	25,1126	24,63	6	3	3	0,244807	0,48261	B8NXT9	B8NXT9	1	AFLA_009090	Nuclear serine protease HtrA2/Nma111, putative
28,5172	28,1975	27,9259	28,2633	28,3694	28,4965		1,34E-59	3,49E+09	8	8	8	73,1	14,415	28,295	28,2135	28,3764	6	3	3	0,425405	-0,162879	B8NXX3	B8NXX3	1	AFLA_009430	Uncharacterized protein
29,8676	29,4284	29,2236	29,5874	29,8302	29,6018		4,15E-24	9,24E+09	4	4	4	34,2	8,5718	29,5898	29,5065	29,6731	6	3	3	0,463288	-0,166579	B8NY04	B8NY04	1	AFLA_009740	Uncharacterized protein
26,5066	26,6185	26,4252	26,3014	25,9352	25,9487	+	9,37E-30	8,07E+08	5	5	5	29,1	34,334	26,2893	26,5168	26,0618	6	3	3	0,026335	0,454989	B8NY47	B8NY47	1	AFLA_010170	Tropinone reductase, putative
24,1517	23,5019	26,3569	NaN	NaN	NaN		2,41E-16	1,65E+08	5	5	5	12,6	54,048	24,6702	24,6702	NaN	3	3	0	1	NaN	B8NY90	B8NY90	1	AFLA_010600	Siderophore biosynthesis acetylase AceI, putative
24,7586	23,6293	25,3136	23,7517	NaN	NaN		3,16E-29	3,29E+08	10	10	10	7,5	229,88	24,3633	24,5672	23,7517	4	3	1	1	0,81543	B8NY92	B8NY92	1	AFLA_010620	Nonribosomal siderophore peptide synthase Sid2
24,6407	25,5185	26,3033	25,827	24,9043	24,761		2,23E-20	5,14E+08	7	7	7	30,9	36,288	25,3258	25,4875	25,1641	6	3	3	0,609804	0,323385	B8NYA7;B8	B8NYA7	2	AFLA_010770	Porphobilinogen deaminase Hem3, putative
31,6175	31,218	31,0756	31,3001	31,528	31,661		3,89E-180	2,95E+10	6	6	6	48,4	13,315	31,4	31,3037	31,4964	6	3	3	0,375593	-0,192663	B8NYC1	B8NYC1	1	AFLA_010910	Peptidyl-prolyl cis-trans isomerase
28,9811	28,2903	27,8982	28,3312	28,823	29,014		5,42E-216	3,8E+09	10	10	10	57,1	28,833	28,5563	28,3898	28,7227	6	3	3	0,426283	-0,33288	B8NYC3	B8NYC3	1	AFLA_010930	Glutathione S-transferase family protein, putative
26,3758	25,5079	26,3682	25,4822	25,9293	25,759		6,27E-83	1,58E+09	8	8	8	42,8	25,3	25,9037	26,0839	25,7235	6	3	3	0,317818	0,360462	B8NYF4	B8NYF4	1	AFLA_011240	Uncharacterized protein
NaN	25,275	26,2392	25,833	25,0719	24,904		2,61E-49	7,29E+08	5	5	5	31,8	26,331	25,4646	25,7571	25,2696	5	2	3	0,413694	0,487511	B8NYG8	B8NYG8	1	AFLA_011380	Uncharacterized protein
NaN	23,1849	23,552	24,0331	24,1877	24,0115	+	2,12E-14	3,3E+08	5	5	5	13,2	64,473	23,7938	23,3685	24,0774	5	2	3	0,019422	-0,708914	B8NYH6	B8NYH6	1	AFLA_011460	GMC oxidoreductase, putative
27,2886	26,0026	24,9291	31,2714	32,0032	32,0819	+	0	1,79E+10	15	15	15	45,7	55,696	28,9295	26,0735	31,7855	6	3	3	0,001434	-5,71204	B8NYI6	B8NYI6	1	AFLA_011560	Phosphatidylglycerol specific phospholipase, putative
26,1688	25,6611	25,2701	26,1655	26,1926	26,5028		8,78E-105	1,35E+09	10	10	10	36,7	42,97	25,9935	25,7	26,2869	6	3	3	0,105646	-0,586927	B8NYJ6	B8NYJ6	1	AFLA_011660	Uncharacterized protein
25,0172	25,8206	26,7595	27,2321	26,3214	25,8265		1,02E-46	1,82E+09	8	8	8	38,9	42,898	26,1629	25,8658	26,46	6	3	3	0,412531	-0,594231	B8NYK4	B8NYK4	1	AFLA_011740	Cystathionine gamma-lyase
30,0856	29,1069	28,5223	28,583	29,4195	29,3014		8,98E-217	5,09E+09	7	7	7	16,8	60,796	29,1698	29,2383	29,1013	6	3	3	0,807286	0,136971	B8NYN2	B8NYN2	1	AFLA_012020	Carboxypeptidase S1, putative
NaN	NaN	23,5304	23,8594	23,9646	23,5291		2,31E-33	2,4E+08	4	4	4	10	60,179	23,7209	23,5304	23,7843	4	1	3	1	-0,25393	B8NYN6	B8NYN6	1	AFLA_012060	Choline oxidase (CodA), putative
25,4771	24,6085	24,3087	25,1196	25,5816	25,3347		3,90E-07	3,11E+08	4	4	4	11,9	54,189	25,0717	24,7981	25,3453	6	3	3	0,21821	-0,547191	B8NYN7	B8NYN7	1	AFLA_012070	Betaine aldehyde dehydrogenase (BadH), putative
26,0145	NaN	24,8156	24,4555	NaN	NaN		2,55E-10	2,33E+08	3	3	3	15,9	39,503	25,0952	25,4151	24,4555	3	2	1	1	0,95956	B8NYN8	B8NYN8	1	AFLA_012080	Glucosamine-6-phosphate isomerase (EC 3.5.99.6) (Glucosamine-6-phosphate deaminase)
24,8128	24,9782	24,9845	24,6694	24,966	24,7765		1,27E-14	3,25E+08	7	7	7	6,6	131,93	24,8646	24,9252	24,8039	6	3	3	0,305729	0,121253	B8NYP1	B8NYP1	1	AFLA_012110	Cleavage and polyadenylation specificity factor subunit A, putative
24,1325	26,693	29,5963	30,1347	27,4475	26,9981		0	6,03E+09	18	18	18	67,2	40,803	27,5003	26,8073	28,1934	6	3	3	0,496972	-1,38615	B8NYP6	B8NYP6	1	AFLA_012160	Acetyl-CoA acetyltransferase, putative
NaN	24,2183	24,7483	24,1631	23,5478	NaN		1,77E-23	3,68E+08	8	7	7	14,7	88,797	24,1694	24,4833	23,8554	4	2	2	0,262075	0,627869	B8NYP7	B8NYP7	1	AFLA_012170	U5 snRNP component Snu114, putative
34,0999	33,9012	33,5563	33,7397	33,7154	33,8729		0	1,5E+11	38	38	38	44,2	96,549	33,8142	33,8525	33,776	6	3	3	0,66935	0,0764669	B8NYQ1	B8NYQ1	1	AFLA_012200	Hsp70 chaperone (HscA), putative
NaN	NaN	NaN	24,2323	24,5589	24,6255		2,64E-07	1,78E+08	2	2	2	9,3	18,627	24,4722	NaN	24,4722	3	0	3	1	NaN	B8NYQ2	B8NYQ2	1	AFLA_012220	Cyclin-dependent kinases regulatory subunit, putative
26,2845	26,4895	27,3993	27,0937	27,4519	27,1412		3,32E-115	2,17E+09	7	7	7	48,6	23,448	26,9767	26,7245	27,2289	6	3	3	0,234316	-0,504465	B8NYQ3	B8NYQ3	1	AFLA_012230	Uncharacterized protein
26,3757	26,2584	25,7542	25,9147	26,2359	26,1647		4,56E-16	7,38E+08	4	4	4	28,7	20,109	26,1173	26,1294	26,1051	6	3	3	0,914985	0,0243327	B8NYQ7	B8NYQ7	1	AFLA_012270	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
NaN	NaN	NaN	23,2952	23,9189	23,3138		2,45E-29	3,74E+08	5	5	5	31	23,258	23,5093	NaN	23,5093	3	0	3	1	NaN	B8N5H5	B8N5H5	1	AFLA_013180	Williams-beuren syndrome chromosome region, putative
22,7042	21,4608	NaN	31,4209	31,5292	31,6738	+	0	3,1E+10	25	25	25	57,4	52,758	27,7578	22,0825	31,5413	5	2	3	0,000273	-9,45874	B8N5M5	B8N5M5	1	AFLA_013680	Phosphatidylglycerol specific phospholipase C, putative
NaN	NaN	NaN	22,7949	22,4155	22,3787		7,60E-94	1,73E+09	6	6	6	27,6	32,989	22,5297	NaN	22,5297	3	0	3	1	NaN	B8N5N1	B8N5N1	1	AFLA_013740	Acid phosphatase, putative
29,5225	28,9404	28,6591	28,7563	29,1136	29,1869		5,94E-173	4,74E+09	9	9	9	32	54,187	29,0298	29,0407	29,0189	6	3	3	0,943227	0,0217444	B8N5Q5	B8N5Q5	1	AFLA_013980	Peptide hydrolase (EC 3.4.-.-)
29,3128	28,9845	28,6666	28,6557	28,9564	29,2357		7,38E-180	5,73E+09	9	9	9	45,8	29,718	28,9686	28,9879	28,9493	6	3	3	0,884872	0,038674	B8N5R2	B8N5R2	1	AFLA_014050	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)
25,2099	24,9814	24,8929	25,5786	26,4061	25,6197	+	9,42E-09	3,4E+08	2	2	2	17,9	11,502	25,4481	25,0281	25,8681	6	3	3	0,042218	-0,840069	B8N5S0	B8N5S0	1	AFLA_014130	Uncharacterized protein
23,6927	24,0179	24,1676	24,4072	24,1771	24,0508		1,06E-25	3,44E+08	9	9	9	25,7	53,612	24,0856	23,9594	24,2117	6	3	3	0,222295	-0,252287	B8N5S1	B8N5S1	1	AFLA_014140	Aldehyde dehydrogenase family protein, putative
25,2329	24,8129	24,2195	26,0628	26,0458	28,0284		1,34E-43	6,93E+08	2	2	2	19,3	14,322	25,7337	24,7551	26,7123	6	3	3	0,05323	-1,95721	B8N5T3	B8N5T3	1	AFLA_014260	Conidial hydrophobin RodB/HypB
25,5418	24,9672	24,4044	NaN	25,3385	25,4482		1,21E-16	3,7E+08	3	3	3	8	57,516	25,14	24,9711	25,3934	5	3	2	0,394512	-0,422252	B8N5T8	B8N5T8	1	AFLA_014310	Acyl-CoA dehydrogenase family protein
24,7727	25,25	25,8959	25,5191	25,2845	25,445		4,24E-67	9,05E+08	9	9	9	43,5	37,713	25,3612	25,3062	25,4162	6	3	3	0,757552	-0,109989	B8N5U3	B8N5U3	1	AFLA_014360	Serine/threonine-protein phosphatase (EC 3.1.3.16)
23,2065	23,1534	22,9718	23,5933	23,6773	23,6369	+	2,38E-07	1,13E+08	2	2	2	18,4	19,631	23,3732	23,1105	23,6358	6	3	3	0,002197	-0,525311	B8N5W1	B8N5W1	1	AFLA_014540	Acetyltransferase, GNAT family, putative
NaN	24,0542	NaN	23,9774	24,7112	24,0862		9,22E-08	1,6E+08	4	4	4	6	86,491	24,2073	24,0542	24,2583	4	1	3	1	-0,204134	B8N5W5	B8N5W5	1	AFLA_014580	Chromatin remodeling complex subunit (Arp5), putative
31,6677	31,3587	31,11	31,6865	31,6096	31,7121		0	3,22E+10	6	6	6	84,1	13,728	31,5241	31,3788	31,6694	6	3	3	0,151444	-0,290632	B8N5W7	B8N5W7	1	AFLA_014600	Profilin
30,863	30,5865	30,3473	30,3375	30,5802	30,6446		0	1,44E+10	22	22	22	42,7	60,722	30,5598	30,5989	30,5208	6	3	3	0,679769	0,0781644	B8N5X8	B8N5X8	1	AFLA_014710	Importin subunit alpha
24,2671	25,3236	23,9605	23,987	23,8981	24,0046		2,51E-25	2,82E+08	6	6	6	4,8	200,15	24,2401	24,517	23,9632	6	3	3	0,252161	0,5538	B8N5Y3	B8N5Y3	1	AFLA_014760	rRNA biogenesis protein RRP5, putative
26,0769	NaN	24,1494	23,689	NaN	NaN		1,56E-14	4,62E+08	5	5	5	8,5	61,681	24,6384	25,1131	23,689	3	2	1	1	1,42412	B8N6G7	B8N6G7	1	AFLA_014800	T-complex protein 1 subunit alpha
28,4784	27,3416	27,1654	26,6839	27,3403	27,6737		2,74E-113	3,09E+09	8	8	8	20,6	66,965	27,4472	27,6618	27,2326	6	3	3	0,442334	0,42915	B8N6G8	B8N6G8	1	AFLA_014810	Prolyl-tRNA synthetase
30,7874	30,5099	30,2858	30,2583	30,4751	30,5944		0	1,63E+10	22	22	22	66,6	46,844	30,4852	30,5277	30,4426	6	3	3	0,652628	0,0851243	B8N6I0	B8N6I0	1	AFLA_014930	Cofactor for methionyl-and glutamyl-tRNA synthetase, putative
29,3662	29,1855	28,7668	29,2242	28,7718	28,9242		4,57E-188	4,72E+09	18	18	18	51,8	44,839	29,0398	29,1062	28,9734	6	3	3	0,581648	0,13276	B8N6I5	B8N6I5	1	AFLA_014980	Uncharacterized protein
27,0393	25,6499	25,4149	26,434	25,8523	25,9889		3,00E-26	8,06E+08	9	9	9	14,7	114,12	26,0632	26,0347	26,0917	6	3	3	0,920462	-0,0570189	B8N6J1	B8N6J1	1	AFLA_015040	Importin beta-5 subunit, putative
NaN	22,3397	NaN	23,0764	23,0235	23,1125		0,000223	76747000	2	2	2	7	32,54	22,888	22,3397	23,0708	4	1	3	1	-0,731127	B8N6J2	B8N6J2	1	AFLA_015050	Methyltransferase family protein
26,6925	26,442	26,3552	26,8051	26,7891	27,0146	+	1,04E-124	1,19E+09	4	4	4	22,3	34,522	26,6831	26,4965	26,8696	6	3	3	0,040088	-0,373042	B8N6J3	B8N6J3	1	AFLA_015060	Phytanoyl-CoA dioxygenase family protein
27,0614	27,2948	27,0051	24,894	25,9488	24,7398	+	4,41E-63	5,53E+08	11	11	11	14,4	115,12	26,1573	27,1204	25,1942	6	3	3	0,007832	1,92623	B8N6J8	B8N6J8	1	AFLA_015110	Uncharacterized protein
26,8818	26,5333	26,0236	25,8649	26,2369	26,545		2,09E-08	8,28E+08	3	3	3	17,1	29,458	26,3476	26,4796	26,2156	6	3	3	0,452359	0,264	B8N6K4	B8N6K4	1	AFLA_015170	SNARE complex subunit (Syn8), putative
27,8647	27,5237	27,1732	27,583	27,8029	27,9823		1,10E-58	2,51E+09	14	14	14	47,3	44,465	27,655	27,5205	27,7894	6	3	3	0,308397	-0,268883	B8N6K9	B8N6K9	1	AFLA_015220	Cell wall biogenesis protein/glutathione transferase (Gto1), putative
31,1224	31,1771	31,1191	31,3164	31,286	31,3712	+	0	2,44E+10	41	41	41	58,9	114,85	31,232	31,1395	31,3245	6	3	3	0,004071	-0,185011	B8N6L0	B8N6L0	1	AFLA_015230	Poly(A)+ RNA transport protein (UbaA), putative
28,3481	28,0737	27,8374	28,095	28,4853	28,3452		5,60E-106	3,26E+09	8	8	8	37,6	38,354	28,1974	28,0864	28,3085	6	3	3	0,299751	-0,222057	B8N6L6	B8N6L6	1	AFLA_015290	Uncharacterized protein
25,9119	25,7032	24,5326	25,1898	24,9331	25,4528		1,84E-31	4,09E+08	4	4	4	43,8	12,738	25,2872	25,3826	25,1919	6	3	3	0,696475	0,190694	B8N6L9	B8N6L9	1	AFLA_015320	Transcription initiation factor IIA subunit 2
27,545	27,3274	27,0907	27,5868	27,646	27,6879		1,84E-43	1,96E+09	11	11	11	28,2	51,849	27,4806	27,321	27,6402	6	3	3	0,076386	-0,319214	B8N6M2	B8N6M2	1	AFLA_015350	Aldehyde dehydrogenase family protein, putative
26,1216	26,0942	27,1876	27,8534	28,3388	28,1102	+	4,74E-149	2,85E+09	20	20	20	32,9	95,766	27,2843	26,4678	28,1008	6	3	3	0,013403	-1,63296	B8N6M3	B8N6M3	1	AFLA_015360	N-methyltransferase, putative
29,8911	29,8056	29,5095	29,8688	29,8014	29,8159		0	9,03E+09	53	53	53	52,4	167,27	29,782	29,7354	29,8287	6	3	3	0,471228	-0,093317	B8N6M9	B8N6M9	1	AFLA_015420	Sulfite reductase, putative
25,6731	25,2096	24,4147	NaN	NaN	24,2479		3,55E-12	2,7E+08	6	6	6	20,7	47,985	24,8863	25,0991	24,2479	4	3	1	1	0,851195	B8N6N3	B8N6N3	1	AFLA_015460	Molybdopterin biosynthesis protein, putative
26,4418	26,3115	26,1476	26,2929	26,1837	26,4549		2,99E-102	8,82E+08	6	6	6	50	18,197	26,3054	26,3003	26,3105	6	3	3	0,934197	-0,0101916	B8N6N7	B8N6N7	1	AFLA_015500	DUF866 domain protein
27,518	27,342	26,8867	25,9822	26,2654	26,0739	+	2,67E-30	1,25E+09	4	4	4	39,8	10,067	26,678	27,2489	26,1072	6	3	3	0,005161	1,1417	B8N6N8	B8N6N8	1	AFLA_015510	Small nuclear ribonucleoprotein F (snRNP-F) (Sm protein F)
31,6746	31,346	30,6111	31,5043	31,7058	31,7501		0	3,09E+10	16	16	16	72,6	28,46	31,432	31,2106	31,6534	6	3	3	0,242697	-0,442828	B8N6P5	B8N6P5	1	AFLA_015580	Sorbitol/xylulose reductase Sou1-like, putative
25,938	26,0326	25,1375	26,5685	26,1176	24,287		2,56E-31	5,14E+08	3	3	3	13,3	37,568	25,6802	25,7027	25,6577	6	3	3	0,955245	0,0449772	B8N6Q6	B8N6Q6	1	AFLA_015690	Uncharacterized protein
26,0032	25,8031	25,2907	24,5498	24,5185	24,6825	+	3,05E-10	4,05E+08	3	3	3	34,7	11,23	25,1413	25,699	24,5836	6	3	3	0,006908	1,11544	B8N5Y8	B8N5Y8	1	AFLA_015720	Small nuclear ribonucleoprotein (LSM2), putative
NaN	24,6347	24,0037	NaN	NaN	NaN		2,93E-10	1,49E+08	2	2	2	4,2	87,437	24,3192	24,3192	NaN	2	2	0	1	NaN	B8N5Z4	B8N5Z4	1	AFLA_015780	Small oligopeptide transporter, OPT family
NaN	NaN	26,6734	28,3044	25,0769	26,0781		9,15E-53	8,52E+08	7	7	7	72,6	14,609	26,5332	26,6734	26,4865	4	1	3	1	0,186949	B8N5Z6	B8N5Z6	1	AFLA_015800	DUF636 domain protein
26,0981	25,7089	25,5064	25,8107	26,3181	26,0383		1,84E-31	7,15E+08	4	4	4	23,9	31,263	25,9134	25,7711	26,0557	6	3	3	0,278765	-0,284604	B8N6N9	B8N649	1	AFLA_016330	Alpha/beta fold family hydrolase, putative
26,3495	25,4535	25,883	25,0878	25,562	25,9468		7,79E-12	4,57E+08	4	4	4	26,9	25,425	25,7138	25,8953	25,5322	6	3	3	0,368603	0,363134	B8N656	B8N656	1	AFLA_016400	Glutathione S-transferase, putative
27,6465	28,4832	28,7865	28,8607	28,8345	28,7022		2,76E-292	5,41E+09	20	20	20	42,1	71,002	28,5523	28,3054	28,7991	6	3	3	0,224999	-0,493719	B8N672	B8N672	1	AFLA_016560	Methionyl-tRNA synthetase
24,0367	24,9023	24,7011	23,7632	23,437	23,458	+	2,82E-101	1,17E+09	11	11	11	42,8	48,89	24,0497	24,5467	23,5527	6	3	3	0,024337	0,993983	B8N6Q7	B8N6Q7	1	AFLA_016600	Uncharacterized protein

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
26,5187	26,5409	26,145	25,901	26,3052	26,3691		7,03E-25	9,4E+08	8	8	8	30,1	41,009	26,2967	26,4015	26,1918	6	3	3	0,342281	0,209781	B8N6S0	B8N6S0	1	AFLA_016730	Alanine racemase
28,5979	28,24	28,0737	27,9608	27,9441	28,141		9,62E-97	2,68E+09	6	6	6	28,6	28,881	28,1596	28,3038	28,0153	6	3	3	0,159128	0,288529	B8N6S7;B8	B8N6S7	2	AFLA_016800	Thioredoxin, putative
NaN	25,8932	26,5679	25,3502	24,7942	24,4546	+	7,41E-82	7,1E+08	11	10	10	31,9	50,409	25,412	26,2305	24,8663	5	2	3	0,047686	1,36421	B8N6T0	B8N6T0	1	AFLA_016830	Tubulin subunit TubB
25,9477	25,7427	25,5789	26,0191	26,0048	25,8261		3,79E-46	5,91E+08	3	3	3	19,6	30,146	25,8532	25,7564	25,95	6	3	3	0,191872	-0,19359	B8N6T8	B8N6T8	1	AFLA_016910	26S proteasome regulatory subunit S5A
27,8999	27,6747	28,0169	28,3146	28,1943	28,1028	+	5,07E-137	3,49E+09	22	22	22	36,2	99,235	28,0339	27,8638	28,2039	6	3	3	0,044559	-0,340044	B8N6U3	B8N6U3	1	AFLA_016960	Acetylglutamate kinase, putative
NaN	24,8176	26,1021	24,1433	24,0411	NaN		3,80E-16	2,52E+08	6	6	6	32,5	33,02	24,776	25,4598	24,0922	4	2	2	0,167775	1,36763	B8N6U6	B8N6U6	1	AFLA_016990	Fibrillarin
26,1884	27,574	28,1064	27,946	27,9192	27,7018		2,18E-110	3,14E+09	16	16	16	48,2	53,17	27,5726	27,2896	27,8557	6	3	3	0,381993	-0,566082	B8N6U8	B8N6U8	1	AFLA_017010	Mitochondrial processing peptidase beta subunit, putative
29,2431	28,9763	28,8737	28,9898	28,9037	28,9493		1,16E-281	5,54E+09	36	36	36	54,7	97,885	28,9893	29,031	28,9476	6	3	3	0,50077	0,0834344	B8N6V6	B8N6V6	1	AFLA_017090	Methyltransferase (Ncl1), putative
27,9749	27,175	26,2081	27,7815	28,6094	28,7735		6,59E-122	2,76E+09	20	20	20	26,7	109,87	27,7537	27,1194	28,3881	6	3	3	0,10032	-1,26877	B8N6V7	B8N6V7	1	AFLA_017100	Probable beta-galactosidase A (EC 3.2.1.23) (Lactase A)
28,6595	28,5029	29,2167	29,6023	28,8856	28,0712		3,05E-293	4,36E+09	21	21	21	42,1	53,022	28,823	28,793	28,8531	6	3	3	0,908894	-0,0600084	B8N6W0	B8N6W0	1	AFLA_017130	Nuclear segregation protein (Bfr1), putative
26,7199	26,8347	26,9361	26,7708	27,0559	26,8561		5,67E-61	1,53E+09	9	9	9	29,5	45,829	26,8622	26,8302	26,8943	6	3	3	0,575034	-0,0640513	B8N6W4	B8N6W4	1	AFLA_017170	Histidinol-phosphate aminotransferase
NaN	NaN	NaN	26,6009	27,3877	NaN		2,72E-12	5,37E+08	3	3	3	16,9	15,333	26,9943	NaN	26,9943	2	0	2	1	NaN	B8N4Q2	B8N4Q2	1	AFLA_017610	Histone H3
25,0394	26,6436	25,6593	28,991	29,555	27,6582	+	1,11E-42	3,48E+09	6	6	1	51,5	11,356	27,2578	25,7808	28,7347	6	3	3	0,015592	-2,95395	B8N4Q3	B8N4Q3	1	AFLA_017620	Histone H4
28,0473	27,0896	26,6839	26,5259	27,5433	27,7359		4,91E-127	2,31E+09	21	21	21	18,8	171,28	27,271	27,2736	27,2684	6	3	3	0,992866	0,0052465	B8N4Q9	B8N4Q9	1	AFLA_017680	Pentafunctional AROM polypeptide [Includes: 3-dehydroquinate synthase (DHQS) (EC 4.2.3.4);3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS); Shikimate kinase (SK) (EC 2.7.1.71); 3-dehydroquinate dehydratase (3-dehydroquinase) (EC 4.2.1.10); Shikimate dehydrogenase (EC .1.1.25)]
28,5828	28,8851	29,5254	29,4019	29,4679	29,5363		0	8,52E+09	38	38	38	50	124,24	29,2332	28,9977	29,4687	6	3	3	0,168517	-0,470975	B8N4R2	B8N4R2	1	AFLA_017710	Isoleucyl-tRNA synthetase, cytoplasmic
27,2073	26,9077	26,8118	26,9257	26,7349	26,479		4,07E-65	1,11E+09	11	11	11	16,8	94,06	26,8444	26,9756	26,7132	6	3	3	0,210029	0,262383	B8N4S3	B8N4S3	1	AFLA_017820	Uncharacterized protein
NaN	25,4827	24,6894	NaN	23,4991	NaN		2,38E-19	2,75E+08	2	2	2	14,3	24,904	24,5571	25,086	23,4991	3	2	1	1	1,58693	B8N4S4	B8N4S4	1	AFLA_017830	Small nuclear ribonucleoprotein complex protein Nhp2, putative
NaN	23,1326	NaN	NaN	23,166	23,4596		7,68E-06	94934000	2	2	2	4	56,521	23,2528	23,1326	23,3128	3	1	2	1	-0,180264	B8N4T0	B8N4T0	1	AFLA_017890	SET domain protein
34,3108	33,9834	33,6926	34,0168	34,1226	34,2375		0	1,83E+11	37	37	37	64,6	74,803	34,0606	33,9956	34,1256	6	3	3	0,530474	-0,130042	B8N4T2	B8N4T2	1	AFLA_017910	Transketolase (EC 2.2.1.1)
32,3667	32,0691	31,8229	32,1084	32,1734	32,31		0	4,99E+10	17	17	17	65	38,725	32,1417	32,0862	32,1972	6	3	3	0,544932	-0,111022	B8N4T3	B8N4T3	1	AFLA_017920	Spermidine synthase
27,7108	28,2736	28,5328	28,686	28,6778	28,6451		4,00E-128	4,39E+09	13	13	13	39,7	43,63	28,421	28,1724	28,6696	6	3	3	0,110098	-0,497262	B8N4V0	B8N4V0	1	AFLA_018090	Arp2/3 complex subunit (Arp2), putative
25,8356	26,3906	26,2813	26,8856	26,4661	26,4311		3,66E-46	9,79E+08	7	7	7	23,9	50,078	26,3817	26,1692	26,5943	6	3	3	0,130441	-0,425117	B8N4V5	B8N4V5	1	AFLA_018140	Mannose-6-phosphate isomerase (EC 5.3.1.8)
28,6934	28,2386	27,7638	27,7094	28,1683	28,38		3,81E-119	2,38E+09	6	6	6	45,8	31,578	28,1589	28,2319	28,0859	6	3	3	0,684061	0,146016	B8N4V7	B8N4V7	1	AFLA_018160	Coatomer subunit epsilon, putative
26,298	26,322	26,3803	26,2277	26,8231	26,3258		1,95E-48	1,02E+09	10	10	10	14,7	113,44	26,3962	26,3334	26,4589	6	3	3	0,536829	-0,125451	B8N4X9	B8N4X9	1	AFLA_018380	Anthranilate synthase multifunctional protein TrpC, putative
26,9952	26,8237	26,2474	26,5028	26,4578	26,6241		1,08E-50	8,83E+08	7	7	7	18,6	46,394	26,6085	26,6888	26,5282	6	3	3	0,526231	0,160543	B8N684	B8N684	1	AFLA_018480	Cytoskeletal adaptor protein SagA
27,4627	27,7876	28,3852	27,7242	28,1056	27,7516		9,36E-275	3,42E+09	19	19	19	34,8	99,725	27,8695	27,8785	27,8605	6	3	3	0,954535	0,0180035	B8N691	B8N691	1	AFLA_018550	Glycogen phosphorylase GlpV/Gph1, putative
29,6119	30,4286	32,0312	29,8336	28,5817	28,9198		0	2,28E+10	16	16	16	60,7	34,613	29,9011	30,6906	29,1117	6	3	3	0,120667	1,57888	B8N6A6	B8N6A6	1	AFLA_018700	60S ribosomal protein L5, putative
22,4869	NaN	NaN	NaN	22,5744	22,3479		1,20E-06	57701000	3	3	3	5	97,516	22,4697	22,4869	22,4611	3	1	2	1	0,0257282	B8N6B7	B8N6B7	1	AFLA_018810	Nitrate reductase
29,7818	29,7448	30,3111	30,182	30,2929	30,1087		0	1,43E+10	18	18	18	57,1	41,862	30,0702	29,9459	30,1945	6	3	3	0,261987	-0,248633	B8N6C1	B8N6C1	1	AFLA_018850	Isocitrate dehydrogenase [NAD] subunit, mitochondrial (EC 1.1.1.41)
27,914	28,027	27,5854	27,7886	27,9455	28,0522		6,65E-76	2,23E+09	9	9	9	24,5	56,764	27,8855	27,8422	27,9288	6	3	3	0,601574	-0,0866089	B8N6C9	B8N6C9	1	AFLA_018930	Adenylyl cyclase-associated protein
24,2592	24,5753	24,4828	22,969	NaN	NaN		1,95E-20	1,78E+08	4	4	4	11,9	44,244	24,0715	24,4391	22,969	4	3	1	1	1,4701	B8N6D2	B8N6D2	1	AFLA_018960	60S ribosomal protein L3
25,0671	26,5717	28,3186	29,1559	26,7073	26,2454		2,96E-56	2,85E+09	4	4	4	33,7	18,052	27,011	26,6525	27,3695	6	3	3	0,61142	-0,717081	B8N6F9	B8N6F9	1	AFLA_019230	Mismatched base pair and cruciform DNA recognition protein, putative
29,0806	28,6764	28,6463	29,043	29,2854	29,1715		3,70E-70	5,13E+09	4	4	4	58,1	17,225	28,9839	28,8011	29,1666	6	3	3	0,079802	-0,365528	B8N6G4	B8N6G4	1	AFLA_019280	Peroxiredoxin, putative
25,041	25,8824	25,9375	25,9747	25,9044	25,7414		1,46E-20	5,99E+08	7	7	7	30,4	39,721	25,7469	25,6203	25,8735	6	3	3	0,443695	-0,253173	B8N6Z7	B8N6Z7	1	AFLA_019300	Uncharacterized protein
29,0522	29,0429	28,4484	29,1895	29,1388	29,289		4,18E-137	6,12E+09	7	7	7	34,9	27,151	29,0268	28,8478	29,2058	6	3	3	0,155048	-0,357937	B8N716	B8N716	1	AFLA_019490	ThiJ/Pfpl family protein
29,4381	29,1154	27,841	28,6909	28,5406	28,7462		6,16E-272	6,9E+09	6	6	6	53,5	18,549	28,7287	28,7982	28,6592	6	3	3	0,791438	0,138922	B8N728	B8N728	1	AFLA_019610	Carboxypeptidase S1, putative
24,7938	24,5706	NaN	NaN	25,3963	25,3369	+	3,40E-12	3,02E+08	4	4	4	39,6	16,977	25,0244	24,6822	25,3666	4	2	2	0,027308	-0,684418	B8N729	B8N729	1	AFLA_019620	Uncharacterized protein
25,5098	25,8787	25,9074	26,0534	26,1561	25,9015		6,72E-33	8,95E+08	15	15	15	22,7	91,568	25,9011	25,7653	26,037	6	3	3	0,140005	-0,271683	B8N732;B8	B8N732	2	AFLA_019650	Phosphoketolase, putative
25,0591	24,3703	25,0032	25,7195	25,4977	25,3908	+	1,13E-13	3,47E+08	5	5	5	17,3	44,079	25,1734	24,8108	25,536	6	3	3	0,039674	-0,725129	B8N736	B8N736	1	AFLA_019690	3-ketoacyl-CoA ketothiolase (Kat1), putative
24,191	NaN	28,4998	30,3703	30,3969	30,3527		0	1,06E+10	26	26	26	51,8	72,622	28,7621	26,3454	30,3733	5	2	3	0,087071	-4,02792	B8N747	B8N747	1	AFLA_019800	Extracellular phytase, putative
26,0664	26,1865	26,0389	26,0908	26,0496	26,1426		6,24E-31	6,93E+08	10	10	10	19,3	76,166	26,0958	26,0973	26,0943	6	3	3	0,9581	0,0029456	B8N782	B8N782	1	AFLA_020150	Glutamate-cysteine ligase Gcs1, putative
30,2015	30,2301	29,7172	30,2084	30,3729	30,4878		1,56E-243	1,19E+10	12	12	12	53,9	22,745	30,203	30,0496	30,3563	6	3	3	0,172832	-0,306737	B8N4Z0	B8N4Z0	1	AFLA_020280	Glycolipid transfer protein HET-C2, putative
28,152	28,0427	27,3684	28,087	28,2212	28,2383		9,61E-170	2,61E+09	13	13	13	59,4	34,977	28,0183	27,8544	28,1822	6	3	3	0,259451	-0,327806	B8N4Z7	B8N4Z7	1	AFLA_020350	Translation initiation factor 2 alpha subunit, putative
24,8186	NaN	NaN	NaN	25,1341	25,3097		3,71E-12	2,21E+08	4	4	4	7	73,913	25,0875	24,8186	25,2219	3	1	2	1	-0,403363	B8N511	B8N511	1	AFLA_020490	Pseudouridylate synthase 3
28,2252	29,1858	30,828	29,8921	29,2475	28,9881		0	1,39E+10	13	13	13	60,5	32,232	29,3944	29,413	29,3759	6	3	3	0,965525	0,0370668	B8N513	B8N513	1	AFLA_020510	40S ribosomal protein S0
25,996	26,418	25,8418	23,4718	23,4541	23,4886	+	1,09E-14	4,96E+08	5	5	5	27	34,242	24,7784	26,0852	23,4715	6	3	3	0,000111	2,61371	B8N514	B8N514	1	AFLA_020520	30S ribosomal protein S15
24,4221	23,9131	23,6174	24,1884	25,5218	24,6954		0,000178	1,75E+08	2	2	2	6,4	44,19	24,393	23,9842	24,8019	6	3	3	0,146138	-0,817685	B8N521	B8N521	1	AFLA_020590	Aldose 1-epimerase, putative
22,554	21,9719	21,5294	22,7808	22,8951	22,8267		4,45E-45	3,22E+08	4	4	4	7,3	78,442	22,4263	22,0184	22,8342	6	3	3	0,05231	-0,815785	B8N531	B8N531	1	AFLA_020690	Extracellular serine-threonine rich protein
26,097	25,8303	26,3062	26,1151	25,1916	25,4843		1,98E-78	2,37E+09	15	15	15	31,4	58,973	25,8374	26,0778	25,597	6	3	3	0,190385	0,480843	B8N538	B8N538	1	AFLA_020760	T-complex protein 1 subunit gamma
28,3406	28,042	27,9076	28,09	28,1942	28,3101		1,13E-79	3,13E+09	6	6	6	59,2	17,288	28,1474	28,0967	28,1981	6	3	3	0,517177	-0,101362	B8N546	B8N546	1	AFLA_020840	Ubiquitin conjugating enzyme (UbcB), putative
26,8495	26,9761	27,2149	27,1779	26,9576	27,0803		7,59E-38	1,62E+09	16	16	16	29,9	76,816	27,0427	27,0135	27,0719	6	3	3	0,663692	-0,0584297	B8N551	B8N551	1	AFLA_020890	Clathrin-coated vesiclec protein (Bud7), putative
32,3547	32,2284	31,6862	32,5131	32,4509	32,5271		0	5,71E+10	28	28	28	65,2	59,368	32,2934	32,0898	32,497	6	3	3	0,119693	-0,407239	B8N562;B8	B8N562	2	AFLA_021000	Uncharacterized protein
25,9667	26,0006	25,5274	25,5932	25,4694	25,5727		1,29E-94	6,46E+08	5	5	5	9,6	79,17	25,6883	25,8316	25,5451	6	3	3	0,142348	0,286485	B8N791	B8N791	1	AFLA_021130	Lupus la ribonucleoprotein, putative
27,2947	27,0685	27,3903	27,642	27,6451	27,719	+	8,47E-52	2,32E+09	10	10	10	46,8	34,545	27,4599	27,2512	27,6687	6	3	3	0,013358	-0,417548	B8N794	B8N794	1	AFLA_021160	Aldehyde reductase (AKR1), putative
24,9501	26,1779	26,0358	26,3199	26,1516	25,5183		2,72E-39	7,92E+08	3	3	3	23,3	24,227	25,8589	25,7213	25,9966	6	3	3	0,580278	-0,275318	B8N799	B8N799	1	AFLA_021210	Ankyrin repeat protein
26,1576	25,9455	26,0123	NaN	25,5894	25,2189	+	1,89E-14	5,97E+08	7	7	7	13,5	92,143	25,7847	26,0384	25,4042	5	3	2	0,028675	0,63425	B8N7A0	B8N7A0	1	AFLA_021220	tRNA ligase
25,593	23,8366	23,1393	23,1631	23,5641	23,6264		2,81E-05	1,25E+08	2	2	2	9,4	43,568	23,8204	24,1896	23,4512	6	3	3	0,377291	0,738432	B8N7B3	B8N7B3	1	AFLA_021350	Transulfuration enzyme family protein, putative
24,7959	24,1348	NaN	23,5485	23,8494	NaN		3,79E-05	1,17E+08	2	2	2	8,9	28,4	24,0821	24,4653	23,6989	4	2	2	0,169295	0,766364	B8N7B4	B8N7B4	1	AFLA_021360	Transcriptional regulator, putative
NaN	24,5529	26,0211	26,409	25,3455	26,319		9,81E-77	7,76E+08	6	6	6	9	113,7	25,7295	25,287	26,0245	5	2	3	0,370532	-0,737494	B8N7C7	B8N7C7	1	AFLA_021490	PAB1 binding protein (Pbp1), putative
26,0436	26,5322	25,9568	26,3684	26,7796	26,4488		3,84E-102	1,17E+09	7	7	7	38,4	27,774	26,3549	26,1775	26,5323	6	3	3	0,180382	-0,354726	B8N7D0	B8N7D0	1	AFLA_021520	N-acetyltransferase complex ARD1 subunit, putative
26,9853	28,279	28,8709	29,267	28,2839	28,0472		8,41E-239	4,09E+09	7	7	7	74,6	14,904	28,2889	28,0451	28,5327	6	3	3	0,507275	-0,487642	B8N7D6	B8N7D6	1	AFLA_021580	Dynein light chain (Tctex1), putative
27,7073	26,9198	26,1623	25,8994	26,5268	26,4488		1,31E-24	9,76E+08	7	7	7	12,4	92,147	26,6107	26,9298	26,2917	6	3	3	0,260918	0,638127	B8N7E5	B8N7E5	1	AFLA_021670	Probable E3 ubiquitin-protein ligase hulA (EC 6.3.2.-) (HECT ubiquitin ligase A)
23,6537	26,0548	26,6122	27,4723	26,2835	25,7261		2,24E-136	1,82E+09	5	5	5	69,6	10,59	25,9671	25,4402	26,494	6	3	3	0,369737	-1,05372	B8N7E6	B8N7E6	1	AFLA_021680	Uncharacterized protein
24,5983	24,9469	24,6721	24,3859	24,8959	24,8444		1,88E-13	3,18E+08	3	3	3	23,1	21,767	24,7239	24,7391	24,7088	6	3	3	0,883125	0,0303402	B8N7E7	B8N7E7	1	AFLA_021690	Vacuolar protein sorting-associated protein 29
31,3717	30,955	30,5519	30,7474	31,1483	31,2808		0	2,05E+10	16	16	16	71,5	41,597	31,0092	30,9595	31,0588	6	3	3	0,745865	-0,0992928	B8N7E8	B8N7E8	1	AFLA_021700	Aminotransferase, class V, putative
27,8694	27,6484	27,5538	28,0382	27,8883	28,0381	+	3,51E-78	2,73E+09	11	11	11	65,5	22,54	27,8394	27,6906	27,9882	6	3	3	0,048459	-0,297607	B8N7G0	B8N7G0	1	AFLA_021820	Nuclear movement protein NudC
31,7114	31,6349	31,0852	31,118	31,3676	31,3723		0	3,11E+10	18	18	16	46,4	45,451	31,3816	31,4772	31,286	6	3	3	0,422811	0,191198	B8N7H4	B8N7H4	1	AFLA_021960	Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)
25,243	25,8815	25,3651	23,2826	22,8335	22,3956	+	4,08E-24	2,87E+08	8	8	8	27	51,308	24,1669	25,4965	22,8373	6	3	3	0,001177	2,65927	B8N570	B8N570	1	AFLA_021980	30S ribosomal subunit S4, putative
26,4123	25,6047	25,3781	25,852	26,191	26,3143		1,55E-43	7,54E+08	5	5	5	33,1	29,961	25,9587	25,7984	26,1191	6	3	3	0,402558	-0,320758	B8N580	B8N580	1	AFLA_022080	Uncharacterized protein
25,9825	25,8372	25,4501	24,8683	25,4182	25,666		1,27E-19	5,11E+08	8	8	8	7,8	162,01	25,537	25,7566	25,3175	6	3	3	0,197275	0,43914	B8N581	B8N581	1	AFLA_022090	Uncharacterized protein
27,6324	27,1797	26,4287	26,9807	27,2909	27,6655		6,95E-26	1,62E+09	8	8	8	15,1	89,195	27,1963	27,0803	27,3124	6	3	3	0,595545	-0,23209	B8N584	B8N584	1	AFLA_022120	C-24(28) sterol reductase
26,3949	26,0596	25,4353	25,4396	26,6645	25,9911		2,02E-18	6,99E+08	8	8	8	22,1	53,768	25,9975	25,9633	26,0317	6	3	3	0,886977	-0,0684751	B8N592	B8N592	1	AFLA_022200	Mitochondrial cytochrome b2, putative
26,1331	25,2218	23,9708	23,5663	23,7788	24,9081		2,11E-16	1,94E+08	5	5	5	30,1	27,431	24,5965	25,1086	24,0844	6	3	3	0,24512	1,02418	B8N595	B8N595	1	AFLA_022230	DSBA-like thioredoxin domain protein
28,3726	27,9547	27,5304	28,046	28,8915	29,0035		3,40E-194	3,83E+09	22	22	22	33,9	88,211	28,2998	27,9526	28,647	6	3	3	0,147919	-0,69442	B8N597	B8N597	1	AFLA_022250	SPX domain protein
29,4855	29,2234	28,8597	28,7552	28,901	29,1076		1,46E-188	5,1E+09	9	9	9	24,3	47,589	29,0554	29,1895	28,9212	6	3	3	0,267139	0,268278	B8N599	B8N599	1	AFLA_022270	Uncharacterized protein
23,3543	NaN	23,2887	NaN	NaN	NaN		1,06E-06	83990000	3	3	3	4,4	95,857	23,3215	23,3215	NaN	2	2	0	1	NaN	B8N5A2	B8N5A2	1	AFLA_022300	Chromosome segregation protein (SepB), putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
28,9677	28,9412	29,0371	28,2789	28,8737	28,6298		0	6,16E+09	45	45	45	32,1	233,2	28,7881	28,982	28,5941	6	3	3	0,090949	0,387867	B8N5A6	B8N5A6	1	AFLA_022340	Glutamate synthase Glt1, putative
34,5972	34,3694	33,9834	34,1343	34,1341	34,3132		0	2,17E+11	39	39	39	65,1	69,704	34,2553	34,3167	34,1939	6	3	3	0,550914	0,122812	B8N5B0	B8N5B0	1	AFLA_022380	Molecular chaperone Hsp70
30,3419	30,5893	30,2966	30,7287	30,3699	30,2634		2,03E-168	1,78E+10	14	14	14	42,3	27,787	30,4316	30,4093	30,454	6	3	3	0,802677	-0,0447483	B8N5B3	B8N5B3	1	AFLA_022410	Coproporphyrinogen III oxidase, putative
NaN	NaN	NaN	24,1966	24,3803	NaN		2,12E-12	1,52E+08	4	4	4	5,3	90,123	24,2885	NaN	24,2885	2	0	2	1	NaN	B8N5B4	B8N5B4	1	AFLA_022420	Microtubule binding protein HOOK3, putative
27,6216	27,5897	27,6674	28,0504	27,9479	27,8263	+	2,58E-103	2,97E+09	11	11	11	44,5	42,51	27,7839	27,6262	27,9415	6	3	3	0,010058	-0,315299	B8N5B8	B8N5B8	1	AFLA_022460	Dimeric dihydrodiol dehydrogenase, putative
30,779	30,6637	30,3509	30,526	30,7367	30,6357		6,69E-201	1,74E+10	17	17	17	59,3	28,463	30,6154	30,5979	30,6328	6	3	3	0,817306	-0,0349382	B8N5B9	B8N5B9	1	AFLA_022470	Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase) (ATP:AMP phosphotransferase) (Adenylate kinase cytosolic and mitochondrial) (Adenylate monophosphate kinase)
27,6146	27,8286	28,5078	28,5011	28,119	28,1105		0	3,78E+09	15	15	15	73,2	39,705	28,1136	27,9837	28,2435	6	3	3	0,433064	-0,259866	B8N5C0	B8N5C0	1	AFLA_022480	26S proteasome regulatory particle subunit Rpn8, putative
26,3707	26,1432	26,0053	26,2353	26,2331	26,2806		3,57E-20	7,96E+08	6	6	6	42,8	29,808	26,2114	26,1731	26,2497	6	3	3	0,516048	-0,0766048	B8N5C5	B8N5C5	1	AFLA_022530	Cell polarity protein (Alp11), putative
22,2095	22,3601	22,8837	NaN	21,44	21,7868		5,34E-07	99990000	3	3	3	25,8	20,598	22,136	22,4844	21,6134	5	3	2	0,059297	0,870966	B8N5D0	B8N5D0	1	AFLA_022580	Zinc knuckle domain protein (Byr3), putative
23,6047	23,5548	23,2298	23,1438	NaN	NaN		2,64E-05	1,31E+08	2	2	2	2,7	84,822	23,3833	23,4631	23,1438	4	3	1	1	0,319291	B8N5D6	B8N5D6	1	AFLA_022640	Protein O-mannosyl transferase
28,1137	27,9097	27,4882	27,5978	27,8151	27,6278		3,37E-94	2,34E+09	22	22	22	29,4	117,53	27,7587	27,8372	27,6802	6	3	3	0,468669	0,156995	B8N5D9	B8N5D9	1	AFLA_022670	Transcription elongation complex subunit (Cdc68)
27,3639	26,5251	26,1557	25,4279	26,4514	26,4642		2,19E-92	8,69E+08	9	9	9	5,5	263,06	26,3981	26,6816	26,1145	6	3	3	0,316337	0,567119	B8N2R2	B8N2R2	1	AFLA_023460	Alpha-1,3-glucan synthase Ags1
23,6832	23,2106	23,1594	NaN	23,0912	NaN		6,45E-05	99927000	3	3	3	5,3	60,431	23,2861	23,3511	23,0912	4	3	1	1	0,259905	B8N2R4	B8N2R4	1	AFLA_023480	Alpha-amylase, putative
25,8424	25,8397	25,9497	25,6182	25,713	25,5539	+	7,37E-209	1,78E+09	5	5	5	55,5	14,434	25,7528	25,8773	25,6284	6	3	3	0,01327	0,248915	B8N2S7	B8N2S7	1	AFLA_023610	Uncharacterized protein
27,916	27,603	27,3089	27,1463	27,3071	27,4294		3,37E-65	1,59E+09	10	10	10	75,2	23,447	27,4518	27,6093	27,2943	6	3	3	0,178898	0,315029	B8N2U0	B8N2U0	1	AFLA_023740	Glutathione S-transferase, putative
27,3134	26,879	27,0184	27,0813	26,6309	26,8919		1,48E-34	1,63E+09	11	11	11	14,3	92,036	26,9691	27,0703	26,868	6	3	3	0,330875	0,202212	B8N0I3	B8N0I3	1	AFLA_024260	Glycosyl hydrolase, putative
29,3324	27,7717	29,8263	22,8134	NaN	23,6589	+	7,76E-200	1,68E+09	12	12	12	34,4	68,812	26,6805	28,9768	23,2362	5	3	2	0,006839	5,74064	B8N0I7;B8	B8N0I7	2	AFLA_024300	Amidase, putative
28,5451	28,7475	29,0054	28,575	28,6921	28,6025		8,94E-169	5,13E+09	19	19	19	37,9	86,1	28,6946	28,766	28,6232	6	3	3	0,358601	0,14282	B8N0K5	B8N0K5	1	AFLA_024480	ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)
NaN	23,7726	24,1818	NaN	NaN	NaN		1,58E-12	2,3E+08	4	4	4	19,8	40,882	23,9772	23,9772	NaN	2	2	0	1	NaN	B8N0P2	B8N0P2	1	AFLA_024850	Deoxyhypusine synthase, putative
27,7741	27,5519	27,2768	27,2013	27,5162	27,5685		2,08E-39	1,77E+09	8	8	8	34,6	25,364	27,4815	27,5343	27,4287	6	3	3	0,596595	0,105607	B8N2W4	B8N2W4	1	AFLA_024880	Uncharacterized protein
25,0367	25,1733	25,2082	24,9184	24,8882	24,8573	+	5,02E-16	4,37E+08	5	5	5	12,7	90,77	25,0137	25,1394	24,888	6	3	3	0,0104	0,251438	B8N2W5	B8N2W5	1	AFLA_024890	Cell differentiation and development protein Fsr1/Pro11
27,5874	27,695	27,5376	27,8037	27,9437	27,9549	+	2,20E-167	2,41E+09	8	8	8	53,7	21,024	27,7537	27,6067	27,9008	6	3	3	0,011943	-0,29406	B8N2X1	B8N2X1	1	AFLA_024950	Actin-related protein 2/3 complex subunit 3 (Arp2/3 complex 21 kDa subunit)
25,4995	25,0874	24,7584	23,9949	24,244	25,1615		1,36E-11	1,77E+08	3	3	3	9,6	65,997	24,7909	25,1151	24,4668	6	3	3	0,192842	0,648273	B8N2Y3	B8N2Y3	1	AFLA_025070	R3H domain protein, putative
32,6593	32,7575	33,7913	33,3653	32,8335	32,6547		0	9,19E+10	19	19	17	72,5	36,3	33,0103	33,0694	32,9512	6	3	3	0,792488	0,118193	B8N2Y6;B8	B8N2Y6	2	AFLA_025100	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
23,6624	24,5262	NaN	NaN	23,6643	NaN		1,27E-05	1,16E+08	3	3	3	11,6	43,18	23,951	24,0943	23,6643	3	2	1	1	0,430029	B8N2Z2	B8N2Z2	1	AFLA_025160	Proline racemase, putative
29,9096	29,7242	29,1799	29,5324	29,7433	29,8402		0	8,61E+09	39	39	39	46,3	134,5	29,6549	29,6046	29,7053	6	3	3	0,692706	-0,100755	B8N2Z3	B8N2Z3	1	AFLA_025170	A-pheromone processing enzyme metallopeptidase Ste23
28,7853	28,1644	28,0379	27,6895	27,9697	28,0598		1,15E-166	2,96E+09	11	11	11	60,4	31,226	28,1178	28,3292	27,9063	6	3	3	0,1745	0,422875	B8N2Z4	B8N2Z4	1	AFLA_025180	Cleavage and polyadenylation specific factor 5
24,534	NaN	NaN	NaN	25,0383	24,6659		5,57E-09	2,45E+08	2	2	2	26,1	14,955	24,7461	24,534	24,8521	3	1	2	1	-0,318119	B8N345	B8N345	1	AFLA_025690	Uncharacterized protein
NaN	24,0595	24,8187	24,4904	NaN	NaN		1,60E-12	3,72E+08	5	5	5	10,4	61,045	24,4562	24,4391	24,4904	3	2	1	1	-0,0513954	B8N350	B8N350	1	AFLA_025750	T-complex protein 1, theta subunit, putative
25,0601	26,3925	26,8782	27,0962	26,4752	26,4527		4,96E-16	7,58E+08	3	3	3	30,4	19,541	26,3925	26,1102	26,6747	6	3	3	0,387742	-0,56445	B8N351	B8N351	1	AFLA_025760	50S ribosomal protein L12
24,0035	26,1805	27,1302	25,7675	25,5285	24,7231		7,85E-21	3,38E+08	6	6	6	17,7	51,634	25,5555	25,7714	25,3397	6	3	3	0,681698	0,431707	B8N0Q0	B8N0Q0	1	AFLA_025850	Kynureninase (EC 3.7.1.3) (Biosynthesis of nicotinic acid protein 5) (L-kynurenine hydrolase)
28,4867	28,4929	28,2759	28,6648	28,5423	28,7008		7,35E-163	4,35E+09	18	18	18	49,7	54,675	28,5272	28,4185	28,636	6	3	3	0,064619	-0,21748	B8N0R3	B8N0R3	1	AFLA_025980	Hsp90 co-chaperone Cdc37
23,6168	24,2769	24,3673	25,7971	24,2386	23,8654		1,17E-157	4,2E+08	4	4	4	27,9	26,199	24,3604	24,087	24,6337	6	3	3	0,439247	-0,546672	B8N0R4	B8N0R4	1	AFLA_025990	Clathrin light chain
26,8795	26,296	24,924	25,2678	26,4661	26,4729		3,60E-16	5,83E+08	4	4	4	16,2	35,085	26,0511	26,0332	26,0689	6	3	3	0,961946	-0,0357666	B8N0R5	B8N0R5	1	AFLA_026000	DUF618 domain protein
31,5819	31,0488	30,6435	30,8714	31,2292	31,2184		0	2,6E+10	15	15	14	73,8	17,013	31,0989	31,0914	31,1064	6	3	3	0,962116	-0,0149625	B8N0R7	B8N0R7	1	AFLA_026020	Calmodulin
27,6319	27,581	26,948	27,768	27,7409	27,7973		3,17E-114	3,68E+09	13	13	13	35,1	54,803	27,5779	27,387	27,7687	6	3	3	0,158549	-0,381734	B8N0S9	B8N0S9	1	AFLA_026140	Alpha-amylase (EC 3.2.1.1)
28,0072	28,0029	27,7261	28,2387	28,3071	28,3689	+	3,62E-124	3,06E+09	10	10	10	16,2	108,76	28,1085	27,9121	28,3049	6	3	3	0,017295	-0,392855	B8N0T0	B8N0T0	1	AFLA_026150	Alpha-glucosidase AgdA, putative
NaN	24,8972	24,8796	23,4731	24,1042	22,9274		3,55E-11	1,61E+08	4	4	4	10,3	71,219	24,0563	24,8884	23,5016	5	2	3	0,050906	1,38683	B8N0T4	B8N0T4	1	AFLA_026190	Signal recognition particle subunit SRP72
28,8312	28,5485	28,1409	28,4864	28,7959	28,9978		5,77E-115	3,16E+09	13	13	13	28,9	65,77	28,6335	28,5069	28,7601	6	3	3	0,36761	-0,253208	B8N0T8	B8N0T8	1	AFLA_026230	Uncharacterized protein
28,3727	27,9593	27,1425	26,3009	26,4615	26,0184	+	3,73E-15	1,53E+09	4	4	4	36,2	12,867	27,0425	27,8248	26,2603	6	3	3	0,015161	1,56453	B8N0U1	B8N0U1	1	AFLA_026260	Small nuclear ribonucleoprotein SmD3, putative
24,6631	26,2192	27,0424	27,1152	26,1302	26,3611		8,04E-32	9,38E+08	7	7	7	37,3	18,406	26,2552	25,9749	26,5355	6	3	3	0,500827	-0,560563	B8N0U4	B8N0U4	1	AFLA_026290	Phosphotransmitter protein Ypd1, putative
NaN	NaN	23,8348	NaN	24,4472	24,3263		5,68E-06	2,12E+08	3	3	3	9,6	47,944	24,2028	23,8348	24,3867	3	1	2	1	-0,551948	B8N0U8	B8N0U8	1	AFLA_026330	CaaX farnesyltransferase beta subunit Ram1
31,2999	31,7447	32,0695	31,8715	31,9008	31,6809		0	4,28E+10	29	29	28	69,5	47,224	31,7612	31,7047	31,8177	6	3	3	0,653669	-0,113012	B8N0W2	B8N0W2	1	AFLA_026470	Aspartate aminotransferase (EC 2.6.1.1)
29,0996	28,9673	28,6116	28,8032	28,8305	28,8734		7,80E-182	5,35E+09	13	13	13	40,4	50,499	28,8643	28,8929	28,8537	6	3	3	0,717385	0,0571696	B8N0W8;B	B8N0W8	2	AFLA_026530	Homocitrate synthase
26,9486	26,5803	26,3487	26,8755	26,9276	27,0708		3,19E-40	1,2E+09	4	4	4	31,4	23,29	26,7919	26,6259	26,958	6	3	3	0,145686	-0,33209	B8N0X3	B8N0X3	1	AFLA_026580	Mitochondrial chaperone Frataxin, putative
26,6544	26,0454	25,5837	24,7058	26,0362	26,0762		4,67E-70	6,3E+08	3	3	3	22,8	25,508	25,8503	26,0945	25,606	6	3	3	0,422143	0,488436	B8N360	B8N360	1	AFLA_026730	Vesicle transport v-snare protein, putative
NaN	NaN	24,2238	24,9669	23,507	NaN		6,66E-10	2,03E+08	5	5	5	17,3	49,641	24,2326	24,2238	24,237	3	1	2	1	-0,0132046	B8N362	B8N362	1	AFLA_026750	AAA family ATPase Pontin, putative
NaN	23,2595	23,4977	23,1963	22,8258	23,1151		5,68E-10	96185000	3	3	3	3,3	123,88	23,1789	23,3786	23,0457	5	2	3	0,145354	0,332881	B8N368	B8N368	1	AFLA_026810	Ubiquitin-protein ligase (Tom1), putative
25,7062	25,2657	29,3902	28,4881	25,7647	26,5187		5,86E-42	1,3E+09	7	7	7	23,6	27,221	26,8556	26,7874	26,9238	6	3	3	0,933619	-0,136449	B8N370	B8N370	1	AFLA_026830	40S ribosomal protein S6
NaN	24,0692	24,5132	25,0211	24,0725	24,0269		3,07E-11	1,88E+08	4	4	4	17,9	36,657	24,3406	24,2912	24,3735	5	2	3	0,86657	-0,0822646	B8N375	B8N375	1	AFLA_026880	Nicotinamide riboside kinase, putative
NaN	NaN	23,7361	23,7095	NaN	24,1191		7,12E-07	1,39E+08	2	2	2	8,7	27,748	23,8549	23,7361	23,9143	3	1	2	1	-0,178141	B8N387	B8N387	1	AFLA_027000	Sit4-associated protein (Sap185), putative
25,9321	25,7451	25,541	26,3292	26,2714	25,6261		9,68E-31	4,58E+08	6	6	6	3,7	213,75	25,9075	25,7394	26,0756	6	3	3	0,25322	-0,336156	B8N391	B8N391	1	AFLA_027040	Nucleoporin SONB, putative
27,2951	27,6136	28,224	28,2948	28,2917	28,2085		6,49E-120	3,78E+09	24	24	24	42,7	78,924	27,988	27,7109	28,265	6	3	3	0,113209	-0,554087	B8N394	B8N394	1	AFLA_027070	Acetyl-coenzyme A synthetase (EC 6.2.1.1)
28,1531	27,7772	27,5683	27,7165	27,4969	27,4738		1,07E-48	2,4E+09	10	10	10	34,4	47,84	27,6977	27,8329	27,5624	6	3	3	0,223098	0,270487	B8N3A4	B8N3A4	1	AFLA_027170	Kynurenine aminotransferase, putative
28,0695	27,3217	25,986	26,5394	27,2217	27,245		4,74E-44	1,01E+09	18	18	18	23,7	127,12	27,0639	27,1258	27,002	6	3	3	0,858681	0,123747	B8N3A7	B8N3A7	1	AFLA_027200	Xanthine dehydrogenase HxA, putative
26,9586	26,9357	26,8352	26,9627	26,9675	27,0416		3,83E-34	1,43E+09	6	6	6	27,6	23,805	26,9502	26,9098	26,9906	6	3	3	0,151947	-0,0807406	B8N3A9	B8N3A9	1	AFLA_027220	Uncharacterized protein
29,983	29,8972	29,7777	30,0817	30,0173	30,0778		0	1,16E+10	36	36	36	42,7	130,32	29,9725	29,886	30,0589	6	3	3	0,051836	-0,172933	B8N3B0	B8N3B0	1	AFLA_027230	L-aminoadipate-semialdehyde dehydrogenase (EC 1.2.1.31) (Alpha-aminoadipate reductase)
24,546	26,017	25,8132	26,3069	25,9843	25,3879		1,10E-56	8,47E+08	6	6	6	32,2	31,172	25,6759	25,4587	25,893	6	3	3	0,460974	-0,434309	B8N3B1	B8N3B1	1	AFLA_027240	Carbonic anhydrase (EC 4.2.1.1)
28,6115	28,002	27,3342	27,1957	27,6362	27,7732		1,59E-55	1,84E+09	12	12	12	41,3	39,105	27,7588	27,9826	27,535	6	3	3	0,334226	0,447532	B8N3B2;B8	B8N3B2	3	AFLA_027250	Aldo-keto reductase, putative
25,7006	26,4313	26,4028	25,7394	26,4161	26,0712		1,87E-36	7,96E+08	14	14	14	9,3	222,86	26,1269	26,1782	26,0756	6	3	3	0,756093	0,102678	B8N3B6	B8N3B6	1	AFLA_027290	Proteasome activator subunit 4, putative
27,0955	28,1467	28,9492	29,2115	29,1401	28,6521		6,25E-148	3,81E+09	14	14	14	53,8	38,911	28,5325	28,0638	29,0013	6	3	3	0,172267	-0,937475	B8N3B8	B8N3B8	1	AFLA_027310	Fructose-1,6-bisphosphatase Fbp1, putative
29,5981	29,4049	28,967	28,935	29,2026	29,3666		4,78E-253	6,87E+09	13	13	13	53,3	36,953	29,2457	29,3233	29,1681	6	3	3	0,528323	0,155251	B8N3C1	B8N3C1	1	AFLA_027340	Aha1 domain family
30,0428	29,9887	30,2751	30,5051	30,4635	30,2853	+	0	1,36E+10	24	24	24	70,4	49,295	30,2601	30,1022	30,418	6	3	3	0,046324	-0,315751	B8N3C2	B8N3C2	1	AFLA_027350	Saccharopine dehydrogenase Lys9, putative
23,7862	23,5515	23,4665	23,6205	23,6283	23,589		6,01E-09	2,21E+08	2	2	2	14,2	18,42	23,607	23,6014	23,6126	6	3	3	0,912704	-0,0112464	B8N3C6	B8N3C6	1	AFLA_027390	Ubiquinol-cytochrome c reductase complex 17 kd protein
24,2035	26,5783	27,1449	26,8704	26,5815	26,2313		1,20E-45	1,17E+09	10	10	10	19,8	100,54	26,2683	25,9756	26,5611	6	3	3	0,559021	-0,585475	B8N3D1	B8N3D1	1	AFLA_027440	Aminotransferase, classes I and II, putative
25,3922	24,7678	25,1347	24,788	25,142	24,5257		3,89E-15	3,54E+08	3	3	3	11,2	39,489	24,9584	25,0983	24,8186	6	3	3	0,333266	0,279707	B8N3D2	B8N3D2	1	AFLA_027450	Sucrase/ferredoxin-like family protein, putative
NaN	23,5375	24,5363	24,0309	23,7203	23,7416		1,03E-92	8,39E+08	7	7	7	30,2	40,13	23,9133	24,0369	23,8309	5	2	3	0,63726	0,206008	B8N3D7	B8N3D7	1	AFLA_027500	Mannose-1-phosphate guanylyltransferase
26,9119	25,9624	25,6264	25,1222	26,1999	26,5316		1,34E-50	7,51E+08	6	6	6	17,9	62,301	26,0591	26,1669	25,9512	6	3	3	0,726071	0,215668	B8N3E0	B8N3E0	1	AFLA_027530	Glycerol kinase, putative
30,7605	30,3155	30,0262	30,1	30,2687	30,4562		1,95E-299	1,58E+10	8	8	8	16,7	93,134	30,3212	30,3674	30,275	6	3	3	0,71654	0,092406	B8N0Y3	B8N0Y3	1	AFLA_027580	Iron superoxide dismutase A, putative
32,9064	32,6605	32,3284	32,8762	32,9417	33,0173		0	7,44E+10	10	10	10	75,9	18,17	32,7884	32,6318	32,9451	6	3	3	0,14326	-0,313291	B8N0Z6	B8N0Z6	1	AFLA_027710	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
30,1316	31,4924	31,8957	32,1283	31,3679	31,3247		0	3,16E+10	24	24	24	68,9	52,838	31,3901	31,1732	31,607	6	3	3	0,505768	-0,433739	B8N0Z7	B8N0Z7	1	AFLA_027720	Phosphatidyl synthase
33,0546	32,8031	32,4903	32,9042	32,894	33,0195		0	7,5E+10	23	23	20	75,7	36,931	32,861	32,7827	32,9392	6	3	3	0,404421	-0,15656	B8N0Z8	B8N0Z8	1	AFLA_027730	Glycerol dehydrogenase (GldB), putative
25,1914	24,4117	29,8403	22,246	23,0295	22,6846		4,01E-172	2E+09	10	10	10	46,7	42,571	24,5672	26,4811	22,6533	6	3	3	0,088731	3,82779	B8N106	B8N106	1	AFLA_027810	Alkaline protease 1 (ALP) (EC 3.4.21.63) (Aspergillopeptidase B) (Aspergillus proteinase B) (Elastase) (Elastinolytic serine proteinase) (Oryzin) (allergen Asp fl 1)
30,2172	29,8661	29,2877	29,094	29,4542	29,5085		1,69E-271	7,47E+09	17	17	16	71,6	36,684	29,5713	29,7903	29,3522	6	3	3	0,218722	0,438087	B8N110;B8	B8N110	2	AFLA_027850	Glyoxylate reductase
NaN	NaN	25,9217	24,8293	NaN	24,8037		2,39E-16	3,71E+08	6	6	6	11,4	72,168	25,1849	25,9217	24,8165	3	1	2	1	1,10525	B8N116	B8N116	1	AFLA_027910	Serine/threonine protein kinase, putative
28,8597	29,1926	28,4971	28,8205	29,1135	29,1643		3,51E-197	7,27E+09	27	27	27	38,6	94,875	28,9413	28,8498	29,0327	6	3	3	0,466622	-0,182933	B8N118	B8N118	1	AFLA_027930	N-terminal acetyltransferase catalytic subunit Nat1, putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
25,2662	25,5319	25,1389	25,5733	25,366	25,4794		3,10E-14	4,67E+08	5	5	5	33	22,026	25,3926	25,3123	25,4729	6	3	3	0,285572	-0,160552	B8N119	B8N119	1	AFLA_027940	Caffeine-induced death protein Cid2, putative
25,6247	24,9278	25,4996	24,634	25,096	24,6697		5,78E-17	2,36E+08	3	3	3	18,6	17,754	25,0753	25,3507	24,7999	6	3	3	0,102328	0,550774	B8N123	B8N123	1	AFLA_027980	NUDIX domain, putative
24,284	25,5966	25,8456	25,9392	26,1528	25,8381		2,46E-50	7,77E+08	6	6	6	27,4	46,545	25,6094	25,2421	25,9767	6	3	3	0,210585	-0,734652	B8N131	B8N131	1	AFLA_028060	Anthranilate phosphoribosyltransferase, putative
28,1193	27,8051	27,2798	27,9897	27,9111	28,103		6,43E-83	2,59E+09	11	11	11	35,5	51,803	27,868	27,7347	28,0013	6	3	3	0,348399	-0,266544	B8N134	B8N134	1	AFLA_028090	Biotin-dependent 2-oxo acid dehydrogenases acyltransferase, putative
NaN	24,6656	24,9133	24,2285	24,553	24,4685		1,35E-09	2,55E+08	3	3	3	11,8	40,182	24,5658	24,7895	24,4167	5	2	3	0,096513	0,372787	B8N139	B8N139	1	AFLA_028140	Vacuolar protein sorting-associated protein 26, putative
28,1235	27,8238	28,048	28,1329	28,2749	28,3256		2,05E-85	2,94E+09	10	10	10	84,2	15,75	28,1215	27,9984	28,2445	6	3	3	0,08279	-0,246044	B8N141	B8N141	1	AFLA_028160	Ubiquitin conjugating enzyme (MmsB), putative
25,9624	25,7374	25,6713	25,4991	25,2483	25,8262		2,37E-15	5,39E+08	3	3	3	19,7	26,568	25,6574	25,7904	25,5245	6	3	3	0,232508	0,265831	B8N143	B8N143	1	AFLA_028180	RWD domain protein (Gir2), putative
NaN	NaN	NaN	24,2299	26,2617	25,5851		7,42E-14	2,96E+08	7	7	7	22,7	44,372	25,3589	NaN	25,3589	3	0	3	1	NaN	B8N151	B8N151	1	AFLA_028260	Probable glucan 1,3-beta-glucosidase A (EC 3.2.1.58) (Exo-1,3-beta-glucanase 1) (Exo-1,3-beta-glucanase A)
26,0485	27,8559	27,0303	26,0565	26,2831	26,427		2,58E-73	1,49E+09	9	9	9	48,1	32,591	26,6169	26,9783	26,2555	6	3	3	0,246905	0,722731	B8N156	B8N156	1	AFLA_028310	Uncharacterized protein
27,3637	27,0808	26,9312	26,2575	26,9012	26,6532		3,42E-60	1,38E+09	7	7	7	24,6	54,156	26,8646	27,1252	26,6039	6	3	3	0,082618	0,521294	B8N163	B8N163	1	AFLA_028380	Uncharacterized protein
25,5416	25,7406	25,3864	25,7397	25,5566	25,7342		1,43E-64	5,47E+08	4	4	4	34,9	14,631	25,6165	25,5562	25,6768	6	3	3	0,367463	-0,120639	B8N3F0	B8N3F0	1	AFLA_028530	Prefoldin subunit 2, putative
26,8001	26,6259	25,8908	26,3645	26,0548	26,0436		4,68E-24	6,58E+08	4	4	4	7,2	98,636	26,2966	26,4389	26,1543	6	3	3	0,393358	0,284618	B8N3F7	B8N3F7	1	AFLA_028600	DNA helicase (EC 3.6.4.12)
24,5554	25,8549	25,2913	23,6008	24,857	23,6769		2,24E-15	2,57E+08	5	5	5	13,1	67,022	24,6394	25,2339	24,0449	6	3	3	0,098401	1,18896	B8N3F9	B8N3F9	1	AFLA_028620	Signal recognition particle subunit SRP68 (SRP68)
27,7771	27,6499	27,0386	27,6883	27,5502	27,6501		1,08E-91	1,7E+09	11	11	11	12,2	118,75	27,559	27,4885	27,6295	6	3	3	0,575609	-0,140985	B8N3G3	B8N3G3	1	AFLA_028660	Mitochondrial translation initiation factor IF-2, putative
NaN	24,59	24,9343	NaN	NaN	NaN		1,37E-08	1,63E+08	4	4	4	26,6	26,433	24,7622	24,7622	NaN	2	2	0	1	NaN	B8N3G8	B8N3G8	1	AFLA_028710	Short chain type dehydrogenase, putative
24,2271	23,355	24,1702	22,3963	24,8131	23,8573		4,75E-231	5,27E+08	4	4	4	19,2	33,983	23,8032	23,9175	23,6889	6	3	3	0,777797	0,228542	B8N3I0	B8N3I0	1	AFLA_028830	FG-GAP repeat protein, putative
NaN	23,3601	23,7374	22,8621	22,915	NaN		2,15E-16	1,04E+08	4	3	3	11	46,976	23,2187	23,5487	22,8886	4	2	2	0,074111	0,660182	B8N3I4	B8N3I4	1	AFLA_028870	Aspartate aminotransferase (EC 2.6.1.1)
31,8059	31,6414	31,4815	31,2991	31,2918	31,2534	+	0	3,13E+10	28	28	28	37,4	77,339	31,4622	31,643	31,2814	6	3	3	0,018826	0,361525	B8N3I8	B8N3I8	1	AFLA_028910	Polyadenylate-binding protein (PABP)
25,99	26,3704	26,3987	24,5549	NaN	NaN		4,42E-20	4,33E+08	4	4	4	13,4	40,373	25,8285	26,253	24,5549	4	3	1	1	1,6981	B8N3J4	B8N3J4	1	AFLA_028970	30S ribosomal protein S7, putative
26,8614	28,0308	31,0261	30,4597	28,2505	28,4266		6,72E-207	4,86E+09	8	8	8	49	22,811	28,8425	28,6394	29,0456	6	3	3	0,790265	-0,40617	B8N3J9	B8N3J9	1	AFLA_029020	40S ribosomal protein S8
25,5043	25,9868	26,2617	NaN	NaN	24,8987		1,59E-15	4,7E+08	5	5	5	17,6	58,287	25,6629	25,9176	24,8987	4	3	1	1	1,0189	B8N3L1	B8N3L1	1	AFLA_029140	Siderophore biosynthesis protein, putative
26,9449	26,6891	26,2921	26,6388	26,7732	26,8062		3,88E-77	1,1E+09	5	5	5	30,4	36,058	26,6907	26,6421	26,7394	6	3	3	0,646633	-0,0973365	B8N3M1	B8N3M1	1	AFLA_029240	NifU-related protein
29,9897	30,5897	30,6484	26,9519	25,7414	26,2005	+	5,21E-111	7,09E+09	7	7	7	22,4	33,628	28,3536	30,4093	26,298	6	3	3	0,00056	4,11131	B8N3M3	B8N3M3	1	AFLA_029260	Ribosomal protein L15
27,2186	27,3151	28,5579	28,5215	28,2482	28,2067		1,11E-161	4,39E+09	10	10	10	39,3	37,684	28,0113	27,6972	28,3255	6	3	3	0,228583	-0,628272	B8N3M8	B8N3M8	1	AFLA_029310	Alcohol dehydrogenase, zinc-containing, putative
29,015	28,7134	28,5042	28,7463	28,7372	28,6268		5,75E-100	4,18E+09	10	10	10	37,6	33,508	28,7238	28,7442	28,7034	6	3	3	0,803139	0,0407861	B8N3N4	B8N3N4	1	AFLA_029390	HMG box protein, putative
30,388	30,0764	29,992	29,4541	29,3312	29,51	+	0	1,44E+10	17	17	17	36,2	62,627	29,792	30,1521	29,4318	6	3	3	0,005408	0,720347	B8N177	B8N177	1	AFLA_029420	Dipeptidyl-peptidase II, putative
30,4368	30,1998	30,326	29,9023	30,2332	30,1285		1,33E-223	1,39E+10	12	12	12	52,3	36,321	30,2044	30,3209	30,088	6	3	3	0,122615	0,232869	B8N179	B8N179	1	AFLA_029440	NADH-cytochrome b5 reductase (EC 1.6.2.2)
30,7709	30,189	31,0186	28,0018	27,757	27,7172	+	0	7,67E+09	11	11	11	38,8	28,509	29,2424	30,6595	27,8253	6	3	3	0,000411	2,83412	B8N180	B8N180	1	AFLA_029450	Ribosomal L18ae protein family
26,5503	27,1038	26,9556	26,6529	26,9585	27,3541		4,11E-39	1,41E+09	5	5	5	50	10,285	26,9292	26,8699	26,9885	6	3	3	0,67404	-0,118613	B8N184	B8N184	1	AFLA_029490	Mitochondrial intermembrane space translocase subunit Tim10, putative
29,1818	28,7991	28,5415	28,8181	28,755	28,8944		6,23E-131	4,56E+09	14	14	14	55,6	38,587	28,8317	28,8408	28,8225	6	3	3	0,928159	0,0182654	B8N186	B8N186	1	AFLA_029510	Uncharacterized protein
27,3283	27,3395	26,8887	26,493	26,9392	26,7661		9,45E-57	1,28E+09	9	9	9	37,2	44,826	26,9591	27,1855	26,7328	6	3	3	0,083376	0,452732	B8N193	B8N193	1	AFLA_029580	Protein phosphatase PP1 regulatory subunit Sds22, putative
25,7194	24,7957	NaN	23,7299	24,59	NaN		3,58E-08	4,2E+08	3	3	3	42,6	11,061	24,7088	25,2576	24,1599	4	2	2	0,224101	1,09763	B8N199	B8N199	1	AFLA_029640	Dynein light chain type 1, putative
28,8025	28,6507	28,6418	28,9468	28,9758	29,0138	+	5,03E-223	5,87E+09	10	10	10	18,2	89,842	28,8386	28,6983	28,9788	6	3	3	0,00727	-0,280514	B8N1A6	B8N1A6	1	AFLA_029710	Proliferating cell nuclear antigen
26,9801	27,2405	26,6433	25,3008	25,7383	25,3957	+	6,11E-47	1,49E+09	7	7	7	46	21,415	26,2165	26,9547	25,4783	6	3	3	0,002482	1,4764	B8N1B1	B8N1B1	1	AFLA_029760	Small monomeric GTPase SarA, putative
NaN	NaN	23,5287	24,261	23,0627	NaN		3,90E-05	1,45E+08	3	3	3	5,5	66,225	23,6175	23,5287	23,6618	3	1	2	1	-0,133096	B8N1B7	B8N1B7	1	AFLA_029820	SAM domain protein
30,0123	28,3752	27,2725	28,0542	29,8395	30,0795		0	2,02E+10	16	16	16	62,4	35,991	28,9389	28,5533	29,3244	6	3	3	0,491973	-0,7711	B8N1C0	B8N1C0	1	AFLA_029850	Cysteine-rich secreted protein
31,145	31,2779	31,2303	31,5089	31,0832	31,1885		0	2,61E+10	16	16	16	42,4	51,72	31,239	31,2177	31,2602	6	3	3	0,766593	-0,0425034	B8N1C3	B8N1C3	1	AFLA_029880	FAD dependent oxidoreductase, putative
26,1928	25,7286	25,2269	25,4221	25,6745	25,2626		2,10E-16	4,49E+08	6	6	6	13	50,892	25,5846	25,7161	25,4531	6	3	3	0,435131	0,263038	B8N1C6	B8N1C6	1	AFLA_029910	Disulfide isomerase, putative
29,2065	29,797	29,8706	29,5849	29,3085	29,2552		0	8,41E+09	27	27	27	31,3	119,79	29,5038	29,6247	29,3828	6	3	3	0,359189	0,241847	B8N1D8	B8N1D8	1	AFLA_030030	Eukaryotic translation initiation factor 3 subunit A (eIF3a) (Eukaryotic translation initiation factor 3 110 kDa subunit homolog) (Translation initiation factor eIF3, p110 subunit homolog)
31,8229	32,0133	31,9106	30,7668	30,238	30,3273	+	0	2,4E+10	10	10	10	48,9	33,441	31,1798	31,9156	30,444	6	3	3	0,001035	1,47159	B8N1E9	B8N1E9	1	AFLA_030140	60S ribosomal protein P0
29,8024	29,6249	29,2067	29,4497	29,5551	29,5708		0	9,07E+09	12	12	12	43	40,766	29,5349	29,5447	29,5252	6	3	3	0,919324	0,0194785	B8N1F1	B8N1F1	1	AFLA_030160	Uroporphyrinogen decarboxylase (EC 4.1.1.37)
26,2026	26,0431	25,8311	25,9716	26,1892	26,4482		6,99E-48	8,06E+08	3	3	3	25,7	16,107	26,1143	26,0256	26,203	6	3	3	0,367556	-0,177402	B8N1F2	B8N1F2	1	AFLA_030170	Cytosine deaminase, putative
28,0513	27,0698	26,19	26,0176	26,7892	27,1218		5,09E-58	1,7E+09	6	6	6	26,9	45,393	26,8733	27,1037	26,6428	6	3	3	0,504523	0,460859	B8N1F3	B8N1F3	1	AFLA_030180	Protein mitochondrial targeting protein (Mas1), putative
25,9597	25,566	25,3449	26,1758	26,0561	26,0409		7,23E-26	5,67E+08	2	2	2	29,5	12,164	25,8572	25,6235	26,0909	6	3	3	0,064692	-0,467401	B8N1G1	B8N1G1	1	AFLA_030260	Uncharacterized protein
24,1174	23,075	23,478	28,5781	28,6952	28,7459	+	0	3,59E+09	8	8	8	48	31,217	26,1149	23,5568	28,673	6	3	3	7,65E-05	-5,11626	B8N1G5	B8N1G5	1	AFLA_030300	Uncharacterized protein
27,9666	28,0448	27,909	28,2145	28,189	28,0346		2,35E-74	3,21E+09	19	19	19	40,8	78,714	28,0598	27,9735	28,146	6	3	3	0,065742	-0,172537	B8N1I0	B8N1I0	1	AFLA_030450	Trehalose synthase (Cre9), putative
25,1233	25,6509	25,8472	25,8225	25,6553	25,5507		5,22E-19	5,8E+08	6	6	6	28,4	28,156	25,6083	25,5405	25,6762	6	3	3	0,587299	-0,135658	B8N1J6	B8N1J6	1	AFLA_030610	Transcription regulator PAB1642, putative
29,599	29,3452	29,0421	29,2533	29,3149	29,4735		3,51E-119	6,63E+09	9	9	9	51,2	26,863	29,338	29,3288	29,3473	6	3	3	0,92045	-0,0184797	B8N1K3	B8N1K3	1	AFLA_030680	Microtubule associated protein EB1, putative
31,092	31,5736	32,0747	32,54	32,5054	32,4033	+	0	4,45E+10	33	33	33	73,5	60,356	32,0315	31,5801	32,4829	6	3	3	0,034529	-0,902805	B8N1K6	B8N1K6	1	AFLA_030710	Phosphoglucomutase PgmA
NaN	NaN	NaN	NaN	24,5609	24,3599		6,37E-06	2,14E+08	3	3	3	20,4	21,449	24,4604	NaN	24,4604	2	0	2	1	NaN	B8N1K7	B8N1K7	1	AFLA_030720	RNA exonuclease Rex2, putative
25,9139	26,0048	25,4817	25,8148	26,2934	26,3943		7,19E-24	6,02E+08	4	4	4	9,6	64,417	25,9838	25,8001	26,1675	6	3	3	0,201765	-0,367404	B8N1K8	B8N1K8	1	AFLA_030730	Uncharacterized protein
29,6008	29,6	29,2867	29,5638	29,5036	29,601		3,95E-246	7,48E+09	15	15	15	52,5	45,843	29,526	29,4959	29,5561	6	3	3	0,607627	-0,060276	B8N1L8	B8N1L8	1	AFLA_030830	Oxysterol binding protein (Osh5), putative
31,1127	30,9404	30,9136	31,048	30,9826	31,031		0	2,17E+10	14	14	14	48,1	40,857	31,0047	30,9889	31,0206	6	3	3	0,653828	-0,0316308	B8N1M4	B8N1M4	1	AFLA_030890	Saccharopine dehydrogenase [NAD(+), L-lysine-forming] (SDH) (EC 1.5.1.7) (Lysine--2-oxoglutarate reductase)
34,175	34,2857	34,0221	34,3793	34,2637	34,3197		0	1,97E+11	26	26	26	86,5	39,721	34,2409	34,1609	34,3209	6	3	3	0,127465	-0,159983	B8N1M8	B8N1M8	1	AFLA_030930	Fructose-bisphosphate aldolase, class II
30,4893	30,1892	29,9777	30,4259	30,4083	30,5326		0	1,35E+10	23	23	23	75,3	38,934	30,3372	30,2187	30,4556	6	3	3	0,197478	-0,236863	B8N1N2	B8N1N2	1	AFLA_030970	Homoserine dehydrogenase (EC 1.1.1.3)
30,5508	30,0619	30,0066	30,0431	30,3708	30,3045		9,56E-178	1,32E+10	6	6	6	54,8	11,945	30,223	30,2064	30,2395	6	3	3	0,876672	-0,0330346	B8N1N5	B8N1N5	1	AFLA_031000	Nucleosome binding protein (Nhp6a), putative
28,001	27,6853	27,5939	28,1238	28,2415	28,3009	+	2,47E-171	2,88E+09	10	10	10	40,1	32,75	27,9911	27,7601	28,2221	6	3	3	0,026013	-0,461995	B8N1Q0	B8N1Q0	1	AFLA_031150	Methylglutaconyl-CoA hydratase, mitochondrial, putative
30,1141	29,8281	29,6931	29,7646	29,7237	29,8304		0	7,88E+09	13	13	13	65,4	35,167	29,8256	29,8784	29,7729	6	3	3	0,455826	0,105532	B8N3N6	B8N3N6	1	AFLA_031200	Arginase (EC 3.5.3.1)
32,3499	32,0359	31,8966	32,0209	32,0844	32,2715		0	4,55E+10	13	13	13	40,1	43,135	32,1099	32,0942	32,1256	6	3	3	0,848113	-0,031402	B8N3P1	B8N3P1	1	AFLA_031250	Aspartic endopeptidase Pep2
NaN	25,9303	26,0536	26,0043	NaN	25,936		1,70E-74	7,26E+08	8	7	7	32,2	48,212	25,9811	25,992	25,9702	4	2	2	0,78614	0,0218134	B8N3P2	B8N3P2	1	AFLA_031260	Proteasome regulatory particle subunit Rpt3, putative
28,9693	29,6839	30,0038	29,7055	29,5472	29,2497		0	9,18E+09	20	20	20	59,9	51,591	29,5266	29,5523	29,5008	6	3	3	0,884748	0,0515397	B8N3P5	B8N3P5	1	AFLA_031290	Eukaryotic translation initiation factor 3 subunit E (eIF3e)
26,87	27,1132	26,949	27,0071	27,0523	27,0842		1,58E-69	1,55E+09	9	9	9	43,4	37,416	27,0126	26,9774	27,0478	6	3	3	0,400917	-0,0704486	B8N3P7	B8N3P7	1	AFLA_031310	ATPase get3 (EC 3.6.-.-) (Arsenical pump-driving ATPase) (Arsenite-stimulated ATPase) (Golgi to ER traffic protein 3) (Guided entry of tail-anchored proteins 3)
30,1839	29,9174	29,5431	29,7181	29,8534	29,985		0	9,73E+09	14	14	14	24,9	74,441	29,8668	29,8815	29,8522	6	3	3	0,891199	0,029314	B8N3Q2	B8N3Q2	1	AFLA_031360	Proteasome component Prs2, putative
26,0272	25,9071	25,2307	25,5414	25,6688	25,7687		2,88E-21	9,18E+08	5	5	5	24,5	48,256	25,6907	25,7217	25,6596	6	3	3	0,820783	0,0620384	B8N3Q4	B8N3Q4	1	AFLA_031380	Class V chitinase, putative
31,0138	30,99	30,4315	30,7785	30,7821	30,776		3,61E-249	2,02E+10	7	7	3	50	17,628	30,7953	30,8118	30,7789	6	3	3	0,871121	0,032896	B8N3Q5;B8	B8N3Q5;B8	2	AFLA_031390	Ubiquitin (UbiC), putative
25,5719	24,6714	NaN	NaN	NaN	NaN		9,65E-08	1,15E+08	4	4	4	19,8	46,735	25,1216	25,1216	NaN	2	2	0	1	NaN	B8N3Q7	B8N3Q7	1	AFLA_031410	Ribonuclease T2 family, putative
32,6696	33,6088	34,2626	33,9729	33,7018	33,3311		0	1,7E+11	27	27	27	79,6	62,926	33,5912	33,5137	33,6686	6	3	3	0,771437	-0,154908	B8N3S3	B8N3S3	1	AFLA_031570	Pyruvate decarboxylase PdcA, putative
NaN	NaN	NaN	NaN	24,4917	24,301		1,56E-16	2,42E+08	5	5	5	7,1	108,52	24,3964	NaN	24,3964	2	0	2	1	NaN	B8N3S6	B8N3S6	1	AFLA_031600	SNARE-dependent exocytosis protein (Sro7), putative
28,1148	27,7222	27,4637	27,8523	27,7786	28,0069		0	1,92E+09	6	6	6	38,6	31,923	27,8231	27,7669	27,8793	6	3	3	0,605749	-0,112373	B8N3S8	B8N3S8	1	AFLA_031620	Histone chaperone
24,114	NaN	23,905	23,9039	NaN	NaN		3,74E-06	1,38E+08	2	2	2	2,9	113,72	23,9743	24,0095	23,9039	3	2	1	1	0,105616	B8N3S9	B8N3S9	1	AFLA_031630	CFIA complex component Rna14, putative
25,6193	NaN	NaN	24,6828	NaN	24,8359		6,90E-07	2,63E+08	3	3	3	7,6	40,709	25,046	25,6193	24,7594	3	1	2	1	0,859938	B8N3T8	B8N3T8	1	AFLA_031720	Peroxisomal membrane protein receptor Pex19, putative
25,2708	24,8308	24,8292	24,9942	25,8984	26,1762		4,94E-16	4,11E+08	5	5	5	10,1	92,445	25,3333	24,977	25,6896	6	3	3	0,138529	-0,712616	B8N3U2	B8N3U2	1	AFLA_031760	Glutaminase, putative
26,4455	27,0827	29,3483	30,2066	27,1106	26,803		6,63E-220	5,94E+09	11	11	11	35,4	31,06	27,8328	27,6255	28,0401	6	3	3	0,781715	-0,414589	B8N3U4	B8N3U4	1	AFLA_031780	Telomere and ribosome associated protein Stm1, putative
29,0416	28,3921	28,0417	28,0302	28,395	28,543		3,02E-79	3,05E+09	10	10	10	54,8	28,662	28,4073	28,4918	28,3227	6	3	3	0,635577	0,169078	B8N3U8	B8N3U8	1	AFLA_031820	Glutathione S-transferase GstA
28,6696	28,9402	28,6386	28,0421	28,9547	29,0973		2,97E-232	6,67E+09	28	28	28	32,5	138,73	28,7238	28,7495	28,698	6	3	3	0,888467	0,0514151	B8N3V1	B8N3V1	1	AFLA_031850	Clustered mitochondria protein homolog (Protein TIF31 homolog)

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
26,6225	25,3222	25,7883	25,2157	25,594	25,2159		4,48E-22	4,47E+08	5	4	4	31,8	27,628	25,6264	25,911	25,3418	6	3	3	0,22851	0,569181	B8N3W1	B8N3W1	1	AFLA_031950	RAB GTPase Vps21/Ypt51, putative
25,9504	26,1407	28,8255	28,2836	26,8149	26,9957		6,84E-34	1,63E+09	7	7	7	40,3	22,775	27,1685	26,9722	27,3648	6	3	3	0,724281	-0,392534	B8N3W2	B8N3W2	1	AFLA_031960	40S ribosomal protein S7e
27,6261	27,9259	27,8703	28,0214	28,1063	28,0996	+	6,16E-296	2,89E+09	9	9	9	76,2	20,442	27,9416	27,8074	28,0758	6	3	3	0,049064	-0,268372	B8N3W5	B8N3W5	1	AFLA_031990	Actin-related protein 2/3 complex subunit 5
29,6717	30,1712	30,4267	30,0013	29,9037	29,9478		0	1,24E+10	13	13	13	45,2	51,026	30,0204	30,0899	29,9509	6	3	3	0,567844	0,138939	B8N3W9;B	B8N3W9	2	AFLA_032030	Hydroxymethylglutaryl-CoA synthase Erg13, putative
27,8605	28,0612	27,4339	27,5377	27,5654	27,7762		9,88E-131	2,24E+09	3	3	3	25,6	14,068	27,7058	27,7852	27,6264	6	3	3	0,471182	0,158749	B8N1S1	B8N1S1	1	AFLA_032250	Nuclear transport factor NTF-2, putative
24,4953	24,1945	23,8048	24,2519	24,4084	NaN		2,55E-08	1,72E+08	2	2	2	4,3	71,329	24,231	24,1649	24,3302	5	3	2	0,576467	-0,165271	B8N1S4	B8N1S4	1	AFLA_032280	Uncharacterized protein
27,9203	27,2017	26,7029	26,9989	27,4383	27,6834		2,21E-71	1,73E+09	8	8	8	43,6	34,316	27,3243	27,275	27,3735	6	3	3	0,820216	-0,0985406	B8N1S7	B8N1S7	1	AFLA_032310	Uncharacterized protein
24,3122	25,4201	25,1353	25,181	25,3459	25,3663		3,59E-22	6,2E+08	7	7	7	10,1	99,561	25,1268	24,9559	25,2977	6	3	3	0,368154	-0,341863	B8N1T0	B8N1T0	1	AFLA_032340	Vacuolar protein sorting-associated protein 35
24,0985	NaN	23,4446	NaN	24,6681	NaN		1,35E-38	6,08E+08	9	9	9	39,6	34,993	24,0704	23,7715	24,6681	3	2	1	1	-0,896581	B8N1U2	B8N1U2	1	AFLA_032460	Pterin-4-alpha-carbinolamine dehydratase, putative
28,8771	28,3263	27,9982	28,3752	28,5172	28,7679		4,18E-202	6,32E+09	10	10	10	73,3	24,935	28,477	28,4005	28,5534	6	3	3	0,615151	-0,152912	B8N1U3	B8N1U3	1	AFLA_032470	Phosphoglycolate phosphatase, putative
24,5737	25,3946	26,6978	27,2211	25,8998	25,8064		3,31E-34	1,29E+09	8	8	8	20,9	58,992	25,9322	25,5553	26,3091	6	3	3	0,382378	-0,753794	B8N1U7	B8N1U7	1	AFLA_032510	Galactokinase
25,7136	25,2093	24,5877	24,6759	25,0464	25,9821		5,06E-18	3,63E+08	9	9	9	4,1	266,87	25,2025	25,1702	25,2348	6	3	3	0,904765	-0,0645994	B8N1V7	B8N1V7	1	AFLA_032610	Ccr4-Not transcription complex subunit (NOT1), putative
NaN	24,0982	24,8068	24,7393	NaN	NaN		3,17E-08	1,4E+08	3	3	3	6,5	82,995	24,5481	24,4525	24,7393	3	2	1	1	-0,286803	B8N1V9	B8N1V9	1	AFLA_032630	Acid phosphatase, putative
26,4842	26,523	26,4493	24,5883	24,6968	24,2798	+	1,23E-16	4,5E+08	4	4	4	13,3	35,184	25,5035	26,4855	24,5216	6	3	3	0,000101	1,96384	B8N1X2	B8N1X2	1	AFLA_032760	Pre-RNA splicing factor Srp2, putative
27,2029	27,0673	26,8473	27,0646	27,0581	27,1528		6,21E-58	1,56E+09	11	11	11	38,4	37,741	27,0655	27,0392	27,0918	6	3	3	0,65179	-0,052599	B8N1X3	B8N1X3	1	AFLA_032770	Dihydroneopterin aldolase domain protein
30,0553	29,6923	29,343	29,6892	29,7573	29,8283		6,03E-290	9,23E+09	15	15	15	47,1	45,104	29,7276	29,6969	29,7583	6	3	3	0,784133	-0,0613798	B8N1Y3	B8N1Y3	1	AFLA_032870	cAMP-dependent protein kinase regulatory subunit
27,7601	27,2706	27,0174	27,3881	27,6674	27,8256		9,33E-84	1,93E+09	6	6	6	27,7	50,762	27,4882	27,3494	27,6271	6	3	3	0,333636	-0,27765	B8N1Y5	B8N1Y5	1	AFLA_032890	Uncharacterized protein
30,1757	30,1684	30,2138	30,5797	30,6247	30,6783	+	0	1,64E+10	20	20	20	75,4	36,716	30,4068	30,186	30,6276	6	3	3	0,000156	-0,441579	B8N3Y7	B8N3Y7	1	AFLA_033100	Phosphatidylinositol transporter, putative
26,288	26,2291	25,8768	24,1274	23,8704	24,28	+	3,99E-28	2,51E+08	7	7	7	16,1	74,805	25,112	26,1313	24,0926	6	3	3	0,000313	2,03871	B8N3Z9	B8N3Z9	1	AFLA_033220	Amidase family protein
24,6399	24,5677	NaN	NaN	24,6264	NaN		9,49E-06	1,51E+08	3	3	3	7,7	52,906	24,6113	24,6038	24,6264	3	2	1	1	-0,0225964	B8N412	B8N412	1	AFLA_033350	Lipin Smp2, putative
29,3071	29,039	29,0757	29,2415	29,174	29,1453		3,22E-254	6,12E+09	23	23	23	40,7	92,27	29,1638	29,1406	29,1869	6	3	3	0,628676	-0,0463384	B8N416	B8N416	1	AFLA_033390	Phosphoribosyl-AMP cyclohydrolase, putative
23,4636	23,8317	NaN	NaN	NaN	NaN		1,01E-21	4,58E+08	3	3	3	26,3	15,049	23,6477	23,6477	NaN	2	2	0	1	NaN	B8N418	B8N418	1	AFLA_033410	Uncharacterized protein
31,0048	30,8172	29,4694	30,3831	30,6088	30,8026		0	2,91E+10	11	11	11	79	23,229	30,5143	30,4304	30,5982	6	3	3	0,753427	-0,167745	B8N419	B8N419	1	AFLA_033420	Superoxide dismutase (EC 1.15.1.1)
28,7492	29,3066	28,9138	28,5637	28,5961	28,6061		0	6,47E+09	16	16	16	62,4	38,059	28,7893	28,9899	28,5886	6	3	3	0,072795	0,401217	B8N426	B8N426	1	AFLA_033490	Nitrilase
26,3849	26,3853	25,0397	24,5244	24,4591	24,7901	+	4,08E-25	3,29E+08	3	3	3	9	48,41	25,2639	25,9366	24,5912	6	3	3	0,042965	1,34544	B8N429	B8N429	1	AFLA_033520	Ubiquitin-like protein DskB, putative
25,209	25,2936	24,7901	24,6787	24,5791	24,3028	+	7,28E-21	3,67E+08	7	7	7	7,9	134,05	24,8089	25,0976	24,5202	6	3	3	0,039677	0,577343	B8N430	B8N430	1	AFLA_033530	Nuclear mRNA splicing factor, putative
29,5506	29,4235	29,0482	29,5544	29,3235	29,297		3,25E-273	8,67E+09	5	5	5	47,8	12,756	29,3662	29,3408	29,3916	6	3	3	0,781676	-0,0508486	B8N439	B8N439	1	AFLA_033620	RNA binding protein, putative
24,7589	26,9757	27,7814	27,8767	27,6214	27,2636		5,95E-33	3,37E+09	7	7	7	29,9	24,083	27,0463	26,5053	27,5872	6	3	3	0,305278	-1,08188	B8N442	B8N442	1	AFLA_033650	GTP-binding nuclear protein Ran, putative
NaN	24,4447	24,8381	27,316	23,9495	24,1749		1,25E-40	3,94E+08	3	3	3	35,7	13,675	24,9446	24,6414	25,1468	5	2	3	0,743832	-0,505368	B8N444	B8N444	1	AFLA_033670	Lipid transfer protein, putative
26,6164	28,262	29,4242	27,0359	25,2716	25,2602		6,81E-24	1,35E+09	6	6	6	37,4	14,069	26,9784	28,1009	25,8559	6	3	3	0,089407	2,24498	B8N446	B8N446	1	AFLA_033690	60S ribosomal protein L31e
29,502	28,7795	28,692	28,4128	28,707	28,9227		7,97E-125	4E+09	13	13	13	57,9	31,788	28,836	28,9912	28,6808	6	3	3	0,353857	0,310338	B8N447	B8N447	1	AFLA_033700	Nitrilase family protein (Nit3), putative
27,5672	27,556	27,2996	27,6782	27,3889	27,5107		2,78E-62	2,16E+09	7	7	7	36,2	25,195	27,5001	27,4743	27,5259	6	3	3	0,691714	-0,0516548	B8N456	B8N456	1	AFLA_033790	3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase) (EC 4.1.99.12)
27,774	27,454	27,2442	27,4969	27,4272	27,5609		2,13E-106	2,05E+09	23	23	23	17,2	227,08	27,4928	27,4907	27,495	6	3	3	0,979762	-0,0042858	B8N458	B8N458	1	AFLA_033810	Filament-forming protein (Tpr/p270), putative
30,9771	31,3758	31,0232	27,5222	26,535	26,7988	+	0	1,46E+10	16	16	16	46,6	29,318	29,0387	31,1254	26,952	6	3	3	0,000202	4,17335	B8N204	B8N204	1	AFLA_033980	Cytosolic large ribosomal subunit protein L7A
24,7857	24,7743	24,5391	24,589	24,5864	25,0391		5,99E-13	2,67E+08	3	3	3	4,5	97,559	24,7189	24,6997	24,7382	6	3	3	0,83274	-0,0384432	B8N205	B8N205	1	AFLA_033990	Spindle pole body component, putative
26,5223	26,8495	25,9997	24,1572	24,2282	24,0797	+	3,36E-73	6,58E+08	5	5	5	27,6	24,22	25,3061	26,4572	24,155	6	3	3	0,000786	2,30213	B8N208	B8N208	1	AFLA_034020	Uncharacterized protein
32,9691	32,9159	32,9568	33,3536	33,3665	33,3344	+	0	9,22E+10	46	46	46	71,6	85,596	33,1494	32,9472	33,3515	6	3	3	2,64E-05	-0,404273	B8N211	B8N211	1	AFLA_034050	Mitochondrial aconitate hydratase, putative
28,0904	28,8087	28,7542	28,893	28,8216	28,8379		1,10E-203	4,76E+09	19	19	19	36,9	99,543	28,701	28,5511	28,8509	6	3	3	0,265782	-0,299747	B8N222	B8N222	1	AFLA_034160	Protein transport protein Sec24, putative
24,6954	25,3017	25,7897	25,7435	25,7905	25,387		5,90E-21	7,54E+08	8	8	8	27,4	40,976	25,4513	25,2623	25,6403	6	3	3	0,330017	-0,378035	B8N223	B8N223	1	AFLA_034170	Mitogen-activated protein kinase (EC 2.7.11.24)
30,941	30,3806	30,6761	28,9999	29,7498	29,8324	+	0	1,03E+10	13	13	13	72,4	27,369	30,0967	30,6659	29,5274	6	3	3	0,021419	1,13856	B8N226	B8N226	1	AFLA_034200	2-heptaprenyl-1,4-naphthoquinone methyltransferase, putative
28,4927	28,1875	28,1233	27,9174	28,1148	28,1646		5,53E-153	3,44E+09	12	12	12	39,1	43,56	28,1667	28,2678	28,0656	6	3	3	0,213039	0,202245	B8N227	B8N227	1	AFLA_034210	Proteasome regulatory particle subunit (Rpn1), putative
29,6769	29,0912	28,8406	29,0896	29,3307	29,5326		3,27E-149	6,96E+09	6	6	6	38,9	26,953	29,2603	29,2029	29,3176	6	3	3	0,701931	-0,114717	B8N230	B8N230	1	AFLA_034240	Dienelactone hydrolase family protein
NaN	23,5289	26,0169	23,18	22,5853	22,4329		3,13E-12	1,08E+08	4	4	4	15,8	20,056	23,5488	24,7729	22,7327	5	2	3	0,126905	2,04017	B8N234	B8N234	1	AFLA_034280	40S ribosomal protein S29, putative
25,0468	25,483	24,8968	25,0692	25,2397	25,435		2,37E-12	4,82E+08	6	6	6	21,9	37,621	25,1951	25,1422	25,248	6	3	3	0,633266	-0,105791	B8N237	B8N237	1	AFLA_034310	Uncharacterized protein
27,4715	27,1045	27,2124	27,5287	27,7568	27,745	+	6,34E-54	2,13E+09	7	7	7	54,4	16,399	27,4698	27,2628	27,6768	6	3	3	0,03477	-0,414032	B8N238	B8N238	1	AFLA_034320	HIT domain protein
24,8089	25,0399	26,887	23,7193	24,4533	24,3094		1,23E-28	4,39E+08	9	9	9	24,6	54,14	24,8696	25,5786	24,1607	6	3	3	0,110875	1,41795	B8N239	B8N239	1	AFLA_034330	Beta-alanine synthase, putative
24,9013	25,1411	27,0779	25,3279	25,3574	25,4539		5,08E-23	1,01E+09	3	3	3	24,8	23,314	25,5432	25,7067	25,3797	6	3	3	0,660308	0,327009	B8N240	B8N240	1	AFLA_034340	40S ribosomal protein S10b
27,5177	27,288	26,7817	27,5518	28,3007	28,1732		2,72E-113	3,12E+09	15	15	15	47,4	53,28	27,6022	27,1958	28,0886	6	3	3	0,062616	-0,812788	B8N244	B8N244	1	AFLA_034380	Catalase, putative
27,4618	26,5689	25,9061	25,9476	26,4653	26,3859		3,85E-43	1,44E+09	6	6	6	19,1	48,326	26,4559	26,6456	26,2662	6	3	3	0,472357	0,379353	B8N247	B8N247	1	AFLA_034410	Aspartate aminotransferase, putative
27,7747	29,4168	30,175	30,0177	29,6326	29,1822		0	1,21E+10	40	40	40	47,4	126,92	29,3665	29,1222	29,6108	6	3	3	0,549422	-0,488655	B8N248	B8N248	1	AFLA_034420	Leucyl-tRNA synthetase
25,9282	26,5169	26,5902	26,8926	26,8895	26,6252		5,71E-58	9,57E+08	10	10	10	28,7	56,957	26,5738	26,3451	26,8024	6	3	3	0,114771	-0,457338	B8N253	B8N253	1	AFLA_034470	Anthranilate synthase component I, putative
31,6763	31,3276	31,1972	29,2447	29,7845	30,0068	+	0	1,23E+10	27	27	26	66,8	75,372	30,5395	31,4003	29,6786	6	3	3	0,003005	1,7217	B8N268	B8N268	1	AFLA_034620	Amine oxidase
22,4877	NaN	29,5672	NaN	20,8521	NaN		3,53E-82	7,24E+08	10	10	10	35,3	53,556	24,3024	26,0275	20,8521	3	2	1	1	5,17539	B8N270	B8N270	1	AFLA_034640	Peptide hydrolase (EC 3.4.-.-)
24,3218	24,8368	24,5912	24,5283	25,0077	25,0304		2,30E-10	2,61E+08	5	5	5	17,3	49,719	24,7194	24,5833	24,8555	6	3	3	0,285883	-0,272187	B8N471;B8	B8N471	2	AFLA_034840	Uncharacterized protein
27,6051	27,6491	27,4452	26,2362	26,5395	26,1732	+	6,53E-94	1,41E+09	3	3	3	45,5	13,43	26,9414	27,5665	26,3163	6	3	3	0,000633	1,25018	B8N488	B8N488	1	AFLA_035010	Small nuclear ribonucleoprotein SmD1, putative
28,6249	28,6314	28,4852	28,3345	28,7613	28,8695		8,87E-193	5,08E+09	15	15	15	43,4	50,269	28,6178	28,5805	28,6551	6	3	3	0,683656	-0,0746078	B8N4A2	B8N4A2	1	AFLA_035150	Proline iminopeptidase
26,2414	26,0284	25,2381	25,5423	25,6364	25,8023		1,01E-19	5,56E+08	7	7	7	18,7	56,337	25,7482	25,836	25,6604	6	3	3	0,606363	0,175617	B8N4A3	B8N4A3	1	AFLA_035160	Tyrosine decarboxylase, putative
23,687	24,2544	23,6217	24,6111	24,6176	24,6778	+	3,07E-09	1,83E+08	3	3	3	9,6	55,155	24,2449	23,8543	24,6355	6	3	3	0,018043	-0,781165	B8N4A4	B8N4A4	1	AFLA_035170	Kelch repeats protein, putative
28,9789	28,822	28,5665	28,6276	28,5639	28,6457		3,58E-101	4,42E+09	13	13	13	46,6	48,762	28,7008	28,7892	28,6124	6	3	3	0,223116	0,176778	B8N4A8	B8N4A8	1	AFLA_035210	KH domain RNA binding protein
26,6449	26,5914	26,1957	26,6951	27,0186	27,0912		1,03E-35	1,08E+09	6	6	6	32,4	24,935	26,7061	26,4773	26,935	6	3	3	0,070421	-0,457694	B8N4A9	B8N4A9	1	AFLA_035220	Uncharacterized protein
26,1357	25,4648	25,244	25,6371	25,7208	25,7747		4,39E-28	5,15E+08	5	5	5	5,6	153,92	25,6628	25,6148	25,7109	6	3	3	0,740935	-0,0960687	B8N4B0	B8N4B0	1	AFLA_035230	Nuclear pore complex subunit Nup159, putative
28,259	27,8963	27,5251	27,7133	27,9153	27,8229		7,21E-161	2,42E+09	10	10	10	49,3	29,518	27,8553	27,8935	27,8172	6	3	3	0,745994	0,0762889	B8N4B1	B8N4B1	1	AFLA_035240	Proteasome subunit beta type (EC 3.4.25.1)
NaN	23,7707	25,4804	24,2229	24,1209	23,2713		1,74E-24	4,16E+08	6	6	6	10,2	78,088	24,1732	24,6255	23,8717	5	2	3	0,387076	0,753858	B8N4C0	B8N4C0	1	AFLA_035330	Translation release factor eRF3, putative
25,0865	24,8854	24,2801	NaN	25,0977	25,4308		1,25E-06	2,12E+08	3	3	3	4,3	82,256	24,9561	24,7507	25,2642	5	3	2	0,224502	-0,51357	B8N4D5	B8N4D5	1	AFLA_035480	Vacuolar sorting-associated protein (Vps27), putative
31,0368	30,0081	28,8249	28,4661	29,811	30,0381		3,15E-156	8,55E+09	7	7	7	63,5	14,54	29,6975	29,9566	29,4384	6	3	3	0,555068	0,518235	B8N4D7	B8N4D7	1	AFLA_035500	Cytochrome b5, putative
27,9876	27,7245	27,0189	27,9612	26,9865	27,5095		5,19E-53	2,28E+09	15	15	15	22,2	104,41	27,5314	27,577	27,4858	6	3	3	0,832282	0,0912253	B8N4D8	B8N4D8	1	AFLA_035510	RNA binding effector protein Scp160, putative
26,4022	26,3735	26,2445	26,0493	26,2211	26,3284		5,59E-25	8,19E+08	5	5	5	14	69,532	26,2698	26,3401	26,1996	6	3	3	0,211876	0,140477	B8N4E1	B8N4E1	1	AFLA_035540	Signal transducing adapter molecule, putative
29,8048	29,5859	29,6195	29,6292	29,5511	29,6032		0	7,64E+09	9	9	9	75,9	20,375	29,6323	29,6701	29,5945	6	3	3	0,352126	0,0755876	B8N4E8	B8N4E8	1	AFLA_035610	DUF967 domain protein
31,9567	31,5926	31,2387	31,1086	31,1958	31,3184		0	2,58E+10	30	30	30	52,1	73,449	31,4018	31,596	31,2076	6	3	3	0,146617	0,388388	B8N4E9	B8N4E9	1	AFLA_035620	Hsp70 chaperone BiP/Kar2, putative
29,056	29,0522	29,0126	29,2583	29,3469	29,3801	+	1,89E-297	6,34E+09	15	15	15	58,7	31,301	29,1844	29,0403	29,3285	6	3	3	0,001776	-0,288161	B8N293	B8N293	1	AFLA_035780	Uncharacterized protein
25,2673	25,4799	25,1486	26,9574	26,6569	26,368	+	3,07E-24	4,62E+08	6	6	6	37,8	25,614	25,9797	25,2986	26,6608	6	3	3	0,002243	-1,36218	B8N2C2	B8N2C2	1	AFLA_036070	Maleylacetoacetate isomerase MaiA
30,0517	29,8409	29,4574	30,6272	30,3125	30,3757	+	0	1,01E+10	18	18	18	68,4	46,876	30,1109	29,7833	30,4384	6	3	3	0,03004	-0,655108	B8N2C3	B8N2C3	1	AFLA_036080	Fumarylacetoacetate hydrolase FahA
29,2876	29,1581	28,762	29,8299	29,5531	29,6712	+	0	5,7E+09	18	18	18	79,7	50,35	29,377	29,0693	29,6847	6	3	3	0,025546	-0,615473	B8N2C4	B8N2C4	1	AFLA_036090	Homogentisate 1,2-dioxygenase (HmgA), putative
25,4816	26,4799	27,0792	28,8616	27,2311	26,6891		8,29E-107	2,1E+09	16	16	16	46,2	45,34	26,9704	26,3469	27,594	6	3	3	0,194965	-1,24708	B8N2C6	B8N2C6	1	AFLA_036110	4-hydroxyphenylpyruvate dioxygenase
NaN	23,9214	25,3986	24,3883	NaN	NaN		6,41E-34	3,72E+08	4	4	4	11,4	63,462	24,5694	24,66	24,3883	3	2	1	1	0,271685	B8N2D2	B8N2D2	1	AFLA_036170	T-complex protein 1, epsilon subunit, putative
25,8131	26,0609	25,9535	26,1474	26,5006	26,4797	+	2,09E-130	1,07E+09	5	5	5	45,9	23,369	26,1592	25,9425	26,3759	6	3	3	0,032605	-0,433446	B8N2D7	B8N2D7	1	AFLA_036220	Uncharacterized protein
24,2836	25,7799	26,6569	26,5878	25,6138	25,7362		9,53E-114	1,61E+09	11	11	11	35,5	48,625	25,7764	25,5735	25,9792	6	3	3	0,620598	-0,405769	B8N2E0	B8N2E0	1	AFLA_036250	GDP-mannose pyrophosphorylase A
28,4465	29,2502	29,3903	29,7208	29,4013	28,8854		0	9,31E+09	22	22	22	50,7	68,796	29,1824	29,029	29,3359	6	3	3	0,466477	-0,306864	B8N2E2	B8N2E2	1	AFLA_036270	Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)
29,6768	29,7969	29,6173	30,6462	31,2973	31,1403	+	0	1,28E+10	27	27	27	65,2	66,547	30,3625	29,697	31,028	6	3	3	0,002807	-1,33096	B8N2F2	B8N2F2	1	AFLA_036370	Phosphoenolpyruvate carboxykinase AcuF

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
27,2001	27,9914	27,915	27,9447	28,0498	27,9886		2,33E-192	2,7E+09	17	17	17	45,4	54,247	27,8483	27,7022	27,9944	6	3	3	0,313769	-0,292208	B8N2F8	B8N2F8	1	AFLA_036430	Proteasome regulatory particle subunit (RpnG), putative
27,4231	27,6453	27,5855	28,0787	27,9659	28,1114	+	1,64E-151	2,69E+09	8	8	8	27,5	54,829	27,8016	27,5513	28,052	6	3	3	0,003277	-0,500666	B8N2F9	B8N2F9	1	AFLA_036440	Alanine aminotransferase, putative
NaN	23,2982	24,4261	25,1787	NaN	NaN		6,18E-10	1,6E+08	2	2	2	18,7	23,738	24,301	23,8622	25,1787	3	2	1	1	-1,31656	B8N2G6	B8N2G6	1	AFLA_036510	Methionine-R-sulfoxide reductase SelR, putative
NaN	24,4029	24,4384	28,0252	28,3331	27,1151	+	9,92E-95	1,71E+09	11	11	11	31,6	57,045	26,4629	24,4206	27,8245	5	2	3	0,005506	-3,4038	B8N4G1	B8N4G1	1	AFLA_036640	PH domain protein
29,1996	28,9078	28,7983	29,1928	29,2374	29,2067		6,29E-254	6,33E+09	16	16	15	67	36,418	29,0904	28,9686	29,2123	6	3	3	0,113168	-0,243731	B8N4G3	B8N4G3	1	AFLA_036660	Lactoylglutathione lyase (EC 4.4.1.5) (Glyoxalase I)
33,5572	33,1554	33,1353	33,0557	33,2528	33,2484		0	1,04E+11	36	36	36	75,8	54,216	33,2341	33,2826	33,1856	6	3	3	0,558051	0,0970001	B8N4I0	B8N4I0	1	AFLA_036840	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
26,3238	25,8346	25,4439	25,49	25,8246	26,0511		4,11E-22	6,24E+08	3	3	3	18,2	26,494	25,828	25,8674	25,7886	6	3	3	0,807108	0,0788352	B8N4I1	B8N4I1	1	AFLA_036850	Uncharacterized protein
25,4565	25,398	25,8965	NaN	25,6164	25,8795		0,000154	5,09E+08	2	2	2	1,3	188,25	25,6494	25,5836	25,748	5	3	2	0,518932	-0,164339	B8N4K1	B8N4K1	1	AFLA_037050	HEAT repeat protein (DRIM), putative
NaN	23,5586	23,736	23,4144	23,448	23,581		5,45E-05	1,18E+08	2	2	2	3,3	61,235	23,5476	23,6473	23,4811	5	2	3	0,172488	0,166202	B8N4K2	B8N4K2	1	AFLA_037060	CwfJ domain protein
29,7816	29,4086	29,0082	29,284	29,3834	29,4449		1,75E-189	7,17E+09	10	10	10	52,4	32,871	29,3851	29,3995	29,3708	6	3	3	0,90607	0,0286681	B8N4K7	B8N4K7	1	AFLA_037110	Proteasome subunit beta type (EC 3.4.25.1)
30,1848	31,1302	31,216	31,3203	30,6034	30,272		0	1,16E+10	13	13	13	51,7	35,109	30,7878	30,8437	30,7319	6	3	3	0,817065	0,111792	B8N4L2	B8N4L2	1	AFLA_037160	Thiazole biosynthesis enzyme Sti35
25,6951	24,9372	24,8324	24,344	25,3998	25,2925		1,96E-22	3,38E+08	5	5	5	10,2	73,648	25,0835	25,1549	25,0121	6	3	3	0,757408	0,142821	B8N4L5	B8N4L5	1	AFLA_037200	Uncharacterized protein
25,3698	25,9065	27,3501	27,1834	26,4537	25,985		1,33E-62	1,54E+09	10	10	10	37,9	45,511	26,3747	26,2088	26,5407	6	3	3	0,65401	-0,331903	B8N4L8	B8N4L8	1	AFLA_037230	Chorismate synthase (EC 4.2.3.5)
26,6384	25,8913	NaN	25,1075	26,077	26,111		2,41E-17	3,01E+08	6	6	6	28,9	39,94	25,965	26,2648	25,7652	5	2	3	0,397722	0,499672	B8N4M0	B8N4M0	1	AFLA_037250	Cyanide hydratase/nitrilase, putative
24,0575	24,4024	24,8802	22,8871	24,1451	24,6103		6,38E-08	1,94E+08	3	3	3	9,8	43,943	24,1638	24,4467	23,8808	6	3	3	0,375009	0,565839	B8N4M5	B8N4M5	1	AFLA_037300	Methionyl-tRNA formyltransferase family protein, putative
25,5979	25,8712	25,7718	25,2985	25,1575	25,3141	+	2,71E-130	1,25E+09	8	8	8	41,5	21,621	25,5018	25,747	25,2567	6	3	3	0,006473	0,490299	B8N4M7	B8N4M7	1	AFLA_037320	Rho GTPase Rho1
25,5634	26,2712	26,5588	25,9226	26,084	26,0181		5,51E-55	7,99E+08	6	6	6	17,8	49,932	26,0697	26,1311	26,0082	6	3	3	0,702484	0,122926	B8N4N0	B8N4N0	1	AFLA_037350	Casein kinase I, putative
29,01	28,6667	28,4289	28,7473	28,8807	28,9365		6,14E-146	4,37E+09	12	12	12	47,4	45,809	28,7784	28,7019	28,8548	6	3	3	0,438096	-0,152953	B8N4P0	B8N4P0	1	AFLA_037450	Probable carboxypeptidase AFLA_037450 (EC 3.4.17.-) (Peptidase M20 domain-containing protein AFLA_037450)
26,3224	26,8787	26,9781	26,7111	26,6724	26,7561		1,94E-44	1,54E+09	12	12	11	40	46,412	26,7198	26,7264	26,7132	6	3	3	0,951724	0,0132357	B8N2H2	B8N2H2	1	AFLA_037470	Proteasome regulatory particle subunit Rpt4, putative
30,9885	32,8444	34,4212	34,808	33,6523	33,3054		0	1,13E+11	19	19	19	54,3	47,406	33,3367	32,7514	33,9219	6	3	3	0,343763	-1,17053	B8N2H3	B8N2H3	1	AFLA_037480	Enolase/allergen Asp F 22
26,8497	27,0541	26,8767	27,2048	27,1172	27,0233		8,96E-120	1,08E+09	5	5	5	30,6	29,688	27,021	26,9268	27,1151	6	3	3	0,085429	-0,188265	B8N2H4	B8N2H4	1	AFLA_037490	Eukaryotic translation initiation factor 3 subunit J (eIF3j) (Eukaryotic translation initiation factor 3 30 kDa subunit homolog)
30,3537	30,3772	30,2035	30,2713	30,2738	30,2732		3,01E-193	1,45E+10	13	12	12	50,2	22,89	30,2921	30,3115	30,2728	6	3	3	0,515986	0,0387274	B8N2H5	B8N2H5	1	AFLA_037500	14-3-3 protein sigma, gamma, zeta, beta/alpha, putative
25,5487	NaN	23,6399	NaN	NaN	23,8287		4,32E-23	2,41E+08	6	6	6	8,3	109,14	24,3391	24,5943	23,8287	3	2	1	1	0,765552	B8N2H6	B8N2H6	1	AFLA_037510	Calcium-transporting ATPase (EC 3.6.3.8)
28,5466	29,039	29,0736	29,4148	29,3575	29,3729	+	2,20E-224	7,2E+09	14	14	14	32,7	76,931	29,1341	28,8864	29,3817	6	3	3	0,044304	-0,495316	B8N2K3	B8N2K3	1	AFLA_037780	Actin-related protein 2/3 complex subunit 1A, putative
28,5829	28,2415	27,8324	28,1568	28,2369	28,3733		1,68E-71	3,18E+09	6	6	6	35,4	28,945	28,2373	28,219	28,2557	6	3	3	0,87885	-0,0366999	B8N2K9	B8N2K9	1	AFLA_037840	Proteasome subunit beta type (EC 3.4.25.1)
29,6964	29,3047	28,8871	29,1185	29,3793	29,4244		3,76E-116	6,48E+09	11	11	11	60,5	28,673	29,3017	29,2961	29,3074	6	3	3	0,966448	-0,0112953	B8N2L0	B8N2L0	1	AFLA_037850	Proteasome component Prs3, putative
24,6044	26,3551	27,11	26,3637	27,0501	26,3687		1,04E-168	3,08E+09	16	16	16	49,2	42,061	26,3087	26,0232	26,5942	6	3	3	0,50284	-0,570982	B8N2L6	B8N2L6	1	AFLA_037910	Isocitrate dehydrogenase [NAD] subunit, mitochondrial (EC 1.1.1.41)
29,8254	29,5183	29,1752	29,4661	29,5066	29,6048		0	7,78E+09	13	13	13	57,7	31,719	29,5161	29,5063	29,5259	6	3	3	0,923746	-0,0195885	B8N2L9	B8N2L9	1	AFLA_037940	Proteasome subunit alpha type (EC 3.4.25.1)
30,4022	30,1523	29,7284	30,071	30,2674	30,2766		0	1,29E+10	8	8	8	62,5	21,722	30,1497	30,0943	30,205	6	3	3	0,622433	-0,110694	B8N2M0	B8N2M0	1	AFLA_037950	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)
23,6363	26,1088	26,9387	25,5692	25,8241	25,6577		0	6,04E+09	29	29	29	49,4	77,127	25,6225	25,5613	25,6837	6	3	3	0,907984	-0,122416	B8N2M1	B8N2M1	1	AFLA_037960	Glucosamine-fructose-6-phosphate aminotransferase
27,4245	26,3567	27,0415	24,5807	24,9304	25,2521	+	4,11E-22	4,39E+08	8	8	8	22	54,086	25,931	26,9409	24,9211	6	3	3	0,005348	2,0198	B8NC44	B8NC44	1	AFLA_038390	Sarcosine oxidase, putative
23,4702	NaN	27,1883	NaN	NaN	NaN		1,45E-49	6,84E+08	9	9	9	20,6	69,301	25,3293	25,3293	NaN	2	2	0	1	NaN	B8NC58	B8NC58	1	AFLA_038530	Extracellular metalloproteinase mep (EC 3.4.24.-) (Elastinolytic metalloproteinase mep) (Fungalysin mep)
29,398	28,8011	28,6607	27,8362	28,1611	28,3295	+	0	7,84E+09	18	18	18	40,9	65,01	28,5311	28,9533	28,1089	6	3	3	0,034652	0,844376	B8NCH3	B8NCH3	1	AFLA_038790	Adenosine deaminase family protein
25,0566	NaN	NaN	23,2502	NaN	23,7905		7,19E-07	1,4E+08	3	3	3	8,3	56,279	24,0325	25,0566	23,5204	3	1	2	1	1,53625	B8NCH7	B8NCH7	1	AFLA_038840	Uncharacterized protein
NaN	NaN	NaN	25,5384	26,0352	25,8052		6,39E-08	2,85E+08	2	2	2	5,9	50,604	25,7929	NaN	25,7929	3	0	3	1	NaN	B8NCN0	B8NCN0	1	AFLA_039370	Acid phosphatase, putative
25,8532	NaN	24,7597	NaN	24,7036	24,891		4,95E-20	1,71E+08	4	4	4	22,3	26,281	25,0519	25,3065	24,7973	4	2	2	0,455551	0,509178	B8NCN4	B8NCN4	1	AFLA_039410	Cell wall serine-threonine-rich galactomannoprotein Mp1
27,4748	27,2631	26,6381	26,9729	26,9648	27,1411		6,41E-139	1,6E+09	3	3	3	22,9	37,182	27,0758	27,1253	27,0263	6	3	3	0,720141	0,0990855	B8NCP9	B8NCP9	1	AFLA_039560	WW domain protein
26,8105	26,3249	25,8094	23,6535	23,4816	23,8801	+	2,19E-35	2,71E+08	5	5	5	15	52,932	24,9933	26,315	23,6717	6	3	3	0,001054	2,64323	B8NAC3	B8NAC3	1	AFLA_039680	Uncharacterized protein
26,4963	25,9572	26,2093	26,34	26,294	26,5427		3,05E-33	8,16E+08	5	5	5	31,2	26,601	26,3066	26,2209	26,3922	6	3	3	0,379203	-0,171327	B8NAC4	B8NAC4	1	AFLA_039690	Phosphoglycerate mutase, putative
25,9183	25,0718	23,953	24,418	24,0786	24,2632		8,15E-18	6,83E+08	5	5	5	24,6	36,352	24,6171	24,981	24,2533	6	3	3	0,276143	0,727757	B8NAC6	B8NAC6	1	AFLA_039710	Quinone oxidoreductase, putative
30,058	30,5309	31,1301	31,0686	30,6648	30,4675		0	2,11E+10	21	21	21	63	45,963	30,6533	30,573	30,7336	6	3	3	0,676164	-0,160616	B8NAG7	B8NAG7	1	AFLA_040120	Flavohemoprotein
30,4971	30,2241	29,7106	30,3118	30,4689	30,5562		0	1,23E+10	20	20	20	52	56,251	30,2948	30,1439	30,4456	6	3	3	0,279462	-0,301708	B8NAJ3	B8NAJ3	1	AFLA_040380	Mannitol dehydrogenase, putative
29,9453	29,5184	29,5024	29,0136	29,0914	29,291	+	0	1,28E+10	12	12	12	37,3	50,7	29,3937	29,6554	29,132	6	3	3	0,035003	0,523361	B8NAJ8	B8NAJ8	1	AFLA_040430	Tripeptidyl-peptidase (TppA), putative
NaN	25,0949	25,4413	24,6792	24,4415	NaN		4,01E-66	1,08E+09	12	12	12	48,9	42,355	24,9142	25,2681	24,5603	4	2	2	0,077907	0,707808	B8NCE8	B8NCE8	1	AFLA_041230	Sterol 24-C-methyltransferase (EC 2.1.1.41) (Delta(24)-sterol C-methyltransferase)
28,3859	28,4657	27,767	28,1671	28,121	28,2612		1,33E-112	2,64E+09	11	11	11	28,8	51,2	28,1947	28,2062	28,1831	6	3	3	0,922994	0,0231133	B8NCF1	B8NCF1	1	AFLA_041260	Ribosome associated DnaJ chaperone Zuotin, putative
27,1748	26,5578	26,1767	31,1604	31,2486	31,369	+	3,00E-277	2,05E+10	8	8	8	27,3	46,686	28,9479	26,6365	31,2593	6	3	3	9,95E-05	-4,62288	B8NCF7	B8NCF7	1	AFLA_041320	Acid phosphatase, putative
26,1382	26,2121	26,0403	26,3211	26,7803	26,6566	+	8,66E-17	8,76E+08	4	3	3	22,7	29,604	26,3581	26,1302	26,586	6	3	3	0,03541	-0,455819	B8NCF9	B8NCF9	1	AFLA_041340	Oxidoreductase, short-chain dehydrogenase/reductase family
27,9106	26,7501	27,1331	27,4654	27,4435	27,4178		2,80E-35	1,55E+09	10	10	10	31,3	50,921	27,3534	27,2646	27,4422	6	3	3	0,630637	-0,177611	B8NCQ6	B8NCQ6	1	AFLA_041410	Aldehyde dehydrogenase family protein, putative
24,1601	24,2838	24,1643	24,903	25,1653	25,1583	+	4,70E-10	2,9E+08	4	4	4	19,8	27,783	24,6391	24,2027	25,0755	6	3	3	0,00079	-0,872804	B8NCQ7	B8NCQ7	1	AFLA_041420	GMP synthase
24,5544	24,5822	24,6662	25,468	25,3381	25,5099	+	4,33E-18	3,48E+08	6	6	6	14,8	52,992	25,0198	24,6009	25,4387	6	3	3	0,00017	-0,837776	B8NCQ8	B8NCQ8	1	AFLA_041430	Glutamine synthetase, putative
24,7682	24,8732	25,7076	25,6979	NaN	25,7533		9,27E-22	4,57E+08	6	6	6	39,8	20,754	25,3601	25,1164	25,7256	5	3	2	0,211002	-0,609254	B8NCS3	B8NCS3	1	AFLA_041580	Estradiol 17 beta-dehydrogenase, putative
28,3197	27,9039	27,7487	27,6068	28,1145	28,2454		2,96E-40	2,6E+09	14	14	14	39,6	54,159	27,9899	27,9908	27,9889	6	3	3	0,994633	0,001852	B8NCS4	B8NCS4	1	AFLA_041590	Peroxisomal multifunctional beta-oxidation protein (MFP), putative
29,6276	30,276	31,2166	28,2164	26,978	27,3119	+	0	7,27E+09	13	13	13	59	29,018	28,9377	30,3734	27,5021	6	3	3	0,008302	2,8713	B8NCT6	B8NCT6	1	AFLA_041710	60S ribosomal protein L7
29,7038	30,1849	30,4257	30,1628	29,961	29,7609		0	1,13E+10	35	35	35	47,2	97,164	30,0332	30,1048	29,9616	6	3	3	0,585433	0,143279	B8NCT8	B8NCT8	1	AFLA_041730	Eukaryotic translation initiation factor 3 subunit C (eIF3c) (Eukaryotic translation initiation factor 3 93 kDa subunit homolog) (Translation initiation factor eIF3, p93 subunit homolog)
30,7771	31,1042	31,3309	30,8318	31,1037	30,9368		0	2,62E+10	38	38	38	56,5	116,05	31,0141	31,0708	30,9575	6	3	3	0,56145	0,113309	B8NCU9	B8NCU9	1	AFLA_041840	Glycine dehydrogenase
27,4115	27,4527	27,9792	27,4503	26,9681	26,9991		1,54E-142	2,82E+09	14	14	14	39,5	60,701	27,3768	27,6145	27,1392	6	3	3	0,118945	0,475327	B8NCV5	B8NCV5	1	AFLA_041900	Amidase family protein
24,7788	27,1793	29,1956	27,0786	25,4827	25,4211		1,33E-44	1,38E+09	8	8	8	33,6	26,174	26,5227	27,0512	25,9941	6	3	3	0,488479	1,05708	B8NCW4	B8NCW4	1	AFLA_041990	60S ribosomal protein L17
27,3925	26,5731	26,3652	26,9542	27,3349	27,4122		1,63E-53	1,13E+09	9	8	8	40,4	35,853	27,0054	26,7769	27,2338	6	3	3	0,254942	-0,456828	B8NCW5	B8NCW5	1	AFLA_042000	Hydroxyisocaproate dehydrogenase, putative
26,0984	25,8174	25,5369	25,3567	25,4568	25,434		5,73E-14	5,41E+08	2	2	2	16,5	14,216	25,6167	25,8176	25,4158	6	3	3	0,071492	0,40176	B8NCX5	B8NCX5	1	AFLA_042100	Small nuclear ribonucleoprotein (LSM7), putative
25,2107	25,5221	25,5895	26,5268	25,3702	24,47		1,06E-99	1,33E+09	11	9	9	39,5	36,003	25,4482	25,4408	25,4556	6	3	3	0,981592	-0,01489	B8NAL4	B8NAL4	1	AFLA_042390	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
27,833	27,4003	27,2101	27,2384	27,6717	27,6637		6,80E-21	1,82E+09	6	6	6	37,9	35,698	27,5029	27,4812	27,5246	6	3	3	0,861424	-0,0434278	B8NAN1	B8NAN1	1	AFLA_042560	Phytanoyl-CoA dioxygenase family protein
24,2043	24,151	23,6452	23,9034	23,4197	24,1948		9,65E-07	1,3E+08	3	3	3	12,3	41,483	23,9197	24,0002	23,8393	6	3	3	0,606025	0,160859	B8NAP7	B8NAP7	1	AFLA_042720	Uncharacterized protein
29,795	29,112	29,1525	27,7735	28,2348	28,4026	+	4,67E-251	3,59E+09	11	11	11	34,8	45,012	28,7451	29,3532	28,1369	6	3	3	0,013823	1,21625	B8NAS6	B8NAS6	1	AFLA_043010	Formamidase FmdS
31,7271	31,0988	31,0474	29,8645	30,0048	30,2584	+	0	1,41E+10	20	20	20	58,4	49,457	30,6668	31,2911	30,0426	6	3	3	0,007213	1,24853	B8NAS7	B8NAS7	1	AFLA_043020	Fructosyl amine:oxygen oxidoreductase
30,7675	30,538	30,2947	30,5081	30,7097	30,6767		0	1,71E+10	13	13	13	49,3	40,858	30,5825	30,5334	30,6315	6	3	3	0,549125	-0,0980962	B8NAS9	B8NAS9	1	AFLA_043040	Peptidyl-prolyl cis-trans isomerase Cpr7, putative
32,0041	32,2712	31,8933	31,9648	32,1658	32,0787		0	5,19E+10	28	28	28	68	54,614	32,063	32,0562	32,0698	6	3	3	0,919703	-0,0135593	B8NAT6	B8NAT6	1	AFLA_043110	Dihydrolipoyl dehydrogenase (EC 1.8.1.4)
26,0663	25,8492	26,056	25,2964	25,5828	25,5614	+	5,17E-27	6,26E+08	5	5	5	14	61,574	25,7354	25,9905	25,4802	6	3	3	0,011738	0,510344	B8NAT7	B8NAT7	1	AFLA_043120	Phosphoglucomutase, putative
26,6402	27,1064	28,3115	27,4693	27,1691	26,7827		4,97E-14	2,4E+09	4	4	4	30,2	13,075	27,2465	27,3527	27,1404	6	3	3	0,712317	0,212312	B8NAU0	B8NAU0	1	AFLA_043150	40S ribosomal protein S10a
26,896	26,5975	26,3782	26,908	26,699	26,7142		2,50E-43	1,23E+09	7	7	7	31,2	34,465	26,6988	26,6239	26,7737	6	3	3	0,413656	-0,149883	B8NAU9	B8NAU9	1	AFLA_043240	Prefoldin subunit 3, putative
28,5624	29,6171	29,6916	30,1273	29,7522	29,2796		0	8,33E+09	18	18	18	55,5	60,75	29,505	29,2903	29,7197	6	3	3	0,383881	-0,429331	B8NAW4	B8NAW4	1	AFLA_043390	Hsp70 chaperone (BiP), putative
NaN	23,7377	NaN	24,0573	24,0927	NaN		1,10E-22	2,18E+08	6	6	6	6,1	151,51	23,9626	23,7377	24,075	3	1	2	1	-0,337331	B8NAW7	B8NAW7	1	AFLA_043420	UDP-glucose:glycoprotein glucosyltransferase, putative
29,1891	28,9775	28,6475	29,6529	29,4774	29,4879	+	2,86E-84	7,08E+09	15	15	15	69,9	31,27	29,2387	28,9381	29,5394	6	3	3	0,022976	-0,601353	B8NAY6	B8NAY6	1	AFLA_043610	Enoyl-CoA hydratase/isomerase family protein
27,7864	27,5919	27,0958	27,5359	27,4422	27,7068		2,79E-119	2E+09	8	8	8	48,2	24,963	27,5265	27,4914	27,5617	6	3	3	0,765006	-0,0703036	B8NAZ4	B8NAZ4	1	AFLA_043690	Phosphoribosylglycinamide formyltransferase, putative
26,8424	26,902	26,3672	26,7296	26,5901	27,1186		4,39E-20	1,01E+09	5	5	5	13,1	51,848	26,7583	26,7038	26,8128	6	3	3	0,662657	-0,10892	B8NAZ8	B8NAZ8	1	AFLA_043730	Nuclear protein export protein Yrb2, putative
NaN	NaN	NaN	NaN	24,1963	23,4775		6,84E-16	1,78E+08	4	4	4	8,8	75,098	23,8369	NaN	23,8369	2	0	2	1	NaN	B8NB18	B8NB18	1	AFLA_043930	MFS phosphate transporter, putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
25,9965	26,4117	26,678	26,7742	26,6831	26,6645		7,43E-26	1,08E+09	6	6	6	13,7	71,123	26,5347	26,3621	26,7073	6	3	3	0,161326	-0,345197	B8NB20	B8NB20	1	AFLA_043950	Serine/threonine protein kinase (YPK1), putative
28,1843	28,2027	28,0174	28,0164	28,1937	28,2387		9,44E-124	2,53E+09	13	13	13	49,6	43,479	28,1422	28,1348	28,1496	6	3	3	0,877079	-0,0148137	B8NB23	B8NB23	1	AFLA_043980	Mannitol-1-phosphate dehydrogenase
28,963	28,193	27,1472	26,6214	27,8996	28,1444		3,15E-104	3,04E+09	20	20	20	37,6	90,789	27,8281	28,1011	27,5551	6	3	3	0,483062	0,545959	B8NB25	B8NB25	1	AFLA_044000	COPI vesicle coat beta' subunit, putative
NaN	24,4035	24,3142	24,7186	23,9135	NaN		2,09E-25	3,44E+08	5	5	5	31,1	26,9	24,3375	24,3589	24,3161	4	2	2	0,925523	0,042779	B8NB26	B8NB26	1	AFLA_044010	NADH-ubiquinone oxidoreductase 299 kDa subunit, putative
32,8596	32,5482	32,2355	31,8553	32,3403	32,4192		0	4,26E+10	19	19	19	68,2	34,24	32,3763	32,5478	32,2049	6	3	3	0,245395	0,342852	B8NB34	B8NB34	1	AFLA_044090	Uricase (EC 1.7.3.3) (Urate oxidase)
25,8737	26,2932	28,3247	27,2091	26,1649	25,9531		7,71E-44	1,25E+09	5	5	5	39,9	15,923	26,6365	26,8306	26,4424	6	3	3	0,671815	0,388174	B8NB36	B8NB36	1	AFLA_044110	40S ribosomal protein Rps16, putative
25,4122	26,1687	29,169	28,0306	26,2685	26,1138		1,07E-126	1,51E+09	7	7	7	52	15,817	26,8605	26,9166	26,8043	6	3	3	0,935359	0,112348	B8NB42	B8NB42	1	AFLA_044170	40S ribosomal protein S11
31,3754	31,3018	31,0993	31,1647	30,9258	31,0317		0	2,34E+10	21	21	21	75,1	44,378	31,1498	31,2588	31,0407	6	3	3	0,112765	0,218088	B8NB44	B8NB44	1	AFLA_044190	Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)
26,8544	28,2825	28,1856	27,5691	27,8237	27,7303		5,10E-153	4,49E+09	14	14	14	48,1	54,745	27,7409	27,7741	27,7077	6	3	3	0,893681	0,0664387	B8NB48	B8NB48	1	AFLA_044230	Eukaryotic translation initiation factor 3 subunit L (eIF3l)
24,3281	24,1462	24,1743	24,0999	24,1955	24,3117		3,76E-07	2,24E+08	3	3	3	8,6	54,862	24,2093	24,2162	24,2024	6	3	3	0,87608	0,0138512	B8NB51	B8NB51	1	AFLA_044260	Kynureninase (EC 3.7.1.3) (Biosynthesis of nicotinic acid protein 5) (L-kynurenine hydrolase)
25,7682	25,5617	25,1388	25,1563	25,3664	25,3794		7,57E-21	5,04E+08	7	7	7	30,6	36,561	25,3951	25,4895	25,3007	6	3	3	0,396037	0,188844	B8NB55	B8NB55	1	AFLA_044300	SH3 domain protein
NaN	NaN	24,4895	26,3616	24,664	24,6863		7,39E-46	5,41E+08	6	6	6	23,2	68,968	25,0504	24,4895	25,2373	4	1	3	1	-0,747781	B8NB56	B8NB56	1	AFLA_044310	SH3 domain protein
29,8108	29,0482	28,8646	28,8556	29,2361	29,2476		3,27E-163	4,73E+09	15	15	15	61,4	36,746	29,1771	29,2412	29,1131	6	3	3	0,70681	0,128107	B8NB58;RE	B8NB58	2	AFLA_044330	Ketoreductase
27,1434	27,5683	27,4071	25,1086	25,1061	24,4081	+	8,72E-38	7,92E+08	10	10	10	29,7	51,166	26,1236	27,3729	24,8743	6	3	3	0,000694	2,49867	B8NB59	B8NB59	1	AFLA_044340	Uncharacterized protein
29,5376	29,1187	28,8278	29,1992	29,458	29,4376		1,22E-243	6,84E+09	15	15	13	73,1	34,609	29,2632	29,1614	29,365	6	3	3	0,411258	-0,20357	B8NB66	B8NB66	1	AFLA_044410	Glycerol dehydrogenase, putative
27,4721	26,7786	25,5211	26,2421	26,7393	27,0572		1,86E-41	1,02E+09	8	8	8	34,6	29,692	26,6351	26,5906	26,6796	6	3	3	0,892545	-0,0889702	B8NB70	B8NB70	1	AFLA_044450	Uncharacterized protein
27,5137	26,6409	25,9234	26,4265	27,1186	26,7136		1,06E-51	8,09E+08	7	7	7	19,6	62,144	26,7228	26,6926	26,7529	6	3	3	0,910164	-0,0602773	B8NB71	B8NB71	1	AFLA_044460	Phenylacetyl-CoA ligase, putative
27,6181	27,0357	26,8448	27,1282	27,5615	27,513		7,61E-46	1,59E+09	13	13	13	62,8	39,389	27,2835	27,1662	27,4009	6	3	3	0,433664	-0,234706	B8NB75	B8NB75	1	AFLA_044500	YjeF domain protein
31,9513	32,1439	32,1406	31,2945	30,8648	30,7891	+	7,10E-271	3,38E+10	8	8	8	95,4	11,087	31,5307	32,0786	30,9828	6	3	3	0,002966	1,09576	B8NB77	B8NB77	1	AFLA_044520	60S acidic ribosomal protein P2/allergen Asp F 8
29,7982	29,4248	29,991	29,6396	28,8511	29,5695		0	7,23E+09	5	5	5	58,2	17,502	29,5457	29,738	29,3534	6	3	3	0,271559	0,384623	B8NB78	B8NB78	1	AFLA_044530	40S ribosomal protein S15, putative
31,8846	31,6609	31,6755	31,8164	31,6978	31,7721		0	3,32E+10	53	53	52	60,1	129,3	31,7512	31,7403	31,7621	6	3	3	0,799079	-0,0217902	B8NB80	B8NB80	1	AFLA_044550	Carbamoyl-phosphate synthase, large subunit
NaN	25,7627	26,485	26,6206	26,9702	26,4306		1,56E-44	8,62E+08	11	11	11	13,4	108,24	26,4538	26,1239	26,6738	5	2	3	0,201991	-0,549913	B8NB84	B8NB84	1	AFLA_044590	Nonsense-mediated mRNA decay protein (Nmd5), putative
32,5814	32,0291	32,5001	32,4429	31,9244	31,8448		0	4,64E+10	35	35	35	58,3	72,467	32,2204	32,3702	32,0707	6	3	3	0,304603	0,299521	B8NB87	B8NB87	1	AFLA_044620	Mitochondrial Hsp70 chaperone (Ssc70), putative
28,3556	27,5425	26,8298	26,3754	27,5707	27,6728		8,55E-45	1,85E+09	11	11	11	27,9	76,31	27,3911	27,576	27,2063	6	3	3	0,575048	0,369701	B8NB89	B8NB89	1	AFLA_044640	Fatty acid activator Faa4, putative
29,8451	29,6667	29,3256	29,2571	29,4169	29,4873		1,15E-236	9,03E+09	11	11	11	40,4	31,538	29,4998	29,6125	29,3871	6	3	3	0,248288	0,225375	B8NB96	B8NB96	1	AFLA_044710	Eukaryotic translation initiation factor 3 subunit G (eIF3g) (Eukaryotic translation initiation factor 3 RNA-binding subunit) (Translation initiation factor eIF3 p33 subunit homolog)
NaN	24,1006	24,5796	24,0271	23,8706	23,9707		3,24E-13	2,46E+08	5	5	5	8,7	95,284	24,1097	24,3401	23,9561	5	2	3	0,133776	0,383993	B8NBA3	B8NBA3	1	AFLA_044780	Rbm25 protein, putative
33,4131	33,3035	33,0756	33,4915	33,4791	33,447		0	1,12E+11	35	35	35	69,4	61,213	33,3683	33,2641	33,4725	6	3	3	0,106175	-0,208486	B8NBA7	B8NBA7	1	AFLA_044820	Glucose-6-phosphate isomerase (EC 5.3.1.9)
27,6992	27,3149	27,2345	27,3973	27,1576	27,3043		4,64E-118	2,03E+09	6	6	6	38,4	26,092	27,3513	27,4162	27,2864	6	3	3	0,461222	0,12982	B8NBB8	B8NBB8	1	AFLA_044930	Superoxide dismutase copper chaperone Lys7, putative
28,747	28,5366	28,5918	29,0093	28,9741	28,9617	+	2,71E-154	4,46E+09	14	14	14	55,1	48,429	28,8034	28,6251	28,9817	6	3	3	0,005257	-0,35656	B8NBC7;B8	B8NBC7	2	AFLA_045020	Aspartate aminotransferase (EC 2.6.1.1)
27,3063	27,2328	27,2159	27,4621	27,329	27,3706	+	9,29E-73	1,62E+09	7	7	7	32	32,556	27,3195	27,2517	27,3872	6	3	3	0,047965	-0,135578	B8NBE2	B8NBE2	1	AFLA_045170	Alpha/beta hydrolase, putative
NaN	NaN	NaN	24,7185	25,3773	25,6684		5,14E-10	4,09E+08	5	5	5	11	74,691	25,2547	NaN	25,2547	3	0	3	1	NaN	B8NBF0	B8NBF0	1	AFLA_045250	Biotin apo-protein ligase, putative
28,9038	29,6203	29,3583	29,6684	29,664	29,5698		4,26E-298	8,16E+09	30	30	30	24,3	147,79	29,4641	29,2942	29,6341	6	3	3	0,183727	-0,339908	B8NBF8	B8NBF8	1	AFLA_045330	Eukaryotic translation initiation factor subunit eIF-4F, putative
27,0945	26,6613	26,2374	25,5855	25,8655	26,1812		6,38E-41	6,81E+08	6	6	6	27,5	27,2	26,2709	26,6644	25,8774	6	3	3	0,059328	0,786975	B8NBJ3	B8NBJ3	1	AFLA_045680	GNAT family acetyltransferase, putative
32,8396	32,7102	32,4377	32,6305	32,5776	32,6842		0	7,48E+10	42	42	42	78,6	62,213	32,6466	32,6625	32,6308	6	3	3	0,808286	0,0317256	B8NBK0	B8NBK0	1	AFLA_045750	Antigenic mitochondrial protein HSP60, putative
25,1799	27,3961	29,2773	27,6885	25,3579	25,4396		3,36E-95	1,87E+09	6	6	6	57,5	11,353	26,7232	27,2844	26,162	6	3	3	0,470273	1,12244	B8NBK4	B8NBK4	1	AFLA_045790	60S ribosomal protein L30, putative
25,4875	25,3918	25,2229	25,5799	26,0917	25,3743		1,45E-21	5,2E+08	6	6	6	11,9	70,047	25,5247	25,3674	25,682	6	3	3	0,237863	-0,314573	B8NBK5	B8NBK5	1	AFLA_045800	M protein, serotype 2.1, putative
NaN	NaN	26,64	26,8071	26,628	26,6094		6,87E-30	9,53E+08	3	3	3	23,4	22,048	26,6711	26,64	26,6815	4	1	3	1	-0,041448	B8NBK6	B8NBK6	1	AFLA_045810	Coatomer subunit zeta, putative
27,0813	26,2273	26,4931	26,5916	26,4308	26,9013		1,62E-17	8,44E+08	4	4	4	42,2	12,542	26,6209	26,6006	26,6412	6	3	3	0,894452	-0,040645	B8NBL0	B8NBL0	1	AFLA_045850	Uncharacterized protein
NaN	23,7788	23,8826	24,9376	23,6777	23,5139		1,02E-09	1,82E+08	3	3	3	12,2	30,065	23,9581	23,8307	24,043	5	2	3	0,739378	-0,212354	B8NBL1	B8NBL1	1	AFLA_045860	NADH-ubiquinone dehydrogenase 24 kDa subunit, putative
23,0887	22,8387	22,9976	23,1469	NaN	23,5524		4,80E-09	1,43E+08	4	4	4	6,5	78,912	23,1249	22,975	23,3496	5	3	2	0,126207	-0,374603	B8NBL5	B8NBL5	1	AFLA_045900	Phenylalanine ammonia-lyase (EC 4.3.1.24)
28,0478	27,3002	26,1512	26,8734	28,1803	28,2532		1,07E-75	2,15E+09	14	14	14	20,6	91,951	27,4677	27,1664	27,769	6	3	3	0,444289	-0,602608	B8NBM2	B8NBM2	1	AFLA_045970	Vacuolar transporter chaperone (Vtc4), putative
32,9401	32,5188	33,711	31,0613	31,0406	31,1508	+	0	5,77E+10	27	27	27	52,7	80,383	32,0704	33,0566	31,0842	6	3	3	0,004914	1,9724	B8NBM3	B8NBM3	1	AFLA_045980	Probable dipeptidyl-peptidase 5 (EC 3.4.14..-) (Dipeptidyl-peptidase V) (DPP V) (DppV)
28,669	28,381	28,0109	27,4156	28,1561	28,0555		2,15E-73	2,78E+09	11	11	11	28,9	46,84	28,1147	28,3536	27,8757	6	3	3	0,186459	0,477905	B8NBM6	B8NBM6	1	AFLA_046010	Eukaryotic translation initiation factor 5, putative
25,4892	25,5848	25,3912	25,6452	25,6732	25,6827	+	1,17E-40	5,56E+08	9	9	9	25,6	54,956	25,5777	25,4884	25,667	6	3	3	0,035051	-0,178672	B8NBM7	B8NBM7	1	AFLA_046020	Thiamine biosynthetic bifunctional enzyme, putative
28,3989	28,692	28,8189	28,3628	28,7067	28,4575		8,08E-100	4,8E+09	11	11	11	60	28,447	28,5728	28,6366	28,509	6	3	3	0,472925	0,127592	B8NBN0	B8NBN0	1	AFLA_046050	GDSL Lipase/Acylhydrolase family protein
26,2878	25,8025	25,8423	26,043	26,1789	26,2566		9,46E-26	7,47E+08	5	5	5	29,8	26,915	26,0685	25,9775	26,1595	6	3	3	0,338698	-0,181964	B8NBN5	B8NBN5	1	AFLA_046100	Dihydrofolate reductase, putative
27,6655	27,0447	26,4294	26,0462	26,9254	27,0998		4,65E-41	1,32E+09	9	9	9	46	36,683	26,8685	27,0465	26,6905	6	3	3	0,502206	0,356057	B8NBQ3	B8NBQ3	1	AFLA_046280	Mitochondrial inner membrane nuclease Nuc1, putative
31,5081	30,6718	31,1099	30,7895	30,7595	30,8227		0	3,19E+10	85	85	85	56	236,61	30,9436	31,0966	30,7906	6	3	3	0,275061	0,30601	B8NBR1	B8NBR1	1	AFLA_046360	Acetyl-CoA carboxylase, putative
26,0436	25,4952	25,4709	25,3182	25,3494	25,398		1,02E-05	4,04E+08	2	2	2	26	20,449	25,5125	25,6699	25,3552	6	3	3	0,170189	0,314694	B8NBS0	B8NBS0	1	AFLA_046450	Small subunit of nuclear cap-binding protein complex
27,5338	27,1801	NaN	NaN	27,3537	27,4206		2,96E-21	1,28E+09	2	2	2	13,3	20,067	27,372	27,3569	27,3872	4	2	2	0,882028	-0,030241	B8NBS2	B8NBS2	1	AFLA_046470	Uncharacterized protein
25,4968	24,7085	24,7452	24,8089	25,0763	25,1413		9,82E-18	4,43E+08	5	5	5	38,8	24,123	24,9962	24,9835	25,0089	6	3	3	0,931283	-0,0253588	B8NBT1	B8NBT1	1	AFLA_046560	Acetyltransferase, CysE/LacA/LpxA/NodL family
25,2182	26,3577	26,626	26,9263	26,4816	26,3295		9,44E-101	1,33E+09	8	8	8	42	25,286	26,3232	26,0673	26,5791	6	3	3	0,334837	-0,511824	B8NBU0	B8NBU0	1	AFLA_046650	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)
29,8047	29,5643	28,623	28,7677	29,1797	29,2454		2,46E-180	5,41E+09	25	25	25	52,1	72,837	29,1975	29,3307	29,0643	6	3	3	0,532402	0,266394	B8NBU9	B8NBU9	1	AFLA_046740	Malic enzyme
28,6998	28,3532	28,003	28,6141	28,6429	28,6411		0	3,85E+09	10	10	10	74,6	13,446	28,4924	28,352	28,6327	6	3	3	0,235728	-0,280713	B8NBV7	B8NBV7	1	AFLA_046820	Tubulin-specific chaperone Rbl2, putative
26,2369	24,7381	27,6625	25,3736	25,4727	25,3367		6,36E-54	5,62E+08	7	7	7	24,9	33,339	25,8034	26,2125	25,3943	6	3	3	0,387869	0,81818	B8NBX2	B8NBX2	1	AFLA_046970	Ribosomal protein L19
29,4539	28,9554	29,1812	29,3313	29,3157	29,0455		1,04E-248	6,67E+09	18	17	17	56,7	58,462	29,2138	29,1968	29,2308	6	3	3	0,852293	-0,0340328	B8NBY3	B8NBY3	1	AFLA_047080	Serine hydroxymethyltransferase (EC 2.1.2.1)
25,0694	23,5346	NaN	NaN	NaN	NaN		8,84E-07	47980000	2	2	2	12	38,961	24,302	24,302	NaN	2	2	0	1	NaN	B8NBY8	B8NBY8	1	AFLA_047130	Uncharacterized protein
25,6868	24,8433	24,4417	25,0376	25,1364	25,6225		1,37E-50	3,32E+08	2	2	2	29,8	9,3906	25,128	24,9906	25,2655	6	3	3	0,538301	-0,274914	B8NBZ1	B8NBZ1	1	AFLA_047160	Cytochrome b5, putative
28,8716	29,3101	30,336	30,7268	30,2163	29,9628		0	1,39E+10	28	28	28	76,9	57,188	29,9039	29,5059	30,302	6	3	3	0,178607	-0,796069	B8NBZ9	B8NBZ9	1	AFLA_047240	Cystathionine beta-synthase (EC 4.2.1.22)
25,8273	24,7825	24,5438	24,6638	24,8499	25,0935		1,73E-10	3,86E+08	3	3	3	24,9	27,241	24,9601	25,0512	24,869	6	3	3	0,682144	0,182168	B8NC02	B8NC02	1	AFLA_047270	Beta-1,6-glucan boisynthesis protein (Knh1), putative
29,5736	29,213	28,6897	29,0458	29,2017	29,4396		3,09E-170	5,99E+09	17	17	17	36,5	75,74	29,1939	29,1588	29,229	6	3	3	0,814861	-0,0702629	B8NC08	B8NC08	1	AFLA_047330	Leukotriene A(4) hydrolase (LTA-4 hydrolase) (EC 3.3.2.6)
30,9119	30,5372	30,0947	30,5814	30,6297	30,7654		0	1,73E+10	25	25	25	66,4	51,607	30,5867	30,5146	30,6588	6	3	3	0,584057	-0,144212	B8NC10	B8NC10	1	AFLA_047350	Probable Xaa-Pro aminopeptidase pepP (EC 3.4.11.9) (Aminoacylproline aminopeptidase) (Prolidase)
30,3868	30,3685	30,3955	30,5532	30,6205	30,5994	+	0	1,45E+10	28	28	28	68,6	53,664	30,4873	30,3836	30,591	6	3	3	0,000637	-0,207429	B8NC16	B8NC16	1	AFLA_047410	Actin-bundling protein Sac6, putative
28,1391	28,259	27,7888	25,6613	26,3241	NaN	+	8,31E-75	1,78E+09	2	2	2	10,8	25,563	27,2345	28,0623	25,9927	5	3	2	0,006658	2,06956	B8NC17	B8NC17	1	AFLA_047420	Uncharacterized protein
29,6524	30,1015	30,4015	25,8646	24,8516	25,4759	+	2,13E-67	5,19E+09	6	6	6	37,5	20,782	27,7246	30,0518	25,3974	6	3	3	0,000222	4,65445	B8NC19	B8NC19	1	AFLA_047440	60S ribosomal protein L18
NaN	25,2129	25,0951	24,8199	24,9046	24,3693		6,45E-13	5,15E+08	4	4	4	12,3	43,656	24,8804	25,154	24,6979	5	2	3	0,128619	0,456065	B8NC20	B8NC20	1	AFLA_047450	Gamma-glutamyl phosphate reductase
26,937	26,4993	29,2366	27,7649	27,0521	27,3781		7,88E-72	2,1E+09	10	10	10	37,5	29,21	27,478	27,5576	27,3983	6	3	3	0,86419	0,159284	B8NSD4	B8NSD4	1	AFLA_047870	40S ribosomal protein S1
28,0607	28,0618	27,7561	27,6534	27,7344	27,6018		6,16E-139	2,48E+09	9	9	9	59	27,683	27,8114	27,9596	27,6632	6	3	3	0,052795	0,296345	B8NSD6	B8NSD6	1	AFLA_047890	Cytosine deaminase-uracil phosphoribosyltransferase fusion protein
29,6329	29,4994	29,5957	29,5558	29,5676	29,6702		0	8,55E+09	21	21	21	59,5	54,003	29,587	29,576	29,5979	6	3	3	0,705578	-0,0218646	B8NSD8	B8NSD8	1	AFLA_048010	Seryl-tRNA synthetase
30,8318	30,5801	30,323	30,4953	30,5965	30,7266		0	1,79E+10	20	20	20	52,9	54,024	30,5922	30,5783	30,6061	6	3	3	0,871639	-0,0277952	B8NSD9	B8NSD9	1	AFLA_048020	D-3-phosphoglycerate dehydrogenase
32,0752	31,7233	31,398	31,6336	31,5441	31,5949		0	2,89E+10	24	24	24	58,8	46,314	31,6615	31,7322	31,5908	6	3	3	0,51331	0,141322	B8NSE2	B8NSE2	1	AFLA_048050	Nucleosome assembly protein Nap1, putative
23,5676	23,8776	22,7848	23,5275	23,4945	23,704		4,92E-31	3,86E+08	11	11	11	10,4	171,18	23,4927	23,41	23,5753	6	3	3	0,644157	-0,165361	B8NSE3	B8NSE3	1	AFLA_048060	Class V myosin (Myo4), putative
28,4488	28,1555	28,1176	28,3396	28,2437	28,3787		4,77E-194	3,77E+09	9	9	9	65,6	20,966	28,2807	28,2407	28,3207	6	3	3	0,514867	-0,0799917	B8NSE4	B8NSE4	1	AFLA_048070	Inosine triphosphate pyrophosphatase (ITPase) (Inosine triphosphatase) (EC 3.6.1.19) (Non-canonical purine NTP pyrophosphatase) (Non-standard purine NTP pyrophosphatase) (Nucleoside-triphosphate diphosphatase) (Nucleoside-triphosphate pyrophosphatase)
28,836	28,7688	28,4935	28,5388	28,6364	28,6942		1,53E-201	4,69E+09	4	4	4	60,2	10,01	28,6613	28,6994	28,6231	6	3	3	0,540646	0,0762793	B8NSF0	B8NSF0	1	AFLA_048130	Mitochondrial intermembrane space translocase subunit Tim10, putative
30,6685	31,0742	30,9058	28,5294	26,7783	27,0226	+	6,41E-114	1,53E+10	8	8	8	37	16,959	29,1631	30,8828	27,4434	6	3	3	0,003564	3,43939	B8NSF1	B8NSF1	1	AFLA_048140	60S ribosomal protein L23
28,4251	28,1741	28,2207	27,773	27,9502	28,1593		5,03E-91	2,88E+09	11	11	11	35,5	48,572	28,1171	28,2733	27,9608	6	3	3	0,082631	0,312489	B8NSF4	B8NSF4	1	AFLA_048170	Peptide chain release factor eRF/aRF, subunit 1

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
27,5903	28,9126	26,6158	25,6323	24,9213	24,8968	+	2,41E-95	1,51E+09	15	15	15	41,8	54,862	26,4282	27,7062	25,1501	6	3	3	0,022541	2,55609	B8NSF7	B8NSF7	1	AFLA_048200	Pseudouridylate synthase family protein
NaN	26,5634	26,925	26,7894	26,1466	25,9641		2,60E-32	8,77E+08	8	8	8	37,7	37,895	26,4777	26,7442	26,3	5	2	3	0,294045	0,444182	B8NSG6	B8NSG6	1	AFLA_048290	Homoserine kinase
29,171	29,7219	29,6922	29,9328	29,6707	29,4452		0	9,27E+09	28	28	28	45,9	80,408	29,6056	29,5284	29,6829	6	3	3	0,53452	-0,154554	B8NSH4	B8NSH4	1	AFLA_048370	Glycyl-tRNA synthetase
26,8729	27,2418	24,8583	27,3538	27,4928	27,5797		6,42E-34	1,31E+09	10	10	10	42,1	30,2	26,8999	26,3244	27,4754	6	3	3	0,196553	-1,15108	B8NSH8	B8NSH8	1	AFLA_048410	BAR adaptor protein RVS161, putative
29,6736	29,5443	29,2154	29,4294	29,2529	29,4008		0	8,84E+09	9	9	9	51,8	26,568	29,4194	29,4778	29,3611	6	3	3	0,471449	0,116723	B8NSI6	B8NSI6	1	AFLA_048490	Eukaryotic translation initiation factor 6 (eIF-6)
29,1215	28,6674	28,6345	29,1776	28,8861	28,8784		3,33E-51	4,68E+09	8	8	8	21,4	47,095	28,8943	28,8078	28,9807	6	3	3	0,404014	-0,17288	B8NSI8	B8NSI8	1	AFLA_048510	UV excision repair protein (RadW), putative
29,2948	29,3361	29,224	29,4681	29,3419	29,403		0	7,49E+09	12	12	12	68,9	18,464	29,3446	29,2849	29,4043	6	3	3	0,071456	-0,119408	B8NSJ0	B8NSJ0	1	AFLA_048530	E3 ubiquitin ligase complex SCF subunit sconC (Sulfur controller C) (Sulfur metabolite repression control protein C)
29,3173	29,2112	29,8398	30,0977	29,6541	29,3065		5,72E-291	9,38E+09	14	14	14	61,5	34,409	29,5711	29,4561	29,6861	6	3	3	0,48639	-0,230007	B8NSJ8	B8NSJ8	1	AFLA_048610	Succinyl-CoA synthetase alpha subunit, putative
NaN	NaN	NaN	24,0118	24,413	NaN		5,62E-08	1,58E+08	4	4	4	9,4	65,081	24,2124	NaN	24,2124	2	0	2	1	NaN	B8NSJ9	B8NSJ9	1	AFLA_048620	Histone acetyltransferase, putative
27,1801	30,809	32,0154	31,831	30,3601	30,0984		0	2,84E+10	19	19	19	78	37,057	30,3823	30,0015	30,7632	6	3	3	0,648866	-0,761674	P41747	P41747	1	AFLA_048690	Alcohol dehydrogenase 1 (EC 1.1.1.1) (Alcohol dehydrogenase I)
NaN	22,8748	29,4044	28,3256	23,4665	NaN		1,04E-107	9,79E+08	6	6	6	40,6	27,435	26,0178	26,1396	25,8961	4	2	2	0,957726	0,243516	B8NRH6	B8NRH6	1	AFLA_048810	60S ribosomal protein L8, putative
31,382	31,1908	31,0543	31,4777	31,6623	31,8063	+	0	3,28E+10	18	18	18	71,7	38,503	31,4289	31,2091	31,6488	6	3	3	0,030762	-0,439738	B8NRH9	B8NRH9	1	AFLA_048840	Adenosine kinase, putative
27,7822	27,5107	27,9572	27,0257	27,3657	27,381	+	1,41E-43	2,15E+09	12	12	12	42,5	42,671	27,5038	27,75	27,2575	6	3	3	0,047401	0,492545	B8NRJ7	B8NRJ7	1	AFLA_049020	Acyl-CoA dehydrogenase family protein
25,809	26,4659	26,5919	26,9772	26,3391	26,2128		1,25E-81	1,97E+09	9	9	9	43	42,286	26,3993	26,289	26,5097	6	3	3	0,550359	-0,220746	B8NRK3	B8NRK3	1	AFLA_049080	Biotin synthase, putative
26,7679	26,7089	26,4928	26,5802	26,8663	26,8353		1,34E-32	1,12E+09	12	12	12	23,2	87,809	26,7086	26,6565	26,7606	6	3	3	0,446168	-0,104083	B8NRK4	B8NRK4	1	AFLA_049090	Onanonoxo-7-onima-8-eninoihtemlysoneda
27,8928	29,5706	29,3097	30,3378	30,4319	30,2497		0	1,06E+10	19	19	19	49,9	51,656	29,6321	28,9244	30,3398	6	3	3	0,053996	-1,41541	B8NRM4	B8NRM4	1	AFLA_049290	Citrate synthase
25,7983	25,7054	25,7905	25,7177	25,8913	25,9088		9,01E-14	6,32E+08	8	8	8	9,1	123,55	25,802	25,7647	25,8393	6	3	3	0,333732	-0,0745525	B8NRM5	B8NRM5	1	AFLA_049300	mRNA-nucleus export ATPase (Elf1), putative
25,6451	25,7319	25,4565	25,8924	25,6748	25,7469		8,18E-37	7,11E+08	10	6	6	26	36,237	25,6912	25,6111	25,7714	6	3	3	0,196356	-0,160213	B8NRM9	B8NRM9	1	AFLA_049340	Aldo/keto reductase, putative
27,8706	27,5955	27,4406	27,7539	27,7328	27,6057		3,21E-69	1,91E+09	6	6	5	30,8	29,823	27,6665	27,6355	27,6975	6	3	3	0,667932	-0,0619348	B8NRN2	B8NRN2	1	AFLA_049370	Short-chain dehydrogenase/reductase family protein, putative
NaN	24,805	25,2592	24,5689	25,9675	25,2757		4,18E-66	1,06E+09	11	11	11	24,9	61,075	25,1753	25,0321	25,2707	5	2	3	0,692708	-0,238595	B8NRN4	B8NRN4	1	AFLA_049390	Malate synthase (EC 2.3.3.9)
29,6979	29,4553	29,1971	29,7431	29,8666	29,8132		1,72E-125	7,33E+09	13	13	13	57,8	27,708	29,6289	29,4501	29,8076	6	3	3	0,074331	-0,35751	B8NSP1	B8NSP1	1	AFLA_049920	Dienelactone hydrolase family protein
29,2279	28,3674	28,6777	28,332	28,6063	28,7086		1,28E-123	3,7E+09	7	7	7	28,7	31,509	28,6533	28,7577	28,549	6	3	3	0,490944	0,208736	B8NSP2	B8NSP2	1	AFLA_049930	Uncharacterized protein
24,0546	24,3576	28,1999	23,4009	NaN	23,5744		4,05E-19	5,96E+08	6	6	6	28,2	22,986	24,7175	25,5374	23,4877	5	3	2	0,319903	2,04972	B8NSP9	B8NSP9	1	AFLA_050000	Ribosomal protein L16a
26,7664	26,6271	26,3393	26,4077	26,6351	26,772		2,65E-14	1,02E+09	4	4	4	8,9	82,71	26,5913	26,5776	26,6049	6	3	3	0,876172	-0,0273329	B8NSQ4	B8NSQ4	1	AFLA_050050	AP-1 adaptor complex subunit gamma, putative
25,0563	24,7144	23,8257	NaN	NaN	24,7874		1,14E-10	2,76E+08	4	4	4	7,8	85,794	24,5959	24,5321	24,7874	4	3	1	1	-0,255218	B8NSQ9	B8NSQ9	1	AFLA_050100	LMBR1 domain protein
27,9869	27,7649	28,202	28,9051	28,7235	28,6762	+	4,41E-36	2,65E+09	6	6	6	57,8	10,968	28,3764	27,9846	28,7683	6	3	3	0,00556	-0,783689	B8NSR1	B8NSR1	1	AFLA_050120	Glutaredoxin Grx1, putative
23,7744	24,9905	25,15	26,1952	26,3511	26,2122	+	1,16E-33	4,71E+08	6	6	6	20,2	45,89	25,4456	24,6383	26,2529	6	3	3	0,020965	-1,61451	B8NSR2	B8NSR2	1	AFLA_050130	Uncharacterized protein
31,2393	31,1475	30,9098	30,9873	30,9647	31,0324		0	2,64E+10	22	22	22	44,8	57,15	31,0468	31,0989	30,9948	6	3	3	0,357265	0,104126	B8NSS6	B8NSS6	1	AFLA_050270	Conserved lysine-rich protein, putative
26,4474	26,096	26,1216	26,2063	26,4483	26,4106		4,58E-53	9,48E+08	4	4	4	40,5	13,392	26,2884	26,2217	26,3551	6	3	3	0,381594	-0,133406	B8NST6	B8NST6	1	AFLA_050370	Prefoldin subunit 1, putative
24,8965	24,026	23,41	23,6958	24,445	24,345		1,10E-07	1,65E+08	4	4	4	27,4	21,518	24,1364	24,1108	24,162	6	3	3	0,922105	-0,0511112	B8NRQ7	B8NRQ7	1	AFLA_050480	ESCRT-II complex component (Vps25), putative
25,1757	25,1437	24,7307	24,951	24,9604	25,0637		3,54E-12	4,05E+08	4	4	4	13,6	36,963	25,0042	25,0167	24,9917	6	3	3	0,874001	0,0249742	B8NRQ8	B8NRQ8	1	AFLA_050490	tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (Transfer RNA methyltransferase 8) (tRNA (guanine(46)-N(7))-methyltransferase) (tRNA(m7G46)-methyltransferase)
27,7535	26,9587	28,4107	27,969	28,1034	27,6845		1,33E-125	2,94E+09	19	19	19	53,4	51,594	27,8133	27,7076	27,919	6	3	3	0,654363	-0,211336	B8NRR9	B8NRR9	1	AFLA_050600	Betaine-aldehyde dehydrogenase, putative
27,1688	26,1288	24,8564	30,3821	30,5189	30,7118	+	5,34E-125	1,05E+10	5	5	5	15,1	49,097	28,2945	26,0514	30,5376	6	3	3	0,002668	-4,48622	B8NRS0	B8NRS0	1	AFLA_050610	Acid phosphatase PHOa
22,7528	23,0281	28,6145	28,6889	23,303	23,5596		6,19E-50	1,03E+09	8	8	8	51,4	16,551	24,9911	24,7985	25,1838	6	3	3	0,889046	-0,385368	B8NRS4;RE	B8NRS4	2	AFLA_050650	40S ribosomal protein S19
25,274	27,7565	27,9777	26,3483	27,1808	NaN		7,38E-225	2,99E+09	6	6	6	22,1	33,843	26,9075	27,0027	26,7645	5	3	2	0,850598	0,23819	B8NRS8	B8NRS8	1	AFLA_050690	Mitochondrial ADP,ATP carrier protein (Ant), putative
29,9498	29,5015	29,8348	29,2593	28,8323	28,6187	+	3,11E-105	9,85E+09	9	9	9	54,7	16,338	29,3327	29,762	28,9035	6	3	3	0,020641	0,85854	B8NRT9	B8NRT9	1	AFLA_050800	40S ribosomal protein S12
27,3634	27,4669	27,3234	27,4506	27,3422	27,4691		1,18E-47	1,54E+09	6	6	6	31,2	40,221	27,4026	27,3846	27,4206	6	3	3	0,56949	-0,0360572	B8NRU2	B8NRU2	1	AFLA_050830	Uridine nucleosidase Urh1, putative
26,873	26,5326	26,7078	26,6132	26,6584	26,408		4,93E-58	1,54E+09	14	14	14	24,7	67,381	26,6322	26,7045	26,5599	6	3	3	0,311278	0,144618	B8NRV1	B8NRV1	1	AFLA_050930	Protein phosphotase 2a 65kd regulatory subunit
24,6785	27,005	27,2259	26,4801	27,1977	26,3134		2,00E-45	1,51E+09	9	9	8	21,5	67,607	26,4834	26,3031	26,6637	6	3	3	0,69612	-0,360616	B8NRV2	B8NRV2	1	AFLA_050940	Phenylalanyl-tRNA synthetase, beta subunit
28,5252	29,5829	31,1405	30,0436	29,1554	28,711		0	1,45E+10	18	18	18	76,7	29,23	29,5264	29,7495	29,3033	6	3	3	0,629167	0,44622	B8NRV3	B8NRV3	1	AFLA_050950	40S ribosomal protein S3, putative
23,9434	23,6786	23,7171	24,4259	24,4798	24,555	+	1,05E-34	3,66E+08	8	8	8	13,7	93,414	24,1333	23,7797	24,4869	6	3	3	0,001459	-0,707136	B8NRX2	B8NRX2	1	AFLA_051140	Probable beta-glucosidase A (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase A) (Cellobiase A) (Gentiobiase A)
27,5114	27,6218	27,2673	27,2374	27,3295	27,4186		1,19E-88	1,97E+09	10	10	10	17,5	79,165	27,3977	27,4668	27,3285	6	3	3	0,302754	0,138332	B8NRY5	B8NRY5	1	AFLA_051270	DnaJ and TPR domain protein
28,6571	29,2151	29,2752	29,5621	29,5752	29,5172		9,53E-274	7,49E+09	19	19	19	53,5	62,412	29,3003	29,0491	29,5515	6	3	3	0,063782	-0,502376	B8NSU4	B8NSU4	1	AFLA_051370	Phosphoribosyl-aminoimidazole carboxylase
27,205	26,7859	26,2393	26,8201	26,9898	27,0336		1,80E-15	1,16E+09	5	5	5	23,8	25,085	26,8456	26,7434	26,9478	6	3	3	0,515766	-0,204396	B8NSV9	B8NSV9	1	AFLA_051520	Uncharacterized protein
30,5627	30,2347	29,7683	30,2635	30,403	30,5706		0	1,2E+10	20	20	20	45,2	63,699	30,302	30,1915	30,4124	6	3	3	0,422255	-0,220864	B8NSW0	B8NSW0	1	AFLA_051530	Methylmalonate-semialdehyde dehydrogenase, putative
29,1457	28,2841	27,8075	27,2766	28,0022	28,1035		0	5,07E+09	12	12	12	32	61,962	28,1033	28,4125	27,7941	6	3	3	0,258886	0,618342	B8NSW1	B8NSW1	1	AFLA_051540	Calnexin
28,4434	28,188	28,0471	28,435	28,6425	28,6397		1,69E-161	4E+09	12	12	12	79,3	27,168	28,3993	28,2262	28,5724	6	3	3	0,062121	-0,346219	B8NSW2	B8NSW2	1	AFLA_051550	Methylthioribulose-1-phosphate dehydratase (MTRu-1-P dehydratase) (EC 4.2.1.109)
25,4552	24,2393	24,5602	24,4508	24,256	24,7617		4,18E-22	2,54E+08	8	8	8	19	64,237	24,6205	24,7516	24,4895	6	3	3	0,540879	0,262056	B8NSW3	B8NSW3	1	AFLA_051560	Vacuolar protein sorting-associated protein Vps5, putative
28,1107	27,4882	27,6968	27,8623	27,8795	27,9753		5,27E-88	2,57E+09	7	7	7	37,8	29,495	27,8355	27,7652	27,9057	6	3	3	0,492761	-0,14047	B8NSX2	B8NSX2	1	AFLA_051650	Phosphoserine phosphatase, putative
24,8279	27,0798	27,0947	27,9534	27,5946	27,5611		2,31E-107	1,93E+09	14	14	14	33,7	65,817	27,0186	26,3341	27,7031	6	3	3	0,147443	-1,36892	B8NSX8	B8NSX8	1	AFLA_051710	Histidyl-tRNA synthetase, mitochondrial
24,3713	24,2453	24,2873	24,3464	24,329	NaN		5,72E-29	3,5E+08	7	7	7	29,2	55,59	24,3159	24,3013	24,3377	5	3	2	0,505969	-0,0363576	B8NSX9	B8NSX9	1	AFLA_051720	Ubiquinone biosynthesis monooxgenase (Coq6), putative
31,9156	31,5738	31,3095	31,2313	31,3094	31,4643		0	2,99E+10	15	15	15	70,8	37,894	31,4673	31,5996	31,335	6	3	3	0,232694	0,264615	B8NSY4	B8NSY4	1	AFLA_051770	Thioredoxin reductase (EC 1.8.1.9)
25,586	27,369	28,7397	27,5361	27,3794	26,5671		0	5,88E+09	19	19	12	67,6	49,813	27,1962	27,2316	27,1609	6	3	3	0,944876	0,0707207	B8NSZ1	B8NSZ1	1	AFLA_051840	Tubulin beta subunit
28,609	29,343	30,2464	29,4656	29,9454	29,3436		0	2,27E+10	18	18	18	54,9	41,944	29,4922	29,3995	29,5849	6	3	3	0,73354	-0,185419	B8NT00	B8NT00	1	AFLA_051930	Glutamine synthetase (EC 6.3.1.2)
27,6273	29,112	30,1682	28,8599	28,5381	28,247		0	1,96E+10	19	19	19	81,3	35,017	28,7588	28,9691	28,5484	6	3	3	0,608355	0,420781	B8NT05	B8NT05	1	AFLA_051980	G-protein complex beta subunit CpcB
25,2848	NaN	NaN	25,1699	25,1573	25,4988		4,36E-19	3,35E+08	4	4	4	8,2	58,248	25,2777	25,2848	25,2754	4	1	3	1	0,0094255	B8NT12	B8NT12	1	AFLA_052050	Calponin domain-containing protein, putative
26,9676	27,5047	27,6863	27,0577	27,3835	27,4358		3,59E-66	1,67E+09	8	8	8	57,9	18,977	27,3393	27,3862	27,2923	6	3	3	0,722227	0,0938695	B8NT21	B8NT21	1	AFLA_052140	Uncharacterized protein
27,358	27,9344	27,5985	26,1587	26,2463	25,8464	+	6,65E-107	1,17E+09	12	12	12	37,9	44,308	26,8571	27,6303	26,0838	6	3	3	0,001702	1,54649	B8NRZ7	B8NRZ7	1	AFLA_052280	Uncharacterized protein
24,2142	23,8425	23,6054	24,0304	24,1228	24,2119		1,39E-08	2,14E+08	3	3	3	11,4	46,226	24,0045	23,8874	24,1217	6	3	3	0,273482	-0,234347	B8NS01	B8NS01	1	AFLA_052320	Aspartic endopeptidase (AP1), putative
25,4356	25,4342	24,64	24,8956	25,1444	25,1031		1,00E-15	4,02E+08	6	6	6	7,1	112,08	25,1088	25,1699	25,0477	6	3	3	0,680667	0,12224	B8NS03	B8NS03	1	AFLA_052340	SNF2 family helicase/ATPase, putative
26,866	26,4901	26,6023	27,0837	27,5256	27,7995	+	3,70E-67	1,71E+09	14	14	14	35,3	60,04	27,0612	26,6528	27,4696	6	3	3	0,025943	-0,816804	B8NS09	B8NS09	1	AFLA_052400	Isocitrate lyase
25,8212	25,9684	26,3183	26,3538	25,4575	25,1786		7,01E-29	6,27E+08	9	9	9	15	86,695	25,8496	26,036	25,6633	6	3	3	0,386699	0,372646	B8NS12	B8NS12	1	AFLA_052430	Trehalase (EC 3.2.1.28) (Alpha-trehalose glucohydrolase)
25,5711	25,4395	26,3522	25,1724	25,9919	25,9251		1,16E-46	8,02E+08	8	8	8	20,3	63,876	25,742	25,7876	25,6965	6	3	3	0,825688	0,091102	B8NS16	B8NS16	1	AFLA_052470	Gamma-glutamyltranspeptidase
28,8621	27,8917	28,0481	27,5822	28,257	28,2823		3,71E-204	4,19E+09	22	22	22	37	82,649	28,1539	28,2673	28,0405	6	3	3	0,581004	0,226824	B8NS24;B8	B8NS24	2	AFLA_052550	Threonyl-tRNA synthetase, putative
29,1002	28,7725	28,5809	28,5986	28,7926	28,8899		2,30E-157	4,52E+09	13	13	12	44,4	48,224	28,7891	28,8178	28,7604	6	3	3	0,757904	0,0574716	B8NS26	B8NS26	1	AFLA_052570	Mitogen-activated protein kinase (EC 2.7.11.24)
27,3946	27,3644	27,4069	28,7295	28,5466	28,2777	+	3,70E-274	2,53E+09	13	13	13	37,1	55,616	27,9533	27,3886	28,518	6	3	3	0,001019	-1,12931	B8NS30	B8NS30	1	AFLA_052610	Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5)
28,3924	28,0101	27,4117	26,0774	26,6422	26,5513	+	6,47E-11	1,52E+09	3	3	3	16,3	11,278	27,1809	27,9381	26,4237	6	3	3	0,010635	1,5144	B8NS34	B8NS34	1	AFLA_052650	Uncharacterized protein
27,6971	27,1201	26,7562	NaN	NaN	NaN		4,28E-09	9,42E+08	2	2	2	17,6	19,894	27,1911	27,1911	NaN	3	3	0	1	NaN	B8NS36	B8NS36	1	AFLA_052670	RNA recognition motif (Rrm) domain containing protein, putative
25,6591	25,4511	25,2173	25,3461	25,3993	25,6346		5,66E-17	4,83E+08	4	4	4	26,5	24,352	25,4513	25,4425	25,46	6	3	3	0,915738	-0,0175006	B8NS53	B8NS53	1	AFLA_052840	Ran-interacting protein Mog1, putative
NaN	20,5933	24,7374	26,0897	23,1489	22,4625		9,60E-27	1,72E+08	2	2	2	25,8	9,5302	23,4064	22,6654	23,9004	5	2	3	0,599291	-1,23499	B8NS55	B8NS55	1	AFLA_052860	Chaperone/heat shock protein Hsp12, putative
28,0573	27,886	27,5901	27,9283	28,081	28,1161		4,65E-136	2,86E+09	10	10	10	42,6	40,212	27,9431	27,8445	28,0418	6	3	3	0,25369	-0,197349	B8NS61	B8NS61	1	AFLA_052920	NGG1 interacting factor Nif3, putative
27,17	28,1414	29,8177	30,3152	29,1704	28,5858		3,94E-248	6,88E+09	11	11	11	61,5	24,287	28,8667	28,3763	29,3571	6	3	3	0,348869	-0,980765	B8NS74	B8NS74	1	AFLA_053060	Peroxiredoxin 5, prdx5, putative
NaN	26,276	26,0653	26,4949	26,5003	26,5313	+	1,57E-06	8,84E+08	2	2	2	16,3	15,924	26,3735	26,1706	26,5088	5	2	3	0,024126	-0,338196	B8NT42	B8NT42	1	AFLA_053250	Uncharacterized protein
26,5774	26,5238	25,8468	26,1369	26,1425	26,279		5,78E-25	7,04E+08	3	3	3	12	34,662	26,2511	26,316	26,1861	6	3	3	0,616646	0,129875	B8NT56	B8NT56	1	AFLA_053390	GPI-anchored cell wall beta-1,3-endoglucanase EglC
25,4227	24,7217	25,6816	24,9367	25,7852	25,7363		1,21E-24	3,06E+08	3	3	3	14,2	45,487	25,3807	25,2753	25,4861	6	3	3	0,623922	-0,210742	B8NT69	B8NT69	1	AFLA_053520	O-methyltransferase, putative
27,749	26,7323	26,6716	25,9948	26,7824	26,9914		1,39E-37	1,06E+09	6	6	6	27,9	31,227	26,8203	27,051	26,5895	6	3	3	0,375193	0,461419	B8NS77	B8NS77	1	AFLA_053990	Class II aldolase/adducin domain protein

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
27,2017	26,2063	25,7228	25,5234	25,9883	26,2289		6,65E-46	5,64E+08	8	8	8	32	35,307	26,1452	26,377	25,9135	6	3	3	0,390833	0,463444	B8NSB2	B8NSB2	1	AFLA_054340	Isoflavone reductase family protein
28,961	28,3792	28,4702	28,5071	28,4807	28,5846		8,14E-102	4,24E+09	16	16	16	50,8	44,623	28,5638	28,6035	28,5241	6	3	3	0,687474	0,0793584	B8NSB3	B8NSB3	1	AFLA_054350	Actin-binding protein Fragmin, putative
24,861	26,1242	25,7298	23,3385	23,3838	23,1413	+	7,97E-19	2,88E+08	4	4	4	13	55,58	24,4298	25,5717	23,2879	6	3	3	0,003877	2,28382	B8NCZ6	B8NCZ6	1	AFLA_054670	Tryptophanyl-tRNA synthetase, putative
28,6813	28,4468	28,0162	28,1358	28,2366	28,3312		6,97E-126	3,6E+09	15	15	15	67,4	34,641	28,308	28,3814	28,2345	6	3	3	0,509012	0,146852	B8NCZ7	B8NCZ7	1	AFLA_054680	Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine-guanosine phosphorylase)
30,8711	30,4805	32,01	32,354	31,5761	31,4654		0	3,03E+10	20	18	18	81	34,679	31,4595	31,1205	31,7985	6	3	3	0,27557	-0,677956	B8ND04	B8ND04	1	AFLA_054750	Malate dehydrogenase, NAD-dependent
27,9634	27,4756	27,8533	27,5184	27,7199	27,9976		1,02E-143	3,49E+09	15	15	15	35,3	63,847	27,7547	27,7641	27,7453	6	3	3	0,930649	0,0187829	B8ND10	B8ND10	1	AFLA_054810	Transcriptional repressor TupA/RocA, putative
28,3905	28,8924	28,5003	28,5856	28,8567	28,9128		1,91E-166	3,69E+09	15	15	15	43,7	45,218	28,6897	28,5944	28,785	6	3	3	0,355885	-0,190633	B8ND13	B8ND13	1	AFLA_054840	Glycogen synthase kinase (Skp1), putative
24,0321	23,5884	23,9396	23,7194	23,761	23,7486		1,08E-06	2,07E+08	4	4	4	8,8	61,463	23,7982	23,8534	23,743	6	3	3	0,46171	0,110365	B8ND16	B8ND16	1	AFLA_054870	6-phosphofructo-2-kinase, putative
26,9404	26,4631	26,1183	26,3314	26,2152	26,1423		4,27E-38	7,98E+08	5	5	5	25,1	30,817	26,3685	26,5073	26,2297	6	3	3	0,319886	0,277604	B8ND19	B8ND19	1	AFLA_054900	ABC transporter, putative
27,7408	27,5509	27,502	27,1452	27,659	27,6583		1,20E-31	1,86E+09	8	8	8	35,3	39,971	27,5427	27,5979	27,4875	6	3	3	0,58478	0,11039	B8ND22	B8ND22	1	AFLA_054930	DUF410 domain protein
24,8801	25,4536	26,0648	26,7104	25,6302	25,3094		7,01E-88	1,28E+09	13	13	13	15,7	123,24	25,6747	25,4662	25,8833	6	3	3	0,486378	-0,41717	B8ND30	B8ND30	1	AFLA_055010	Homoaconitase, mitochondrial (EC 4.2.1.36) (Homoaconitate hydratase)
31,5192	31,0407	30,5129	32,3898	32,2883	32,3916	+	0	4,87E+10	22	22	20	72,3	40,145	31,6904	31,0243	32,3566	6	3	3	0,010392	-1,33232	B8ND35	B8ND35	1	AFLA_055060	NAD-dependent formate dehydrogenase AciA/Fdh
29,6508	29,2474	28,9932	29,2154	29,2895	29,4432		1,91E-255	6,46E+09	12	12	12	69,5	28,518	29,3066	29,2971	29,316	6	3	3	0,930295	-0,0188904	B8ND48	B8ND48	1	AFLA_055190	Proteasome subunit alpha type (EC 3.4.25.1)
27,8136	27,5782	27,2442	27,4637	27,5196	27,6836		7,24E-75	2,17E+09	8	8	8	51,4	23,558	27,5505	27,5453	27,5557	6	3	3	0,956403	-0,010348	B8ND51	B8ND51	1	AFLA_055220	Hsp70 nucleotide exchange factor (Fes1), putative
28,9381	29,594	29,9338	29,7396	29,2853	29,1522		0	1,56E+10	19	19	16	68,8	41,639	29,4405	29,4886	29,3924	6	3	3	0,792352	0,0962626	B8ND52;C0	B8ND52	2	AFLA_055230	Actin Act1
29,3436	29,2542	28,8332	28,793	29,2604	29,2835		0	6,74E+09	18	18	18	33	86,584	29,128	29,1437	29,1123	6	3	3	0,895462	0,0313867	B8ND53	B8ND53	1	AFLA_055240	Bifunctional purine biosynthetic protein Ade1, putative
24,2783	24,1626	24,1504	23,8257	24,122	23,6545		1,94E-13	1,95E+08	6	6	6	9,3	91,575	24,0323	24,1971	23,8674	6	3	3	0,08172	0,329718	B8ND54	B8ND54	1	AFLA_055250	Mitochondrial mRNA processing protein PET127, putative
33,3406	33,2901	32,9795	33,3355	33,2545	33,3577		0	1,09E+11	31	31	31	68,8	46,388	33,2596	33,2034	33,3159	6	3	3	0,39126	-0,112509	B8NDQ4	B8NDQ4	1	AFLA_055450	Translation elongation factor eEF-1 subunit gamma, putative
26,6098	26,814	26,2816	24,2622	24,2739	24,0779	+	6,08E-44	5,42E+08	7	7	7	32,2	34,813	25,3866	26,5685	24,2047	6	3	3	0,000147	2,36378	B8NDQ5	B8NDQ5	1	AFLA_055460	37S ribosomal protein S9
27,0132	26,5859	26,2647	26,9319	26,4811	26,2105		5,67E-81	8,07E+08	5	5	5	38,5	23,231	26,5812	26,6213	26,5412	6	3	3	0,804075	0,0800743	B8NDQ7	B8NDQ7	1	AFLA_055480	Calcineurin Ca2+-binding regulatory subunit CnaB
25,4771	25,4369	25,7907	26,3522	26,1089	26,0557	+	1,35E-37	5,02E+08	7	7	7	27,4	52,927	25,8702	25,5682	26,1723	6	3	3	0,013865	-0,604063	B8NDQ9	B8NDQ9	1	AFLA_055500	SET domain protein
27,5759	26,8811	27,0526	27,1801	27,1748	27,3113		1,26E-60	1,61E+09	8	8	8	51,7	20,811	27,196	27,1699	27,2221	6	3	3	0,819059	-0,0521927	B8NDR9	B8NDR9	1	AFLA_055600	ARD/ARD family protein, putative
NaN	27,2454	26,7823	NaN	NaN	NaN		0,00016	3,57E+08	2	2	2	10,3	38,792	27,0138	27,0138	NaN	2	2	0	1	NaN	B8NDS7	B8NDS7	1	AFLA_055680	Esterase, putative
27,2372	27,553	27,893	28,0877	28,1059	28,1373	+	3,80E-86	2,52E+09	17	17	17	25,3	108,39	27,8357	27,5611	28,1103	6	3	3	0,044476	-0,549245	B8NDT9	B8NDT9	1	AFLA_055800	Chromosome segregation protein Cse1, putative
27,9442	27,6418	27,3309	27,9867	28,0084	27,9287		1,26E-49	2,4E+09	13	13	13	49,9	51,881	27,8068	27,639	27,9746	6	3	3	0,133516	-0,335594	B8NDV6	B8NDV6	1	AFLA_055970	Fad NAD binding oxidoreductase, putative
27,9671	27,6087	27,2246	27,657	27,3245	27,3305		3,49E-129	2,18E+09	18	18	18	33,3	92,748	27,5187	27,6002	27,4373	6	3	3	0,536087	0,16285	B8NDV7	B8NDV7	1	AFLA_055980	Mannosyl-oligosaccharide glucosidase, putative
28,7961	28,4803	28,2935	28,7684	29,0912	28,9774		5,12E-241	5,97E+09	30	30	30	57	83,859	28,7345	28,5233	28,9457	6	3	3	0,072742	-0,42234	B8NDX6	B8NDX6	1	AFLA_056170	Catalase (EC 1.11.1.6)
27,6021	27,5674	29,9751	27,3876	26,9752	26,7032		5,24E-186	2,23E+09	7	7	7	43	17,028	27,7018	28,3815	27,022	6	3	3	0,173208	1,35953	B8NDY4	B8NDY4	1	AFLA_056250	Ribosomal protein L14
31,0878	31,3448	31,2496	31,1021	30,7598	30,8336		0	2,72E+10	11	11	11	80,7	21,804	31,0629	31,2274	30,8985	6	3	3	0,062339	0,328912	B8ND65	B8ND65	1	AFLA_056260	Nascent polypeptide-associated complex (NAC) subunit, putative
29,1911	29,5284	30,5999	31,1599	30,9681	30,5768		0	1,84E+10	29	29	29	58,9	61,708	30,3374	29,7731	30,9016	6	3	3	0,069426	-1,12845	B8ND74	B8ND74	1	AFLA_056350	2-methylcitrate dehydratase, putative
25,335	25,0497	24,5591	24,6917	26,0915	25,8116		2,84E-46	8,62E+08	6	6	6	32,4	24,789	25,2564	24,9813	25,5316	6	3	3	0,318957	-0,550355	B8ND83	B8ND83	1	AFLA_056440	Uncharacterized protein
28,7571	28,5104	28,2848	28,3864	28,4174	28,4779		1,93E-109	3,75E+09	14	14	14	45,8	56,772	28,4723	28,5174	28,4272	6	3	3	0,551849	0,0901998	B8ND96	B8ND96	1	AFLA_056570	Glutathione synthetase (GSH-S) (EC 6.3.2.3)
31,8968	31,6432	31,5406	31,7457	31,8857	31,8809		0	3,06E+10	28	28	28	69,1	57,221	31,7655	31,6936	31,8374	6	3	3	0,280488	-0,143864	B8NDA6	B8NDA6	1	AFLA_056670	4-aminobutyrate transaminase GatA
26,5083	26,6274	26,9146	27,1907	26,8596	26,8663		1,24E-39	1,43E+09	13	13	13	39,7	55,765	26,8278	26,6834	26,9722	6	3	3	0,150612	-0,288772	B8NDA8	B8NDA8	1	AFLA_056690	Serine/threonine-protein phosphatase (EC 3.1.3.16)
28,0235	27,8022	27,32	27,7446	27,8178	28,0844		1,91E-73	2,29E+09	11	11	11	32,4	53,407	27,7987	27,7152	27,8822	6	3	3	0,511332	-0,167002	B8NDA9	B8NDA9	1	AFLA_056700	DUF89 domain protein
30,6535	30,0335	29,4357	29,308	29,5504	29,7403		0	9,22E+09	13	13	13	30,8	67,479	29,7869	30,0409	29,5329	6	3	3	0,245024	0,508022	B8NDC0	B8NDC0	1	AFLA_056810	Carboxypeptidase S1, putative
27,0987	27,278	25,6412	24,7721	26,4953	26,7874		1,10E-86	7,34E+08	8	8	8	15,4	81,967	26,3454	26,6726	26,0183	6	3	3	0,466968	0,65435	B8NDC1	B8NDC1	1	AFLA_056820	Geranylgeranyl pyrophosphate synthase, putative
24,4299	NaN	NaN	NaN	24,2963	24,4601		4,57E-06	94144000	4	4	4	5,7	70,292	24,3954	24,4299	24,3782	3	1	2	1	0,0516729	B8NDC8	B8NDC8	1	AFLA_056890	Uncharacterized protein
29,9071	29,1182	28,7208	29,113	29,2999	29,3231		1,06E-196	5,15E+09	12	12	12	55,3	37,563	29,247	29,2487	29,2454	6	3	3	0,992926	0,0033474	B8NDF3	B8NDF3	1	AFLA_057140	Nucleoside-diphosphate-sugar epimerase, putative
31,1232	30,9472	30,6597	30,2343	30,5978	30,6763		0	1,55E+10	12	12	12	47,7	38,179	30,7064	30,91	30,5028	6	3	3	0,100992	0,407221	B8NDZ3	B8NDZ3	1	AFLA_057240	RNP domain protein
25,9246	26,078	25,9829	25,4713	26,5285	25,9842		6,34E-45	1,01E+09	11	11	11	33,5	51,609	25,9949	25,9952	25,9947	6	3	3	0,99883	0,0004813	B8NE05	B8NE05	1	AFLA_057360	Proteasome regulatory particle subunit Rpt2, putative
26,116	26,162	26,0047	26,257	26,4929	26,5884	+	5,03E-20	7,05E+08	6	6	6	49,6	27,18	26,2701	26,0942	26,4461	6	3	3	0,032024	-0,351863	B8NE06	B8NE06	1	AFLA_057370	Ubiquitin conjugating enzyme (UbcA), putative
26,8264	27,5739	28,297	28,4192	28,025	27,7848		1,05E-102	2,23E+09	13	13	13	26,3	69,005	27,8211	27,5658	28,0763	6	3	3	0,332092	-0,510575	B8NE08	B8NE08	1	AFLA_057390	Ribosome biogenesis ABC transporter Arb1, putative
28,2036	28,3879	28,8061	27,8103	28,2046	28,3726		0	1,05E+10	17	17	17	65,8	39,876	28,2975	28,4658	28,1292	6	3	3	0,239739	0,336686	B8NE10	B8NE10	1	AFLA_057410	NAD binding Rossmann fold oxidoreductase, putative
27,7231	27,367	27,6501	25,8946	27,0002	27,1517		7,76E-114	1,14E+09	15	15	15	29,7	76,548	27,1311	27,5801	26,6822	6	3	3	0,094148	0,897876	B8NE30	B8NE30	1	AFLA_057610	Amine oxidase
24,9625	23,8974	23,7805	NaN	NaN	24,106		1,95E-09	1,4E+08	3	3	3	7,6	52,328	24,1866	24,2135	24,106	4	3	1	1	0,107504	B8NE31	B8NE31	1	AFLA_057620	CCR4-NOT core complex subunit Caf1, putative
28,9584	28,7581	28,4332	28,6543	28,7073	28,7056		3,65E-189	3,82E+09	19	18	18	54,1	53,051	28,7028	28,7166	28,6891	6	3	3	0,866886	0,0275141	B8NE43	B8NE43	1	AFLA_057740	Aldehyde dehydrogenase, putative
26,8993	27,2385	27,084	27,3902	27,2396	27,3399		4,12E-49	1,57E+09	5	5	5	16,4	45,792	27,1986	27,0739	27,3233	6	3	3	0,081359	-0,249315	B8NE44	B8NE44	1	AFLA_057750	FAD binding domain protein
28,4198	28,1603	28,0046	27,9112	28,0295	27,9958		1,53E-91	3,28E+09	5	5	5	61,7	14,42	28,0869	28,1949	27,9789	6	3	3	0,161777	0,216059	B8NE67	B8NE67	1	AFLA_057980	Uncharacterized protein
31,5319	31,0917	30,8204	29,2128	29,306	29,4598	+	0	1,37E+10	9	9	9	29,7	43,181	30,2371	31,148	29,3262	6	3	3	0,00115	1,82181	B8NE68	B8NE68	1	AFLA_057990	Purine nucleoside permease, putative
26,2973	24,9343	24,5345	26,2662	26,7636	26,8999		7,60E-34	7,23E+08	5	5	5	36,5	21,537	25,9493	25,2553	26,6432	6	3	3	0,070714	-1,38788	B8NEU7	B8NEU7	1	AFLA_058110	Cupin domain protein
32,3838	32,7022	32,4833	32,544	31,7294	31,764		0	5,28E+10	25	25	25	57,8	58,35	32,2678	32,5231	32,0125	6	3	3	0,144529	0,510628	B8NEV1	B8NEV1	1	AFLA_058150	Myo-inositol-phosphate synthase, putative
NaN	24,7678	26,5631	NaN	23,8451	23,856		4,13E-08	1,58E+08	3	3	3	12,8	38,278	24,758	25,6655	23,8505	4	2	2	0,180554	1,81496	B8NEV2	B8NEV2	1	AFLA_058160	1-aminocyclopropane-1-carboxylate deaminase, putative
24,1872	25,917	27,7133	27,8384	26,7718	26,112		1,17E-152	2,38E+09	13	13	13	55,8	40,28	26,4233	25,9392	26,9074	6	3	3	0,441858	-0,968217	B8NEW7;B	B8NEW7	3	AFLA_058310	S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284)
NaN	24,5913	24,8918	NaN	NaN	NaN		1,56E-08	2,67E+08	2	2	2	20,7	16,051	24,7416	24,7416	NaN	2	2	0	1	NaN	B8NEW9	B8NEW9	1	AFLA_058330	Mitochondrial intermembrane space translocase subunit Tim9, putative
29,9754	29,356	28,4006	29,7177	30,2447	30,2441		0	9,1E+09	13	13	13	33,3	48,268	29,6564	29,244	30,0688	6	3	3	0,16796	-0,824816	B8NEY4	B8NEY4	1	AFLA_058480	1,3-beta-glucanosyltransferase (EC 2.4.1.-)
28,2455	29,0108	28,9478	28,7698	29,1544	29,2172		3,54E-170	4,82E+09	17	17	17	52,4	53,32	28,8909	28,7347	29,0471	6	3	3	0,330538	-0,312429	B8NEZ3	B8NEZ3	1	AFLA_058570	ATP dependent RNA helicase (Dbp5), putative
28,4725	28,4732	28,5774	28,3358	28,5205	28,5108		1,56E-143	3,59E+09	19	19	19	64,8	49,534	28,4817	28,5077	28,4557	6	3	3	0,49548	0,0519848	B8NEZ4	B8NEZ4	1	AFLA_058580	GTP cyclohydrolase II, putative
27,0534	26,9653	27,6824	25,1328	26,7516	26,7987		1,13E-33	7,87E+08	6	6	6	26,3	34,238	26,7307	27,2337	26,2277	6	3	3	0,164674	1,00597	B8NEZ5	B8NEZ5	1	AFLA_058590	Dihydrodipicolinate synthetase family protein
28,166	27,803	27,5916	27,8945	27,9736	28,0849		1,32E-87	2,56E+09	13	13	13	54,8	31,309	27,9189	27,8535	27,9843	6	3	3	0,499897	-0,130831	B8NF27	B8NF27	1	AFLA_058910	Uncharacterized protein
27,9072	28,0435	27,8514	27,1821	27,2537	27,343	+	1,18E-63	1,89E+09	16	16	16	39,6	75,183	27,5968	27,934	27,2596	6	3	3	0,000788	0,674463	B8NDM0	B8NDM0	1	AFLA_059590	Amine oxidase
NaN	NaN	NaN	27,5088	27,4891	27,6653		1,06E-42	1,57E+09	4	4	4	32,2	19,57	27,5544	NaN	27,5544	3	0	3	1	NaN	B8NDN7	B8NDN7	1	AFLA_059760	Uncharacterized protein
25,1516	25,4603	NaN	24,8264	26,7491	26,4684		7,26E-35	2,92E+08	6	6	6	18,1	56,375	25,7312	25,3059	26,0146	5	2	3	0,431901	-0,708716	B8NE86	B8NE86	1	AFLA_059950	Oxidoreductase, FAD-binding, putative
32,2674	31,9181	30,6686	31,432	32,5512	32,6538		0	3,44E+10	13	13	13	60,6	32,512	31,9152	31,6181	32,2123	6	3	3	0,394424	-0,594282	B8NE88	B8NE88	1	AFLA_059970	Short-chain dehydrogenase, putative
29,3326	29,647	27,0998	29,5361	31,2923	31,0663		0	7,46E+09	33	33	33	42,9	113,65	29,6623	28,6931	30,6316	6	3	3	0,117214	-1,93844	B8NE90	B8NE90	1	AFLA_059990	O-methyltransferase, putative
26,2859	25,4721	28,7585	24,2723	24,2274	23,5927		2,57E-32	8,64E+08	7	7	7	39,6	15,129	25,4348	26,8388	24,0308	6	3	3	0,050124	2,80801	B8NEA6	B8NEA6	1	AFLA_060150	Ribosomal protein L26
25,8891	25,5673	26,1816	26,0431	25,451	25,6474		8,20E-09	5,86E+08	5	5	5	24,2	30,447	25,7966	25,8793	25,7138	6	3	3	0,541958	0,165508	B8NEB8	B8NEB8	1	AFLA_060270	Enoyl-CoA hydratase/isomerase family protein
31,5042	30,8205	31,4511	31,4883	31,2421	31,192		0	2,37E+10	19	19	19	55	44,422	31,283	31,2586	31,3075	6	3	3	0,847286	-0,0488637	B8NEC1	B8NEC1	1	AFLA_060300	Ketol-acid reductoisomerase
26,3421	26,4356	26,5891	26,1704	26,0791	26,1957	+	5,62E-15	7,49E+08	6	6	6	26,2	41,443	26,302	26,4556	26,1484	6	3	3	0,018637	0,307168	B8NED9	B8NED9	1	AFLA_060480	Phenazine biosynthesis protein, putative
31,2696	30,7442	30,2784	29,358	29,3359	29,6638	+	0	1,12E+10	18	18	18	25,2	105,17	30,1083	30,7641	29,4526	6	3	3	0,01268	1,31152	B8NEE0	B8NEE0	1	AFLA_060490	Pyridine nucleotide-disulphide oxidoreductase family protein
NaN	25,2471	24,7419	NaN	NaN	NaN		6,80E-09	2,65E+08	2	2	2	17,4	21,01	24,9945	24,9945	NaN	2	2	0	1	NaN	B8NEE9	B8NEE9	1	AFLA_060580	NEDD8 conjugating enzyme (UbcL), putative
28,8452	28,86	28,8721	28,9645	29,1685	29,0971	+	5,28E-171	6,82E+09	25	25	25	46,9	71,048	28,9679	28,8591	29,0767	6	3	3	0,022558	-0,2176	B8NEF6	B8NEF6	1	AFLA_060650	Glutaminyl-tRNA synthetase
NaN	23,8496	NaN	23,9368	23,7416	24,4345		7,46E-33	5,58E+08	8	8	8	30,5	51,349	23,9906	23,8496	24,0376	4	1	3	1	-0,188068	B8NEF9	B8NEF9	1	AFLA_060680	Dimethylallyl tryptophan synthase, putative
26,1831	25,9741	25,6957	26,1424	26,0095	26,5055		1,53E-58	2,18E+09	13	13	13	28,9	77,148	26,0851	25,951	26,2191	6	3	3	0,260343	-0,268167	B8NEG1	B8NEG1	1	AFLA_060700	Phenylalanine ammonia-lyase, putative
29,1181	28,6332	28,1888	28,469	28,7897	28,862		9,36E-204	5,16E+09	17	17	17	56,9	48,016	28,6768	28,6467	28,7069	6	3	3	0,847948	-0,0601794	B8NEG2	B8NEG2	1	AFLA_060710	Toxin biosynthesis protein, putative
26,2891	27,4127	27,4119	27,1209	27,6534	27,4245		2,85E-61	1,82E+09	12	12	12	29,8	77,193	27,2187	27,0379	27,3996	6	3	3	0,422217	-0,361702	B8NF31	B8NF31	1	AFLA_060750	Golgi transport protein Sly1, putative
24,2706	NaN	25,0007	25,3595	25,6684	25,6706		7,39E-54	6,56E+08	7	7	7	40,5	33,455	25,194	24,6357	25,5661	5	2	3	0,054538	-0,930466	B8NF67	B8NF67	1	AFLA_061110	Mono-and diacylglycerol lipase, putative
23,2957	24,1362	23,6868	23,7093	23,1635	23,1813		1,45E-10	1,28E+08	3	3	3	5,8	73,65	23,5288	23,7062	23,3514	6	3	3	0,304702	0,354852	B8NFA3	B8NFA3	1	AFLA_061470	DSB repair complex subunit Ku70, putative
23,6373	23,9637	23,7981	NaN	NaN	NaN		8,49E-21	2,93E+08	5	5	5	15,6	53,058	23,7997	23,7997	NaN	3	3	0	1	NaN	B8NFA6	B8NFA6	1	AFLA_061500	Squalene monooxygenase Erg1

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
29,1882	28,8006	28,3818	28,4134	28,57	28,4307		1,55E-178	4,16E+09	7	7	7	47,9	15,65	28,6308	28,7902	28,4714	6	3	3	0,251548	0,318787	B8NEG5	B8NEG5	1	AFLA_061630	SsDNA binding protein, putative
30,8466	30,509	30,3193	30,401	30,4394	30,5134		0	1,55E+10	23	23	23	59	72,825	30,5048	30,5583	30,4513	6	3	3	0,534628	0,107005	B8NEI6	B8NEI6	1	AFLA_061840	Probable Xaa-Pro aminopeptidase P (AMPP) (Aminopeptidase P) (EC 3.4.11.9) (Aminoacylproline aminopeptidase) (Prolidase)
30,8418	30,808	30,5214	30,9081	30,7509	30,5742		0	2,24E+10	20	20	20	84,2	32,984	30,734	30,7237	30,7444	6	3	3	0,890012	-0,0206394	B8NEJ0	B8NEJ0	1	AFLA_061880	Pyridoxine biosynthesis protein
25,0181	24,6835	25,139	24,9937	24,5774	24,5336		1,13E-11	2,24E+08	5	5	5	16,1	48,922	24,8242	24,9469	24,7016	6	3	3	0,287568	0,245296	B8NEJ3	B8NEJ3	1	AFLA_061910	Arginine biosynthesis bifunctional protein ArgJ, mitochondrial [Cleaved into: Arginine biosynthesis bifunctional protein ArgJ alpha chain; Arginine biosynthesis bifunctional protein ArgJ beta chain] [Includes: Glutamate N-acetyltransferase (GAT) (EC 2.3.1.35) (Ornithine acetyltransferase) (OATase) (Ornithine transacetylase); Amino-acid acetyltransferase (EC 2.3.1.1) (N-acetylglutamate synthase) (AGS)]
NaN	24,0378	23,4446	NaN	22,2967	NaN		1,15E-26	2,81E+08	4	4	4	10,5	52,195	23,2597	23,7412	22,2967	3	2	1	1	1,44442	B8NEJ4	B8NEJ4	1	AFLA_061920	Protein transport protein Sec61 alpha subunit, putative
NaN	24,8047	24,5262	24,877	24,7417	NaN		1,64E-11	3,29E+08	3	3	3	14,3	39,939	24,7374	24,6654	24,8094	4	2	2	0,450698	-0,143934	B8NEJ7	B8NEJ7	1	AFLA_061950	Autophagy-related protein 3
23,5572	27,4163	27,1994	29,6554	27,6424	27,3953		0	2,55E+09	10	10	10	41,4	38,305	27,1443	26,0576	28,2311	6	3	3	0,206215	-2,17345	B8NEK6	B8NEK6	1	AFLA_062040	Stress protein DDR48, putative
27,248	26,939	26,5429	26,7638	26,9655	27,2505		8,91E-22	1,17E+09	5	5	5	44,9	23,102	26,9516	26,91	26,9933	6	3	3	0,753849	-0,0833416	B8NEL1	B8NEL1	1	AFLA_062090	MutT/nudix family protein
30,6713	30,181	30,059	30,243	30,3153	30,3522		0	1,29E+10	13	13	13	54,3	28,717	30,3036	30,3038	30,3035	6	3	3	0,998651	0,0003414	B8NEL2	B8NEL2	1	AFLA_062100	HAD superfamily hydrolase, putative
25,0299	24,9489	24,4517	24,6981	24,739	24,7273		2,99E-10	2,51E+08	4	4	4	8,4	74,268	24,7658	24,8101	24,7215	6	3	3	0,650114	0,0886771	B8NEL5	B8NEL5	1	AFLA_062130	Alpha-actinin, sarcomeric (F-actin cross linking protein)
27,391	27,2011	26,5929	24,86	25,1521	25,5167	+	2,77E-48	9,75E+08	5	5	5	21,7	36,186	26,119	27,0617	25,1763	6	3	3	0,003548	1,8854	B8NEL6	B8NEL6	1	AFLA_062140	RNA binding protein, putative
28,34	28,1946	27,9834	27,9005	28,034	28,2244		1,02E-105	3,64E+09	14	14	14	23,4	84,821	28,1128	28,1727	28,053	6	3	3	0,440305	0,119673	B8NEL8	B8NEL8	1	AFLA_062160	Polyubiquitin binding protein (Doa1/Ufd3), putative
22,8681	23,3738	24,8578	24,4216	24,0261	23,928		3,96E-10	1,73E+08	3	3	3	24	28,61	23,9126	23,6999	24,1252	6	3	3	0,527759	-0,425326	B8NEL9	B8NEL9	1	AFLA_062170	AI-8P family protein
26,6341	26,4183	26,1295	24,9647	25,2437	NaN	+	1,65E-58	6,32E+08	4	4	4	64,1	11,564	25,8781	26,3939	25,1042	5	3	2	0,009335	1,28971	B8NEM0	B8NEM0	1	AFLA_062180	37S ribosomal protein S16
25,5162	24,8487	24,7576	24,4917	NaN	24,6976		1,21E-07	2,5E+08	3	3	3	4,6	64,422	24,8623	25,0408	24,5947	5	3	2	0,255363	0,446155	B8NEM1	B8NEM1	1	AFLA_062190	RNA binding protein
27,4766	27,6662	27,39	25,2561	25,3826	24,6681	+	7,93E-57	1,24E+09	10	10	10	35,8	44,771	26,3066	27,5109	25,1022	6	3	3	0,000509	2,4087	B8NEM2	B8NEM2	1	AFLA_062200	Uncharacterized protein
24,1108	23,8632	23,7915	NaN	NaN	23,7676		4,54E-08	2,07E+08	4	4	4	9,9	70,661	23,8833	23,9218	23,7676	4	3	1	1	0,154252	B8NEN9	B8NEN9	1	AFLA_062370	Mitochondrial outer membrane translocase receptor (TOM70), putative
28,956	28,4693	28,5767	28,7744	28,8167	28,768		5,38E-152	4,5E+09	17	17	17	44,1	49,068	28,7268	28,6673	28,7864	6	3	3	0,467454	-0,119034	B8NEP1	B8NEP1	1	AFLA_062390	Tryptophanyl-tRNA synthetase
NaN	NaN	NaN	27,2497	27,6974	27,6582		7,84E-34	1,07E+09	9	9	9	20	74,118	27,5351	NaN	27,5351	3	0	3	1	NaN	B8NEP7	B8NEP7	1	AFLA_062450	Sphingomyelin phosphodiesterase
25,7533	25,5403	25,3161	25,3305	25,5452	25,7044		3,42E-47	5,04E+08	7	7	7	15,7	72,065	25,5316	25,5366	25,5267	6	3	3	0,955474	0,0098807	B8NEQ3	B8NEQ3	1	AFLA_062510	Myosin heavy chain, embryonic smooth muscle isoform, putative
NaN	NaN	NaN	25,3229	25,2405	25,716		1,14E-11	4,08E+08	2	2	2	12	26,52	25,4264	NaN	25,4264	3	0	3	1	NaN	B8NFD0	B8NFD0	1	AFLA_062640	Uncharacterized protein
26,8323	26,3541	25,6783	25,0126	24,8458	26,0729		1,65E-20	5,56E+08	6	6	6	21	38,576	25,7994	26,2883	25,3104	6	3	3	0,127468	0,977809	B8NFE6	B8NFE6	1	AFLA_062800	Aldo-keto reductase, putative
24,1829	23,8556	26,5081	23,5729	23,8771	24,0062		8,90E-27	3,54E+08	8	8	8	24,4	51,673	24,3338	24,8489	23,8187	6	3	3	0,289679	1,03016	B8NFE9;B8	B8NFE9	2	AFLA_062830	Monoxygenase, putative
25,0149	24,7177	24,1019	24,9614	25,4838	25,103		1,16E-17	3,77E+08	6	6	6	30,4	24,559	24,8971	24,6115	25,1827	6	3	3	0,139971	-0,571211	B8NFJ8	B8NFJ8	1	AFLA_063320	Uncharacterized protein
26,4551	24,7685	24,8497	NaN	24,5729	24,6058		8,25E-26	2,24E+08	3	3	3	19	35,133	25,0504	25,3578	24,5893	5	3	2	0,357831	0,768408	B8NES9	B8NES9	1	AFLA_063660	Polysaccharide deacetylase family protein
28,7051	28,8547	29,9473	27,9499	28,3175	28,0149		1,19E-91	4,69E+09	10	10	10	45,9	34,031	28,6316	29,169	28,0941	6	3	3	0,057741	1,07489	B8NI45	B8NI45	1	AFLA_064500	Uncharacterized protein
25,8966	25,6782	26,5028	23,2843	24,6635	24,4795	+	1,65E-12	4,8E+08	5	5	5	28	28,345	25,0842	26,0259	24,1424	6	3	3	0,019371	1,88343	B8NI48	B8NI48	1	AFLA_064530	Glutathione S-transferase GliG-like, putative
29,5954	29,4879	29,4998	29,7309	29,6048	29,7182	+	0	8,39E+09	28	28	28	60,5	62,245	29,6062	29,5277	29,6847	6	3	3	0,040481	-0,156956	B8NJ76	B8NJ76	1	AFLA_065080	Phosphoglucomutase, putative
24,9033	24,775	26,4225	27,6445	28,1505	28,0507	+	7,36E-77	2,36E+09	10	10	10	37,1	45,706	26,6578	25,3669	27,9486	6	3	3	0,009424	-2,58163	B8NJ90	B8NJ90	1	AFLA_065230	Glycerophosphoryl diester phosphodiesterase family protein
24,6899	25,0008	25,19	25,1271	25,557	25,3663		3,11E-263	1,76E+09	7	7	7	29,6	46,178	25,1552	24,9602	25,3501	6	3	3	0,111615	-0,389903	B8NJC1	B8NJC1	1	AFLA_065540	Peptide hydrolase (EC 3.4.-.-)
27,7191	27,5115	27,3289	26,9889	27,0623	27,236	+	1,50E-145	2,77E+09	13	13	13	45,4	44,316	27,3078	27,5198	27,0957	6	3	3	0,034367	0,424077	B8NJC4	B8NJC4	1	AFLA_065570	O-methyltransferase family protein
28,4343	27,9191	28,1241	26,9104	27,7718	28,0803		8,57E-107	1,56E+09	16	16	16	51,5	50,833	27,8733	28,1592	27,5875	6	3	3	0,207636	0,571672	B8NJE0	B8NJE0	1	AFLA_065730	Guanine deaminase, putative
27,3843	24,4821	24,9229	23,3499	23,8384	23,8966		2,33E-22	3,26E+08	3	3	3	8,5	45,369	24,6457	25,5964	23,695	6	3	3	0,107461	1,90146	B8NJE1	B8NJE1	1	AFLA_065740	7-dehydrocholesterol reductase, putative
27,1035	25,6147	25,8383	25,7097	26,1185	26,325		6,37E-36	7,04E+08	9	9	9	30,2	47,815	26,1183	26,1855	26,0511	6	3	3	0,800385	0,134423	B8NI96	B8NI96	1	AFLA_065920	Uncharacterized protein
30,4635	29,8047	29,7286	29,4342	29,8615	30,1187		0	1,27E+10	7	7	7	91,2	15,031	29,9019	29,9989	29,8048	6	3	3	0,561592	0,194123	B8NI98	B8NI98	1	AFLA_065940	Glyoxalase family protein
28,6244	28,699	28,4089	28,8796	28,4211	28,5436		2,55E-141	3,99E+09	14	14	14	47,1	45,979	28,5961	28,5774	28,6148	6	3	3	0,829231	-0,037365	B8NIA6	B8NIA6	1	AFLA_066020	12-oxophytodienoate reductase, putative
28,4295	28,4701	28,6026	28,523	28,5048	28,4647		1,27E-175	4,54E+09	11	11	11	61,8	37,136	28,4991	28,5007	28,4975	6	3	3	0,956294	0,0032088	B8NIB4	B8NIB4	1	AFLA_066100	Uncharacterized protein
29,832	29,8204	29,6229	29,7352	29,545	29,4989		3,18E-292	9,13E+09	19	19	19	52,9	42,938	29,6757	29,7584	29,593	6	3	3	0,17068	0,16538	B8NID1	B8NID1	1	AFLA_066270	RNA-binding La domain protein
24,1066	23,8038	NaN	23,5907	24,785	NaN		1,01E-08	2,86E+08	2	2	2	6,6	40,824	24,0715	23,9552	24,1879	4	2	2	0,74201	-0,232645	B8NIF9	B8NIF9	1	AFLA_066550	Alcohol dehydrogenase, putative
25,2242	25,2109	24,477	24,9835	25,5291	25,2224		7,08E-10	3,16E+08	4	4	4	19,3	37,635	25,1079	24,9707	25,245	6	3	3	0,4023	-0,274295	B8NJF2	B8NJF2	1	AFLA_066730	Alcohol dehydrogenase, putative
NaN	24,5656	24,4881	25,3937	25,1179	24,4315		1,59E-08	2,25E+08	4	4	4	16,5	36,622	24,7993	24,5268	24,981	5	2	3	0,307628	-0,454216	B8NJL3	B8NJL3	1	AFLA_067340	Uncharacterized protein
29,5987	29,3639	29,1708	28,7523	29,4746	29,3458		0	9,17E+09	21	21	21	54,6	48,308	29,2844	29,3778	29,1909	6	3	3	0,50349	0,186893	B8NJL5	B8NJL5	1	AFLA_067360	Elongation factor Tu
29,2699	28,7878	29,3403	29,5569	28,2302	28,7507		2,77E-94	6,67E+09	3	3	3	25,4	18,467	28,9893	29,1327	28,8459	6	3	3	0,535241	0,286724	B8NJM4	B8NJM4	1	AFLA_067450	Glycine cleavage system H protein
26,2635	26,5945	26,8798	25,7798	26,4289	26,1888		2,90E-18	7,77E+08	6	6	6	19,3	51,722	26,3559	26,5793	26,1325	6	3	3	0,160895	0,446758	B8NIH3	B8NIH3	1	AFLA_067600	Nuclear and cytoplasmic polyadenylated RNA-binding protein pub1
25,8944	26,574	26,9563	26,8961	26,9214	26,7349		1,43E-55	1,4E+09	11	11	11	23,9	68,175	26,6628	26,4749	26,8508	6	3	3	0,299921	-0,375923	B8NIJ3	B8NIJ3	1	AFLA_067800	Mitochondrial processing peptidase alpha subunit, putative
28,1814	27,9038	27,6659	28,4053	28,3069	28,3362	+	1,50E-56	3,01E+09	9	9	9	27,7	44,468	28,1332	27,917	28,3495	6	3	3	0,046447	-0,432439	B8NIJ9	B8NIJ9	1	AFLA_067860	Tyrosinase, putative
NaN	NaN	24,368	24,0913	22,5463	NaN		5,71E-07	86327000	4	4	4	13,5	45,802	23,6685	24,368	23,3188	3	1	2	1	1,04919	B8NIK6	B8NIK6	1	AFLA_067930	Nucleoside hydrolase, putative
30,5965	30,6596	30,9785	27,4041	26,9891	27,5533	+	3,41E-219	1,26E+10	12	12	12	51,2	24,222	29,0302	30,7449	27,3155	6	3	3	7,64E-05	3,42934	B8NIL3	B8NIL3	1	AFLA_068000	Ribosomal protein
25,6129	25,9633	26,315	25,0573	25,3857	25,9934		1,02E-57	1,33E+09	6	6	6	36,1	20,972	25,7213	25,9637	25,4788	6	3	3	0,228052	0,484917	B8NIL7;B8	B8NIL7	2	AFLA_068040	ADP-ribosylation factor, putative
26,9594	26,6196	26,126	25,6693	25,2932	25,6965	+	3,61E-110	7,07E+08	7	7	7	23,6	47,87	26,0607	26,5683	25,553	6	3	3	0,020912	1,01529	B8NIN1	B8NIN1	1	AFLA_068180	Ethanolamine kinase, putative
26,6944	26,7771	26,7493	27,2211	27,083	27,0296	+	2,57E-20	1,55E+09	8	8	8	36,4	34,857	26,9258	26,7403	27,1113	6	3	3	0,003924	-0,370981	B8NIN2	B8NIN2	1	AFLA_068190	CORD and CS domain protein
26,4278	26,3155	24,3826	26,1513	26,2014	26,0667		3,32E-09	6,79E+08	3	3	3	40	12,545	25,9242	25,7086	26,1398	6	3	3	0,552067	-0,431158	B8NIN3	B8NIN3	1	AFLA_068200	Uncharacterized protein
30,8895	30,6915	30,5235	30,6642	30,6727	30,6931		1,89E-214	1,66E+10	6	6	6	54,5	17,871	30,6891	30,7015	30,6767	6	3	3	0,826865	0,0247752	B8NIP0	B8NIP0	1	AFLA_068270	Uncharacterized protein
26,2944	NaN	NaN	NaN	26,1678	26,137		2,70E-13	6,68E+08	4	4	4	17,1	33,454	26,1997	26,2944	26,1524	3	1	2	1	0,142003	B8NIP3	B8NIP3	1	AFLA_068300	1,3-beta-glucanosyltransferase Bgt1
28,179	28,4881	28,3686	28,1337	28,3948	27,8879		1,31E-183	4,39E+09	25	25	24	29,2	135,59	28,242	28,3452	28,1388	6	3	3	0,295856	0,206415	B8NIP7	B8NIP7	1	AFLA_068340	Cell wall biogenesis protein phosphatase Ssd1, putative
29,5947	29,6481	31,125	29,2951	28,4485	28,3752		4,97E-212	6,16E+09	13	13	13	59	21,955	29,4144	30,1226	28,7063	6	3	3	0,071662	1,41633	B8NIQ5	B8NIQ5	1	AFLA_068420	60S ribosomal protein L6
28,9132	28,4694	28,1687	28,2889	28,6186	28,7848		1,49E-165	3,6E+09	11	11	11	54,9	41,418	28,5406	28,5171	28,5641	6	3	3	0,865807	-0,0469716	B8NJN3	B8NJN3	1	AFLA_068430	Adhesion regulating molecule, putative
26,169	25,9503	25,7791	25,7747	25,7912	25,8227		1,77E-13	5,95E+08	3	3	3	22,4	18,183	25,8812	25,9661	25,7962	6	3	3	0,209463	0,169887	B8NJP6	B8NJP6	1	AFLA_068560	Mago nashi domain protein
NaN	26,691	27,7703	26,0029	25,186	24,4371		4,88E-219	2,41E+09	19	12	12	58,7	50,544	26,0175	27,2306	25,2087	5	2	3	0,064991	2,02194	B8NJQ2;CC	B8NJQ2	2	AFLA_068620	Tubulin beta, putative
26,0944	25,1217	25,3729	25,6246	25,5775	25,3037		1,09E-25	5,4E+08	4	4	4	14,1	44,344	25,5158	25,5296	25,502	6	3	3	0,932793	0,0276655	B8NJQ3	B8NJQ3	1	AFLA_068630	Nuclear mRNA splicing factor-associated protein, putative
27,2414	26,9568	27,9761	28,5612	28,1748	28,0739		6,55E-93	1,87E+09	5	5	5	79,3	10,245	27,8307	27,3914	28,2699	6	3	3	0,060106	-0,878531	B8NJR3	B8NJR3	1	AFLA_068730	Ubiquitin-like modifier SUMO, putative
27,9874	28,4549	29,0124	29,321	28,8868	28,7908		0	5,76E+09	8	8	8	61,1	23,675	28,7422	28,4849	28,9995	6	3	3	0,202717	-0,514635	B8NJR9	B8NJR9	1	AFLA_068790	Adenylyl-sulfate kinase (EC 2.7.1.25)
26,2675	26,7629	26,8286	26,676	27,1719	27,0457		4,83E-33	1,07E+09	7	7	7	24	43,682	26,7921	26,6197	26,9645	6	3	3	0,210243	-0,344875	B8NJS0	B8NJS0	1	AFLA_068800	Vacuolar ATP synthase subunit c
30,7433	30,4645	30,214	30,3884	30,4531	30,5784		0	1,56E+10	19	19	19	50,7	51,545	30,4736	30,4739	30,4733	6	3	3	0,997067	0,0006364	B8NJS4	B8NJS4	1	AFLA_068840	Aminomethyltransferase (EC 2.1.2.10)
NaN	26,1664	25,9857	26,1226	25,9835	26,0332		2,06E-35	7,03E+08	5	5	5	34,9	18,559	26,0583	26,076	26,0464	5	2	3	0,751541	0,0296351	B8NJT0	B8NJT0	1	AFLA_068900	Prefoldin subunit 5, putative
23,8791	23,8727	24,8857	25,0077	25,4062	25,0684		2,85E-09	2,15E+08	4	4	4	19,1	25,299	24,6866	24,2125	25,1608	6	3	3	0,057371	-0,948247	B8NJT4	B8NJT4	1	AFLA_068940	Proteasome regulatory particle subunit (Nas6), putative
26,2937	27,7411	27,8706	27,8633	27,7579	27,58		7,41E-80	2,24E+09	11	11	11	24,8	53,058	27,5178	27,3018	27,7337	6	3	3	0,446527	-0,431921	B8NJT6	B8NJT6	1	AFLA_068960	Vacuolar ATP synthase subunit H, putative
26,8777	29,3235	30,2664	30,667	28,8361	28,4604		0	1,43E+10	20	20	20	76,7	42,482	29,0719	28,8225	29,3212	6	3	3	0,703282	-0,498662	B8NJU1	B8NJU1	1	AFLA_069010	S-adenosylmethionine synthase (EC 2.5.1.6)
25,2006	24,8241	23,7407	24,002	24,0079	24,1		1,38E-09	1,77E+08	4	4	4	9,1	65,231	24,3125	24,5884	24,0366	6	3	3	0,276909	0,551819	B8NJU8	B8NJU8	1	AFLA_069080	Nuclear localization protein, putative
NaN	NaN	NaN	26,6398	26,5628	26,7352		4,15E-67	1,19E+09	5	5	5	22,3	39,792	26,6459	NaN	26,6459	3	0	3	1	NaN	B8NJU9	B8NJU9	1	AFLA_069090	GPI anchored protein, putative
NaN	25,1862	26,4455	26,5346	NaN	NaN		1,99E-06	5,24E+08	3	3	3	17,7	25,724	26,0554	25,8158	26,5346	3	2	1	1	-0,718718	B8NJV1	B8NJV1	1	AFLA_069110	Glycerol-3-phosphate phosphatase (GppA), putative
27,4661	27,9398	29,1133	24,337	23,8529	23,8823	+	1,50E-36	1,43E+09	7	7	7	33,1	14,625	26,0986	28,1731	24,0241	6	3	3	0,00128	4,14898	B8NJV8	B8NJV8	1	AFLA_069180	60S ribosomal protein L35
30,3572	30,8815	32,8796	33,1159	31,5228	31,451		0	3,33E+10	30	30	30	68,6	44,369	31,7013	31,3727	32,0299	6	3	3	0,523501	-0,657154	B8NIQ9	B8NIQ9	1	AFLA_069370	Phosphoglycerate kinase (EC 2.7.2.3)
25,8315	25,4813	24,3978	24,2407	25,2055	25,0897		3,48E-11	2,82E+08	5	5	5	7	94,493	25,0411	25,2369	24,8453	6	3	3	0,499437	0,391603	B8NIR2	B8NIR2	1	AFLA_069400	Formin binding protein (FNB3), putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
25,7233	25,2318	25,2808	25,0502	25,669	25,7442		2,26E-41	7,03E+08	8	8	8	17,7	68,069	25,4499	25,4119	25,4878	6	3	3	0,792474	-0,0758711	B8NIR3	B8NIR3	1	AFLA_069410	RNase L inhibitor of the ABC superfamily, putative
26,154	24,7076	24,6158	26,3338	26,6088	27,1175	+	1,04E-26	5,55E+08	11	11	11	39,7	34,644	25,9229	25,1591	26,6867	6	3	3	0,049561	-1,52756	B8NIR6	B8NIR6	1	AFLA_069440	Pyridoxal reductase (AKR8), putative
24,9241	24,7836	NaN	NaN	25,1648	24,7562		4,12E-06	2,13E+08	2	2	2	6	56,002	24,9072	24,8538	24,9605	4	2	2	0,670454	-0,106634	B8NIS7	B8NIS7	1	AFLA_069550	Pre-mRNA splicing factor (Prp31), putative
33,0887	32,6617	32,6401	32,7171	33,2099	33,13		0	1,08E+11	31	31	31	61,5	48,931	32,9079	32,7968	33,019	6	3	3	0,352425	-0,222167	B8NIT1	B8NIT1	1	AFLA_069590	Adenosylhomocysteinase (EC 3.3.1.1)
27,1593	27,0339	25,5066	28,2344	28,4499	28,5881	+	6,92E-114	2,68E+09	3	3	3	38,6	13,55	27,4954	26,5666	28,4241	6	3	3	0,02647	-1,85752	B8NIT4	B8NIT4	1	AFLA_069620	Uncharacterized protein
28,7004	28,3815	28,1902	28,7225	28,7587	28,8615		3,56E-140	4,25E+09	8	8	8	39,8	30,254	28,6025	28,424	28,7809	6	3	3	0,082072	-0,356875	B8NIT8	B8NIT8	1	AFLA_069660	TIM-barrel enzyme family protein
27,921	27,454	26,989	26,6933	27,4289	26,8816		9,02E-40	1,36E+09	6	6	6	20,2	36,753	27,228	27,4547	27,0013	6	3	3	0,26247	0,453445	B8NIU5	B8NIU5	1	AFLA_069730	HMG box protein, putative
28,2827	28,4852	28,5336	28,6582	28,352	28,1037		1,04E-85	3,53E+09	14	14	14	40	40,919	28,4026	28,4338	28,3713	6	3	3	0,742931	0,0625006	B8NIU9	B8NIU9	1	AFLA_069770	Eukaryotic translation initiation factor 3 subunit H (eIF3h)
24,6278	24,4428	24,1214	24,1366	NaN	24,3513		3,10E-05	1,89E+08	2	2	2	9,8	33,689	24,336	24,3973	24,2439	5	3	2	0,512571	0,153399	B8NIV0	B8NIV0	1	AFLA_069780	Kynurenine formamidase (KFA) (KFase) (EC 3.5.1.9) (Arylformamidase) (N-formylkynurenine formamidase)
26,0926	26,222	25,8124	25,5124	25,4498	25,1866	+	1,38E-39	5,49E+08	5	5	5	30,5	34,445	25,7126	26,0423	25,3829	6	3	3	0,013628	0,659414	B8NIV1	B8NIV1	1	AFLA_069790	Casein kinase 2 beta' regulatory subunit Ckb2, putative
33,6165	33,2789	32,9814	33,0112	32,8952	33,0442		0	9,52E+10	28	28	28	84,2	33,487	33,1379	33,2923	32,9835	6	3	3	0,177561	0,308784	B8NIV7;B8	B8NIV7	2	AFLA_069850	Glycerol dehydrogenase Gcy1, putative
31,4346	31,1501	30,9246	30,9049	30,9654	31,0778		0	2,36E+10	28	28	28	70,6	43,579	31,0762	31,1698	30,9827	6	3	3	0,296632	0,187097	B8NIW4	B8NIW4	1	AFLA_069920	Obg-like ATPase 1
29,8319	29,6174	29,3247	29,4793	29,6099	29,6947		2,89E-290	8,05E+09	13	13	13	50,3	40,044	29,593	29,5913	29,5946	6	3	3	0,984483	-0,0033067	B8NIW7	B8NIW7	1	AFLA_069950	Hsc70 cochaperone (SGT), putative
27,2066	26,6529	26,417	26,0794	26,7579	26,2197		1,19E-34	8,95E+08	2	2	2	38,5	8,7148	26,5556	26,7588	26,3523	6	3	3	0,262884	0,406511	B8NIX3	B8NIX3	1	AFLA_070010	Uncharacterized protein
25,4611	25,7812	25,3416	26,0678	25,5828	25,4291		4,04E-08	4,72E+08	2	2	2	8	28,278	25,6106	25,5279	25,6932	6	3	3	0,517261	-0,165252	B8NIY1	B8NIY1	1	AFLA_070090	Uncharacterized protein
26,3596	27,7923	28,3062	28,0778	28,2774	27,9744		6,40E-183	2,95E+09	26	26	26	34,9	120,48	27,798	27,486	28,1099	6	3	3	0,349373	-0,623837	B8NIY2	B8NIY2	1	AFLA_070100	Importin beta-4 subunit, putative
26,8904	26,7987	27,3986	26,8322	26,7749	27,0556		5,92E-32	9,91E+08	7	7	7	10,5	106,25	26,9584	27,0292	26,8876	6	3	3	0,528034	0,141678	B8NIY9	B8NIY9	1	AFLA_070170	Lysosomal alpha-glucosidase, putative
26,1495	25,8511	25,7515	26,2311	25,976	26,1526		5,90E-39	7,3E+08	4	4	4	12,7	51,384	26,0186	25,9174	26,1199	6	3	3	0,225306	-0,202518	B8NK20	B8NK20	1	AFLA_070690	Cystathionine gamma-synthase
32,2218	32,24	32,01	32,5251	32,7075	32,6564	+	0	6,44E+10	28	28	28	67,1	56,313	32,3935	32,1572	32,6297	6	3	3	0,006727	-0,472418	B8NK50	B8NK50	1	AFLA_070990	UTP-glucose-1-phosphate uridylyltransferase Ugp1, putative
28,6157	28,2571	27,6857	27,8243	27,7071	28,0367		1,71E-181	2,9E+09	19	19	19	19,8	166,52	28,0211	28,1861	27,856	6	3	3	0,314867	0,33009	B8NK51	B8NK51	1	AFLA_071000	Membrane bound C2 domain protein (Vp115), putative
31,0897	30,8215	30,5468	30,8209	31,0105	31,0584		0	2,09E+10	28	28	28	52,5	64,085	30,8913	30,8193	30,9633	6	3	3	0,451484	-0,143918	B8NK52	B8NK52	1	AFLA_071010	Heat shock protein (Sti1), putative
27,4605	27,1512	27,0996	27,1907	27,1009	27,3198		7,15E-30	1,76E+09	9	9	9	32,1	55,01	27,2205	27,2371	27,2038	6	3	3	0,809488	0,0333169	B8NK55	B8NK55	1	AFLA_071040	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)
24,8813	24,9771	NaN	25,0893	24,9778	25,1124		2,50E-16	3,52E+08	6	6	6	13,7	55,939	25,0076	24,9292	25,0598	5	2	3	0,135706	-0,130649	B8NJ01	B8NJ01	1	AFLA_071180	Indoleamine 2,3-dioxygenase family protein
25,8769	25,7681	25,6855	25,6302	26,2921	26,284		9,33E-25	6,21E+08	3	3	3	18,4	21,535	25,9228	25,7768	26,0688	6	3	3	0,266377	-0,291957	B8NJ02	B8NJ02	1	AFLA_071190	Vacuolar ATP synthase subunit G, putative
24,6153	25,2839	25,5642	27,2808	27,5638	27,3517	+	1,59E-28	8,89E+08	11	11	11	22,9	72,59	26,2766	25,1545	27,3988	6	3	3	0,001582	-2,24434	B8NJ06	B8NJ06	1	AFLA_071230	AIF-like mitochondrial oxidoreductase (Nfrl), putative
24,8057	24,8212	NaN	NaN	NaN	24,3853		5,86E-09	2,32E+08	4	4	4	11,3	53,513	24,6707	24,8134	24,3853	3	2	1	1	0,428148	B8NJ17	B8NJ17	1	AFLA_071340	Cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative
32,1453	31,9435	32,1332	32,5755	32,5687	32,6037	+	0	4,96E+10	30	30	30	79,1	56,165	32,3283	32,074	32,5826	6	3	3	0,001546	-0,508618	B8NJ18	B8NJ18	1	AFLA_071350	UDP-N-acetylglucosamine pyrophosphorylase
23,5882	24,1056	24,4025	23,126	22,7711	23,425	+	2,24E-34	3,02E+08	4	4	4	26,1	24,268	23,5697	24,0321	23,1074	6	3	3	0,038274	0,924714	B8NJ19	B8NJ19	1	AFLA_071360	Zinc knuckle nucleic acid binding protein, putative
31,1459	30,6648	30,3666	30,137	30,3516	30,484		0	1,42E+10	11	11	11	33,7	45,881	30,525	30,7258	30,3242	6	3	3	0,181465	0,401527	B8NJ22	B8NJ22	1	AFLA_071390	mRNA binding post-transcriptional regulator (Csx1), putative
24,6775	24,8496	NaN	NaN	NaN	24,2966		7,40E-11	2,13E+08	5	5	5	20	33,095	24,6079	24,7636	24,2966	3	2	1	1	0,466932	B8NJ26	B8NJ26	1	AFLA_071430	U5 snRNP complex subunit, putative
NaN	NaN	NaN	23,9876	NaN	22,4329		1,30E-10	1,28E+08	4	4	4	21,3	28,879	23,2103	NaN	23,2103	2	0	2	1	NaN	B8NJ29	B8NJ29	1	AFLA_071460	Uncharacterized protein
26,181	27,0768	27,6902	27,7005	27,383	26,9295		2,45E-44	2,37E+09	7	7	7	52,6	23,223	27,1602	26,9827	27,3377	6	3	3	0,510471	-0,355035	B8NJ30	B8NJ30	1	AFLA_071470	Adenine phosphoribosyltransferase 1
30,6304	29,9164	29,9871	30,1153	30,1732	30,1308		3,25E-165	1,07E+10	6	6	6	59,4	17,394	30,1589	30,178	30,1398	6	3	3	0,874847	0,0382366	B8NJ33	B8NJ33	1	AFLA_071500	Translation initiation inhibitor, putative
26,2154	23,8022	NaN	NaN	NaN	24,0213		1,42E-13	1,48E+08	3	3	3	18,1	31,57	24,6797	25,0088	24,0213	3	2	1	1	0,987512	B8MVS8	B8MVS8	1	AFLA_072750	Pyrroline-5-carboxylate reductase, putative
30,1366	29,607	29,0978	27,7892	29,3899	29,3718		0	4,48E+09	19	19	19	44,8	65,751	29,232	29,6138	28,8503	6	3	3	0,278528	0,763533	B8MVT0	B8MVT0	1	AFLA_072770	Pyrroline-5-carboxylate dehydrogenase, putative
26,4273	27,5057	28,2464	28,7217	28,5034	28,3397		2,65E-122	2,67E+09	10	9	9	39,8	39,492	27,9573	27,3931	28,5216	6	3	3	0,104692	-1,12843	B8MVY2	B8MVY2	1	AFLA_073290	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) (DAHP synthase) (Phospho-2-keto-3-deoxyheptonate aldolase)
29,8676	29,52	29,6738	28,1225	28,6653	28,6684	+	6,77E-158	4,75E+09	20	19	19	44,4	78,235	29,0863	29,6872	28,4854	6	3	3	0,004414	1,20175	B8MVZ8	B8MVZ8	1	AFLA_073450	Amine oxidase
24,4609	26,9345	26,6968	25,5034	26,3344	25,5749		5,37E-161	1,52E+09	12	12	12	34,9	58,819	25,9175	26,0307	25,8042	6	3	3	0,798809	0,226508	B8MVZ9;B8	B8MVZ9	2	AFLA_073460	Cyclopropane-fatty-acyl-phospholipid synthase, putative
31,5395	31,6005	31,4816	31,6685	31,6811	31,7231	+	0	3,46E+10	13	13	13	70,8	18,83	31,6157	31,5405	31,6909	6	3	3	0,016869	-0,150349	B8MW01	B8MW01	1	AFLA_073480	Tropomyosin, putative
27,1608	26,5751	25,7816	25,7143	26,6927	26,6144		1,73E-31	8,1E+08	10	10	10	15,9	98,082	26,4232	26,5058	26,3405	6	3	3	0,761196	0,16535	B8MW10	B8MW10	1	AFLA_073570	RhoGAP and Fes/CIP4 domain protein
25,0964	24,705	24,4722	25,3402	25,4701	24,944		2,18E-19	3,4E+08	6	6	6	20,6	58,784	25,0047	24,7579	25,2514	6	3	3	0,110217	-0,493562	B8MW12	B8MW12	1	AFLA_073590	UBX domain protein (Ubx5), putative
26,991	27,2145	27,4383	25,596	25,8747	25,5202	+	7,62E-21	1,64E+09	8	8	8	22,4	55,064	26,4391	27,2146	25,6636	6	3	3	0,000769	1,55096	B8MW24	B8MW24	1	AFLA_073710	Mitochondrial ribosomal protein DAP3, putative
29,5891	29,4261	29,0839	29,8413	29,8786	29,8989	+	0	8,69E+09	16	16	16	14,6	152,65	29,6197	29,3664	29,873	6	3	3	0,027745	-0,5066	B8MW29	B8MW29	1	AFLA_073760	DNA mismatch repair protein Msh3
26,1302	25,5821	25,49	25,7622	25,8654	25,8714		5,77E-19	8,7E+08	6	6	6	23,7	38,82	25,7836	25,7341	25,833	6	3	3	0,651594	-0,0988859	B8MW33	B8MW33	1	AFLA_073800	Short chain dehydrogenase/reductase family
29,343	29,0388	28,5997	28,8836	28,9732	29,0466		1,64E-130	5,37E+09	8	8	8	44	24,89	28,9808	28,9938	28,9678	6	3	3	0,911791	0,0260487	B8MW52	B8MW52	1	AFLA_073990	Proteasome subunit beta type (EC 3.4.25.1)
28,0544	27,5733	27,1719	26,1577	26,6132	26,8018	+	1,23E-74	9,43E+08	7	7	7	17,8	62,965	27,062	27,5998	26,5242	6	3	3	0,027938	1,07561	B8MW63	B8MW63	1	AFLA_074100	Gamma-glutamyltranspeptidase
28,4605	26,9762	26,3767	26,212	26,9039	27,2936		1,23E-43	1,41E+09	11	11	11	23,2	58,726	27,0371	27,2711	26,8032	6	3	3	0,53789	0,467943	B8MWJ5	B8MWJ5	1	AFLA_074520	Probable alpha-galactosidase A (EC 3.2.1.22) (Melibiase A)
28,3854	27,4888	27,0092	26,1405	27,1747	27,4432		4,51E-34	1,43E+09	6	6	6	18,5	62,782	27,2736	27,6278	26,9195	6	3	3	0,278939	0,708338	B8MWP0	B8MWP0	1	AFLA_074980	Splicing factor u2af large subunit
25,9765	25,8128	28,7062	27,3844	26,332	27,7226		8,36E-50	1,05E+09	6	6	6	39,7	16,816	26,9891	26,8318	27,1463	6	3	3	0,774822	-0,314499	B8MWP5	B8MWP5	1	AFLA_075030	40S ribosomal protein S13
28,498	28,5127	28,0301	25,8226	26,0485	25,8662	+	3,13E-49	1,83E+09	10	10	10	42,5	35,332	27,1297	28,3469	25,9125	6	3	3	0,000148	2,43446	B8MWP8	B8MWP8	1	AFLA_075060	Transformer-SR ribonucleoprotein, putative
29,4808	29,0864	29,0604	29,3833	29,4633	29,5735		2,17E-183	7,35E+09	15	15	15	69	31,585	29,3413	29,2092	29,4734	6	3	3	0,146177	-0,264199	B8MWQ7	B8MWQ7	1	AFLA_075150	Esterase, putative
27,2628	27,2893	27,3978	27,1	27,0894	26,8879	+	4,35E-125	1,79E+09	9	9	9	31,1	43,873	27,1712	27,3166	27,0258	6	3	3	0,022433	0,290857	B8MWW3	B8MWW3	1	AFLA_075500	Uncharacterized protein
NaN	NaN	24,3348	NaN	24,6268	25,6235		5,00E-18	2,24E+08	5	5	5	12,1	60,752	24,8617	24,3348	25,1252	3	1	2	1	-0,790316	B8MWW4	B8MWW4	1	AFLA_075510	General amidase, putative
26,6391	26,218	26,0857	26,1578	26,7925	25,8196		2,53E-81	1,29E+09	3	3	3	27,3	21,81	26,2855	26,3142	26,2567	6	3	3	0,870108	0,0575822	B8MWX6	B8MWX6	1	AFLA_075630	Uncharacterized protein
27,2892	26,9954	NaN	27,0624	26,7869	27,0113		1,11E-20	7,1E+08	6	6	6	15,3	61,969	27,029	27,1423	26,9535	5	2	3	0,309424	0,188769	B8MWZ2	B8MWZ2	1	AFLA_075800	Uncharacterized protein
25,577	25,9128	25,4457	25,9165	26,109	25,9976		3,16E-52	7,67E+08	4	4	4	56,9	13,302	25,8264	25,6452	26,0077	6	3	3	0,072807	-0,362513	B8MX15	B8MX15	1	AFLA_076020	Tropomyosin-1, putative
27,6693	27,6024	27,2911	27,0323	27,2605	27,084	+	8,84E-62	1,48E+09	12	12	12	25,6	70,64	27,3233	27,5209	27,1256	6	3	3	0,043304	0,395342	B8MX19	B8MX19	1	AFLA_076060	Structure-specific recognition protein, putative
25,9232	27,2247	27,7003	27,1906	27,0051	27,0713		3,57E-188	2,51E+09	11	10	10	32,5	59,145	27,0192	26,9494	27,089	6	3	3	0,80666	-0,13959	B8MX20	B8MX20	1	AFLA_076070	Septin AspB
NaN	25,4369	NaN	25,9565	25,5981	25,6969		0,00011	3,25E+08	2	2	2	13,1	41,912	25,6721	25,4369	25,7505	4	1	3	1	-0,313571	B8MX23	B8MX23	1	AFLA_076100	Uncharacterized protein
NaN	25,8149	26,7776	NaN	NaN	NaN		0,000171	2,15E+08	2	2	2	11,5	25,038	26,2962	26,2962	NaN	2	2	0	1	NaN	B8MX33	B8MX33	1	AFLA_076200	HAD superfamily hydrolase, putative
27,4584	27,3253	27,4174	27,3306	27,3247	27,4343		4,63E-76	2,43E+09	7	7	7	30	43,337	27,3818	27,4004	27,3632	6	3	3	0,5219	0,0371901	B8MX56	B8MX56	1	AFLA_076430	SUN domain protein (Uth1), putative
24,7912	25,8033	26,0359	25,6873	25,6434	25,6293		3,64E-10	5,6E+08	4	4	4	23,4	25,648	25,5984	25,5435	25,6533	6	3	3	0,788138	-0,109893	B8MX61	B8MX61	1	AFLA_076480	Glutathione S-transferase, putative
26,5085	25,9977	NaN	26,2122	26,0206	26,0729		5,75E-21	6,87E+08	9	9	9	15,9	73,932	26,1624	26,2531	26,1019	5	2	3	0,512758	0,151166	B8MX62	B8MX62	1	AFLA_076490	RSC complex subunit (RSC8), putative
32,8644	32,7785	32,8369	33,1615	33,1978	33,2429	+	0	9,09E+10	62	62	62	74,4	117,9	33,0137	32,8266	33,2007	6	3	3	0,000415	-0,374147	B8MX73	B8MX73	1	AFLA_076600	Translation elongation factor eEF-3, putative
26,0858	25,6375	25,4976	25,6985	26,1061	25,8025		2,82E-19	5,97E+08	4	4	4	31,5	25,589	25,8047	25,7403	25,8691	6	3	3	0,582261	-0,128766	B8MX75	B8MX75	1	AFLA_076620	Siroheme synthase Met8, putative
28,8229	28,7123	27,9427	28,6423	28,9101	28,902		0	6,74E+09	24	24	24	42,4	95,892	28,6554	28,4926	28,8181	6	3	3	0,325181	-0,325476	B8MX77	B8MX77	1	AFLA_076640	Phospholipase PldA, putative
30,032	31,899	31,193	31,4758	31,4257	31,2984		0	2,61E+10	15	15	15	50,1	51,618	31,2206	31,0413	31,4	6	3	3	0,547746	-0,35863	B8MX81	B8MX81	1	AFLA_076680	Acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)
34,5781	34,2992	34,0414	34,3677	34,3642	34,3915		0	2,24E+11	22	22	20	65	44,515	34,3404	34,3062	34,3745	6	3	3	0,682771	-0,068264	B8MX84	B8MX84	1	AFLA_076710	Malate dehydrogenase, NAD-dependent
NaN	NaN	24,8541	25,438	23,8125	NaN		1,48E-06	3,24E+08	2	2	2	20,5	16,838	24,7015	24,8541	24,6252	3	1	2	1	0,228874	B8MX88	B8MX88	1	AFLA_076750	Uncharacterized protein
24,5233	25,2874	25,7799	25,5375	NaN	NaN		1,33E-22	4,14E+08	5	5	5	17,9	36,068	25,282	25,1969	25,5375	4	3	1	1	-0,340638	B8MX91	B8MX91	1	AFLA_076780	Ribonucleoprotein, putative
30,0062	29,6981	29,4285	29,5533	29,739	29,8191		1,41E-256	8,61E+09	11	11	11	67,7	30,174	29,7074	29,7109	29,7038	6	3	3	0,970972	0,0071449	B8MX97	B8MX97	1	AFLA_076840	Proteasome subunit alpha type (EC 3.4.25.1)
28,5221	25,8216	25,2274	24,5784	25,9431	25,9385		1,88E-57	9,1E+08	6	6	4	17,3	51,944	26,0052	26,5237	25,4867	6	3	3	0,403396	1,03705	B8MXA1	B8MXA1	1	AFLA_076880	Stearic acid desaturase (SdeA), putative
30,4211	30,2642	30,1483	30,3545	30,6115	30,6519		0	1,56E+10	29	29	29	52	81,691	30,4086	30,2779	30,5393	6	3	3	0,099092	-0,261422	B8MXA2	B8MXA2	1	AFLA_076890	Metallopeptidase MepB
27,8108	27,7118	26,7651	27,165	27,4064	27,4937		3,23E-107	2,21E+09	12	11	11	88,5	15,333	27,3921	27,4292	27,355	6	3	3	0,841339	0,0742073	B8MXA4	B8MXA4	1	AFLA_076910	Cytokinesis EF-hand protein Cdc4, putative
25,0049	26,0553	25,8039	25,9376	25,8698	25,8149		8,76E-18	6,25E+08	10	10	10	11,3	115,13	25,7477	25,6214	25,8741	6	3	3	0,472092	-0,25272	B8MXA6	B8MXA6	1	AFLA_076930	Importin, putative
26,2117	26,1625	25,7806	23,8974	24,396	24,9421	+	5,46E-11	4,87E+08	4	4	4	50,5	10,64	25,2317	26,0516	24,4118	6	3	3	0,007741	1,63978	B8MXA7	B8MXA7	1	AFLA_076940	Small nuclear ribonucleoprotein SmE, putative
27,1954	27,1496	27,0524	27,7188	27,3802	27,5238	+	5,34E-48	1,68E+09	6	6	6	44,5	20,11	27,3367	27,1324	27,5409	6	3	3	0,018693	-0,408513	B8MXB0	B8MXB0	1	AFLA_076970	Uncharacterized protein

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
28,4284	28,3363	27,982	28,3198	28,0209	28,1176		4,08E-246	3,14E+09	17	17	17	50,1	46,285	28,2008	28,2489	28,1528	6	3	3	0,584936	0,0961482	B8MXB5	B8MXB5	1	AFLA_077020	DNA damage-inducible v-SNARE binding protein Ddi1, putative
24,8922	25,0013	24,8516	25,009	24,3504	24,6351		6,09E-06	3,83E+08	3	3	3	25,7	25,879	24,7899	24,915	24,6648	6	3	3	0,270543	0,250221	B8MXD7	B8MXD7	1	AFLA_077240	Uncharacterized protein
28,0893	27,5951	27,4665	25,8266	26,3498	26,2066	+	1,36E-60	1,45E+09	14	14	14	27,7	78,204	26,9223	27,717	26,1277	6	3	3	0,002945	1,58932	B8MXD8	B8MXD8	1	AFLA_077250	Acyl-coenzyme A oxidase
29,4927	28,9216	28,5272	28,6742	28,8578	28,921		3,96E-159	2,97E+09	18	18	17	61,9	45,256	28,8991	28,9805	28,8177	6	3	3	0,604362	0,162795	B8MXE0;B	B8MXE0	2	AFLA_077270	NADH-dependent flavin oxidoreductase, putative
23,9076	23,8574	22,5438	25,3155	25,8902	26,013	+	4,64E-25	2,52E+08	6	6	6	17,8	59,924	24,5879	23,4363	25,7396	6	3	3	0,009673	-2,30329	B8MXJ8	B8MXJ8	1	AFLA_077850	Phenylalanine ammonia-lyase (EC 4.3.1.24)
27,6069	26,6356	27,1858	26,7532	27,3027	27,9484		2,78E-163	1,72E+09	13	13	13	39,7	48,158	27,2388	27,1428	27,3347	6	3	3	0,688691	-0,19196	B8MXJ9	B8MXJ9	1	AFLA_077860	Uncharacterized protein
26,141	25,7214	25,1776	25,3779	25,9295	26,3162		7,20E-09	3,42E+08	3	3	3	15,2	37,604	25,7772	25,68	25,8745	6	3	3	0,643827	-0,194568	B8MXL2	B8MXL2	1	AFLA_077990	Zinc-binding oxidoreductase ToxD, putative
26,0516	NaN	22,9709	NaN	22,8439	22,7887		8,55E-06	1,04E+08	2	2	2	17,1	23,787	23,6638	24,5112	22,8163	4	2	2	0,385979	1,69494	B8MXL7	B8MXL7	1	AFLA_078040	(S)-2-haloacid dehalogenase IVA, putative
23,5901	23,515	23,486	23,8735	23,269	23,4454		1,76E-24	2,39E+08	3	3	3	8	61,824	23,5298	23,5304	23,5293	6	3	3	0,995646	0,0010573	B8MXP5	B8MXP5	1	AFLA_078320	Probable beta-glucosidase btgE (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase btgE) (Cellobiase btgE) (Gentiobiase btgE)
24,6625	27,5931	28,0294	27,8613	28,143	27,6925		1,33E-252	3,93E+09	17	17	17	55,2	58,058	27,3303	26,7616	27,8989	6	3	3	0,345848	-1,13726	B8MXQ1	B8MXQ1	1	AFLA_078380	Acetyl-coA hydrolase Ach1, putative
25,6043	25,6138	25,2217	25,7081	25,5772	25,8872		3,44E-15	4,37E+08	5	5	5	4,7	178,78	25,6021	25,4799	25,7242	6	3	3	0,195501	-0,244252	B8MXQ2	B8MXQ2	1	AFLA_078390	Transcription factor (Sin3), putative
27,5595	27,3284	26,6862	26,7717	27,1408	27,2744		1,38E-47	1,7E+09	9	9	9	22,9	54,547	27,1268	27,1914	27,0623	6	3	3	0,690513	0,129084	B8MXQ3	B8MXQ3	1	AFLA_078400	Protein phosphatase PP2A regulatory subunit B
27,2273	28,5195	28,285	29,1538	29,444	29,2296	+	3,92E-148	5,5E+09	18	18	18	33,6	67,874	28,6432	28,0106	29,2758	6	3	3	0,035884	-1,26518	B8MXQ5	B8MXQ5	1	AFLA_078420	Fumarate reductase Osm1, putative
25,7592	25,8926	25,474	25,492	25,9428	26,0593		1,06E-26	6,16E+08	8	8	8	27,2	45,433	25,77	25,7086	25,8314	6	3	3	0,594504	-0,122751	B8MXQ8	B8MXQ8	1	AFLA_078450	COP9 signalosome subunit CsnD
28,9072	28,5428	26,7093	27,6926	28,3543	28,5984		2,80E-169	2,58E+09	17	17	17	43,6	54,228	28,1341	28,0531	28,2151	6	3	3	0,835672	-0,162007	B8MXR1	B8MXR1	1	AFLA_078480	Cysteine protease, putative
NaN	NaN	NaN	25,4028	25,778	NaN		7,40E-07	1,55E+08	3	3	3	22,3	22,33	25,5904	NaN	25,5904	2	0	2	1	NaN	B8MXS2	B8MXS2	1	AFLA_078590	Extracellular matrix protein, putative
27,2826	27,383	27,5105	27,6699	27,3566	27,563		3,65E-107	2,03E+09	10	10	10	48,5	37,292	27,4609	27,392	27,5298	6	3	3	0,290336	-0,137757	B8MXS7	B8MXS7	1	AFLA_078640	Methylenetetrahydrofolate dehydrogenase
29,163	31,1656	31,4891	31,4141	31,2769	31,2086		0	2,92E+10	25	25	25	51,3	59,938	30,9529	30,6059	31,2999	6	3	3	0,395598	-0,693964	B8MXS8	B8MXS8	1	AFLA_078650	ATP synthase subunit alpha
24,8323	NaN	25,0932	25,5296	25,1667	25,2196		1,31E-12	3,21E+08	3	3	3	23,6	21,459	25,1683	24,9628	25,3053	5	2	3	0,146063	-0,342529	B8MXT0	B8MXT0	1	AFLA_078670	RNA polymerase II subunit 7
26,2349	25,9499	26,0388	26,767	26,2182	26,5825		2,12E-21	8,49E+08	5	5	5	13,9	56,668	26,2985	26,0745	26,5226	6	3	3	0,069423	-0,448042	B8MXT1	B8MXT1	1	AFLA_078680	Uncharacterized protein
26,856	27,1506	27,006	26,6402	27,3962	26,9469		1,70E-32	1,71E+09	6	6	6	13,5	73,106	26,9993	27,0042	26,9944	6	3	3	0,968742	0,0098152	B8MXT5	B8MXT5	1	AFLA_078720	Peroxisomal targeting receptor pex5, putative
26,5382	25,9663	25,66	25,9294	26,1915	26,3529		6,61E-26	7,06E+08	12	12	12	24,7	64,064	26,1064	26,0548	26,1579	6	3	3	0,736154	-0,103118	B8MXT7	B8MXT7	1	AFLA_078740	2-hydroxyphytanoyl-CoA lyase, putative
24,7904	NaN	23,0477	NaN	NaN	NaN		1,08E-06	1,03E+08	2	2	2	4	68,226	23,9191	23,9191	NaN	2	2	0	1	NaN	B8MXU4	B8MXU4	1	AFLA_078810	Oxidoreductin
30,1624	29,59	29,2442	29,0908	29,3534	29,449		0	9,25E+09	22	22	22	47,7	67,541	29,4816	29,6656	29,2977	6	3	3	0,271105	0,367861	B8MXV3	B8MXV3	1	AFLA_078900	Beta-hexosaminidase (EC 3.2.1.52)
28,4499	28,7299	28,352	27,9074	27,9597	27,7471	+	3,16E-135	3,14E+09	12	12	12	45,2	39,263	28,191	28,5106	27,8714	6	3	3	0,007951	0,639219	B8MXX7	B8MXX7	1	AFLA_079140	Casein kinase, putative
27,9148	28,3372	29,1739	29,2865	29,2491	29,1925		4,36E-152	5,91E+09	23	23	23	29,3	119,42	28,859	28,4753	29,2427	6	3	3	0,107398	-0,767426	B8MXX8	B8MXX8	1	AFLA_079150	Valyl-tRNA synthetase
23,2484	23,4539	23,0619	NaN	NaN	NaN		2,05E-09	1,54E+08	4	4	4	10,9	37,363	23,2547	23,2547	NaN	3	3	0	1	NaN	B8MXX9	B8MXX9	1	AFLA_079160	Ribosome biogenesis protein, putative
25,9255	26,5566	26,2075	26,1516	26,5855	26,1363		7,08E-96	1,5E+09	25	25	25	27,2	137,48	26,2605	26,2299	26,2911	6	3	3	0,806849	-0,0612513	B8MY03	B8MY03	1	AFLA_079400	NRPS-like enzyme, putative
26,6738	26,7292	27,4185	27,4991	27,3888	27,2575		1,35E-38	1,43E+09	6	6	6	53,1	26,272	27,1612	26,9405	27,3818	6	3	3	0,1517	-0,441263	B8MY08	B8MY08	1	AFLA_079450	Ureidoglycolate hydrolase, putative
27,1897	26,7652	26,2986	26,308	26,8218	26,6583		5,53E-31	9,45E+08	12	12	12	7,1	249,12	26,6736	26,7512	26,596	6	3	3	0,630838	0,155149	B8MY10	B8MY10	1	AFLA_079470	Pre-mRNA splicing helicase, putative
26,9259	27,3454	26,3949	27,298	27,4476	27,5304		6,19E-73	1,72E+09	10	10	10	21,6	78,809	27,157	26,8887	27,4253	6	3	3	0,131118	-0,536605	B8MY11	B8MY11	1	AFLA_079480	Oligopeptidase family protein
26,8818	25,4058	24,6017	24,2669	24,8408	25,9211		9,55E-22	6,33E+08	6	6	6	8,7	93,504	25,3197	25,6298	25,0096	6	3	3	0,494115	0,620179	B8MY31	B8MY31	1	AFLA_079680	Vesicular fusion ATPase, putative
27,8179	27,4347	27,4406	27,6099	27,741	27,7956		6,12E-64	2,39E+09	17	17	17	46,6	61,121	27,6399	27,5644	27,7155	6	3	3	0,335736	-0,151094	B8MY33	B8MY33	1	AFLA_079700	Protein arginine methyltransferase RmtB
27,5837	26,9206	26,5392	26,7556	27,1863	26,9966		1,17E-14	1,51E+09	8	8	8	17,6	71,422	26,997	27,0145	26,9795	6	3	3	0,920501	0,0350208	B8MY40	B8MY40	1	AFLA_079770	Endothelin-converting enzyme
30,7568	30,84	30,705	29,4784	28,8326	28,8116	+	2,21E-42	8,56E+09	6	6	6	46	14,147	29,9041	30,7673	29,0409	6	3	3	0,001483	1,72639	B8MY51	B8MY51	1	AFLA_079880	60S ribosomal protein L22, putative
25,4483	25,7684	25,8855	24,8764	25,1578	25,1986	+	5,41E-18	5,47E+08	6	6	6	25,8	33,516	25,3892	25,7007	25,0776	6	3	3	0,019624	0,623128	B8MY53	B8MY53	1	AFLA_079900	Recombination hotspot-binding protein (Translin), putative
29,8697	29,9146	30,1226	30,2839	30,1882	30,2118	+	6,46E-64	1,1E+10	9	9	9	34	28,156	30,0985	29,969	30,228	6	3	3	0,035585	-0,259019	B8MY54	B8MY54	1	AFLA_079910	Glutathione peroxidase
NaN	26,7061	27,7025	27,458	26,6026	26,0634		2,76E-196	1,91E+09	8	8	8	40,1	32,288	26,9065	27,2043	26,708	5	2	3	0,496015	0,496326	B8MY65	B8MY65	1	AFLA_080020	ATP synthase subunit gamma
25,2246	NaN	NaN	23,531	24,5906	NaN		6,99E-09	1,15E+08	4	4	4	5,2	100,79	24,4488	25,2246	24,0608	3	1	2	1	1,16382	B8MY66	B8MY66	1	AFLA_080030	Topoisomerase I
26,9821	28,2673	29,2138	29,1097	28,3689	27,9152		0	7,02E+09	22	22	22	48	85,571	28,3095	28,1544	28,4646	6	3	3	0,694482	-0,310199	B8MY76	B8MY76	1	AFLA_080130	Protein transport protein Sec23, putative
30,4844	30,5277	30,4712	29,2864	28,74	28,8897	+	1,23E-47	8,01E+09	5	5	5	35,8	17,937	29,7332	30,4944	28,972	6	3	3	0,000747	1,52239	B8MY77	B8MY77	1	AFLA_080140	60S ribosomal protein L12
25,4934	25,8493	27,4139	27,9832	26,6363	26,2287		4,16E-102	1,87E+09	2	2	2	17,6	17,669	26,6008	26,2522	26,9494	6	3	3	0,428975	-0,697208	B8MY87	B8MY87	1	AFLA_080240	ATP synthase delta chain, mitochondrial, putative
28,6715	28,4696	28,3939	28,8497	28,9325	28,9992	+	1,88E-133	3,89E+09	7	7	7	38	25,59	28,7194	28,5117	28,9271	6	3	3	0,011286	-0,415482	B8MY92	B8MY92	1	AFLA_080290	DUTPase (Dut), putative
NaN	24,0368	24,1546	24,1558	23,914	23,5914		1,04E-07	2,36E+08	4	4	4	21,8	37,787	23,9705	24,0957	23,8871	5	2	3	0,404529	0,208653	B8MY93	B8MY93	1	AFLA_080300	Pyridoxal kinase, putative
30,9468	30,6708	30,5251	31,0292	31,0182	31,0229		0	1,97E+10	14	14	14	85	29,031	30,8688	30,7142	31,0234	6	3	3	0,066822	-0,309219	B8MYA2	B8MYA2	1	AFLA_080390	6-phosphogluconolactonase, putative
27,1129	27,0888	27,0913	27,1171	27,1421	27,1718		1,70E-57	2,05E+09	8	8	8	36,4	38,083	27,1207	27,0977	27,1437	6	3	3	0,058672	-0,0459989	B8MYC0	B8MYC0	1	AFLA_080570	F-actin capping protein beta subunit
24,928	NaN	23,9208	23,6575	NaN	NaN		2,17E-05	1,89E+08	3	3	3	5,7	80,629	24,1688	24,4244	23,6575	3	2	1	1	0,766895	B8MYC2	B8MYC2	1	AFLA_080590	Transcription initiation factor TFIID subunit, putative
26,0263	25,9518	25,7563	26,1975	25,7615	25,9017		1,75E-70	8,12E+08	5	5	5	13,1	66,988	25,9325	25,9115	25,9535	6	3	3	0,795246	-0,0420628	B8MYC5	B8MYC5	1	AFLA_080620	Endoplasmic reticulum and nuclear membrane proteinc Npl4, putative
31,1012	30,4207	29,8645	30,0108	30,6429	30,7302		9,84E-299	1,25E+10	9	9	9	70	21,813	30,4617	30,4622	30,4613	6	3	3	0,998474	0,0008615	B8MYC6	B8MYC6	1	AFLA_080630	NADH-quinone oxidoreductase Pst2, putative
30,2294	29,1182	30,6719	NaN	24,4705	24,9859	+	1,13E-163	2,83E+09	10	10	10	39,9	39,669	27,8952	30,0065	24,7282	5	3	2	0,003514	5,2783	B8MYC9	B8MYC9	1	AFLA_080660	L-asparaginase
27,2469	28,0483	28,1792	28,2643	28,3208	28,2667		1,32E-100	3,76E+09	14	14	14	56,9	36,893	28,0544	27,8248	28,2839	6	3	3	0,190954	-0,459139	B8MYD7	B8MYD7	1	AFLA_080750	ARP2/3 complex 34 kDa subunit, putative
27,7575	27,9064	27,8067	27,7339	27,8583	27,7964		1,74E-45	2,44E+09	11	11	11	26,3	65,149	27,8099	27,8236	27,7962	6	3	3	0,654412	0,0273514	B8MYE1	B8MYE1	1	AFLA_080790	TPR domain protein
25,5504	26,4588	26,3058	26,6901	25,9242	26,1201		5,58E-37	8,25E+08	9	9	9	22,8	59,662	26,1749	26,105	26,2448	6	3	3	0,719543	-0,139819	B8MYE7	B8MYE7	1	AFLA_080850	rRNA processing protein Pwp1, putative
26,4237	28,7785	29,6353	28,7784	27,96	27,2554		0	7,56E+09	19	19	18	66,7	50,168	28,1385	28,2792	27,9979	6	3	3	0,803192	0,281229	B8MYF4	B8MYF4	1	AFLA_080920	Tubulin alpha-1 subunit
28,3564	28,335	28,4154	28,4961	28,7154	28,4959		9,43E-254	3,06E+09	18	18	18	19,8	132,4	28,469	28,3689	28,5691	6	3	3	0,059969	-0,200211	B8MYF5	B8MYF5	1	AFLA_080930	EF hand domain protein
26,149	25,8378	25,5439	25,696	25,7755	25,9895		9,07E-57	6,19E+08	6	6	6	18,7	40,183	25,832	25,8436	25,8203	6	3	3	0,911095	0,0232379	B8MYG4	B8MYG4	1	AFLA_081020	Ubiquitin fusion degradation protein Ufd1, putative
24,1184	24,6402	NaN	NaN	NaN	24,3886		8,39E-21	1,39E+08	2	2	2	6	51,454	24,3824	24,3793	24,3886	3	2	1	1	-0,009346	B8MYG6	B8MYG6	1	AFLA_081040	AAA family ATPase Rvb2/Reptin, putative
23,7234	24,2351	23,448	23,8813	23,9513	24,0995		1,56E-05	1,46E+08	2	2	2	7,4	40,508	23,8897	23,8021	23,9774	6	3	3	0,504812	-0,175216	B8MYI8	B8MYI8	1	AFLA_081260	60S ribosome biogenesis protein Brx1, putative
28,046	27,5847	27,5203	27,0811	27,2064	27,3971		1,11E-85	1,99E+09	10	10	10	55	23,473	27,4726	27,717	27,2282	6	3	3	0,061206	0,488806	B8MYJ0	B8MYJ0	1	AFLA_081280	Ras GTPase Rab11, putative
NaN	24,8142	24,8051	NaN	24,1681	24,1625	+	9,12E-12	2,91E+08	4	4	4	12,6	54,068	24,4875	24,8096	24,1653	4	2	2	6,90E-05	0,644386	B8MYJ5	B8MYJ5	1	AFLA_081330	Glycerol-3-phosphate dehydrogenase [NAD(+)] (EC 1.1.1.8)
28,2227	27,7055	27,3922	27,6225	28,2203	28,2934		1,01E-130	2,78E+09	25	25	25	23,8	172,72	27,9094	27,7735	28,0454	6	3	3	0,446157	-0,271926	B8MYJ6	B8MYJ6	1	AFLA_081340	Glycogen debranching enzyme Gdb1, putative
28,8435	29,1156	28,8552	29,3793	29,5306	29,4869	+	1,13E-278	6,92E+09	17	17	16	67,3	40,626	29,2018	28,9381	29,4656	6	3	3	0,006093	-0,527497	B8MYJ8	B8MYJ8	1	AFLA_081360	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) (DAHP synthase) (Phospho-2-keto-3-deoxyheptonate aldolase)
31,7257	31,4752	30,9468	30,679	30,9438	31,1056		0	2,71E+10	36	36	36	60,1	84,29	31,146	31,3826	30,9095	6	3	3	0,144168	0,473111	B8MYK4	B8MYK4	1	AFLA_081430	Eukaryotic translation initiation factor 3 subunit B (eIF3b) (Eukaryotic translation initiation factor 3 90 kDa subunit homolog) (Translation initiation factor eIF3, p90 subunit homolog)
NaN	NaN	24,4636	24,8551	24,8711	25,2204		2,58E-06	2,6E+08	2	2	2	13,7	20	24,8525	24,4636	24,9822	4	1	3	1	-0,518592	B8MYK9	B8MYK9	1	AFLA_081480	IgE-binding protein
25,85	25,3681	24,7843	25,0937	25,3438	25,4547		8,89E-13	3,68E+08	3	3	3	9,4	39,141	25,3158	25,3341	25,2974	6	3	3	0,915873	0,036672	B8MYL0	B8MYL0	1	AFLA_081490	Nucleoside diphosphatase Gda1
24,6823	24,5138	24,5807	24,6604	24,8556	24,662		5,46E-07	1,54E+08	3	3	3	21	25,794	24,6591	24,5923	24,726	6	3	3	0,17509	-0,133718	B8MYM3	B8MYM3	1	AFLA_081620	Uncharacterized protein
24,9206	26,8075	27,0708	26,8271	26,5956	26,7985		6,52E-129	2,12E+09	8	8	8	23,3	60,343	26,5034	26,2663	26,7404	6	3	3	0,524662	-0,474105	B8MYN6	B8MYN6	1	AFLA_081750	T-complex protein 1, beta subunit, putative
27,6106	27,2811	27,7318	27,7519	27,9719	27,4235		4,97E-84	2,15E+09	12	12	12	42,3	41,189	27,6285	27,5412	27,7158	6	3	3	0,449679	-0,17461	B8MYP9	B8MYP9	1	AFLA_081880	Branched-chain amino acid aminotransferase
29,2401	30,6883	31,2052	31,3044	31,1955	30,9135		0	2,57E+10	9	9	9	48,6	19,708	30,7578	30,3779	31,1378	6	3	3	0,273731	-0,759931	B8MYW2	B8MYW2	1	AFLA_082510	TCTP family protein
NaN	NaN	23,2128	23,028	NaN	24,5733		1,00E-06	1,47E+08	3	3	3	4,9	96,417	23,6047	23,2128	23,8007	3	1	2	1	-0,587827	B8MYW6	B8MYW6	1	AFLA_082550	Cleavage and polyadenylation specifity factor, 73 kDa subunit
26,4264	26,0171	25,6692	25,6052	25,562	25,6864		1,57E-34	6,25E+08	12	12	12	19	80,072	25,8277	26,0376	25,6179	6	3	3	0,131503	0,419673	B8MYY0	B8MYY0	1	AFLA_082690	Pseudouridine synthase TruD/Pus7, putative
25,7743	25,1879	25,2221	25,21	25,9487	26,0095		3,19E-24	4,06E+08	7	7	7	20,3	45,561	25,5587	25,3947	25,7227	6	3	3	0,36281	-0,327962	B8MYZ2	B8MYZ2	1	AFLA_082810	Uncharacterized protein
27,4075	26,8201	26,4688	28,3054	28,6848	28,6901	+	5,84E-71	2,56E+09	7	7	7	25	34,953	27,7294	26,8988	28,5601	6	3	3	0,005326	-1,6613	B8MZ00	B8MZ00	1	AFLA_082890	Ribonuclease T2, putative
27,8135	27,544	27,6864	27,8024	27,7805	27,915		1,87E-60	2,58E+09	8	8	8	34,4	40,11	27,7569	27,6813	27,8326	6	3	3	0,161664	-0,151322	B8MZ09	B8MZ09	1	AFLA_082980	Dihydroorotase, homodimeric type
NaN	NaN	28,7934	28,9301	23,3526	22,8118		3,76E-24	9,86E+08	4	4	4	31,5	9,9816	25,972	28,7934	25,0315	4	1	3	1	3,76193	B8MZ16	B8MZ16	1	AFLA_083050	40S ribosomal protein S25, putative
26,9563	26,9378	26,3637	26,2117	26,6054	26,5117		1,82E-71	1,23E+09	14	14	14	34,3	58,524	26,5978	26,7526	26,4429	6	3	3	0,245768	0,309649	B8MZ19	B8MZ19	1	AFLA_083080	Histidine acid phosphatase, putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
29,4708	28,9656	28,611	29,136	29,5119	29,7716		1,44E-123	7,04E+09	5	5	5	59,6	11,926	29,2445	29,0158	29,4732	6	3	3	0,214515	-0,457326	B8MZ23	B8MZ23	1	AFLA_083120	Thioredoxin
28,0034	27,5749	27,5823	27,2791	27,2735	27,351	+	9,41E-32	1,61E+09	6	6	6	25	44,689	27,5107	27,7202	27,3012	6	3	3	0,043504	0,419008	B8MZ47	B8MZ47	1	AFLA_083360	Extracellular cell wall glucanase Crf1/allergen Asp F9
30,7682	30,2976	30,0123	30,1919	30,4176	30,4996		0	1,4E+10	18	18	18	51,1	60,985	30,3645	30,3593	30,3697	6	3	3	0,967424	-0,0103772	B8MZ48	B8MZ48	1	AFLA_083370	Glutathione oxidoreductase Glr1, putative
22,4239	22,0115	21,7122	29,7705	30,0022	30,2119	+	0	8,35E+09	18	18	18	48,1	69,417	26,022	22,0492	29,9949	6	3	3	5,17E-06	-7,94565	B8MZ53	B8MZ53	1	AFLA_083420	Non-hemolytic phospholipase C, putative
26,3916	26,1463	26,1091	25,9854	26,2985	26,3622		9,00E-22	7,88E+08	7	7	7	26,4	35,022	26,2155	26,2157	26,2153	6	3	3	0,998293	0,0003332	B8MZ55	B8MZ55	1	AFLA_083440	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)
24,391	24,4136	29,3914	28,8623	26,3564	27,0186		6,29E-48	2,59E+09	3	3	3	36,8	7,6649	26,7389	26,0653	27,4124	6	3	3	0,501218	-1,3471	B8MZ58	B8MZ58	1	AFLA_083470	Ribosomal protein S28e
25,0774	25,1879	24,6269	25,0894	25,3892	25,3672		5,01E-15	3,32E+08	4	4	4	7,7	82,41	25,123	24,9641	25,2819	6	3	3	0,181582	-0,317878	B8MZ59	B8MZ59	1	AFLA_083480	Importin beta-2 subunit, putative
24,1446	24,8654	25,409	25,4328	25,4096	24,9372		3,47E-85	5,3E+08	7	7	7	18	57,211	25,0331	24,8063	25,2599	6	3	3	0,320408	-0,453552	B8MZ66	B8MZ66	1	AFLA_083550	Coatomer subunit delta, putative
29,1012	28,7719	27,6148	26,8604	28,0199	28,3196		0	2,15E+09	6	6	6	24,3	46,201	28,1146	28,496	27,7333	6	3	3	0,294891	0,762663	B8MZ70	B8MZ70	1	AFLA_083590	Fatty acid hydroxylase, putative
25,1881	25,7921	24,7573	23,9946	24,1597	24,4006	+	5,21E-13	3,71E+08	5	5	5	10,9	64,216	24,7154	25,2458	24,185	6	3	3	0,030215	1,06081	B8MZ71	B8MZ71	1	AFLA_083600	RNA splicing factor (Pad-1), putative
26,3366	27,2353	28,1911	27,3772	27,1279	27,0278		3,57E-58	1,58E+09	6	6	6	56,9	14,737	27,216	27,2543	27,1777	6	3	3	0,895013	0,0766621	B8MZ85	B8MZ85	1	AFLA_083740	40S ribosomal protein S22
27,5885	28,2465	28,1018	27,9942	28,7041	28,5366		2,67E-132	4,28E+09	22	22	22	33,3	96,049	28,1953	27,9789	28,4117	6	3	3	0,213577	-0,432725	B8MZ86	B8MZ86	1	AFLA_083750	Importin beta-1 subunit
28,8699	28,5657	28,0048	28,8145	28,8319	28,8339		1,18E-176	4,76E+09	9	9	9	51,2	37,506	28,6534	28,4801	28,8268	6	3	3	0,24319	-0,34664	B8MZA0	B8MZA0	1	AFLA_083890	Oxidoreductase, zinc-binding dehydrogenase family, putative
28,5072	28,7225	28,7025	28,3072	29,246	29,329		1,79E-128	5,05E+09	18	18	18	51,2	46,282	28,8024	28,6441	28,9607	6	3	3	0,397808	-0,316619	B8MZA3	B8MZA3	1	AFLA_083920	Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)
24,851	26,4526	26,8219	26,5546	26,3374	26,2391		2,75E-25	5,95E+08	4	4	4	17,4	23,974	26,2094	26,0418	26,3771	6	3	3	0,612978	-0,335255	B8MZC7	B8MZC7	1	AFLA_084160	DUF1014 domain protein
25,8526	26,5986	26,314	25,9841	26,5597	26,2519		1,14E-12	4,31E+08	5	5	5	19,3	41,007	26,2601	26,2551	26,2652	6	3	3	0,972218	-0,0101407	B8MZD4	B8MZD4	1	AFLA_084230	Homoserine acetyltransferase family protein
25,1023	24,7236	25,0037	NaN	25,1386	24,9752		3,03E-19	2,97E+08	5	5	5	12	68,153	24,9887	24,9432	25,0569	5	3	2	0,525228	-0,113673	B8MZD5	B8MZD5	1	AFLA_084240	Poly(A) polymerase Pap
NaN	25,4063	25,9211	23,9452	24,8438	NaN		1,05E-26	6,69E+08	5	5	5	18,9	32,749	25,0291	25,6637	24,3945	4	2	2	0,133848	1,26917	B8MZE3;B8	B8MZE3	2	AFLA_084330	Mitochondrial phosphate carrier protein (Mir1), putative
24,7133	24,1777	23,5656	23,9927	24,3933	24,3555		2,21E-11	2,47E+08	5	5	5	19,9	36,327	24,1997	24,1522	24,2472	6	3	3	0,802417	-0,0949891	B8MZF4	B8MZF4	1	AFLA_084440	Autophagy protein Atg27, putative
28,8236	28,1928	27,8944	28,6198	28,9469	28,9291		1,72E-91	3,22E+09	16	16	16	47,7	42,38	28,5678	28,3036	28,832	6	3	3	0,146481	-0,528348	B8MZF5	B8MZF5	1	AFLA_084450	Uncharacterized protein
28,5982	28,4506	28,2331	28,4384	28,5154	28,6233		2,74E-157	3,62E+09	22	22	22	32,9	102,84	28,4765	28,4273	28,5257	6	3	3	0,454181	-0,0984097	B8MZF6	B8MZF6	1	AFLA_084460	Heat shock protein Hsp98/Hsp104/ClpA, putative
28,0919	27,9023	27,6632	27,7494	27,7184	27,7819		4,11E-98	3,15E+09	22	22	22	30,5	107,67	27,8178	27,8858	27,7499	6	3	3	0,339416	0,135909	B8MZG9	B8MZG9	1	AFLA_084590	Hsp70 family chaperone Lhs1/Orp150, putative
24,3423	25,8558	28,4269	25,1624	24,8968	25,3934		1,26E-57	2,02E+09	10	10	10	46,3	23,866	25,6796	26,2084	25,1508	6	3	3	0,428238	1,05752	B8MZH2	B8MZH2	1	AFLA_084620	40S ribosomal protein S5, putative
28,1569	27,6819	27,3946	27,7808	28,1512	28,125		1,12E-78	3,03E+09	11	11	11	80,5	26,482	27,8817	27,7445	28,019	6	3	3	0,337638	-0,274551	B8MZH5	B8MZH5	1	AFLA_084650	Palmitoyltransferase with autoacylation activity Pfa4, putative
30,082	30,1713	30,0358	30,3518	30,1661	30,2498		0	1,31E+10	30	30	30	57,5	71,114	30,1761	30,0963	30,2559	6	3	3	0,075313	-0,159585	B8MZH6	B8MZH6	1	AFLA_084660	2-isopropylmalate synthase
26,2059	26,0593	25,4943	25,6688	26,0275	25,956		1,00E-16	6,27E+08	6	6	6	16,7	55,816	25,902	25,9198	25,8841	6	3	3	0,890354	0,0356941	B8MZI5	B8MZI5	1	AFLA_084750	Probable Xaa-Pro aminopeptidase AFLA_084750 (EC 3.4.11.9) (Aminoacylproline aminopeptidase) (Prolidase)
29,4186	29,0884	28,5534	29,3303	29,4254	29,4151		2,25E-152	5,89E+09	13	13	13	44,4	47,607	29,2052	29,0201	29,3902	6	3	3	0,218644	-0,370113	B8MZJ2	B8MZJ2	1	AFLA_084820	Acyl-CoA dehydrogenase, putative
25,0071	24,6966	24,0641	24,202	24,9245	25,4514		1,81E-10	2,57E+08	3	3	3	9,2	52,445	24,7243	24,5892	24,8593	6	3	3	0,585704	-0,270064	B8MZJ4	B8MZJ4	1	AFLA_084840	Uncharacterized protein
23,1648	23,3272	NaN	NaN	23,0346	23,2929		3,35E-05	76860000	2	2	2	6,2	49,373	23,2049	23,246	23,1638	4	2	2	0,643939	0,0822086	B8MZK1	B8MZK1	1	AFLA_084910	Exosome complex exonuclease Rrp6, putative
25,7202	25,4898	25,813	NaN	24,1901	24,1029	+	4,78E-07	1,77E+08	2	2	2	8,1	37,827	25,0632	25,6743	24,1465	5	3	2	0,001271	1,52779	B8MZL2	B8MZL2	1	AFLA_085020	Class II aldolase/adducin domain protein
25,8671	25,8152	25,4267	25,7999	25,6162	25,8147		7,06E-23	5,95E+08	3	3	3	27	13,408	25,7233	25,703	25,7436	6	3	3	0,80357	-0,0406354	B8MZL4	B8MZL4	1	AFLA_085040	Uncharacterized protein
25,7149	24,9757	26,3913	26,1402	25,8149	25,5351		9,79E-74	1,08E+09	12	12	12	18,4	110,69	25,762	25,694	25,8301	6	3	3	0,774781	-0,136099	B8MZM3	B8MZM3	1	AFLA_085130	Sec23/Sec24 family protein
NaN	22,9565	23,6506	NaN	NaN	NaN		6,07E-27	2,91E+08	3	3	3	7,6	58,844	23,3036	23,3036	NaN	2	2	0	1	NaN	B8MZN7	B8MZN7	1	AFLA_085270	T-complex protein 1, zeta subunit, putative
NaN	NaN	24,9674	25,4293	25,4627	25,3503		8,10E-30	4,07E+08	4	4	4	19,3	38,204	25,3024	24,9674	25,4141	4	1	3	1	-0,446657	B8MZP5	B8MZP5	1	AFLA_085350	AMMECR1 family protein
26,4714	26,4001	26,3657	26,4921	26,4427	26,6839		2,65E-24	1,06E+09	4	4	4	38,3	13,319	26,476	26,4124	26,5396	6	3	3	0,18671	-0,127155	B8MZP9	B8MZP9	1	AFLA_085390	Prefoldin subunit 6, putative
31,9553	32,8641	32,9116	33,351	32,7465	32,8288		0	7,77E+10	37	37	37	82,7	57,288	32,7762	32,577	32,9754	6	3	3	0,335413	-0,398451	B8MZQ0	B8MZQ0	1	AFLA_085400	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent
28,7465	30,0527	30,1719	28,867	30,1492	29,6201		0	1,39E+10	25	25	24	67,2	51,863	29,6012	29,657	29,5454	6	3	3	0,858896	0,111629	B8MZQ2	B8MZQ2	1	AFLA_085420	Serine hydroxymethyltransferase (EC 2.1.2.1)
25,8498	26,8043	27,4878	27,1294	27,1266	26,9498		3,55E-115	1,98E+09	6	6	6	33,1	28,051	26,8913	26,714	27,0686	6	3	3	0,49994	-0,354631	B8MZQ5	B8MZQ5	1	AFLA_085450	Eukaryotic translation initiation factor 3 subunit K (eIF3k) (eIF-3 p25)
26,7326	26,2569	25,5051	24,9025	25,7706	26,0576		2,20E-30	5,46E+08	3	3	3	40	14,692	25,8709	26,1648	25,5769	6	3	3	0,303349	0,58797	B8MZR4	B8MZR4	1	AFLA_085540	Uncharacterized protein
25,4771	24,8841	24,5678	24,8955	25,2518	26,0167		9,65E-25	4,59E+08	5	5	5	33,8	29,098	25,1822	24,9763	25,388	6	3	3	0,387332	-0,411676	B8MZS0	B8MZS0	1	AFLA_085600	Uncharacterized protein
28,577	27,9974	27,6477	27,8939	28,212	28,3385		6,25E-87	2,97E+09	11	11	11	86,3	16,691	28,1111	28,074	28,1481	6	3	3	0,817959	-0,0741081	B8MZT0	B8MZT0	1	AFLA_085700	Arsenate reductase (Arc2), putative
27,5243	27,5938	27,2722	27,4985	27,2418	27,5108		4,36E-32	1,96E+09	7	7	7	21,8	44,288	27,4402	27,4635	27,417	6	3	3	0,741407	0,046435	B8MZU4	B8MZU4	1	AFLA_085840	Tubulin-specific chaperone c, putative
NaN	NaN	NaN	26,123	27,431	27,535		1,35E-58	8,57E+08	6	6	6	21,6	50,64	27,0297	NaN	27,0297	3	0	3	1	NaN	B8MZU5	B8MZU5	1	AFLA_085850	Uncharacterized protein
29,5682	29,1812	28,5701	28,7958	29,1446	29,2457		0	4,91E+09	20	20	20	23,7	135,61	29,0843	29,1065	29,062	6	3	3	0,896475	0,0444698	B8MZV1	B8MZV1	1	AFLA_085910	Coatomer subunit alpha
30,1791	30,1432	29,9382	29,6304	29,5414	29,6524	+	0	1,11E+10	11	11	11	53,5	34,847	29,8475	30,0868	29,6081	6	3	3	0,004361	0,478753	B8MZV8	B8MZV8	1	AFLA_085980	Regulatory protein SUAPRGA1
29,3561	29,24	28,8933	28,8927	29,0866	29,2341		0	5,83E+09	11	11	11	51,4	31,14	29,1171	29,1631	29,0712	6	3	3	0,618437	0,0919615	B8MZX7	B8MZX7	1	AFLA_086170	Proteasome regulatory particle subunit (RpnL), putative
27,8272	25,7835	24,7442	24,0759	25,3698	26,5456		3,99E-41	4,77E+08	7	7	7	31	44,506	25,7244	26,1183	25,3304	6	3	3	0,53186	0,787835	B8MZY1	B8MZY1	1	AFLA_086210	Epoxide hydrolase, putative
26,6422	26,5866	26,2789	26,9022	26,6036	26,673		1,73E-27	1,02E+09	7	7	7	15,8	85,073	26,6144	26,5026	26,7263	6	3	3	0,196784	-0,223682	B8MZZ0	B8MZZ0	1	AFLA_086300	Vacuolar import and degRadation protein, putative
30,7449	30,5562	30,9463	30,5975	30,6891	30,6626		1,35E-248	1,8E+10	29	29	29	55,3	55,825	30,6994	30,7491	30,6498	6	3	3	0,43956	0,0993506	B8N000	B8N000	1	AFLA_086400	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)
29,0865	28,7556	29,1753	29,2061	28,936	29,0042		1,44E-270	6,16E+09	27	27	27	31,1	112	29,0273	29,0058	29,0487	6	3	3	0,790604	-0,0429408	B8N001	B8N001	1	AFLA_086410	C1 tetrahydrofolate synthase, putative
30,2273	30,0296	29,4748	29,3769	29,5734	29,6593		8,51E-265	9,69E+09	16	16	16	70,7	37,317	29,7236	29,9106	29,5365	6	3	3	0,194509	0,374031	B8N002	B8N002	1	AFLA_086420	Eukaryotic translation initiation factor 3 subunit I (eIF3i) (Eukaryotic translation initiation factor 3 39 kDa subunit homolog)
27,1716	27,0625	27,3573	27,3805	27,0844	27,1877		5,36E-28	9,43E+08	4	4	4	20,6	16,934	27,2073	27,1971	27,2175	6	3	3	0,87566	-0,0203781	B8N003	B8N003	1	AFLA_086430	Coactivator bridging factor 1 (Mbf1), putative
NaN	24,3229	24,5601	25,011	24,5442	24,7358		3,95E-13	4,38E+08	3	3	3	15,7	26,982	24,6348	24,4415	24,7637	5	2	3	0,198711	-0,322179	B8N004	B8N004	1	AFLA_086440	SH3 domain protein
31,3716	31,0734	30,8656	30,023	30,4432	30,4277	+	7,69E-293	1,6E+10	4	4	4	40,2	13,622	30,7007	31,1035	30,298	6	3	3	0,016081	0,80553	B8N014	B8N014	1	AFLA_086540	Glycine-rich RNA-binding protein, putative
25,9911	25,9051	25,3055	25,4482	25,6079	25,7477		7,51E-17	5,6E+08	8	8	8	10,7	110,4	25,6676	25,7339	25,6013	6	3	3	0,598557	0,132662	B8N020	B8N020	1	AFLA_086600	Morphogenesis protein (Msb1), putative
31,6404	31,4278	31,2024	31,1778	31,7406	31,686		0	3,09E+10	40	40	40	73,7	57,904	31,4792	31,4235	31,5348	6	3	3	0,638677	-0,111241	B8N022	B8N022	1	AFLA_086620	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
25,7418	26,0758	28,8145	26,2342	24,7357	24,7779		4,18E-76	9,83E+08	5	5	5	49,5	12,429	26,0633	26,8774	25,2493	6	3	3	0,209877	1,62812	B8N023	B8N023	1	AFLA_086630	60S ribosomal protein L35Ae
26,7419	27,0266	26,9228	27,3261	27,4804	27,4413	+	4,75E-29	1,29E+09	7	7	7	52,2	19,711	27,1565	26,8971	27,4159	6	3	3	0,00551	-0,51883	B8N027	B8N027	1	AFLA_086670	Cystathionine beta-synthase (Beta-thionase), putative
22,4794	NaN	24,319	24,5695	NaN	NaN		2,14E-07	1,8E+08	3	3	3	18,2	19,572	23,7893	23,3992	24,5695	3	2	1	1	-1,17033	B8N030	B8N030	1	AFLA_086700	tRNA dihydrouridine synthase (Smm1), putative
32,6544	32,4767	32,3122	32,3814	32,2547	32,4761		0	5,87E+10	21	21	21	59	43,623	32,4259	32,4811	32,3707	6	3	3	0,401772	0,110392	B8N031	B8N031	1	AFLA_086710	Inorganic diphosphatase, putative
27,026	26,5576	26,467	26,4448	26,5267	26,9736		2,58E-48	9,51E+08	6	6	6	22,2	33,592	26,6659	26,6835	26,6484	6	3	3	0,889989	0,0351798	B8N034	B8N034	1	AFLA_086740	4-nitrophenylphosphatase
24,7419	24,5865	24,2669	24,1338	24,458	24,5252		0,000131	2,92E+08	2	2	2	19,9	28,306	24,452	24,5317	24,3723	6	3	3	0,436989	0,159432	B8N036	B8N036	1	AFLA_086760	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)
27,4019	27,4808	27,7222	27,9267	28,0289	27,7964	+	2,03E-178	3,58E+09	15	15	15	47	53,991	27,7262	27,5349	27,9174	6	3	3	0,03126	-0,382406	B8N038	B8N038	1	AFLA_086780	Aspartyl aminopeptidase
27,7689	27,5628	27,8011	27,4455	28,1751	28,1957		1,18E-59	2,22E+09	13	13	13	53,3	39,312	27,8248	27,7109	27,9388	6	3	3	0,42669	-0,22783	B8N040	B8N040	1	AFLA_086800	Epoxide hydrolase, putative
27,037	28,9003	28,3158	28,7574	28,5228	28,2703		5,37E-155	3,28E+09	11	11	11	48,1	31,082	28,3006	28,0844	28,5169	6	3	3	0,488733	-0,432502	B8N042	B8N042	1	AFLA_086820	Pyruvate dehydrogenase complex component Pdx1, putative
27,5195	26,7995	26,4525	26,9711	27,9076	27,953		2,68E-44	1,82E+09	15	15	15	20	123,51	27,2672	26,9238	27,6106	6	3	3	0,200455	-0,686759	B8N050	B8N050	1	AFLA_086900	Alpha-mannosidase (EC 3.2.1.-)
27,9039	29,4256	30,1174	30,0345	28,7867	28,5129		0	1,81E+10	17	17	16	44,9	49,384	29,1302	29,149	29,1114	6	3	3	0,964944	0,0376059	B8N054	B8N054	1	AFLA_086940	Eukaryotic translation initiation factor 4, putative
28,7784	28,2649	27,8657	27,7189	28,1897	28,3764		3,41E-97	2,63E+09	9	9	9	41,1	26,115	28,199	28,303	28,095	6	3	3	0,561179	0,208045	B8N056	B8N056	1	AFLA_086960	Fumarylacetoacetate hydrolase family protein
25,8715	25,3144	25,647	25,4266	25,675	25,6139		1,42E-10	4,97E+08	4	4	4	35,8	16,872	25,5914	25,611	25,5718	6	3	3	0,836972	0,0391343	B8N071	B8N071	1	AFLA_087110	Polymerase (RNA) II (DNA directed) polypeptide D
24,9505	24,6423	24,8027	24,8804	25,651	24,26		2,24E-08	3,11E+08	4	4	4	15,8	54,176	24,8645	24,7985	24,9305	6	3	3	0,764766	-0,131979	B8N072	B8N072	1	AFLA_087120	tRNA (guanine(37)-N1)-methyltransferase (EC 2.1.1.228) (M1G-methyltransferase) (tRNA [GM37] methyltransferase) (tRNA methyltransferase 5)
29,27	28,8258	29,3134	28,7742	29,1396	29,2026		0	6,23E+09	17	17	17	40,7	85,922	29,0876	29,1364	29,0388	6	3	3	0,659144	0,0976105	B8N077	B8N077	1	AFLA_087170	Extracellular serine-rich protein, putative
28,0166	28,0837	27,915	27,6141	27,7152	27,6197	+	5,04E-51	2,76E+09	11	11	11	36,7	31,135	27,8274	28,0051	27,6497	6	3	3	0,003823	0,355385	B8N083	B8N083	1	AFLA_087240	Glutathione S-transferase, putative
26,1354	25,9804	26,071	26,0591	26,279	26,3161		2,78E-36	6,68E+08	4	4	4	12,7	47,261	26,1402	26,0623	26,2181	6	3	3	0,165408	-0,155774	B8N090	B8N090	1	AFLA_087310	Uncharacterized protein
26,6082	26,0351	25,6677	25,9462	26,6998	26,404		9,40E-41	7,72E+08	10	10	10	37	46,008	26,2268	26,1037	26,35	6	3	3	0,521094	-0,24632	B8N099	B8N099	1	AFLA_087400	Oxysterol binding protein (Osh7), putative
29,1899	28,8087	28,4292	28,7337	28,8666	28,919		5,71E-154	5,08E+09	6	6	6	59,7	14,523	28,8245	28,8093	28,8398	6	3	3	0,899416	-0,0304788	B8N0A7	B8N0A7	1	AFLA_087480	Peptidyl-prolyl cis-trans isomerase
26,8939	26,266	25,9512	26,3042	26,5434	26,6792		1,75E-54	8,69E+08	5	5	5	27,5	38,458	26,4396	26,3703	26,5089	6	3	3	0,666046	-0,138597	B8N0B7	B8N0B7	1	AFLA_087580	DUF52 domain protein

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
30,2399	29,6593	29,0674	29,5532	29,7502	29,873		9,37E-133	5,67E+09	12	12	12	44,6	33,63	29,6905	29,6555	29,7255	6	3	3	0,851838	-0,0699247	B8N0C1	B8N0C1	1	AFLA_087620	NmrA family transcriptional regulator, putative
NaN	25,1752	25,0662	24,9762	25,2696	24,3428		2,10E-38	7,85E+08	8	8	5	22,8	53,831	24,966	25,1207	24,8629	5	2	3	0,520609	0,257843	B8N0C2	B8N0C2	1	AFLA_087630	Alpha,alpha-trehalose-phosphate synthase (UDP-forming) (EC 2.4.1.15) (Trehalose-6-phosphate synthase)
23,9952	23,7594	23,1997	23,939	23,704	23,6729		1,21E-14	1,35E+08	2	2	2	2,8	76,372	23,7117	23,6514	23,772	6	3	3	0,655341	-0,120555	B8N0C4	B8N0C4	1	AFLA_087650	Chromatin assembly factor 1 subunit B, putative
27,68	27,3944	28,9959	26,5979	26,343	26,4452	+	1,47E-39	1,33E+09	5	5	5	29,4	18,491	27,2427	28,0234	26,462	6	3	3	0,035148	1,5614	B8N0D5	B8N0D5	1	AFLA_087760	40S ribosomal protein S11
26,0322	26,5258	26,4764	27,1012	27,7581	26,6811		4,50E-96	1,53E+09	11	11	11	44,1	39,208	26,7625	26,3448	27,1801	6	3	3	0,075732	-0,835324	B8MW92	B8MW92	1	AFLA_087820	Cell wall integrity signaling protein Lsp1/Pil1, putative
30,6311	30,8276	31,5586	32,4185	32,0477	31,8304	+	0	3,89E+10	31	31	31	66,9	58,086	31,5523	31,0058	32,0988	6	3	3	0,029671	-1,09306	B8MWA0	B8MWA0	1	AFLA_087900	Pyruvate kinase (EC 2.7.1.40)
25,1643	25,1467	24,8488	24,4076	NaN	24,5095	+	1,10E-13	3,06E+08	6	6	6	18,5	51,882	24,8154	25,0533	24,4586	5	3	2	0,02278	0,594677	B8MWA2	B8MWA2	1	AFLA_087920	F-box domain protein
30,2977	30,1364	30,1183	30,2069	30,3729	30,4331		1,39E-168	1,08E+10	19	19	19	48,1	41,263	30,2609	30,1841	30,3376	6	3	3	0,157747	-0,153493	B8MWA5	B8MWA5	1	AFLA_087950	Isocitrate dehydrogenase LysB
26,1613	26,3705	26,1261	NaN	23,9914	23,2131	+	1,84E-16	4,33E+08	6	6	6	54,7	18,499	25,1725	26,2193	23,6022	5	3	2	0,003368	2,61707	B8MWA9	B8MWA9	1	AFLA_087990	40S ribosomal protein S8
27,0386	26,7351	26,4216	26,6319	26,6779	26,622		1,30E-24	1,23E+09	7	7	7	22,8	44,789	26,6878	26,7318	26,6439	6	3	3	0,649151	0,087862	B8MWB2	B8MWB2	1	AFLA_088020	Methionine aminopeptidase 1 (MAP 1) (MetAP 1) (EC 3.4.11.18) (Peptidase M 1)
24,2014	24,1286	23,8664	23,9232	23,8283	24,0662		3,14E-06	1,79E+08	2	2	2	10,4	45,208	24,0024	24,0655	23,9393	6	3	3	0,362849	0,126221	B8MWB8	B8MWB8	1	AFLA_088080	Aspartate aminotransferase, putative
27,8932	27,911	27,3422	25,4256	25,7199	25,4279	+	9,71E-45	1,58E+09	7	7	7	50	33,532	26,62	27,7155	25,5245	6	3	3	0,000483	2,19103	B8MWC5	B8MWC5	1	AFLA_088150	Fe superoxide dismutase, putative
29,0729	29,7671	29,9057	29,8486	29,5649	29,2818		0	8,67E+09	13	13	13	52,8	37,175	29,5735	29,5819	29,5651	6	3	3	0,958665	0,0168311	B8MWD6	B8MWD6	1	AFLA_088260	Eukaryotic translation initiation factor 3 subunit F (eIF3f)
29,0611	29,3206	29,2588	29,1409	29,0393	29,2342		5,77E-154	6,21E+09	14	14	14	53,2	33,913	29,1758	29,2135	29,1381	6	3	3	0,477858	0,0753886	B8MWE2	B8MWE2	1	AFLA_088320	Protein phosphatase 2C, putative
27,4014	27,644	29,933	28,0281	27,4525	27,4127		1,94E-51	3,49E+09	10	10	10	62,5	21,888	27,9786	28,3261	27,6311	6	3	3	0,449812	0,695023	B8MWE7	B8MWE7	1	AFLA_088370	60S ribosomal protein L9, putative
28,9978	29,26	29,0831	29,7572	29,1062	28,9119		1,18E-284	6,6E+09	11	11	11	61	20,02	29,186	29,1137	29,2584	6	3	3	0,616496	-0,144761	B8MWG7	B8MWG7	1	AFLA_088570	Uncharacterized protein
28,899	28,5334	28,0644	27,9971	28,4654	28,5925		9,79E-131	3,79E+09	13	13	13	49,9	39,699	28,4253	28,4989	28,3517	6	3	3	0,651189	0,147263	B8MWG9	B8MWG9	1	AFLA_088590	Nuclear pore complex protein (SonA), putative
29,8914	29,7155	29,4385	29,7521	29,6815	29,7649		0	9,96E+09	16	16	16	70	41,427	29,7073	29,6818	29,7328	6	3	3	0,723158	-0,0510737	B8MWH2	B8MWH2	1	AFLA_088620	UPF0160 domain protein MYG1, putative
NaN	NaN	24,0718	24,1458	23,9541	23,7165		3,11E-10	1,68E+08	4	4	4	23,1	23,68	23,972	24,0718	23,9388	4	1	3	1	0,132984	B8MWH6	B8MWH6	1	AFLA_088660	DUF431 domain protein
26,0889	25,8688	25,5064	25,9439	25,9517	26,0954		1,35E-14	6,58E+08	2	2	2	40,5	8,3184	25,9092	25,8214	25,997	6	3	3	0,376755	-0,175641	B8MWS2	B8MWS2	1	AFLA_088720	Iron/copper transporter Atx1, putative
24,4422	24,9915	26,079	25,1129	24,803	24,5156		2,36E-93	7,75E+08	5	5	5	37,7	19,685	24,9907	25,1709	24,8105	6	3	3	0,519484	0,360401	B8MWS6	B8MWS6	1	AFLA_088760	Septin
28,356	28,9148	28,6832	29,1736	28,7869	28,749		2,42E-101	4,6E+09	11	11	11	55,2	25,898	28,7772	28,6513	28,9031	6	3	3	0,299323	-0,25184	B8MWS7	B8MWS7	1	AFLA_088770	Guanylate kinase
NaN	24,9103	24,8695	25,037	25,5085	25,5192		2,29E-30	5,71E+08	9	9	9	11,2	123,33	25,1689	24,8899	25,3549	5	2	3	0,108987	-0,465009	B8MWT5	B8MWT5	1	AFLA_088850	Exportin KapK
24,0109	23,4908	NaN	NaN	NaN	NaN		2,14E-05	74033000	2	2	2	4,1	77,122	23,7509	23,7509	NaN	2	2	0	1	NaN	B8MWT6	B8MWT6	1	AFLA_088860	Acetyltransferase, putative
24,3617	23,7449	23,9969	24,2052	24,2615	24,458		8,61E-07	1,55E+08	2	2	2	12,6	32,787	24,1714	24,0345	24,3082	6	3	3	0,232568	-0,273747	B8NL76	B8NL76	1	AFLA_089120	Inositol monophosphatase, putative
31,7115	33,0503	33,132	31,0918	32,5096	32,0942		0	8,62E+10	99	99	99	66,4	232,14	32,2649	32,6312	31,8985	6	3	3	0,305327	0,732683	B8NL80	B8NL80	1	AFLA_089160	Fatty acid synthase beta subunit, putative
30,7605	32,559	32,5073	30,2343	31,1933	30,5528		0	5,23E+10	80	80	79	56,6	204,29	31,3012	31,9423	30,6601	6	3	3	0,12186	1,28215	B8NL81	B8NL81	1	AFLA_089170	Fatty acid synthase alpha subunit FasA
32,1161	31,8426	31,4439	31,4016	31,6742	31,6776		0	3,68E+10	14	14	14	54,8	40,402	31,6927	31,8009	31,5845	6	3	3	0,372181	0,216394	B8NL85	B8NL85	1	AFLA_089210	Pyruvate dehydrogenase E1 beta subunit PdbA, putative
26,891	26,4208	25,9317	26,092	26,3487	26,6043		1,43E-29	7,74E+08	6	6	6	13,9	70,711	26,3814	26,4145	26,3483	6	3	3	0,843304	0,0661977	B8NL86	B8NL86	1	AFLA_089220	Ser/Thr protein phosphatase family
29,9989	29,6577	29,1897	29,5448	29,631	29,7376		2,65E-298	8,44E+09	20	20	19	47,7	64,283	29,6266	29,6154	29,6378	6	3	3	0,930541	-0,0223662	B8NK82;B8	B8NK82	2	AFLA_089560	Pyruvate decarboxylase, putative
28,5165	28,0726	27,4743	27,76	28,0038	28,2431		3,11E-31	2,19E+09	6	6	6	42,3	14,649	28,0117	28,0211	28,0023	6	3	3	0,95768	0,0187804	B8NK85	B8NK85	1	AFLA_089590	Uncharacterized protein
28,8956	28,8834	29,1448	29,3376	29,1096	28,9979		7,65E-129	5,78E+09	15	15	15	44,1	42,417	29,0615	28,9746	29,1484	6	3	3	0,256349	-0,173775	B8NKA1	B8NKA1	1	AFLA_089750	Tyrosine--tRNA ligase (EC 6.1.1.1) (Tyrosyl-tRNA synthetase)
27,265	27,0609	27,0108	27,1907	27,1802	27,1225		3,13E-30	1,67E+09	6	6	6	48,1	17,269	27,1383	27,1122	27,1644	6	3	3	0,552353	-0,0522035	B8NKC0	B8NKC0	1	AFLA_089940	Thioredoxin, putative
25,103	25,1707	24,7669	NaN	24,2204	24,984		2,91E-19	3,49E+08	5	5	5	13,8	73,101	24,849	25,0135	24,6022	5	3	2	0,297533	0,411297	B8NLB1	B8NLB1	1	AFLA_090380	Chromatin remodeling complex subunit (Arp9), putative
25,9221	25,5111	26,569	24,6678	25,0753	25,1869	+	2,77E-21	3,64E+08	7	7	7	9,8	117,64	25,4887	26,0008	24,9767	6	3	3	0,041561	1,02407	B8NLC2	B8NLC2	1	AFLA_090490	Alpha,alpha-trehalose glucohydrolase TreA/Ath1
28,6053	28,0431	28,0829	27,1183	27,1388	27,2818	+	7,33E-105	1,64E+09	16	16	14	27,5	89,135	27,7117	28,2438	27,1796	6	3	3	0,004829	1,06414	B8NLD2	B8NLD2	1	AFLA_090590	Alpha-1,2-mannosidase, putative subfamily
32,0197	31,3201	31,4275	31,1325	31,5576	31,7522		0	3,56E+10	25	25	25	47,3	79,838	31,5349	31,5891	31,4808	6	3	3	0,722451	0,108342	B8NLE2	B8NLE2	1	AFLA_090690	Mycelial catalase Cat1
27,0785	26,9036	26,6819	26,9933	27,0686	27,075		8,52E-29	1,01E+09	6	6	6	43,9	19,124	26,9668	26,888	27,0456	6	3	3	0,251459	-0,157653	B8NLE9	B8NLE9	1	AFLA_090760	Ankyrin repeat protein
32,8277	33,2961	33,2156	33,551	32,8139	32,8677		0	1,08E+11	21	21	21	53,3	50,067	33,0953	33,1131	33,0775	6	3	3	0,904291	0,0355759	B8NLF1	B8NLF1	1	AFLA_090780	Elongation factor 1-alpha
NaN	23,5507	23,7774	23,0462	23,1023	23,6043		5,62E-25	3,72E+08	6	6	6	19,6	47,21	23,4162	23,6641	23,2509	5	2	3	0,189207	0,413131	B8NLF5	B8NLF5	1	AFLA_090820	Aminotransferase, putative
28,3772	28,2814	28,2332	28,0065	28,3366	28,287		1,20E-269	2,54E+09	8	8	8	39,4	26,044	28,2537	28,2973	28,21	6	3	3	0,476322	0,0872669	B8NLG2	B8NLG2	1	AFLA_090890	ATP synthase subunit E, putative
34,0919	33,7472	33,4437	33,4011	33,5186	33,6518		1,36E-297	1,42E+11	13	13	13	83,3	18,618	33,6424	33,7609	33,5238	6	3	3	0,303096	0,237071	B8NLH9	B8NLH9	1	AFLA_091060	Allergen Asp F3
25,8459	25,477	24,8817	25,1374	25,3142	25,4862		7,65E-19	4,02E+08	4	4	4	32,5	18,57	25,3571	25,4015	25,3126	6	3	3	0,780534	0,0889206	B8NLI0	B8NLI0	1	AFLA_091070	Uncharacterized protein
26,6958	27,4322	27,6244	27,7265	27,6911	27,7031		0	2,33E+09	5	5	5	42,6	19,583	27,4788	27,2508	27,7069	6	3	3	0,182525	-0,456135	B8NLJ1	B8NLJ1	1	AFLA_091180	ARP2/3 complex 20 kDa subunit (P20-ARC), putative
27,0783	27,3992	27,7213	27,8153	27,7899	27,7811		3,49E-77	1,95E+09	13	13	13	32	63,917	27,5975	27,3996	27,7955	6	3	3	0,100277	-0,395876	B8NKF3	B8NKF3	1	AFLA_091190	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)
25,6121	27,0567	27,3825	28,0152	27,8283	27,694		1,67E-115	1,92E+09	5	5	5	62,4	16,988	27,2648	26,6838	27,8458	6	3	3	0,103032	-1,16204	B8NKF7	B8NKF7	1	AFLA_091230	Ubiquitin conjugating enzyme (UbcM), putative
28,7595	28,3412	27,7494	28,1123	28,2329	28,4481		3,03E-106	3,35E+09	8	8	8	57,6	21,331	28,2739	28,2834	28,2644	6	3	3	0,954026	0,0189578	B8NKG0	B8NKG0	1	AFLA_091260	Glucosamine 6-phosphate acetyltransferase, putative
28,1619	28,335	29,916	30,0897	29,824	29,3818		0	8,4E+09	14	14	14	40,6	59,683	29,2847	28,8043	29,7651	6	3	3	0,181667	-0,960842	B8NKG1	B8NKG1	1	AFLA_091270	Fumarate hydratase, putative
26,2094	26,3989	26,0344	26,2744	26,3454	26,308		1,99E-28	8,15E+08	7	7	7	23	46,047	26,2618	26,2142	26,3093	6	3	3	0,425441	-0,095047	B8NKG4	B8NKG4	1	AFLA_091300	Chitin biosynthesis protein (Chs5), putative
25,811	26,8572	27,1523	27,4796	27,2378	26,7409		2,32E-31	1,05E+09	6	6	6	38,9	17,264	26,8798	26,6068	27,1528	6	3	3	0,302239	-0,54592	B8NKG5	B8NKG5	1	AFLA_091310	Eukaryotic translation initiation factor eIF-1A subunit, putative
27,3965	27,0842	26,7903	27,1823	27,26	27,2459		4,57E-26	1,3E+09	10	10	10	44,4	26,85	27,1599	27,0903	27,2294	6	3	3	0,475061	-0,139094	B8NKH2	B8NKH2	1	AFLA_091380	Phosphoglycerate mutase family protein
28,9784	29,0209	28,761	28,6929	28,8167	28,949		8,19E-116	5,93E+09	15	15	15	44,2	49,499	28,8698	28,9201	28,8195	6	3	3	0,409486	0,100574	B8NKH6	B8NKH6	1	AFLA_091420	ATP dependent RNA helicase (Sub2), putative
30,2047	30,6848	30,7133	30,7266	30,2785	29,7822		0	1,47E+10	13	13	13	48,9	25,169	30,3983	30,5342	30,2625	6	3	3	0,441928	0,271784	B8NKJ4	B8NKJ4	1	AFLA_091600	Nascent polypeptide-associated complex subunit beta
26,3535	25,5911	25,4811	26,0447	26,297	26,3521		1,08E-15	6,55E+08	5	5	5	25,1	23,162	26,0199	25,8086	26,2313	6	3	3	0,218895	-0,422699	B8NKJ6	B8NKJ6	1	AFLA_091620	Uncharacterized protein
28,5011	28,899	28,8897	29,1227	29,1453	29,2073	+	2,43E-130	5,48E+09	13	13	13	71,9	26,804	28,9608	28,7633	29,1584	6	3	3	0,041599	-0,395128	B8NKJ7	B8NKJ7	1	AFLA_091630	Phospholipase, putative
27,4812	26,8903	26,0561	26,4734	26,5943	27,0588		3,30E-34	1,19E+09	9	9	9	29,9	43,451	26,759	26,8092	26,7088	6	3	3	0,834506	0,100377	B8NKK2	B8NKK2	1	AFLA_091680	Uncharacterized protein
26,5575	26,7761	27,1725	27,9247	27,6069	27,2256		3,37E-136	2,64E+09	14	14	14	31,8	67,951	27,2105	26,8353	27,5857	6	3	3	0,050174	-0,750399	B8NKK3	B8NKK3	1	AFLA_091690	Isocitrate lyase
28,9081	28,9263	28,5863	28,9542	28,8719	28,9656		6,47E-250	4,99E+09	8	8	8	70,1	15,646	28,8687	28,8069	28,9306	6	3	3	0,340145	-0,123651	B8NKK9	B8NKK9	1	AFLA_091750	Uncharacterized protein
NaN	24,5129	24,5236	NaN	NaN	NaN		1,74E-14	2,91E+08	5	5	5	9,5	80,72	24,5183	24,5183	NaN	2	2	0	1	NaN	B8NKL5	B8NKL5	1	AFLA_091810	Uncharacterized protein
27,8976	28,4682	28,4946	28,0253	28,255	27,8474		3,29E-233	6,37E+09	19	19	19	65,2	43,248	28,1647	28,2868	28,0426	6	3	3	0,343792	0,244253	B8NKM2	B8NKM2	1	AFLA_091880	Septin AspA, putative
25,2835	24,9631	24,8952	24,7617	24,7753	24,9475		1,54E-26	3,48E+08	3	3	3	8,6	57,01	24,9377	25,0473	24,8282	6	3	3	0,176906	0,219114	B8NKM7	B8NKM7	1	AFLA_091930	Homoserine O-acetyltransferase
34,3594	34,2265	33,9991	34,3833	34,3804	34,4776		0	2,41E+11	10	10	10	60,9	23,525	34,3044	34,195	34,4138	6	3	3	0,117452	-0,218779	B8NKN3	B8NKN3	1	AFLA_091990	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
25,8628	25,6268	25,311	25,9578	25,7568	25,5274		1,42E-52	6,28E+08	6	6	6	12,3	55,099	25,6738	25,6002	25,7473	6	3	3	0,507771	-0,14712	B8NKP0	B8NKP0	1	AFLA_092060	Golgi to endosome transport protein (Ent3), putative
31,2502	31,1919	30,849	31,0429	30,8231	30,903		0	2,5E+10	25	25	25	71,2	58,021	31,01	31,097	30,923	6	3	3	0,283675	0,17403	B8NLJ4	B8NLJ4	1	AFLA_092100	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)
25,6592	28,5623	30,5211	30,4633	28,8545	27,5062		4,67E-159	8,1E+09	5	5	5	56,8	10,007	28,5944	28,2476	28,9413	6	3	3	0,695893	-0,693768	B8NLJ6	B8NLJ6	1	AFLA_092120	40S ribosomal protein S21
NaN	25,3589	26,658	26,6333	25,1689	NaN		3,09E-62	8,63E+08	10	10	10	31,3	58,513	25,9547	26,0084	25,9011	4	2	2	0,922664	0,107371	B8NLJ7	B8NLJ7	1	AFLA_092130	Phenylalanyl-tRNA synthetase beta chain cytoplasmic
NaN	24,3882	24,8269	25,1427	24,8866	24,7599		2,44E-17	3,84E+08	4	4	4	10,7	69,82	24,8009	24,6076	24,9297	5	2	3	0,237169	-0,322192	B8NLK8	B8NLK8	1	AFLA_092240	Calcium/calmodulin-dependent protein kinase, putative
25,2123	24,9753	25,2323	24,543	24,6539	24,7426	+	8,33E-09	3,09E+08	3	3	3	6,3	60,549	24,8932	25,1399	24,6465	6	3	3	0,008052	0,493455	B8NLL1	B8NLL1	1	AFLA_092270	Penicillin-binding protein, putative
24,795	25,5161	26,9773	27,2796	26,194	25,8227		1,04E-32	9,78E+08	6	6	6	27,5	37,348	26,0974	25,7628	26,4321	6	3	3	0,437385	-0,669299	B8NLL9	B8NLL9	1	AFLA_092350	Proteasome regulatory particle subunit (RpnK), putative
NaN	24,9557	28,5077	25,932	25,3012	NaN		1,85E-12	7,08E+08	5	5	5	43,9	14,677	26,1741	26,7317	25,6166	4	2	2	0,599459	1,11513	B8NLM1	B8NLM1	1	AFLA_092370	Alkaline serine protease
33,0651	33,0688	32,865	32,9623	32,9804	33,01		0	9,46E+10	23	23	22	74,8	26,869	32,9919	32,9996	32,9842	6	3	3	0,833514	0,0154241	B8NLM9	B8NLM9	1	AFLA_092450	14-3-3 family protein ArtA, putative
27,2588	27,5988	27,2362	27,1118	26,942	27,1709		3,80E-64	1,64E+09	4	4	4	46,2	17,393	27,2197	27,3646	27,0749	6	3	3	0,099975	0,28967	B8NLN2	B8NLN2	1	AFLA_092480	RNA binding protein (Rbm8A), putative
24,9858	25,7319	25,869	25,6887	25,8025	25,9236		1,05E-11	5,34E+08	5	5	5	44,4	21,258	25,6669	25,5289	25,8049	6	3	3	0,38417	-0,27599	B8NLN5	B8NLN5	1	AFLA_092510	Uncharacterized protein
27,8831	27,6108	27,1337	27,8515	27,7337	27,7883		4,04E-26	2,24E+09	7	7	7	57,7	19,665	27,6669	27,5425	27,7912	6	3	3	0,324758	-0,248635	B8NLP3	B8NLP3	1	AFLA_092590	Peptide methionine sulfoxide reductase
28,4865	27,9967	27,665	27,1721	27,3278	27,3846	+	3,23E-28	1,87E+09	6	6	6	14,8	46,883	27,6721	28,0494	27,2948	6	3	3	0,037811	0,754562	B8NLP7	B8NLP7	1	AFLA_092630	Cell wall glucanase (Utr2), putative
26,3331	25,9426	25,8484	25,775	26,2974	26,2817		5,77E-45	7,95E+08	6	6	6	15,7	66,631	26,0797	26,0413	26,118	6	3	3	0,752245	-0,0767028	B8NLP8	B8NLP8	1	AFLA_092640	Alkaline phosphatase (EC 3.1.3.1)
28,6238	27,7481	27,5452	27,3351	27,7091	27,7823		6,35E-197	3,13E+09	17	17	17	25,8	100,98	27,7906	27,9723	27,6088	6	3	3	0,368216	0,363526	B8NLQ7	B8NLQ7	1	AFLA_092730	26S proteasome regulatory submit Mts4, putative
28,0213	27,8887	27,731	27,8957	27,736	27,7636		1,02E-60	2,41E+09	10	10	10	38,3	36,547	27,8394	27,8803	27,7984	6	3	3	0,447068	0,081941	B8NLR0	B8NLR0	1	AFLA_092760	Hydroxymethylbilane synthase, putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
23,5404	23,4114	23,0328	23,381	23,213	23,3778		2,98E-10	1,42E+08	3	3	3	11	40,817	23,3261	23,3282	23,324	6	3	3	0,980282	0,0042623	B8NLR1	B8NLR1	1	AFLA_092770	TOR signaling pathway regulator (TapA), putative
23,0113	23,6072	23,1815	23,575	23,5598	23,1447		5,15E-05	1,01E+08	2	2	2	3,1	97,176	23,3466	23,2666	23,4265	6	3	3	0,519213	-0,15983	B8NLR9	B8NLR9	1	AFLA_092850	WD repeat protein
26,2623	29,0689	29,3925	29,3462	29,4226	28,9829		0	7,01E+09	12	12	12	52,4	42,001	28,7459	28,2413	29,2506	6	3	3	0,37124	-1,00931	B8NLS4	B8NLS4	1	AFLA_092900	Oxidative stress protein Svf1, putative
24,6762	24,7173	24,1414	NaN	NaN	24,3346		9,82E-20	3,02E+08	5	5	5	6,4	105,72	24,4674	24,5116	24,3346	4	3	1	1	0,17707	B8NLS8	B8NLS8	1	AFLA_092940	DNA repair and transcription protein (Xab2), putative
24,1057	24,033	24,2326	22,5802	NaN	NaN		6,24E-09	92011000	2	2	2	9,5	36,615	23,7379	24,1237	22,5802	4	3	1	1	1,54349	B8NKP2	B8NKP2	1	AFLA_092960	Small nuclear ribonucleoprotein, putative
28,8386	25,9649	25,9249	24,8671	26,5313	26,9394		3,99E-49	9,58E+08	10	10	10	68,7	22,593	26,511	26,9095	26,1126	6	3	3	0,527922	0,796857	B8NKR2	B8NKR2	1	AFLA_093160	Rab small monomeric GTPase Rab7, putative
29,7429	29,7253	29,7791	30,3799	29,9096	29,8063		0	1,03E+10	22	22	22	62,4	53,168	29,8905	29,7491	30,0319	6	3	3	0,185782	-0,282801	B8NKR8	B8NKR8	1	AFLA_093220	Ran-specific GTPase-activating protein 1, putative
26,8039	27,6209	27,963	27,1583	27,2563	27,4419		1,22E-140	1,6E+09	7	7	7	28	41,309	27,374	27,4626	27,2855	6	3	3	0,64289	0,177113	B8NKS2	B8NKS2	1	AFLA_093260	Oxidoreductase, 2OG-Fe(II) oxygenase family, putative
27,3391	27,2393	26,8782	26,9477	27,2364	27,1874		3,54E-30	1,41E+09	7	7	7	30,3	30,443	27,138	27,1522	27,1238	6	3	3	0,872699	0,0283464	B8NKS3	B8NKS3	1	AFLA_093270	Uncharacterized protein
30,4107	30,0197	29,6405	29,9106	29,8531	29,9546		1,52E-218	1,3E+10	19	19	19	59,6	39,916	29,9649	30,0236	29,9061	6	3	3	0,627907	0,117556	B8NKS4	B8NKS4	1	AFLA_093280	Disulfide isomerase (TigA), putative
NaN	NaN	23,8085	23,5326	NaN	22,5926		2,35E-10	1,21E+08	4	4	4	12,3	45,501	23,3112	23,8085	23,0626	3	1	2	1	0,745945	B8NKS8	B8NKS8	1	AFLA_093320	Pseudouridine synthase
25,1848	25,484	25,6405	25,8764	25,5953	26,1073		9,43E-32	4,89E+08	5	5	5	30,5	20,676	25,648	25,4364	25,8597	6	3	3	0,101141	-0,423239	B8NKT0	B8NKT0	1	AFLA_093340	Uncharacterized protein
25,8655	26,1263	26,0748	26,7698	26,4142	26,4416	+	1,07E-29	9,34E+08	9	9	9	29,9	45,901	26,282	26,0222	26,5418	6	3	3	0,020305	-0,519636	B8NKT3	B8NKT3	1	AFLA_093370	Ribonucleotide reductase small subunit RnrA, putative
25,2914	24,799	24,2758	24,4992	NaN	NaN		4,56E-10	2,49E+08	3	3	3	12,5	49,653	24,7163	24,7887	24,4992	4	3	1	1	0,289555	B8NKU4	B8NKU4	1	AFLA_093480	Aminomethyl transferase, putative
29,3255	28,7516	28,757	27,8323	28,641	28,6724		0	4,41E+09	12	12	12	55,4	36,305	28,6633	28,9447	28,3819	6	3	3	0,16771	0,562791	B8NKU8	B8NKU8	1	AFLA_093520	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase, putative
28,6237	28,1403	28,4972	27,2556	27,847	27,855	+	6,27E-102	2,31E+09	12	12	12	45,3	39,245	28,0365	28,4204	27,6525	6	3	3	0,035327	0,767886	B8NKU9	B8NKU9	1	AFLA_093530	Oxidoreductase, 2OG-Fe(II) oxygenase family
25,615	24,2822	NaN	24,1046	24,6439	24,7656		2,20E-06	1,3E+08	2	2	2	8,9	31,827	24,6823	24,9486	24,5047	5	2	3	0,487058	0,443887	B8NKV0	B8NKV0	1	AFLA_093540	Short chain dehydrogenase/reductase family
26,7506	26,4147	26,0567	26,0508	26,016	25,9711		1,05E-65	8,47E+08	3	3	3	39,6	10,908	26,21	26,4073	26,0126	6	3	3	0,121949	0,394709	B8NKW0	B8NKW0	1	AFLA_093640	U6 small nuclear ribonucleoprotein (Lsm3), putative
24,8829	24,2082	24,1416	24,2064	25,2601	25,1391		9,77E-12	1,96E+08	6	6	6	12,3	63,286	24,6397	24,4109	24,8686	6	3	3	0,325299	-0,457666	B8NKX5	B8NKX5	1	AFLA_093790	Dihydroxyacetone kinase (DakA), putative
26,1371	26,6486	26,1072	24,4544	24,6195	24,1401	+	3,80E-25	5,2E+08	3	3	3	42,6	13,05	25,3511	26,2976	24,4046	6	3	3	0,001093	1,89297	B8NKX6	B8NKX6	1	AFLA_093800	Small nuclear ribonucleoprotein SmD2, putative
23,8286	24,5147	24,7801	25,3378	25,0379	25,0176		1,62E-14	3,17E+08	3	3	3	31,7	13,373	24,7528	24,3744	25,1311	6	3	3	0,066246	-0,756652	B8NKX8	B8NKX8	1	AFLA_093820	SsDNA binding protein Ssb3, putative
27,727	27,3336	27,3739	27,5417	27,5855	27,5808		2,03E-50	1,92E+09	10	10	10	52	28,36	27,5237	27,4782	27,5693	6	3	3	0,508567	-0,0911388	B8NLT5	B8NLT5	1	AFLA_093910	Hydroxyacylglutathione hydrolase, putative
26,3248	26,5591	25,5442	24,7399	25,0755	23,8537	+	3,30E-21	5,29E+08	9	9	9	21,7	48,134	25,3495	26,1427	24,5564	6	3	3	0,029112	1,58634	B8NLT8	B8NLT8	1	AFLA_093940	Mitochondrial large ribosomal subunit YmL35, putative
28,3128	28,2453	28,0929	27,6927	27,6622	27,5712	+	1,71E-139	2,49E+09	10	10	10	34,8	55,183	27,9295	28,217	27,6421	6	3	3	0,001524	0,574922	B8NLU0	B8NLU0	1	AFLA_093960	Mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative
27,7779	27,6808	27,2725	27,954	27,8832	27,9935		4,02E-125	2,3E+09	11	11	11	41,1	42,069	27,7603	27,5771	27,9435	6	3	3	0,081427	-0,366463	B8NLU8	B8NLU8	1	AFLA_094040	CRAL/TRIO domain protein
24,2307	24,0283	23,4636	23,7866	24,2243	24,1324		0,000276	1,49E+08	2	2	2	7,2	28,588	23,9776	23,9075	24,0478	6	3	3	0,625125	-0,140258	B8NLW3	B8NLW3	1	AFLA_094190	Uncharacterized protein
27,5603	27,0715	26,8675	27,2018	27,4691	27,4063		5,51E-215	1,59E+09	10	10	10	54,1	30,536	27,2628	27,1665	27,3591	6	3	3	0,432296	-0,192623	B8NLW5	B8NLW5	1	AFLA_094210	Chorismate mutase
30,4457	28,4763	27,988	27,5805	28,7137	28,9121		0	2,82E+09	9	9	9	51,5	42,308	28,6861	28,97	28,4021	6	3	3	0,544261	0,567907	B8NLX2	B8NLX2	1	AFLA_094280	Agmatinase, putative
31,8547	31,404	30,2754	30,2868	30,4948	30,746		0	5,92E+10	19	19	19	63,9	42,313	30,8436	31,178	30,5092	6	3	3	0,242457	0,668828	B8NLY9	B8NLY9	1	AFLA_094450	Aspartic protease pep1 (EC 3.4.23.18) (Aspergillopepsin A) (Aspergillopepsin I)
NaN	26,4143	27,135	27,3503	26,4395	26,3686		2,11E-58	1,17E+09	10	10	10	24,7	60,647	26,7415	26,7746	26,7195	5	2	3	0,917239	0,0551567	B8NLZ3	B8NLZ3	1	AFLA_094490	Protein phosphatase 2C, putative
29,2085	29,0073	28,631	29,2335	29,2512	29,3725		2,92E-131	6,78E+09	6	6	6	48,5	18,026	29,1173	28,9489	29,2858	6	3	3	0,126223	-0,336817	B8NM00	B8NM00	1	AFLA_094560	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
33,7774	33,6839	33,3538	33,7174	33,645	33,7081		0	1,38E+11	17	17	17	82,5	27,414	33,6476	33,605	33,6902	6	3	3	0,549694	-0,0851415	B8NM07	B8NM07	1	AFLA_094630	Triosephosphate isomerase (EC 5.3.1.1)
27,1212	27,2078	27,0494	25,5732	25,825	25,6162	+	1,36E-176	1,47E+09	6	6	6	40,9	27,781	26,3988	27,1261	25,6714	6	3	3	8,66E-05	1,45467	B8NM09	B8NM09	1	AFLA_094650	60S acidic ribosomal protein P0, putative
27,336	26,8733	26,575	26,5797	26,6046	27,0142		1,11E-57	1,29E+09	5	5	5	20,7	49,642	26,8305	26,9281	26,7329	6	3	3	0,498185	0,195248	B8NM13	B8NM13	1	AFLA_094690	Cell cycle control protein (Cwf8), putative
NaN	NaN	NaN	25,1091	25,1069	24,5207		2,82E-08	1,92E+08	5	5	5	22,6	27,235	24,9123	NaN	24,9123	3	0	3	1	NaN	B8NM17	B8NM17	1	AFLA_094730	Exosome complex subunit Csl4, putative
NaN	NaN	26,214	25,686	25,4968	NaN		5,45E-36	5,44E+08	8	8	8	19	62,607	25,7989	26,214	25,5914	3	1	2	1	0,622573	B8NM53	B8NM53	1	AFLA_094850	Glucose-methanol-choline (Gmc) oxidoreductase, putative
28,9102	28,3073	28,8038	29,1156	28,6519	28,6342		1,33E-111	3,21E+09	8	8	8	35,2	25,832	28,7372	28,6738	28,8005	6	3	3	0,630308	-0,126758	B8NMC5	B8NMC5	1	AFLA_095570	RNA annealing protein Yra1, putative
30,7447	30,553	30,3879	30,6603	30,5461	30,7481		5,67E-117	1,74E+10	9	9	9	43,6	27,256	30,6067	30,5619	30,6515	6	3	3	0,491714	-0,0896034	B8NMC7	B8NMC7	1	AFLA_095590	Hsp90 binding co-chaperone (Sba1), putative
26,2995	25,6819	25,3058	24,6624	24,7967	24,93	+	9,21E-13	3,52E+08	7	7	7	24,1	38,345	25,2794	25,7624	24,7964	6	3	3	0,032205	0,966012	B8NMD1	B8NMD1	1	AFLA_095630	FAD dependent oxidoreductase superfamily
25,8601	25,462	25,2658	25,066	25,167	25,672		1,65E-15	4,77E+08	4	4	4	21,7	33,761	25,4155	25,5293	25,3017	6	3	3	0,424717	0,227615	B8NL00	B8NL00	1	AFLA_095840	Fe-S cluster assembly protein dre2 (Anamorsin homolog)
31,6764	32,2872	32,2126	32,5307	32,2914	32,301		0	6,48E+10	45	45	45	64,7	79,792	32,2166	32,0587	32,3744	6	3	3	0,20317	-0,315655	B8NL13	B8NL13	1	AFLA_095970	Hsp70 chaperone Hsp88
NaN	24,377	NaN	25,8596	25,9604	25,0461		0	6,92E+09	9	9	9	69,4	12,309	25,3108	24,377	25,622	4	1	3	1	-1,24508	B8NL17	B8NL17	1	AFLA_096010	Uncharacterized protein
NaN	23,7729	24,1405	22,8744	23,911	23,6825		4,25E-56	3,19E+08	5	5	5	11,6	80,695	23,6763	23,9567	23,4893	5	2	3	0,355095	0,467392	B8NU54	B8NU54	1	AFLA_097260	Dynamin family GTPase, putative
26,3683	25,8727	NaN	25,4552	26,0991	26,2596		6,08E-24	6,67E+08	5	5	5	24,3	39,966	26,011	26,1205	25,938	5	2	3	0,653277	0,182523	B8NU58	B8NU58	1	AFLA_097300	Uncharacterized protein
28,4536	28,18	28,194	27,5535	27,9265	27,772	+	3,11E-214	3,02E+09	8	8	8	47,2	27,811	28,0133	28,2758	27,7507	6	3	3	0,019961	0,525177	B8NTC5	B8NTC5	1	AFLA_097650	Uncharacterized protein
NaN	24,3204	24,0057	NaN	23,9082	24,0082		5,80E-25	4,36E+08	5	5	5	16,1	51,057	24,0606	24,1631	23,9582	4	2	2	0,340455	0,204844	B8NTD8	B8NTD8	1	AFLA_097780	Isoamyl alcohol oxidase, putative
28,7178	28,34	27,9904	29,0576	29,1993	29,2388	+	6,31E-223	6,24E+09	12	12	12	33	67,134	28,7573	28,3494	29,1652	6	3	3	0,019823	-0,815831	B8NTE9	B8NTE9	1	AFLA_097890	Glycosyl hydrolases family 32 superfamily
26,936	27,6763	27,6279	28,0694	27,9435	27,8404		1,49E-61	2,2E+09	11	11	11	50,9	29,624	27,6822	27,4134	27,9511	6	3	3	0,096099	-0,537736	B8NTF4	B8NTF4	1	AFLA_097940	AhpC/TSA family thioredoxin peroxidase, putative
25,5242	25,4486	25,3429	NaN	25,9507	NaN		2,88E-11	4,91E+08	4	4	4	27,5	26,051	25,5666	25,4386	25,9507	4	3	1	1	-0,512129	B8NTG4	B8NTG4	1	AFLA_098040	Aldo-keto reductase (AKR), putative
25,8265	26,1573	26,1652	26,6411	25,6947	25,3673		3,52E-20	5,55E+08	5	5	5	25,8	33,125	25,9754	26,0497	25,901	6	3	3	0,727676	0,148644	B8NTG5	B8NTG5	1	AFLA_098050	Gamma-cysteine synthetase regulatory subunit, putative
26,9182	26,9198	24,8221	27,2215	26,8141	27,4279		4,18E-30	1,19E+09	7	7	7	18,5	55,226	26,6873	26,22	27,1545	6	3	3	0,26516	-0,934472	B8NTG9	B8NTG9	1	AFLA_098090	BAR adaptor protein RVS167, putative
NaN	NaN	NaN	NaN	24,0153	24,0315		2,75E-08	1,26E+08	3	3	3	7,2	62,91	24,0234	NaN	24,0234	2	0	2	1	NaN	B8NTI4	B8NTI4	1	AFLA_098240	Probable D-xylulose kinase A (Xylulokinase A) (EC 2.7.1.17)
25,1296	25,199	NaN	NaN	21,9163	21,556	+	4,12E-11	2,05E+08	2	2	2	9,8	28,186	23,4502	25,1643	21,7362	4	2	2	0,002852	3,42808	B8NTI7	B8NTI7	1	AFLA_098270	RNase III domain protein
27,2556	27,1274	27,2534	27,4002	27,3912	27,4506	+	1,63E-112	1,45E+09	10	10	10	28,2	55,205	27,3131	27,2121	27,414	6	3	3	0,011989	-0,201863	B8NTJ2	B8NTJ2	1	AFLA_098320	Conserved fungal protein
26,8151	26,4324	26,6019	26,6803	26,5493	26,5655		2,99E-54	1,25E+09	12	12	12	20,8	98,489	26,6074	26,6165	26,5984	6	3	3	0,885658	0,0180963	B8NTJ5	B8NTJ5	1	AFLA_098350	Cysteinyl-tRNA synthetase
24,8302	23,9889	NaN	25,8991	26,3248	26,5989	+	8,17E-30	3,15E+08	2	2	2	8,8	23,433	25,5284	24,4095	26,2743	5	2	3	0,019797	-1,86471	B8NTJ8	B8NTJ8	1	AFLA_098380	Conidial hydrophobin RodA/RolA
27,2371	26,599	26,0366	26,0874	26,8954	26,922		8,35E-19	1,46E+09	4	4	4	20,5	35,409	26,6296	26,6242	26,6349	6	3	3	0,981892	-0,0106697	B8NU93	B8NU93	1	AFLA_098550	Nitrilase, putative
29,5424	29,3543	29,0221	29,3483	29,4023	29,5375		1,79E-181	7,39E+09	12	12	12	43,9	40,713	29,3678	29,3063	29,4294	6	3	3	0,490137	-0,123112	B8NUA2	B8NUA2	1	AFLA_098640	Isoflavone reductase family protein
29,3373	28,2308	27,7514	28,6145	29,0328	29,3106		8,12E-79	4,28E+09	5	5	5	28	31,386	28,7129	28,4399	28,986	6	3	3	0,3457	-0,546087	B8NUA8	B8NUA8	1	AFLA_098700	Carbonyl reductase, putative
25,9285	25,9502	25,8786	26,004	NaN	26,1202		8,28E-27	7,27E+08	5	5	5	29,3	32,471	25,9763	25,9191	26,0621	5	3	2	0,06832	-0,142977	B8NUB0	B8NUB0	1	AFLA_098720	Uncharacterized protein
27,5074	27,2319	26,9537	26,9761	26,9964	27,1226		1,48E-57	1,38E+09	10	10	10	33,7	59,093	27,1313	27,231	27,0317	6	3	3	0,296784	0,199328	B8NUB3	B8NUB3	1	AFLA_098750	Serine/threonine-protein phosphatase (EC 3.1.3.16)
NaN	23,6569	24,233	26,5761	23,6334	NaN		1,77E-06	5,22E+08	2	2	2	6,1	38,612	24,5249	23,9449	25,1048	4	2	2	0,520088	-1,15986	B8NUC3	B8NUC3	1	AFLA_098850	Uncharacterized protein
27,0794	26,9037	26,8825	27,2561	27,3297	27,3405	+	2,97E-59	1,68E+09	11	11	11	36,3	46,932	27,132	26,9552	27,3088	6	3	3	0,006448	-0,353566	B8NUD7	B8NUD7	1	AFLA_098990	Phosphatidylinositol transporter, putative
31,5111	31,3036	31,7398	31,7859	31,8668	31,7628		0	2,19E+10	9	9	9	82,5	16,008	31,6617	31,5182	31,8051	6	3	3	0,091618	-0,28697	B8NUD8	B8NUD8	1	AFLA_099000	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)
34,1764	33,8921	33,4924	33,782	33,7902	33,915		0	1,51E+11	26	26	26	63,3	35,496	33,8413	33,8536	33,8291	6	3	3	0,909538	0,0245603	B8NUD9	B8NUD9	1	AFLA_099010	Transaldolase (EC 2.2.1.2)
32,2198	31,7104	31,3031	31,2849	31,6264	31,5386		0	2,79E+10	12	12	12	47,9	52,4	31,6139	31,7444	31,4833	6	3	3	0,410222	0,261136	B8NUE0	B8NUE0	1	AFLA_099020	Autophagic serine protease Alp2
28,0487	27,2878	26,3832	27,6132	27,9721	28,2169		4,50E-122	2,24E+09	2	2	2	25,2	12,024	27,587	27,2399	27,9341	6	3	3	0,246918	-0,694171	B8NUF3	B8NUF3	1	AFLA_099150	Thioredoxin
25,1627	25,1334	24,3574	25,426	25,3863	25,4073		1,19E-19	5,14E+08	4	4	4	39,2	17,83	25,1455	24,8845	25,4065	6	3	3	0,11911	-0,521996	B8NUF7	B8NUF7	1	AFLA_099190	Uncharacterized protein
NaN	NaN	NaN	24,3513	25,0113	24,9895		8,71E-16	1,67E+08	3	3	3	12,8	40,381	24,784	NaN	24,784	3	0	3	1	NaN	B8NUG2	B8NUG2	1	AFLA_099240	D-arabinitol dehydrogenase ArbD, putative
27,5609	26,8891	26,6536	26,4048	26,5283	27,1197		5,58E-113	1,72E+09	12	12	12	27	77,885	26,8594	27,0345	26,6843	6	3	3	0,373652	0,350272	B8NUG3	B8NUG3	1	AFLA_099250	3-methylcrotonyl-CoA carboxylase subunit alpha (MccA), putative
29,4712	29,4654	29,0787	29,2413	29,5726	29,3364		4,15E-153	7,49E+09	17	17	17	49,5	46,755	29,3609	29,3384	29,3835	6	3	3	0,795966	-0,0450452	B8NUG5	B8NUG5	1	AFLA_099270	Isovaleryl-CoA dehydrogenase IvdA, putative
27,6597	27,7154	27,7874	28,2006	27,9857	27,7236		3,27E-111	3,03E+09	11	11	11	37,8	48,351	27,8454	27,7208	27,97	6	3	3	0,156044	-0,249113	B8NUG6	B8NUG6	1	AFLA_099280	3-methylcrotonyl-CoA carboxylase, beta subunit (MccB), putative
27,4199	26,4427	26,3808	26,8896	27,0022	26,8267		2,61E-40	1,46E+09	8	8	8	19,7	56,603	26,827	26,7478	26,9062	6	3	3	0,665955	-0,158375	B8NTN4	B8NTN4	1	AFLA_099650	Woronin body major protein, putative
NaN	22,9789	22,7872	NaN	24,0394	23,1007		2,37E-19	44187000	3	3	3	12,6	43,845	23,2266	22,883	23,5701	4	2	2	0,287973	-0,68701	B8NTP4	B8NTP4	1	AFLA_099750	Epoxide hydrolase, putative
NaN	25,3022	NaN	NaN	26,1696	25,5929		4,76E-05	8,25E+08	3	3	3	1,2	276,97	25,6882	25,3022	25,8813	3	1	2	1	-0,579128	B8NTQ4	B8NTQ4	1	AFLA_099850	Myosin type II heavy chain, putative
NaN	24,6333	24,4373	NaN	24,3608	NaN		2,71E-07	1,59E+08	2	2	2	9,9	29,157	24,4772	24,5553	24,3608	3	2	1	1	0,174455	B8NTQ5	B8NTQ5	1	AFLA_099860	Pre-mRNA splicing factor, putative
30,4038	30,3892	30,2942	30,6254	30,691	30,6643	+	0	1,82E+10	24	24	24	62,3	52,019	30,5113	30,3624	30,6602	6	3	3	0,001621	-0,297872	B8NTR5	B8NTR5	1	AFLA_099960	Argininosuccinate lyase
27,084	27,6141	27,7471	27,3378	27,4799	27,1771		2,26E-162	2,55E+09	20	20	20	43,7	71,038	27,4067	27,4817	27,3316	6	3	3	0,533634	0,150103	B8NTR8	B8NTR8	1	AFLA_099990	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1)
26,7024	26,6955	27,0866	26,3455	26,2379	26,0272	+	1,73E-61	1,46E+09	15	15	15	38,3	48,944	26,5159	26,8282	26,2035	6	3	3	0,017301	0,624626	B8NTR9	B8NTR9	1	AFLA_100000	Proteasome regulatory particle subunit Rpt1, putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
27,4075	26,5853	25,7555	25,3642	26,3415	26,7372		1,77E-91	1,45E+09	12	12	12	34,6	57,591	26,3652	26,5828	26,1476	6	3	3	0,526255	0,435143	B8NTS0	B8NTS0	1	AFLA_100010	T-complex protein 1 subunit delta
29,7651	29,9713	29,8813	25,1314	24,9765	24,5285	+	0	6,55E+09	11	11	11	21,3	55,822	27,3757	29,8726	24,8788	6	3	3	1,25E-05	4,99378	B8NTS2	B8NTS2	1	AFLA_100030	Nucleolin protein Nsr1, putative
29,8745	29,6651	29,3851	29,7407	29,5653	29,7054		3,86E-298	7,93E+09	16	16	16	50,8	46,086	29,656	29,6415	29,6705	6	3	3	0,857973	-0,0289148	B8NTS5	B8NTS5	1	AFLA_100060	Ran GTPase activating protein 1 (RNA1 protein)
25,6716	24,8397	NaN	24,4864	NaN	24,9577		4,41E-11	2,93E+08	4	4	4	13,8	33,554	24,9889	25,2556	24,7221	4	2	2	0,380519	0,533558	B8NTS7	B8NTS7	1	AFLA_100080	Transcription elongation factor S-II
26,8846	26,8277	27,1267	25,2786	26,5756	26,2823		8,64E-271	2,49E+09	16	16	16	25,6	93,812	26,4959	26,9463	26,0455	6	3	3	0,089215	0,900841	B8NTT0;B8	B8NTT0	2	AFLA_100110	Plasma membrane H+-ATPase Pma1
23,8794	NaN	23,6396	23,984	24,1033	24,0098		2,55E-06	1,49E+08	3	3	3	14,8	37,59	23,9232	23,7595	24,0324	5	2	3	0,073507	-0,272825	B8NTT3	B8NTT3	1	AFLA_100140	Metallo-beta-lactamase superfamily protein
24,3995	24,5706	24,1068	24,2683	24,4267	24,3335		0,00031	2,55E+08	2	2	2	10	38,17	24,3509	24,359	24,3428	6	3	3	0,91551	0,016154	B8NTT6	B8NTT6	1	AFLA_100170	Complex I intermediate associated protein (Cia30), putative
28,5882	28,3006	28,1649	28,6335	28,5887	28,5962		8,67E-193	3,43E+09	15	15	15	62,3	34,153	28,4787	28,3513	28,6062	6	3	3	0,112215	-0,254878	B8NTT7	B8NTT7	1	AFLA_100180	Phosphoribosyl-aminoimidazole-succinocarboxamide synthase
23,1196	23,1786	23,2721	25,7325	24,4701	24,5863	+	1,27E-13	2,12E+08	5	5	5	13,3	66,502	24,0599	23,1901	24,9296	6	3	3	0,012721	-1,73956	B8NTU3	B8NTU3	1	AFLA_100240	Glucose dehydrogenase, putative
29,6592	29,6069	29,0936	30,2753	30,115	30,1009	+	0	1,03E+10	16	16	16	51,2	54,684	29,8085	29,4532	30,1637	6	3	3	0,019764	-0,710486	B8NTU4	B8NTU4	1	AFLA_100250	Catalase (EC 1.11.1.6)
NaN	28,1206	29,3927	29,5912	28,7796	28,1711		6,98E-102	5,96E+09	2	2	2	34,9	7,1109	28,811	28,7566	28,8473	5	2	3	0,906724	-0,0906525	B8NUL0	B8NUL0	1	AFLA_100630	Uncharacterized protein
30,7566	30,2616	29,098	29,7612	29,8518	30,0839		0	1,34E+10	6	6	6	22,1	54,876	29,9688	30,0387	29,8989	6	3	3	0,793995	0,139804	B8NUL2	B8NUL2	1	AFLA_100650	Serine carboxypeptidase (CpdS), putative
28,846	28,3734	28,8448	28,4169	28,7416	28,1558		0	1,01E+10	23	23	23	58,6	57,696	28,5631	28,6881	28,4381	6	3	3	0,34046	0,24999	B8NUL4	B8NUL4	1	AFLA_100670	ATP sulphurylase
28,0835	27,9808	27,8602	27,6958	27,8127	27,8312		1,11E-130	2,7E+09	13	13	13	33,3	57,52	27,8774	27,9748	27,7799	6	3	3	0,065059	0,194952	B8NUM6	B8NUM6	1	AFLA_100790	Proteasome regulatory particle subunit (RpnE), putative
27,2399	26,8334	26,9653	26,8677	26,9127	26,8923		5,45E-34	1,4E+09	9	9	9	58,9	30,67	26,9519	27,0129	26,8909	6	3	3	0,368492	0,121965	B8NUM7	B8NUM7	1	AFLA_100800	Dihydrofolate reductase
NaN	NaN	NaN	24,9468	24,8329	24,2013		1,04E-20	4,42E+08	3	3	3	27	26,851	24,6603	NaN	24,6603	3	0	3	1	NaN	B8NUN1	B8NUN1	1	AFLA_100840	Pyridoxamine phosphate oxidase, putative
29,1483	29,2058	29,0518	29,1471	29,0268	29,1167		9,81E-273	5,89E+09	12	12	12	50,4	39,182	29,1161	29,1353	29,0969	6	3	3	0,541457	0,0384343	B8NUP8;B8	B8NUP8	2	AFLA_101010	Aspartate-semialdehyde dehydrogenase
26,4142	25,8031	28,5262	26,6828	25,8268	26,0658		4,79E-40	1,22E+09	8	8	8	30,3	29,222	26,5532	26,9145	26,1918	6	3	3	0,449697	0,7227	B8NUP9	B8NUP9	1	AFLA_101020	40S ribosomal protein S4
26,5326	26,1319	25,6851	25,7041	26,1677	26,6769		5,76E-10	6,47E+08	3	3	3	25,4	16,755	26,1497	26,1165	26,1829	6	3	3	0,867191	-0,0664183	B8NUQ4	B8NUQ4	1	AFLA_101070	Sorting nexin Snx3, putative
26,2245	25,5672	24,9172	24,8906	25,0744	25,3545		4,48E-10	4,11E+08	3	3	3	15,2	42,101	25,3381	25,5696	25,1065	6	3	3	0,312166	0,463135	B8NUQ7	B8NUQ7	1	AFLA_101100	RRM domain protein
26,0333	26,3263	29,3204	24,9988	23,6411	24,2396		1,16E-110	1,01E+09	6	6	6	43,7	18,044	25,7599	27,2267	24,2931	6	3	3	0,05904	2,93353	B8NUR2	B8NUR2	1	AFLA_101150	60S ribosomal protein L21, putative
24,4268	25,4288	27,7558	24,878	24,6196	24,6519		8,77E-122	1,24E+09	8	8	8	32,1	22,173	25,2935	25,8705	24,7165	6	3	3	0,308286	1,15396	B8NUR3	B8NUR3	1	AFLA_101160	40S ribosomal protein S9
NaN	24,6794	24,8811	24,7342	24,7133	24,9657		9,01E-09	3,5E+08	3	3	3	17,8	32,364	24,7947	24,7802	24,8044	5	2	3	0,862973	-0,0241642	B8NTU8	B8NTU8	1	AFLA_101190	Uncharacterized protein
24,816	25,4521	24,7953	24,2388	24,8552	24,324		1,90E-16	2,59E+08	5	5	5	12,6	58,533	24,7469	25,0211	24,4727	6	3	3	0,13081	0,548477	B8NTV0	B8NTV0	1	AFLA_101210	Septin
31,0839	30,3486	30,067	29,1636	29,5708	29,7497	+	0	7,72E+09	14	14	14	34	66,878	29,9973	30,4998	29,4947	6	3	3	0,045103	1,00511	B8NTV3	B8NTV3	1	AFLA_101240	Vacuolar carboxypeptidase Cps1, putative
27,4878	27,9073	27,8744	28,0823	28,2747	27,935		4,91E-48	2,7E+09	9	9	9	33,2	45,072	27,9269	27,7565	28,0973	6	3	3	0,110491	-0,340803	B8NTV8	B8NTV8	1	AFLA_101290	FAD binding domain protein
29,6944	28,7581	28,1947	29,2503	29,9106	29,9464		0	1,14E+10	24	24	24	54,6	70,783	29,2924	28,8824	29,7024	6	3	3	0,171201	-0,820031	B8NUO7	B8NUO7	1	AFLA_101780	NADH-cytochrome B5 reductase, putative
24,1839	24,4152	22,1021	23,855	24,5158	24,6501		9,00E-181	1,53E+09	9	9	8	31	38,786	23,9537	23,5671	24,3403	6	3	3	0,375142	-0,77323	B8NUZ7	B8NUZ7	1	AFLA_101980	Tartrate dehydrogenase, putative
25,5785	25,5915	24,3975	25,8655	26,5557	26,5576		2,75E-20	5,19E+08	7	7	7	22	47,268	25,7577	25,1891	26,3263	6	3	3	0,068013	-1,13713	B8NU30	B8NU30	1	AFLA_102010	Class V chitinase, putative
26,6587	26,3541	26,0918	26,4948	27,3311	27,4324		2,07E-31	1,11E+09	11	11	11	28,8	68,621	26,7271	26,3682	27,0861	6	3	3	0,101781	-0,717884	B8NUU0	B8NUU0	1	AFLA_102340	Oligo-1,6-glucosidase
27,9282	27,3447	27,014	27,1859	27,5649	27,7845		5,76E-112	1,73E+09	13	13	13	36,2	63,638	27,4704	27,429	27,5118	6	3	3	0,808273	-0,0827764	B8NUU5	B8NUU5	1	AFLA_102390	Uncharacterized protein
26,5327	26,3195	26,0096	25,6905	25,9343	26,2716		2,10E-45	8,3E+08	7	7	7	17,2	72,541	26,1264	26,2873	25,9655	6	3	3	0,228938	0,321822	B8NUZ1	B8NUZ1	1	AFLA_102850	Rho GTPase activator (Rgd1), putative
NaN	24,0621	26,1543	26,9519	25,0827	24,6013		2,34E-56	9,04E+08	4	4	4	30,7	13,011	25,3705	25,1082	25,5453	5	2	3	0,741889	-0,437121	B8NUZ4	B8NUZ4	1	AFLA_102880	Translation initiation factor SUI1, putative
27,7953	27,8751	27,8406	28,3568	28,0889	28,1956	+	2,02E-95	2,22E+09	5	5	5	44,1	15,474	28,0254	27,837	28,2138	6	3	3	0,009751	-0,376769	B8NV07	B8NV07	1	AFLA_103010	DsDNA-binding protein PDCD5, putative
25,5386	NaN	24,2552	NaN	24,8377	24,97		4,39E-07	2,17E+08	3	3	3	7,2	59,719	24,9004	24,8969	24,9038	4	2	2	0,992379	-0,0069532	B8NV09	B8NV09	1	AFLA_103030	Pre-mRNA splicing factor, putative
30,3972	30,0284	29,7014	29,3137	29,8662	29,9658		5,24E-278	1,01E+10	34	34	34	41	127,63	29,8788	30,0423	29,7152	6	3	3	0,315856	0,327099	B8NV28	B8NV28	1	AFLA_103220	Cytoskeleton assembly control protein Sla2, putative
NaN	23,8758	24,4995	24,3528	NaN	NaN		1,31E-17	2,11E+08	6	6	6	11,9	69,182	24,2427	24,1877	24,3528	3	2	1	1	-0,165137	B8NV31	B8NV31	1	AFLA_103250	Proteasome regulatory particle subunit (RpnC), putative
27,8753	27,8229	NaN	27,2172	28,0678	27,5739		1,46E-18	1,69E+09	3	3	3	15,1	18,155	27,7114	27,8491	27,6196	5	2	3	0,523891	0,229441	B8NV35	B8NV35	1	AFLA_103290	Histone H1
28,8832	28,8876	28,4205	28,4665	28,7293	28,7163		9,84E-65	3,99E+09	3	3	3	10,5	58,197	28,6839	28,7305	28,6374	6	3	3	0,6267	0,0931034	B8NV39	B8NV39	1	AFLA_103330	Glutaryl-CoA dehydrogenase, putative
29,201	29,1605	28,8364	28,6245	28,6666	28,8946		0	5,94E+09	16	16	16	37,1	74,988	28,8973	29,066	28,7286	6	3	3	0,077243	0,337397	B8NV47	B8NV47	1	AFLA_103410	Eukaryotic translation initiation factor subunit eIF2A, putative
28,1696	27,7402	27,3293	27,4375	27,506	27,5759		1,23E-76	1,8E+09	21	21	21	20,7	163,73	27,6264	27,7464	27,5065	6	3	3	0,384421	0,239907	B8NV55	B8NV55	1	AFLA_103490	Transcription elongation factor SPT6, putative
28,3113	27,9128	27,6902	28,0301	28,3625	28,5368		6,02E-258	3,12E+09	12	12	12	52,1	37,028	28,1406	27,9714	28,3098	6	3	3	0,22283	-0,338387	B8NV70	B8NV70	1	AFLA_103650	Aldose 1-epimerase, putative
NaN	23,4977	24,2882	23,5353	NaN	NaN		4,91E-20	2,25E+08	6	6	6	20,8	33,121	23,7737	23,8929	23,5353	3	2	1	1	0,357646	B8NV71	B8NV71	1	AFLA_103660	Nicotinate-nucleotide pyrophosphorylase
30,4242	30,9908	31,5229	28,1911	27,3704	27,7701	+	1,66E-190	9,17E+09	8	8	8	49,7	16,827	29,3783	30,9793	27,7772	6	3	3	0,00127	3,20212	B8NV82	B8NV82	1	AFLA_103770	60S ribosomal protein L27a, putative
26,9499	26,5403	26,2986	26,0752	26,5962	26,6954		8,09E-36	8,79E+08	7	7	7	14,9	81,138	26,5259	26,5963	26,4556	6	3	3	0,630285	0,14072	B8NV84	B8NV84	1	AFLA_103790	Chitin synthase activator (Chs3), putative
27,132	26,3288	26,5502	27,0741	26,6918	26,7562		2,99E-58	1,42E+09	9	9	9	40,4	36,363	26,7555	26,6703	26,8407	6	3	3	0,558261	-0,170364	B8NV88	B8NV88	1	AFLA_103830	OTU-like cysteine protease, putative
24,1272	24,5665	24,9224	25,216	24,9812	24,7314		2,38E-13	3,74E+08	5	5	5	15,3	66,553	24,7575	24,5387	24,9762	6	3	3	0,179398	-0,437536	B8NV95	B8NV95	1	AFLA_103900	Cystathionine gamma-synthase, putative
29,4083	30,64	31,1909	31,1658	30,9159	30,8305		0	2,06E+10	28	28	28	78,2	52,912	30,6919	30,4131	30,9708	6	3	3	0,357271	-0,557682	B8NV99	B8NV99	1	AFLA_103940	Glutamate carboxypeptidase, putative
30,0284	29,7956	29,4127	29,6002	29,6131	29,7203		4,39E-286	9,45E+09	16	16	16	41,5	50,724	29,6951	29,7456	29,6445	6	3	3	0,61104	0,10107	B8NVA6	B8NVA6	1	AFLA_104010	Dihydrolipoamide succinyltransferase, putative
NaN	25,3462	24,8921	29,4939	29,6535	28,1187	+	1,57E-16	2,26E+09	3	3	3	29,3	14,092	27,5009	25,1192	29,0887	5	2	3	0,008874	-3,96953	B8NVA8;B8	B8NVA8	2	AFLA_104030	Histone H2A
26,3918	27,9108	27,3845	29,9385	30,0177	29,1827	+	1,24E-134	4,14E+09	5	5	5	31,9	14,972	28,471	27,229	29,713	6	3	3	0,008725	-2,48392	B8NVA9	B8NVA9	1	AFLA_104040	Histone H2B
29,1856	28,6991	28,565	27,0618	27,5958	27,4143	+	1,67E-68	2,7E+09	8	8	8	30,4	32,116	28,0869	28,8166	27,3573	6	3	3	0,003998	1,45931	B8N7K8	B8N7K8	1	AFLA_104510	Methyltransferase family protein
31,0267	30,5492	30,0807	29,4291	29,524	29,7409	+	0	1,01E+10	10	10	10	31,1	56,806	30,0584	30,5522	29,5647	6	3	3	0,02664	0,987531	B8N7M4	B8N7M4	1	AFLA_104670	Serine peptidase, putative
NaN	NaN	NaN	28,1967	28,514	28,7807		0	6,87E+09	12	12	12	45,2	54,633	28,4971	NaN	28,4971	3	0	3	1	NaN	B8N7N3	B8N7N3	1	AFLA_104760	Purple acid phosphatase (EC 3.1.3.2)
27,6188	27,3415	27,5388	25,5577	26,698	26,9132		4,68E-25	9,03E+08	9	9	9	31,8	37,43	26,9447	27,4997	26,3897	6	3	3	0,060677	1,11003	B8N7P3	B8N7P3	1	AFLA_104860	Leucoanthocyanidin dioxygenase, putative
28,7522	28,9396	28,9731	29,0997	29,0242	28,9729		2,10E-218	5,41E+09	15	15	15	44,5	46,039	28,9603	28,8883	29,0323	6	3	3	0,13861	-0,14399	B8N7T9	B8N7T9	1	AFLA_105320	Phosphoserine aminotransferase
24,3564	24,2628	NaN	NaN	24,4983	NaN		7,70E-09	1,06E+08	4	4	4	16,3	34,595	24,3725	24,3096	24,4983	3	2	1	1	-0,188663	B8N7U0	B8N7U0	1	AFLA_105330	Uncharacterized protein
30,1816	29,8325	29,5852	29,8361	29,77	29,9111		0	9,92E+09	22	22	22	53,8	68,258	29,8528	29,8664	29,8391	6	3	3	0,885203	0,0273399	B8N7U5	B8N7U5	1	AFLA_105380	Coronin
28,8961	28,7926	28,5088	28,6991	28,6678	28,7507		4,05E-268	4,6E+09	13	13	12	34	65,522	28,7192	28,7325	28,7059	6	3	3	0,832727	0,0266546	B8N7W8	B8N7W8	1	AFLA_105610	Dihydroxy acid dehydratase Ilv3, putative
25,9601	26,7714	27,3522	26,64	26,8902	26,6003		1,53E-61	1,32E+09	9	9	9	28,4	48,634	26,7024	26,6946	26,7102	6	3	3	0,971731	-0,0156002	B8N7Y1	B8N7Y1	1	AFLA_105740	Sulfide quinone reductase, putative
25,3959	25,0552	NaN	NaN	25,0623	25,2834		2,61E-12	2,65E+08	5	5	5	9,6	70,731	25,1992	25,2256	25,1728	4	2	2	0,819338	0,0527582	B8N802	B8N802	1	AFLA_105960	Autophagy protein Atg20, putative
29,6123	29,2483	28,9928	29,3187	29,3332	29,4582		0	6,96E+09	15	15	15	81,2	32,366	29,3273	29,2845	29,37	6	3	3	0,668027	-0,085544	B8N831	B8N831	1	AFLA_106250	HAD superfamily hydrolase, putative
25,0969	28,7209	30,3406	30,7371	28,1766	27,6849		4,10E-59	4,76E+09	5	5	5	61,5	11,246	28,4595	28,0528	28,8662	6	3	3	0,677421	-0,8134	B8N837	B8N837	1	AFLA_106310	Chaperonin, putative
32,5621	32,6547	32,8775	32,9685	32,8783	32,8928		0	7,43E+10	24	24	24	62,8	52,764	32,8057	32,6981	32,9132	6	3	3	0,0925	-0,215099	B8N841	B8N841	1	AFLA_106350	ATP citrate lyase subunit (Acl), putatibe
24,5006	23,1807	NaN	NaN	NaN	24,7281		3,20E-06	2,83E+08	3	3	3	39,3	9,934	24,1365	23,8407	24,7281	3	2	1	1	-0,887435	B8N844	B8N844	1	AFLA_106380	Nuclear pore complex subunit, putative
30,5762	30,3315	30,0417	30,2471	30,2014	30,3539		1,16E-172	1,37E+10	14	14	14	65,1	29,12	30,292	30,3165	30,2675	6	3	3	0,776038	0,0489941	B8N845	B8N845	1	AFLA_106390	Ribose 5-phosphate isomerase A
28,1928	27,7503	27,4087	27,719	27,9741	28,0387		1,06E-94	2,6E+09	18	18	18	44,3	61,895	27,8473	27,7839	27,9106	6	3	3	0,635136	-0,126685	B8N846	B8N846	1	AFLA_106400	Ubiquitin-like activating enzyme (UlaA), putative
24,4668	24,6521	24,7842	24,8291	24,5051	24,6114		9,70E-15	3,35E+08	4	4	4	22,1	22,845	24,6415	24,6344	24,6486	6	3	3	0,920009	-0,0141703	B8N861	B8N861	1	AFLA_106550	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
28,1944	27,7524	27,5331	27,7676	27,5598	27,6206		3,52E-283	3,12E+09	13	13	13	40,8	52,592	27,738	27,8266	27,6493	6	3	3	0,433852	0,177302	B8N862	B8N862	1	AFLA_106560	Zinc finger protein ZPR1
NaN	23,9949	25,0976	25,9135	25,2339	24,4151		2,49E-19	5,07E+08	6	6	6	8,4	98,488	24,931	24,5463	25,1875	5	2	3	0,423648	-0,641237	B8N863	B8N863	1	AFLA_106570	Cullin binding protein CanA, putative
NaN	NaN	23,9075	23,5859	23,7486	23,6264		3,61E-05	61010000	2	2	2	6,3	32,17	23,7171	23,9075	23,6536	4	1	3	1	0,253836	B8N873	B8N873	1	AFLA_106670	Tip120, putative
28,799	28,606	28,3659	28,2651	28,1927	28,3099		2,73E-182	4E+09	16	16	16	46,3	49,785	28,4231	28,5903	28,2559	6	3	3	0,061638	0,334365	B8N886	B8N886	1	AFLA_106800	Guanine deaminase, putative
29,3275	28,7939	28,3828	28,5687	28,7831	28,6635		2,15E-146	3,31E+09	15	15	15	57,1	39,009	28,7533	28,8347	28,6718	6	3	3	0,592275	0,162992	B8N888	B8N888	1	AFLA_106820	FAD dependent oxidoreductase superfamily
31,5915	31,1603	30,5422	31,0579	31,1758	31,2543		0	2,46E+10	15	15	15	60,2	36,511	31,1303	31,098	31,1627	6	3	3	0,844886	-0,0646515	B8N894	B8N894	1	AFLA_106880	Aldehyde reductase (AKR1), putative
26,3238	26,0059	25,6006	25,6886	25,5791	25,6977		7,08E-79	8,37E+08	6	6	6	26,6	54,465	25,8159	25,9767	25,6552	6	3	3	0,205141	0,321585	B8N8A6	B8N8A6	1	AFLA_107000	Ribosome biogenesis protein (Rrb1), putative
28,887	28,5007	28,4246	28,6334	28,695	28,8528		6,37E-128	4,23E+09	9	9	9	55,7	29,976	28,6656	28,6041	28,7271	6	3	3	0,478155	-0,12296	B8N8C6	B8N8C6	1	AFLA_107200	F-actin capping protein alpha subunit, putative
32,3531	31,9518	32,1433	31,4712	31,5126	31,5694	+	0	2,9E+10	26	26	26	68,8	48,57	31,8336	32,1494	31,5177	6	3	3	0,006113	0,631673	B8N8D0	B8N8D0	1	AFLA_107240	Fructosyl amine: oxygen oxidoreductase
23,7644	23,6731	24,0223	24,1054	23,8954	NaN		2,04E-11	3,29E+08	3	3	3	29,2	21,547	23,8921	23,8199	24,0004	5	3	2	0,331047	-0,180496	B8N8D6	B8N8D6	1	AFLA_107300	3-hydroxyanthranilate 3,4-dioxygenase (EC 1.13.11.6) (3-hydroxyanthranilate oxygenase) (3-hydroxyanthranilic acid dioxygenase) (Biosynthesis of nicotinic acid protein 1)

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
26,274	26,1182	25,9731	25,7972	25,8503	26,0359		8,28E-14	7,81E+08	5	5	5	15,8	56,376	26,0081	26,1218	25,8945	6	3	3	0,114763	0,227301	B8N8E2	B8N8E2	1	AFLA_107360	Pre-mRNA splicing factor, putative
28,859	28,5918	27,9289	28,2286	28,3803	28,2884		1,23E-94	3,3E+09	9	9	9	26,9	45,682	28,3795	28,4599	28,2991	6	3	3	0,596522	0,160792	B8N8E4	B8N8E4	1	AFLA_107380	PWWP domain protein
26,127	24,9243	24,8599	26,4911	25,3076	24,8231		1,68E-57	4,86E+08	6	6	6	4,7	172,52	25,4222	25,3038	25,5406	6	3	3	0,731835	-0,236831	B8N8F0	B8N8F0	1	AFLA_107440	Cytoskeleton assembly control protein Sla1, putative
NaN	NaN	NaN	NaN	23,1509	23,2382		9,47E-07	55611000	2	2	2	10,6	33,212	23,1945	NaN	23,1945	2	0	2	1	NaN	B8N8F1	B8N8F1	1	AFLA_107450	Pirin, putative
NaN	23,3384	23,9758	NaN	NaN	NaN		3,74E-08	1,7E+08	4	4	4	15,6	41,918	23,6571	23,6571	NaN	2	2	0	1	NaN	B8N8G5	B8N8G5	1	AFLA_107590	3-methyl-2-oxobutanoate dehydrogenase, putative
24,4592	NaN	25,3271	NaN	24,1185	24,2998		4,77E-13	4,77E+08	6	6	6	10,8	85,746	24,5511	24,8931	24,2092	4	2	2	0,262822	0,683983	B8N8I6	B8N8I6	1	AFLA_107800	Exo-beta-1,3-glucanase, putative
31,3867	31,0641	30,8687	30,2682	30,3513	30,7671	+	3,46E-217	2,2E+10	4	4	4	48,8	13,13	30,7844	31,1065	30,4622	6	3	3	0,040581	0,64432	B8N8I7	B8N8I7	1	AFLA_107810	Heteregeneous nuclear ribonucleoprotein G, putative
25,2559	25,7218	25,6985	25,8544	26,155	26,2429		1,17E-32	1,22E+09	8	8	8	17,6	64,958	25,8214	25,5587	26,0841	6	3	3	0,051997	-0,525368	B8N8J0	B8N8J0	1	AFLA_107840	AMP dependent CoA ligase, putative
29,157	30,6337	31,1528	31,4335	30,8136	30,5071		0	2,63E+10	21	21	21	57,1	46,804	30,6163	30,3145	30,9181	6	3	3	0,410267	-0,603546	B8N8L6	B8N8L6	1	AFLA_108100	Argininosuccinate synthase
29,4936	29,3376	29,047	28,7221	28,7954	28,9274	+	6,60E-298	6,78E+09	9	9	9	65,3	26,615	29,0539	29,2927	28,815	6	3	3	0,029441	0,477738	B8N8N3	B8N8N3	1	AFLA_108270	Formyltetrahydrofolate deformylase, putative
25,6011	25,0476	24,4188	24,9674	25,0899	24,9743		1,33E-10	3,14E+08	4	4	4	11,9	60,716	25,0165	25,0225	25,0106	6	3	3	0,973946	0,0119476	B8N8P1	B8N8P1	1	AFLA_108350	Alpha/beta hydrolase, putative
NaN	NaN	NaN	NaN	25,3324	24,9761		9,07E-77	2,12E+08	4	4	4	11,4	75,17	25,1543	NaN	25,1543	2	0	2	1	NaN	B8N8P3	B8N8P3	1	AFLA_108370	Tyrosinase, putative
27,827	27,0718	26,5908	26,9325	27,2586	27,3668		2,09E-89	1,3E+09	9	9	9	37,6	44,286	27,1746	27,1632	27,186	6	3	3	0,955438	-0,0227566	B8N8P6	B8N8P6	1	AFLA_108410	Dipeptidase (EC 3.4.13.19)
NaN	24,6491	24,0375	24,9699	NaN	24,951		7,22E-12	2,69E+08	3	3	3	16,2	24,284	24,6519	24,3433	24,9605	4	2	2	0,181149	-0,617185	B8N8P7	B8N8P7	1	AFLA_108420	NUDIX domain protein
24,8348	25,0625	24,7836	NaN	24,5571	NaN		1,70E-11	2,92E+08	5	5	5	15,8	43,37	24,8095	24,8936	24,5571	4	3	1	1	0,336489	B8N8Q0	B8N8Q0	1	AFLA_108450	Serine/threonine-protein phosphatase (EC 3.1.3.16)
25,4934	24,0637	NaN	NaN	23,6436	23,5532		2,53E-09	88692000	3	3	3	7,3	44,699	24,1885	24,7786	23,5984	4	2	2	0,241187	1,18018	B8N8Q9	B8N8Q9	1	AFLA_108540	NADH oxidase, putative
26,5992	26,4257	26,1638	25,8081	26,6232	26,9638		1,00E-19	1,28E+09	6	6	6	23,7	46,238	26,4306	26,3962	26,465	6	3	3	0,859835	-0,0688082	B8N8S4	B8N8S4	1	AFLA_108690	Uncharacterized protein
29,1311	28,4463	27,6211	28,5451	29,2122	29,4178		4,77E-44	3,53E+09	4	4	4	59,8	11,573	28,7289	28,3995	29,0584	6	3	3	0,265848	-0,658889	B8N8S9	B8N8S9	1	AFLA_108740	Uncharacterized protein
31,7663	31,1153	30,6546	31,1758	31,4372	31,6705		0	4,35E+10	28	28	28	74,8	53,981	31,3033	31,1787	31,4278	6	3	3	0,519028	-0,249092	B8N8T4	B8N8T4	1	AFLA_108790	Aldehyde dehydrogenase AldA, putative
24,681	24,4606	26,224	24,1837	NaN	24,1363		2,91E-07	2,19E+08	3	3	3	10,4	51,484	24,7371	25,1218	24,16	5	3	2	0,271929	0,961846	B8N8U1	B8N8U1	1	AFLA_108860	1,3-beta-glucanosyltransferase (EC 2.4.1.-)
25,1399	23,9849	NaN	23,5727	23,8766	23,6052		1,22E-10	3,23E+08	5	5	5	39,4	18,668	24,0358	24,5624	23,6848	5	2	3	0,145063	0,877518	B8N8U3	B8N8U3	1	AFLA_108880	Mitochondrial import receptor subunit (Tom20), putative
25,5507	25,7206	NaN	27,7446	27,9553	28,0361	+	9,14E-136	1,9E+09	13	13	13	45,8	51,072	27,0015	25,6356	27,912	5	2	3	0,000395	-2,27635	B8N8U9	B8N8U9	1	AFLA_108950	Histidine acid phosphatase, putative
28,9674	27,8194	27,855	26,9918	27,6431	27,6815		8,99E-181	4,2E+09	41	40	40	21,5	279,52	27,8264	28,2139	27,4388	6	3	3	0,15171	0,775109	B8N8V0	B8N8V0	1	AFLA_108960	Bifunctional pyrimidine biosynthesis protein (PyrABCN), putative
27,5284	27,2313	27,4641	27,5264	27,7589	27,6726		5,94E-172	2,76E+09	11	11	11	50,6	35,175	27,5303	27,4079	27,6526	6	3	3	0,096082	-0,244708	B8N8X0	B8N8X0	1	AFLA_109160	Isopentenyl-diphosphate delta-isomerase
26,2706	26,5718	25,9198	26,4577	26,6371	26,6461		3,92E-13	8,42E+08	5	5	5	23,2	28,801	26,4172	26,254	26,5803	6	3	3	0,174967	-0,326258	B8N8X3	B8N8X3	1	AFLA_109190	Possible replication factor-a protein
28,3266	27,7794	27,1414	27,7963	27,9173	28,005		1,19E-113	1,88E+09	11	11	11	37,2	39,317	27,8277	27,7491	27,9062	6	3	3	0,674934	-0,157064	B8N8Y6	B8N8Y6	1	AFLA_109320	3-hydroxyisobutyrate dehydrogenase
27,1255	26,0599	25,6039	24,7884	25,6728	25,3736		1,02E-64	1,03E+09	13	13	13	27,5	76,636	25,7707	26,2631	25,2783	6	3	3	0,131329	0,984849	B8N8Y9	B8N8Y9	1	AFLA_109350	NADPH--cytochrome P450 reductase (EC 1.6.2.4)
30,0422	29,6007	29,3016	29,5598	29,5024	29,615		0	7E+09	11	11	11	54,5	24,59	29,6036	29,6482	29,5591	6	3	3	0,703222	0,0890624	B8N9A0	B8N940	1	AFLA_109860	Translation elongation factor eEF-1B gamma subunit, putative
26,3981	26,2467	26,2989	26,5909	26,4696	26,5266	+	2,13E-17	8,8E+08	6	6	6	30,8	38,043	26,4218	26,3146	26,529	6	3	3	0,019247	-0,214437	B8N947	B8N947	1	AFLA_109930	D-lactate dehydrogenase, putative
23,8482	NaN	25,589	NaN	NaN	NaN		5,58E-12	57945000	5	5	5	19,3	41,531	24,7186	24,7186	NaN	2	2	0	1	NaN	B8N950	B8N950	1	AFLA_109960	Uncharacterized protein
27,2463	26,2478	25,7955	25,6183	27,1195	27,1558		4,26E-09	8,59E+08	4	4	4	25,3	27,489	26,5305	26,4299	26,6312	6	3	3	0,77667	-0,20135	B8N953	B8N953	1	AFLA_109990	SNARE protein Ykt6, putative
28,4043	27,7417	27,9405	27,0921	27,517	27,6322		2,09E-90	2,01E+09	12	12	12	30,6	86,874	27,7213	28,0288	27,4138	6	3	3	0,074106	0,615036	B8N970	B8N970	1	AFLA_110160	Probable dipeptidyl peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV) (DPP IV) (DppIV)
26,0694	26,0514	26,7135	26,9402	27,3992	27,1502	+	1,71E-107	2,64E+09	24	24	24	48	69,275	26,7206	26,2781	27,1632	6	3	3	0,025551	-0,885099	B8N980	B8N980	1	AFLA_110260	Flavin-binding monooxygenase-like protein
29,5629	29,8464	30,0474	30,2572	30,1484	30,1504		0	1,24E+10	22	22	22	68,4	50,261	30,0021	29,8189	30,1853	6	3	3	0,064936	-0,366435	B8N997;B8	B8N997	2	AFLA_110430	L-ornithine aminotransferase Car2, putative
25,428	26,146	26,517	26,2763	26,8464	26,4596		3,77E-71	1,58E+09	14	14	14	33,1	67,5	26,2789	26,0303	26,5274	6	3	3	0,240676	-0,497084	B8N9A0	B8N9A0	1	AFLA_110460	mRNA splicing protein (Prp39), putative
25,9946	26,1703	25,9359	24,6189	24,2005	NaN	+	4,82E-24	4,43E+08	4	4	4	19,2	33,102	25,3841	26,0336	24,4097	5	3	2	0,002899	1,62391	B8N9A8	B8N9A8	1	AFLA_110540	Uncharacterized protein
33,4804	33,0954	32,7149	33,0522	33,226	33,3511		0	9,51E+10	48	48	48	57,8	106,78	33,1533	33,0969	33,2098	6	3	3	0,659127	-0,112907	B8N9B4	B8N9B4	1	AFLA_110600	Aminopeptidase
29,6682	29,2738	28,8321	29,0729	29,0752	29,2939		8,64E-267	6,44E+09	16	16	16	70,1	35,782	29,2027	29,258	29,1474	6	3	3	0,683592	0,110688	B8N9C1	B8N9C1	1	AFLA_110670	Thioredoxin, putative
28,0479	27,9011	27,1846	27,074	28,1274	28,0505		1,97E-119	2,38E+09	10	10	10	38,1	40,025	27,7309	27,7112	27,7506	6	3	3	0,931628	-0,0393918	B8N9C3	B8N9C3	1	AFLA_110690	Cytochrome c peroxidase Ccp1, putative
28,6464	28,277	27,9367	28,2258	28,3261	28,4657		1,02E-71	3,74E+09	9	9	9	66,9	17,881	28,3129	28,2867	28,3392	6	3	3	0,820303	-0,0524832	B8N9D1	B8N9D1	1	AFLA_110770	DUF757 domain protein
30,7078	30,453	30,1159	30,6292	30,623	30,7094		0	1,63E+10	16	16	16	68,7	34,911	30,5397	30,4256	30,6539	6	3	3	0,258967	-0,228278	B8N9D5	B8N9D5	1	AFLA_110810	Possible apospory-associated protein c
23,5138	24,546	24,4646	24,8497	24,1558	23,7379		4,09E-58	4,43E+08	7	7	7	18,4	55,557	24,2113	24,1748	24,2478	6	3	3	0,882536	-0,0729809	B8N9E3	B8N9E3	1	AFLA_110890	FAD-dependent oxygenase, putative
28,4204	28,1923	28,204	28,6219	28,4154	28,5147		7,19E-177	4,6E+09	14	14	14	48,6	52,321	28,3948	28,2723	28,5173	6	3	3	0,061622	-0,245061	B8N9E7	B8N9E7	1	AFLA_110930	Phospho-2-dehydro-3-deoxyheptonate aldolase, class II
24,2578	23,9339	23,5806	23,7169	23,6923	23,7973		1,96E-09	1,75E+08	4	4	4	6,1	69,165	23,8298	23,9241	23,7355	6	3	3	0,394989	0,188606	B8N9F0	B8N9F0	1	AFLA_110960	Lysophospholipase Plb1
24,2088	NaN	NaN	28,7785	29,2932	29,3174		3,03E-266	4,42E+09	5	5	5	17,5	54,729	27,8995	24,2088	29,1297	4	1	3	1	-4,92087	B8N9F8	B8N9F8	1	AFLA_111040	Phytase
27,273	26,9216	26,8044	26,8156	27,0258	27,1815		1,46E-46	1,17E+09	9	9	9	32,1	34,893	27,0036	26,9997	27,0076	6	3	3	0,966235	-0,0079384	B8N9G0	B8N9G0	1	AFLA_111060	Calcium homeostasis protein Regucalcin, putative
29,0791	29,2243	29,0692	29,3038	29,1279	29,3284		3,22E-230	6,89E+09	22	22	19	51,2	54,164	29,1888	29,1242	29,2533	6	3	3	0,184551	-0,129129	B8N9G1	B8N9G1	1	AFLA_111070	Aldehyde dehydrogenase, putative
28,8003	28,3777	28,0569	28,1467	28,3618	28,3524		3,44E-90	3,16E+09	8	8	8	30,6	34,3	28,3493	28,4116	28,2869	6	3	3	0,61112	0,124704	B8N9G2	B8N9G2	1	AFLA_111080	AT DNA binding protein (Thy28), putative
31,3208	31,2213	31,2195	31,7295	31,6396	31,6397	+	0	2,78E+10	14	14	14	38,5	37,964	31,4617	31,2538	31,6696	6	3	3	0,000757	-0,415757	B8N9G4	B8N9G4	1	AFLA_111100	Mitochondrial peroxiredoxin Prx1, putative
25,1943	NaN	NaN	25,2588	24,9081	25,1406		1,13E-14	4,49E+08	7	7	7	31	43,419	25,1254	25,1943	25,1025	4	1	3	1	0,0918535	B8N9G7	B8N9G7	1	AFLA_111130	Pantetheine-phosphate adenylyltransferase family protein
25,2935	24,5979	24,4928	24,441	24,2619	24,2376		2,02E-14	2,07E+08	6	6	6	7,6	96,177	24,5541	24,7948	24,3135	6	3	3	0,137038	0,481239	B8N9H1	B8N9H1	1	AFLA_111170	Transcription initiation protein spt5
26,1286	27,0787	27,4486	27,8909	27,1315	26,8405		7,15E-110	2,34E+09	19	19	19	21,9	124,65	27,0865	26,8853	27,2877	6	3	3	0,468233	-0,402347	B8N9H5	B8N9H5	1	AFLA_111210	26S proteasome regulatory subunit Rpn2, putative
23,2621	23,1366	23,4283	23,4276	NaN	23,2205		1,31E-09	1,66E+08	4	4	4	10,4	62,23	23,295	23,2757	23,3241	5	3	2	0,741076	-0,048426	B8N9I7	B8N9I7	1	AFLA_111330	Aspartyl-tRNA synthetase, putative
NaN	NaN	NaN	25,6679	26,0469	26,1643		5,28E-12	4,69E+08	4	4	4	17,7	37,584	25,9597	NaN	25,9597	3	0	3	1	NaN	B8N9K7	B8N9K7	1	AFLA_111530	Zinc-containing alcohol dehydrogenase, putative
23,7152	25,9583	27,4983	24,6785	24,5287	23,9048		4,29E-35	3,17E+08	9	9	9	26,5	50,005	25,0473	25,7239	24,3707	6	3	3	0,294827	1,35327	B8N9L1	B8N9L1	1	AFLA_111570	Salicylate hydroxylase, putative
29,1943	28,7782	28,3252	28,3324	28,7398	28,9818		1,42E-169	4,48E+09	9	9	9	45,5	32,025	28,7253	28,7659	28,6847	6	3	3	0,808893	0,0812372	B8N9L6	B8N9L6	1	AFLA_111620	Succinate-semialdehyde dehydrogenase Uga2, putative
27,3874	27,4355	27,1325	27,1753	27,2069	27,1851		1,65E-54	1,67E+09	10	10	10	42,9	38,268	27,2538	27,3185	27,1891	6	3	3	0,242776	0,129344	B8N9L9	B8N9L9	1	AFLA_111650	Threonine dehydratase (EC 4.3.1.19) (Threonine deaminase)
27,8119	27,2014	26,7902	26,6425	27,4222	27,3482		4,35E-73	1,97E+09	9	9	9	14,3	88,836	27,2027	27,2678	27,1377	6	3	3	0,753553	0,130176	B8N9M2	B8N9M2	1	AFLA_111680	Elongation factor G, mitochondrial (EF-Gmt) (Elongation factor G 1, mitochondrial) (mEF-G 1) (Elongation factor G1)
NaN	25,3147	25,7761	25,8787	25,399	25,4345		1,13E-44	1E+09	9	9	9	25,2	56,896	25,5606	25,5454	25,5707	5	2	3	0,929294	-0,0253627	B8N9M6	B8N9M6	1	AFLA_111720	Glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97)
27,3186	27,1864	26,9544	26,6917	26,6127	26,8882	+	1,12E-29	1,67E+09	7	7	6	38,1	23,795	26,942	27,1531	26,7309	6	3	3	0,03472	0,422276	B8N9M9	B8N9M9	1	AFLA_111750	RAB GTPase Ypt5, putative
27,7349	27,6528	27,6808	28,0029	27,63	27,6328		9,31E-79	2,49E+09	17	17	17	23,4	117,4	27,7224	27,6895	27,7552	6	3	3	0,629787	-0,0657527	B8N9P4	B8N9P4	1	AFLA_111900	Pitrilysin family metalloprotease (Cym1), putative
23,3344	23,2231	23,2077	23,3492	23,1182	23,3856		1,79E-06	1,18E+08	4	4	4	18	27,414	23,2697	23,2551	23,2844	6	3	3	0,768022	-0,029281	B8N9P9	B8N9P9	1	AFLA_111950	Uncharacterized protein
25,0019	24,8515	24,8478	25,2797	25,6477	25,3125	+	6,78E-46	4,49E+08	4	4	4	17,5	40,552	25,1569	24,9004	25,4133	6	3	3	0,016074	-0,512899	B8N9Q6	B8N9Q6	1	AFLA_112020	CaaX farnesyltransferase alpha subunit Ram2
27,9075	27,6179	27,5312	25,6869	26,5304	25,7127	+	1,56E-64	1,32E+09	5	5	5	35,5	19,836	26,8311	27,6855	25,9767	6	3	3	0,00466	1,70888	B8N9R2	B8N9R2	1	AFLA_112080	Small nuclear ribonucleoprotein SmB, putative
27,3634	28,1478	29,9721	27,1647	26,3219	25,5227		1,04E-96	2,14E+09	8	8	8	45,1	20,059	27,4154	28,4945	26,3364	6	3	3	0,075957	2,15802	B8N9R3	B8N9R3	1	AFLA_112090	60S ribosomal protein L11
30,4571	30,2387	30,2896	29,2787	30,3534	30,0552		0	1,7E+10	38	38	38	42,2	131,2	30,1121	30,3284	29,8958	6	3	3	0,256409	0,432676	B8N9R6	B8N9R6	1	AFLA_112120	Pyruvate carboxylase (EC 6.4.1.1)
29,4201	29,7549	29,7555	30,2001	29,8055	29,591		0	1,24E+10	52	52	52	45,7	199,56	29,7545	29,6435	29,8656	6	3	3	0,350849	-0,222074	B8N9R7	B8N9R7	1	AFLA_112130	Clathrin heavy chain
31,6666	31,4062	31,2855	31,6532	31,5756	31,679		0	3,1E+10	32	32	32	72,3	65,045	31,5444	31,4528	31,6359	6	3	3	0,191469	-0,183146	B8N9R9	B8N9R9	1	AFLA_112150	Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP
28,8337	29,55	29,0813	27,5395	27,8819	27,9697	+	1,54E-195	4,51E+09	21	21	20	34	71,973	28,476	29,155	27,797	6	3	3	0,005387	1,35797	B8N9S2	B8N9S2	1	AFLA_112180	ATP dependent RNA helicase (Dbp1), putative
27,7414	27,4297	27,0191	27,3248	27,3968	27,4147		9,85E-158	2,02E+09	6	6	6	34,8	21,941	27,3878	27,3967	27,3788	6	3	3	0,936278	0,0179501	B8N9S3	B8N9S3	1	AFLA_112190	Cyclophilin, putative
28,353	28,0574	27,4999	28,0012	28,0715	28,2627		1,43E-147	2,18E+09	16	16	16	18,5	117,67	28,041	27,9701	28,1118	6	3	3	0,617469	-0,141665	B8N9S7	B8N9S7	1	AFLA_112230	Zinc metalloprotease, putative
25,5852	26,3394	25,8362	26,7238	26,673	26,3271		4,82E-39	8,76E+08	8	8	8	25,9	55,879	26,2474	25,9203	26,5746	6	3	3	0,061815	-0,654348	B8N9T1	B8N9T1	1	AFLA_112270	Translation initiation factor EF-2 gamma subunit, putative
28,8049	28,4922	28,1422	28,2539	28,5866	28,625		1,40E-114	3,73E+09	7	7	7	37,4	22,613	28,4841	28,4798	28,4885	6	3	3	0,970754	-0,0087662	B8N9T8	B8N9T8	1	AFLA_112340	Proteasome subunit beta type (EC 3.4.25.1)
29,2772	29,8472	30,2209	26,9979	25,9408	26,0707	+	4,91E-22	4,39E+09	5	5	5	39	11,978	28,0591	29,7818	26,3365	6	3	3	0,001332	3,44532	B8N9U3	B8N9U3	1	AFLA_112390	60S ribosomal protein L36
24,7855	24,7753	24,4268	24,8935	24,5381	24,7882		5,91E-08	2,58E+08	4	4	4	9,6	55,154	24,7012	24,6625	24,7399	6	3	3	0,650216	-0,0773869	B8N9U4	B8N9U4	1	AFLA_112400	UBX domain protein, putative
28,8914	28,6262	28,3156	28,4462	28,5354	28,5727		2,58E-211	3,83E+09	5	5	5	44,7	22,466	28,5646	28,6111	28,5181	6	3	3	0,614803	0,0929432	B8N9U5	B8N9U5	1	AFLA_112410	Proteasome subunit beta type (EC 3.4.25.1)
33,9559	33,4974	33,5295	33,6335	34,1213	34,1654		0	1,8E+11	55	55	55	75,6	87,163	33,8172	33,6609	33,9734	6	3	3	0,238218	-0,31248	B8N9V1	B8N9V1	1	AFLA_112470	Cobalamin-independent methionine synthase MetH/D
26,361	26,3464	25,9021	25,6727	26,1153	26,3672		9,38E-28	7,33E+08	11	11	11	12,8	121,52	26,1275	26,2032	26,0517	6	3	3	0,581408	0,151423	B8N9V3	B8N9V3	1	AFLA_112490	Ubiquitin fusion degradation protein UfdB, putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
24,9965	25,2946	24,9387	NaN	NaN	NaN		2,92E-57	2,03E+08	8	8	8	34,1	30,478	25,0766	25,0766	NaN	3	3	0	1	NaN	B8N9W4	B8N9W4	1	AFLA_112600	37S ribosomal protein S25, mitochondrial
26,8763	26,4935	26,0478	26,1206	26,4775	26,5644		8,50E-26	9,82E+08	6	6	6	13,1	64,29	26,43	26,4725	26,3875	6	3	3	0,772751	0,085043	B8N9W7	B8N9W7	1	AFLA_112630	KH domain protein
26,5836	27,5869	28,0201	28,0318	27,7075	27,318		1,91E-70	2,07E+09	11	11	11	49,7	35,221	27,5413	27,3969	27,6858	6	3	3	0,57426	-0,28886	B8N9W8	B8N9W8	1	AFLA_112640	Mitochondrial acetolactate synthase small subunit, putative
29,0362	28,7629	28,3694	28,6502	28,8252	28,9282		1,46E-239	4,78E+09	12	12	12	47,8	40,452	28,762	28,7228	28,8012	6	3	3	0,727775	-0,0783609	B8N9X0	B8N9X0	1	AFLA_112660	Ornithine carbamoyltransferase
30,7046	30,4457	30,2753	30,6641	30,5957	30,716		0	1,67E+10	23	23	23	80,9	43,129	30,5669	30,4752	30,6586	6	3	3	0,2299	-0,183386	B8N9X6	B8N9X6	1	AFLA_112720	Diphosphomevalonate decarboxylase
26,2702	25,3832	NaN	NaN	25,5156	25,5833		1,69E-13	2,34E+08	2	2	2	8,1	30,666	25,6881	25,8267	25,5495	4	2	2	0,596733	0,277205	B8N9X8	B8N9X8	1	AFLA_112740	SNARE domain protein
23,3258	NaN	24,5429	24,4141	25,0399	24,3612		1,05E-09	2,33E+08	4	4	4	12,8	51,872	24,3368	23,9343	24,6051	5	2	3	0,297836	-0,670722	B8N9Y3	B8N9Y3	1	AFLA_112790	Acyl-CoA thioester hydrolase, putative
NaN	21,8936	25,0861	26,0478	22,9643	22,5009		1,19E-11	1,32E+08	4	4	4	17,8	27,534	23,6986	23,4899	23,8377	5	2	3	0,863991	-0,347844	B8N9Z5	B8N9Z5	1	AFLA_112910	Uncharacterized protein
26,9945	26,8059	26,6524	27,1739	27,0258	26,9503		4,41E-62	1,4E+09	10	10	10	39,5	34,894	26,9338	26,8176	27,05	6	3	3	0,12199	-0,232387	B8NA03	B8NA03	1	AFLA_112990	UBX domain protein, putative
28,1751	27,2124	26,8065	26,2596	27,2401	27,4225		1,78E-28	1,44E+09	5	5	5	22,5	30,771	27,186	27,398	26,9741	6	3	3	0,478765	0,423917	B8NA04	B8NA04	1	AFLA_113000	Integral ER membrane protein Scs2, putative
27,7207	28,2641	28,3872	28,2471	27,8763	27,9056		6,50E-122	3,86E+09	12	12	12	43,4	48,527	28,0668	28,124	28,0097	6	3	3	0,654557	0,114311	B8NA06	B8NA06	1	AFLA_113020	Methionine aminopeptidase 2-1 (MAP 2-1) (MetAP 2-1) (EC 3.4.11.18) (Peptidase M)
NaN	24,0893	24,5601	NaN	24,5776	24,1245		6,55E-25	5E+08	4	4	4	14,5	37,064	24,3379	24,3247	24,351	4	2	2	0,943061	-0,0263491	B8NA08	B8NA08	1	AFLA_113040	Outer mitochondrial membrane protein porin
23,1852	24,8663	25,4849	24,2593	24,9196	25,0648		1,24E-75	1,17E+09	7	7	7	18,5	64,711	24,63	24,5121	24,7479	6	3	3	0,763	-0,235792	B8NA09	B8NA09	1	AFLA_113050	Asparagine synthetase Asn2, putative
28,451	27,9236	27,3997	28,2045	28,47	28,5038		9,81E-60	2,7E+09	14	14	14	31,4	56,094	28,1588	27,9248	28,3928	6	3	3	0,214967	-0,468019	B8NA12	B8NA12	1	AFLA_113080	Coenzyme A synthetase, putative
28,3902	27,8226	27,3431	28,1594	28,2779	28,3016		2,06E-16	2,94E+09	3	3	3	20,5	17,792	28,0491	27,852	28,2463	6	3	3	0,266765	-0,394322	B8NA13	B8NA13	1	AFLA_113090	Uncharacterized protein
23,1857	22,5171	22,8478	NaN	22,855	NaN		2,68E-16	1,34E+08	4	4	4	11,2	46,831	22,8514	22,8502	22,855	4	3	1	1	-0,004783	B8NA14	B8NA14	1	AFLA_113100	N-glycosyl-transferase
31,9868	31,5682	31,1011	31,501	31,6268	31,7643		0	3,07E+10	12	12	12	33,9	41,463	31,5914	31,552	31,6307	6	3	3	0,782827	-0,0786686	B8NA16	B8NA16	1	AFLA_113120	GPI-anchored cell wall organization protein Ecm33
NaN	23,8223	23,9259	25,8306	24,9193	24,2199		5,83E-05	1,92E+08	3	3	3	28,9	16,778	24,5436	23,8741	24,99	5	2	3	0,161455	-1,11587	B8NA21	B8NA21	1	AFLA_113170	Iron-sulfur cofactor synthesis protein (Isu1), putative
NaN	24,8352	25,3555	24,9782	23,2823	22,9658		9,96E-100	1,27E+09	16	16	16	30,3	95,646	24,2834	25,0954	23,7421	5	2	3	0,201324	1,35324	B8NA29	B8NA29	1	AFLA_113250	Ribonucleoside-diphosphate reductase (EC 1.17.4.1)
35,1754	34,929	34,5838	34,6488	34,7049	34,8044		0	2,9E+11	28	28	28	81,7	49,333	34,8077	34,8961	34,7194	6	3	3	0,375838	0,176715	B8NA36	B8NA36	1	AFLA_113320	Glutamate dehydrogenase
24,8045	24,375	NaN	NaN	NaN	NaN		7,79E-15	1,95E+08	5	5	5	7,7	81,936	24,5898	24,5898	NaN	2	2	0	1	NaN	B8NA76	B8NA76	1	AFLA_113720	Ribosome biogenesis (Nop4), putative
26,8362	26,2017	25,9558	26,1619	26,4033	26,4925		3,17E-21	1,02E+09	6	6	6	56,2	13,708	26,3419	26,3312	26,3526	6	3	3	0,942895	-0,0213642	B8NA77	B8NA77	1	AFLA_113730	Progesterone binding protein, putative
25,4463	25,6438	25,5175	24,7562	25,0039	24,802	+	1,43E-35	3,77E+08	4	4	4	17,5	39,67	25,195	25,5359	24,8541	6	3	3	0,002038	0,6818	B8NA82	B8NA82	1	AFLA_113780	Casein kinase II subunit beta (CK II beta)
28,5669	28,7012	28,7975	28,8998	28,6853	28,5828		4,05E-300	4,46E+09	14	14	14	51,9	45,268	28,7056	28,6885	28,7226	6	3	3	0,781337	-0,0341015	B8NA84	B8NA84	1	AFLA_113800	Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)
29,5724	29,1379	28,6532	29,1953	29,277	29,3936		0	6,53E+09	17	17	17	52,9	39,319	29,2049	29,1212	29,2886	6	3	3	0,570974	-0,16743	B8NA87	B8NA87	1	AFLA_113830	Dipeptidyl peptidase, putative
25,4934	26,9445	27,3426	27,1868	26,9485	26,5676		4,57E-144	3,08E+09	11	11	11	45,6	34,16	26,7472	26,5935	26,9009	6	3	3	0,629874	-0,307472	B8NA93	B8NA93	1	AFLA_113890	Nuclear pore complex subunit (SEC13), putative
NaN	23,26	22,9379	22,9698	NaN	23,0749		1,39E-08	1,13E+08	4	4	4	9,2	83,008	23,0606	23,0989	23,0223	4	2	2	0,695406	0,0766106	B8NA96	B8NA96	1	AFLA_113920	Translation initiation regulator (Gcn20), putative
NaN	NaN	NaN	24,4964	24,4219	NaN		1,41E-24	3,39E+08	8	8	8	11,7	97,024	24,4592	NaN	24,4592	2	0	2	1	NaN	B8NAA2	B8NAA2	1	AFLA_113980	Cyclin dependent kinase inhibitor Pho81, putative
28,2482	28,0213	28,0706	27,9233	28,0441	28,1771		2,01E-92	2,61E+09	13	13	13	51,8	49,825	28,0808	28,1134	28,0482	6	3	3	0,552217	0,0651957	B8NAA9	B8NAA9	1	AFLA_114050	Phosphoethanolamine
27,6522	27,1887	26,9857	27,2311	27,1566	27,308		2,71E-34	1,44E+09	3	3	3	32,1	15,135	27,2537	27,2755	27,2319	6	3	3	0,839759	0,0435823	B8NYT2	B8NYT2	1	AFLA_114440	L-PSP endoribonuclease family protein Brt1, putative
NaN	NaN	NaN	23,7777	NaN	24,6947		8,11E-07	1,28E+08	3	3	3	18,6	35,485	24,2362	NaN	24,2362	2	0	2	1	NaN	B8NYT7	B8NYT7	1	AFLA_114490	Histidinol-phosphatase
27,2515	27,4169	27,5856	24,8292	26,5341	25,9757	+	5,04E-41	7,17E+08	8	8	8	21,4	61,89	26,5988	27,418	25,7797	6	3	3	0,032711	1,63836	B8NYW3	B8NYW3	1	AFLA_114750	Glutamyl-tRNA(Gln) amidotransferase subunit A, putative
26,7695	26,9001	27,0965	27,0509	27,0963	26,9785		1,92E-58	1,34E+09	8	8	8	36,7	43,147	26,982	26,922	27,0419	6	3	3	0,301111	-0,119855	B8NYX1	B8NYX1	1	AFLA_114830	Leucine aminopeptidase 1 (EC 3.4.11.-) (Leucyl aminopeptidase 1) (LAP1)
25,259	25,2019	25,1251	25,1171	25,3029	25,0908		4,44E-12	4,29E+08	5	5	5	18,2	50,034	25,1828	25,1953	25,1703	6	3	3	0,761616	0,0250765	B8NYX7	B8NYX7	1	AFLA_114890	Queuine tRNA-ribosyltransferase (EC 2.4.2.29)
NaN	23,7848	NaN	23,5844	23,69	NaN		6,95E-09	1,61E+08	3	3	3	9,9	37,175	23,6864	23,7848	23,6372	3	1	2	1	0,147577	B8NYX8	B8NYX8	1	AFLA_114900	Thymidylate synthase
NaN	NaN	25,2325	24,2473	23,9945	NaN		2,33E-07	2,12E+08	5	5	5	5,1	158,06	24,4914	25,2325	24,1209	3	1	2	1	1,11166	B8NYY7	B8NYY7	1	AFLA_114990	DEAD helicases superfamily protein (Aquarius), putative
30,4012	30,9258	31,5159	27,7354	26,4745	26,7871	+	0	9,39E+09	15	15	15	47,3	25,677	28,9733	30,9476	26,999	6	3	3	0,001363	3,94864	B8NYZ9	B8NYZ9	1	AFLA_115110	60S ribosomal protein L13
28,7274	29,0087	29,5851	29,7783	29,3947	29,3543		0	1,1E+10	21	21	21	54,8	53,189	29,3081	29,1071	29,5091	6	3	3	0,232957	-0,402026	B8NZ05	B8NZ05	1	AFLA_115170	Succinyl-CoA ligase subunit beta (EC 6.2.1.-)
26,0215	27,508	28,1645	28,0416	27,684	27,1441		7,42E-149	3,9E+09	11	11	11	74	22,939	27,4273	27,2313	27,6232	6	3	3	0,598106	-0,39191	B8NZ08	B8NZ08	1	AFLA_115200	Xanthine-guanine phosphoribosyl transferase Xpt1, putative
27,0006	25,7875	26,0523	25,853	25,5204	25,6896		2,93E-58	8,67E+08	10	9	9	32,1	43,417	25,9839	26,2801	25,6877	6	3	3	0,194515	0,59245	B8NZ22	B8NZ22	1	AFLA_115340	Proteasome regulatory particle subunit Rpt6, putative
29,1468	28,833	28,4502	28,6582	28,6016	28,8256		1,17E-105	4,52E+09	12	12	12	40,9	55,471	28,7526	28,81	28,6951	6	3	3	0,617335	0,114842	B8NZ30	B8NZ30	1	AFLA_115420	Ran exchange factor Prp20/Pim1, putative
28,7562	28,4687	29,2016	29,3492	28,9151	28,8554		0	7,29E+09	11	11	11	80,1	16,359	28,9244	28,8088	29,0399	6	3	3	0,430772	-0,231064	B8NXA7	B8NXA7	1	AFLA_115930	Uncharacterized protein
24,7666	25,2187	24,8516	24,4483	24,9989	25,1575		3,05E-16	4,28E+08	2	2	2	8	41,753	24,9069	24,9457	24,8682	6	3	3	0,777173	0,0774409	B8NVJ1	B8NVJ1	1	AFLA_116780	Homocysteine S-methyltransferase, putative
28,348	28,1034	27,5894	27,5866	27,5259	27,7031		3,20E-165	2,11E+09	12	12	12	50,9	36,155	27,8094	28,0136	27,6052	6	3	3	0,14981	0,408397	B8NVM0	B8NVM0	1	AFLA_117070	Kelch repeat protein
25,5776	25,4587	25,6285	25,4707	25,4538	25,3751		5,15E-10	4,74E+08	5	5	5	29,1	23,51	25,4941	25,555	25,4332	6	3	3	0,105011	0,121745	B8NVN9	B8NVN9	1	AFLA_117260	N-acetyltransferase, GNAT family, putative
23,7553	NaN	28,4655	NaN	NaN	NaN		3,78E-64	9,46E+08	5	5	5	39,1	20,206	26,1104	26,1104	NaN	2	2	0	1	NaN	B8NVQ0	B8NVQ0	1	AFLA_117370	Uncharacterized protein
NaN	24,1415	24,2629	25,1786	25,0519	25,0125	+	4,58E-21	4,14E+08	9	9	9	15,2	68,837	24,7295	24,2022	25,081	5	2	3	0,001554	-0,87878	B8NVS5	B8NVS5	1	AFLA_117620	Uncharacterized protein
NaN	24,0456	25,2079	24,3207	24,7357	24,3414		2,27E-12	9,02E+08	2	2	2	29,9	11,998	24,5303	24,6267	24,466	5	2	3	0,753308	0,160781	B8NVS7	B8NVS7	1	AFLA_117640	CipC-like antibiotic stress responsive protein
30,2361	29,9794	28,9112	26,154	26,7371	26,4545	+	7,56E-218	4,87E+09	11	11	11	26,9	57,28	28,0787	29,7089	26,4485	6	3	3	0,001758	3,26038	B8NVT9	B8NVT9	1	AFLA_117760	Phytase, putative
26,5078	26,3612	25,899	26,5135	26,4395	26,6002		7,40E-61	1,04E+09	7	7	7	19,8	53,852	26,3869	26,256	26,5177	6	3	3	0,23882	-0,261716	B8NVU0	B8NVU0	1	AFLA_117770	DnaJ domain protein
26,5777	27,1118	27,3207	27,4355	27,622	27,4718		7,39E-143	1,68E+09	10	10	10	36	38,785	27,2566	27,0034	27,5098	6	3	3	0,090982	-0,506353	B8NW40	B8NW40	1	AFLA_117870	Thiosulfate sulfurtransferase, putative
26,054	27,6615	29,3168	27,4101	26,9349	26,9662		1,73E-184	2,81E+09	11	11	11	50,2	28,274	27,3906	27,6774	27,1037	6	3	3	0,580161	0,573671	B8NW52	B8NW52	1	AFLA_117990	Ribosomal protein S5
28,3202	28,246	28,233	28,3991	28,3119	28,3363		9,81E-147	3,65E+09	9	9	9	56,7	27,707	28,3078	28,2664	28,3491	6	3	3	0,092616	-0,0827058	B8NW54	B8NW54	1	AFLA_118010	Cap binding protein
28,2325	26,8934	25,6777	25,2873	26,7112	27,0976		1,51E-97	8,7E+08	4	4	4	20,4	32,476	26,65	26,9345	26,3654	6	3	3	0,569828	0,569173	B8NW67	B8NW67	1	AFLA_118140	SNARE domain protein
25,5691	25,4582	25,0392	25,275	25,7401	25,8922		1,80E-13	4,9E+08	4	4	4	9,3	66,744	25,4956	25,3555	25,6358	6	3	3	0,318132	-0,280266	B8NW69	B8NW69	1	AFLA_118160	AMP-binding enzyme, putative
27,5097	26,5704	26,4747	25,1832	26,1128	26,3659		1,47E-56	8,17E+08	6	6	6	15,6	59,389	26,3695	26,8516	25,8873	6	3	3	0,119439	0,964287	B8NW87	B8NW87	1	AFLA_118340	Flavin containing polyamine oxidase, putative
24,8001	24,822	24,3835	24,5918	24,4298	24,6012		6,38E-09	2,12E+08	4	4	4	18,8	35,987	24,6047	24,6685	24,5409	6	3	3	0,451472	0,127607	B8NWB0	B8NWB0	1	AFLA_118570	Short-chain dehydrogenases/reductase, putative
25,8071	25,9294	NaN	NaN	NaN	25,7184		5,23E-10	4,39E+08	5	5	5	17,8	45,494	25,8183	25,8683	25,7184	3	2	1	1	0,149851	B8NVY4	B8NVY4	1	AFLA_119120	Beta-lactamase family protein
NaN	25,6676	26,2213	NaN	24,1301	NaN		3,65E-167	1,63E+09	13	13	13	30	70,001	25,3397	25,9445	24,1301	3	2	1	1	1,81433	B8NW02	B8NW02	1	AFLA_119290	Phosphofructokinase, putative
NaN	25,121	25,1872	25,647	24,6977	24,6516		3,31E-37	4,14E+08	4	4	4	24	36,013	25,0609	25,1541	24,9988	5	2	3	0,735735	0,155358	B8NW03	B8NW03	1	AFLA_119310	Uncharacterized protein
28,5368	28,4669	28,3119	28,7828	29,0834	28,9844	+	3,03E-283	6,76E+09	18	18	18	80,5	23,726	28,6944	28,4385	28,9502	6	3	3	0,009839	-0,511686	B8NW05	B8NW05	1	AFLA_119330	Glutathione-S-transferase theta, GST, putative
NaN	NaN	NaN	24,508	24,7829	NaN		7,14E-09	3,55E+08	4	4	4	7,7	78,476	24,6454	NaN	24,6454	2	0	2	1	NaN	B8NW15	B8NW15	1	AFLA_119430	Sec1 family superfamily
28,0867	29,9345	30,5113	30,3472	29,6635	28,889		0	1,83E+10	18	18	18	78,1	25,65	29,572	29,5108	29,6332	6	3	3	0,89169	-0,122405	B8NW18	B8NW18	1	AFLA_119460	UDP-glucose 4-epimerase
NaN	23,4229	23,3088	23,9264	23,0431	23,2631		4,61E-07	1,36E+08	3	3	3	4,1	92,574	23,3929	23,3659	23,4109	5	2	3	0,904546	-0,0450141	B8NW19	B8NW19	1	AFLA_119470	Topoisomerase II associated protein (Pat1), putative
26,4387	26,7871	25,9063	26,6468	26,9333	26,727		1,63E-83	1,17E+09	6	6	6	23,7	44,853	26,5732	26,3774	26,769	6	3	3	0,22042	-0,391668	B8NW28	B8NW28	1	AFLA_119560	Pyridoxamine phosphate oxidase, putative
31,9247	31,7115	31,4458	31,7854	31,7567	31,8264		0	3,71E+10	9	9	9	67,8	16,985	31,7417	31,694	31,7895	6	3	3	0,532376	-0,0955486	B8NWC7	B8NWC7	1	AFLA_119640	Cofilin
28,8819	30,958	31,9273	32,0829	31,142	30,7362		0	3,2E+10	25	25	25	74,3	55,402	30,9547	30,5891	31,3204	6	3	3	0,49818	-0,731289	B8NWC9	B8NWC9	1	AFLA_119660	ATP synthase subunit beta (EC 3.6.3.14)
26,5005	27,6174	28,0244	27,8711	28,5383	28,2859		2,76E-140	3,08E+09	14	14	14	73,6	30,978	27,8063	27,3807	28,2318	6	3	3	0,160902	-0,851011	B8NWD0	B8NWD0	1	AFLA_119670	Glycogen branching enzyme GbeA, putative
NaN	NaN	NaN	27,3167	28,3767	28,4127		3,55E-141	2,03E+09	12	12	12	25,9	85,243	28,0353	NaN	28,0353	3	0	3	1	NaN	B8NWD3	B8NWD3	1	AFLA_119700	Alpha-1,2-mannosidase family protein
24,175	NaN	25,0388	NaN	NaN	NaN		5,12E-69	8,92E+08	3	3	3	22,5	30,301	24,6069	24,6069	NaN	2	2	0	1	NaN	B8NWE1	B8NWE1	1	AFLA_119780	Neutral protease 2 homolog AFLA_119780 (EC 3.4.24.39) (Deuterolysin AFLA_119780)
29,9897	29,3973	28,4971	28,2525	28,431	28,9842		4,53E-279	7,25E+09	9	9	8	23,2	57,753	28,9253	29,2947	28,5559	6	3	3	0,203575	0,738809	B8NWI1	B8NWI1	1	AFLA_120180	Carboxypeptidase (EC 3.4.16.-)
25,5834	25,2197	25,1219	27,4858	28,069	28,3951	+	6,16E-154	3,27E+09	12	12	12	51,7	29,585	26,6458	25,3084	27,9833	6	3	3	0,000883	-2,67492	B8NWI5	B8NWI5	1	AFLA_120220	Uncharacterized protein
28,6179	28,1706	28,0105	27,864	27,8528	28,0445		2,11E-134	3,21E+09	8	8	8	44,3	24,327	28,0934	28,2663	27,9204	6	3	3	0,146066	0,345907	B8NWI9	B8NWI9	1	AFLA_120260	Nitroreductase family protein, putative
26,9059	26,5021	26,2354	25,5188	26,0465	25,9512	+	3,76E-21	9,77E+08	7	7	7	23,4	41,897	26,1933	26,5478	25,8389	6	3	3	0,049069	0,708928	B8NWK8	B8NWK8	1	AFLA_120450	Porphyromonas-type peptidyl-arginine deiminase superfamily
29,7937	29,3306	29,1088	30,9832	30,765	30,7766	+	0	1,48E+10	19	17	17	61,3	43,173	30,1263	29,411	30,8416	6	3	3	0,002598	-1,43056	B8NWM6	B8NWM6	1	AFLA_120630	Glyoxylate/hydroxypyruvate reductase, putative
27,1722	27,5113	27,1182	28,0479	27,9562	28,0345	+	8,31E-169	3,36E+09	11	11	11	65,3	24,748	27,6401	27,2672	28,0129	6	3	3	0,004121	-0,745626	B8NWR2	B8NWR2	1	AFLA_120990	O-methyltransferase, putative
27,116	26,9086	26,5053	26,3625	26,341	26,3698		1,89E-34	9,84E+08	6	6	6	52,2	20,222	26,6005	26,8433	26,3578	6	3	3	0,053837	0,485532	B8NWR6	B8NWR6	1	AFLA_121030	GNAT family N-acetyltransferase, putative
30,9122	31,0149	30,7835	31,2671	31,0096	31,0437		1,26E-107	2,07E+10	11	11	11	78,1	12,539	31,0052	30,9035	31,1068	6	3	3	0,124727	-0,203266	B8NWS2	B8NWS2	1	AFLA_121090	Uncharacterized protein
24,9074	25,0935	NaN	23,3612	NaN	22,746	+	6,60E-17	2,32E+08	4	4	4	9,8	64,728	24,027	25,0005	23,0536	4	2	2	0,026181	1,94689	B8NWT6	B8NWT6	1	AFLA_121230	L-amino acid oxidase LaoA

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
27,3577	26,6759	26,0462	26,7907	27,4483	27,3189		7,28E-225	5,66E+09	7	7	7	20,6	45,559	26,9396	26,6933	27,186	6	3	3	0,31461	-0,492687	B8NWT9	B8NWT9	1	AFLA_121260	Aspartic-type endopeptidase, putative
26,1533	24,6347	24,691	24,2854	24,4138	24,3869		1,85E-06	2,6E+08	3	3	3	10,2	31,025	24,7609	25,1597	24,362	6	3	3	0,184915	0,79766	B8NWV7	B8NWV7	1	AFLA_121440	Fumarylacetoacetate hydrolase, putative
23,6358	NaN	22,959	NaN	NaN	NaN		5,25E-06	76535000	2	2	2	5,4	51,017	23,2974	23,2974	NaN	2	2	0	1	NaN	B8NX26;B8	B8NX26;B8	2	AFLA_122130	Mannan endo-1,6-alpha-mannosidase DCW1, putative
24,1106	NaN	25,0047	NaN	NaN	NaN		1,99E-09	1,62E+08	3	3	3	4,9	83,122	24,5576	24,5576	NaN	2	2	0	1	NaN	B8NX31	B8NX31	1	AFLA_122180	Uncharacterized protein
24,8067	24,6661	24,4605	24,8057	25,475	25,5106		1,02E-158	9,04E+08	10	10	10	24,7	65,47	24,9541	24,6444	25,2637	6	3	3	0,068659	-0,619323	B8NX52	B8NX52	1	AFLA_122400	Glucoamylase (EC 3.2.1.3) (1,4-alpha-D-glucan glucohydrolase) (Glucan 1,4-alpha-glucosidase)
26,8359	26,2061	NaN	24,2495	23,5217	23,7787	+	1,65E-25	5,04E+08	8	8	8	16,2	63,696	24,9184	26,521	23,8499	5	2	3	0,005131	2,67109	B8NX59	B8NX59	1	AFLA_122470	CobW domain protein
25,5786	25,6045	25,3675	25,5417	25,8452	25,7321		8,32E-38	4,71E+08	4	4	4	39,7	21,287	25,6116	25,5169	25,7064	6	3	3	0,177945	-0,189497	B8NX71	B8NX71	1	AFLA_122590	Translation machinery-associated protein 22
25,8826	24,7669	24,7788	24,8022	25,0366	25,3632		3,16E-18	2,78E+08	4	4	4	38,9	21,849	25,105	25,1428	25,0673	6	3	3	0,861018	0,0754286	B8NX75	B8NX75	1	AFLA_122630	Cytidine deaminase, putative
28,3525	28,5352	28,1793	28,6338	28,4633	28,6343		2,53E-142	3,84E+09	15	15	15	45,4	56,078	28,4664	28,3556	28,5771	6	3	3	0,132406	-0,221495	B8NX84	B8NX84	1	AFLA_122720	Actin binding protein, putative
25,3948	24,7556	24,8642	22,855	23,3669	23,1142	+	2,68E-05	1,55E+08	2	2	2	3,9	65,705	24,0584	25,0049	23,112	6	3	3	0,001551	1,89284	B8NMX2	B8NMX2	1	AFLA_123160	Laccase, putative
26,4784	26,3935	26,148	25,6622	26,1772	25,7443		7,51E-88	1,49E+09	8	8	8	55,5	23,667	26,1006	26,34	25,8612	6	3	3	0,063504	0,478764	B8NMK2	B8NMK2	1	AFLA_124380	Uncharacterized protein
29,3796	28,6452	28,5507	24,08	NaN	24,1284	+	5,88E-146	1,28E+09	9	9	9	24	74,712	26,9568	28,8585	24,1042	5	3	2	0,000783	4,75426	B8NMK6	B8NMK6	1	AFLA_124420	Amine oxidase, putative
24,696	24,2241	24,2347	24,4133	24,8066	24,7768		2,76E-32	4,72E+08	4	4	4	25,8	23,215	24,5252	24,3849	24,6655	6	3	3	0,234147	-0,280616	B8NMM0	B8NMM0	1	AFLA_124560	Uncharacterized protein
NaN	NaN	NaN	NaN	26,0367	25,9783		5,20E-32	4,36E+08	5	5	5	31,5	34,269	26,0075	NaN	26,0075	2	0	2	1	NaN	B8NN48;B8	B8NN48	2	AFLA_124820	Uncharacterized protein
NaN	26,8129	28,3775	26,7566	25,7482	26,7665		0	4,56E+09	8	8	8	52,5	16,407	26,8923	27,5952	26,4238	5	2	3	0,20603	1,17139	B8NNY3	B8NNY3	1	AFLA_125890	40S ribosomal protein S17, putative
NaN	NaN	24,1066	25,0915	25,0173	NaN		2,30E-22	5,94E+08	9	9	9	33,2	32,784	24,7385	24,1066	25,0544	3	1	2	1	-0,947772	B8NMM6	B8NMM6	1	AFLA_126390	Oxidoreductase 2-nitropropane dioxygenase family, putative
26,7842	26,278	25,9903	26,8788	26,9828	26,569		2,36E-90	1,43E+09	8	8	8	38,1	32,663	26,5805	26,3508	26,8102	6	3	3	0,155913	-0,459361	B8NMQ3	B8NMQ3	1	AFLA_126660	Ankyrin repeat protein
26,3356	26,5719	25,8809	26,3214	26,5567	26,5062		1,07E-83	1,31E+09	6	6	6	50,3	19,467	26,3621	26,2628	26,4614	6	3	3	0,407794	-0,198659	B8NMQ4	B8NMQ4	1	AFLA_126670	Uncharacterized protein
25,9268	24,6118	25,314	25,4499	25,8856	25,6587		1,29E-73	8,11E+08	9	9	9	19,9	59,701	25,4745	25,2842	25,6647	6	3	3	0,395541	-0,380517	B8NMQ5	B8NMQ5	1	AFLA_126680	WD repeat-containing protein, putative
26,3042	26,013	25,3187	25,7572	26,3528	25,9932		7,58E-55	1,21E+09	5	5	5	23,5	33,303	25,9565	25,8786	26,0344	6	3	3	0,670323	-0,155807	B8NMQ6	B8NMQ6	1	AFLA_126690	Uncharacterized protein
25,08	24,6787	26,2837	27,4691	25,4898	25,4474		9,55E-36	1,21E+09	6	6	6	48,3	18,988	25,7415	25,3475	26,1354	6	3	3	0,392597	-0,787934	B8NMR6	B8NMR6	1	AFLA_126790	Threonine synthase Thr4, putative
24,856	25,0297	24,4364	24,7395	25,182	24,9772		6,17E-42	7,65E+08	12	12	12	27,6	74,726	24,8701	24,774	24,9662	6	3	3	0,427052	-0,1922	B8NMS3	B8NMS3	1	AFLA_126860	Cell wall cysteine-rich protein
27,8503	27,4645	27,2134	27,4616	27,4417	27,587		6,32E-24	2,21E+09	3	3	3	35,2	11,497	27,5031	27,5094	27,4968	6	3	3	0,950468	0,0126082	B8NMS5	B8NMS5	1	AFLA_126880	Peptidyl-prolyl cis-trans isomerase
23,2276	24	25,3597	24,9002	24,4187	24,8051		2,15E-58	5,39E+08	5	5	5	32,5	21,151	24,4519	24,1957	24,708	6	3	3	0,468585	-0,512241	B8NMV8	B8NMV8	1	AFLA_127210	Pathogenesis associated protein Cap20, putative
28,1488	29,5291	30,38	27,485	26,6826	26,7169	+	2,17E-105	5,04E+09	8	8	8	47,4	15,612	28,1571	29,3526	26,9615	6	3	3	0,026987	2,39116	B8NMV9	B8NMV9	1	AFLA_127220	60S ribosomal protein L27
25,5382	26,5351	26,7725	26,382	26,9207	26,8025		5,63E-19	1,3E+09	5	5	5	14,7	42,33	26,4918	26,2819	26,7017	6	3	3	0,365812	-0,419794	B8NNB5	B8NNB5	1	AFLA_127260	Cop9 signalosome complex subunit, putative
24,5615	23,7928	23,4176	23,09	23,5498	23,7757		0,000101	1,02E+08	2	2	2	3,8	49,076	23,6979	23,924	23,4718	6	3	3	0,31344	0,452188	B8NNC0	B8NNC0	1	AFLA_127310	CAIB/BAIF family enzyme
27,3286	27,3577	27,139	27,4774	27,3321	27,3446		4,96E-60	1,88E+09	5	5	5	35,2	25,024	27,3299	27,2751	27,3847	6	3	3	0,25649	-0,109589	B8NNC1	B8NNC1	1	AFLA_127320	Riboflavin synthase, alpha subunit
27,0701	28,0084	29,2748	29,4736	28,59	27,9896		6,98E-171	4,72E+09	16	16	16	42,4	58,657	28,4011	28,1178	28,6844	6	3	3	0,502924	-0,566637	B8NNC4	B8NNC4	1	AFLA_127350	N-acetylglucosamine-phosphate mutase
27,3016	27,4966	27,6713	27,7185	27,67	27,5652		9,02E-62	3,22E+09	12	12	12	43,5	38,926	27,5705	27,4899	27,6512	6	3	3	0,236403	-0,161386	B8NNC6	B8NNC6	1	AFLA_127370	Histone H4 arginine methyltransferase RmtA
25,013	24,2787	25,2167	24,8601	25,0856	23,9301		1,12E-21	4,06E+08	6	6	6	19,3	51,465	24,7307	24,8361	24,6253	6	3	3	0,666524	0,210866	B8NNC8	B8NNC8	1	AFLA_127390	Proteasome regulatory particle subunit Rpt5, putative
NaN	23,8342	23,2648	NaN	24,1101	24,4549		1,06E-07	1,11E+08	2	2	2	2,3	122,38	23,916	23,5495	24,2825	4	2	2	0,158543	-0,732967	B8NND9	B8NND9	1	AFLA_127500	Cytochrome P450, putative
NaN	NaN	NaN	NaN	27,5362	27,6342		3,18E-09	8,43E+08	3	3	3	14,1	31,401	27,5852	NaN	27,5852	2	0	2	1	NaN	B8NNE2	B8NNE2	1	AFLA_127530	BCAS2 family protein
26,1584	26,2865	26,178	24,0663	24,0835	NaN	+	3,27E-28	3,86E+08	5	5	5	17,8	52,303	25,3545	26,2076	24,0749	5	3	2	3,16E-05	2,13272	B8NNE9	B8NNE9	1	AFLA_127600	40S ribosomal protein S2, putative
25,8202	25,2511	25,2158	26,0074	25,4183	25,4266		5,49E-19	4,84E+08	8	8	8	16,5	69,73	25,5232	25,429	25,6174	6	3	3	0,532857	-0,188407	B8NNF9	B8NNF9	1	AFLA_127700	VHS domain protein
25,3022	25,6068	25,6687	25,2563	25,5582	25,3121		7,82E-30	5,58E+08	5	5	5	14,7	55,437	25,4507	25,5259	25,3755	6	3	3	0,362359	0,150392	B8NNG1	B8NNG1	1	AFLA_127720	CBS domain protein
27,5207	26,6648	NaN	25,9951	26,9492	26,9238		2,41E-28	9,91E+08	4	4	4	14,5	44,199	26,8107	27,0928	26,6227	5	2	3	0,429221	0,470072	B8NNG3	B8NNG3	1	AFLA_127740	Metacaspase CasA
23,8058	24,2053	24,6083	23,8555	24,048	23,9491		1,93E-43	8,3E+08	9	9	9	21,8	61,088	24,0787	24,2065	23,9509	6	3	3	0,343778	0,255599	B8NNG4	B8NNG4	1	AFLA_127750	T-complex protein 1, eta subunit, putative
NaN	23,5398	28,0684	26,6398	NaN	NaN		1,05E-09	4,67E+08	3	3	3	24,5	16,505	26,0826	25,8041	26,6398	3	2	1	1	-0,835684	B8NNG9	B8NNG9	1	AFLA_127800	40S ribosomal protein S26
25,3942	26,41	26,8307	27,063	27,479	26,9438		4,14E-58	1,3E+09	20	20	20	25,5	121,58	26,6868	26,2117	27,1619	6	3	3	0,105662	-0,950281	B8NNH1	B8NNH1	1	AFLA_127820	Importin beta-3 subunit, putative
25,6154	26,0319	27,0888	27,342	26,6427	26,4568		3,56E-59	1,42E+09	11	11	11	23,2	85,381	26,5296	26,2454	26,8138	6	3	3	0,33141	-0,568402	B8NNH3	B8NNH3	1	AFLA_127840	Aconitate hydratase, mitochondrial
27,388	27,3105	26,9047	27,0291	27,168	27,1559		2,70E-89	1,41E+09	9	9	9	31,8	50,501	27,1594	27,2011	27,1176	6	3	3	0,621674	0,0834611	B8NNH4	B8NNH4	1	AFLA_127850	Uncharacterized protein
29,6618	30,5151	31,2796	30,436	29,1597	28,9607		3,90E-184	1,5E+10	5	5	5	27,8	24,904	30,0022	30,4855	29,5188	6	3	3	0,21528	0,966704	B8NNH5	B8NNH5	1	AFLA_127860	60S acidic ribosomal protein P1
24,9916	25,4149	NaN	NaN	NaN	NaN		3,80E-05	3,07E+08	2	2	2	3,5	80,926	25,2033	25,2033	NaN	2	2	0	1	NaN	B8NP31	B8NP31	1	AFLA_128140	Sister chromatid separation protein (Src1), putative
24,6329	26,4098	24,7319	26,6433	26,255	24,4579		1,19E-52	5,25E+08	4	4	4	11,9	51,306	25,5218	25,2582	25,7854	6	3	3	0,583979	-0,527187	B8NP37	B8NP37	1	AFLA_128200	FK506-binding protein (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase)
29,409	30,4251	30,2871	30,3801	30,1657	30,0895		0	1,48E+10	42	42	42	38,9	131,45	30,1261	30,0404	30,2118	6	3	3	0,630902	-0,171335	B8NP45	B8NP45	1	AFLA_128280	M protein repeat protein
23,4849	23,6967	23,535	23,6652	23,5538	23,8951		8,57E-07	1,12E+08	3	3	3	8,8	52,116	23,6385	23,5722	23,7047	6	3	3	0,32818	-0,13251	B8NP48	B8NP48	1	AFLA_128310	Serine/threonine-protein phosphatase 2A activator (EC 5.2.1.8) (Phosphotyrosyl phosphatase activator)
30,4298	29,9867	29,6759	29,9525	30,1796	30,3338		0	1,2E+10	12	12	12	53,7	40,3	30,0931	30,0308	30,1553	6	3	3	0,638296	-0,124505	B8NP67	B8NP67	1	AFLA_128500	5'-methylthioadenosine phosphorylase (Meu1), putative
31,6906	31,3492	31,0607	31,4403	31,595	31,6956		0	2,84E+10	27	27	27	67,1	62,341	31,4719	31,3668	31,577	6	3	3	0,345422	-0,210118	B8NP70	B8NP70	1	AFLA_128530	Delta-1-pyrroline-5-carboxylate dehydrogenase PrnC
25,8355	24,9754	27,0579	25,5824	25,884	25,5872		5,14E-21	5,3E+08	7	7	7	22,8	38,431	25,8204	25,9563	25,6845	6	3	3	0,680145	0,271752	B8NP72	B8NP72	1	AFLA_128550	Proline utilization protein PrnX, putative
24,1013	25,5356	25,9613	26,4828	25,9989	25,8204		4,69E-45	8,79E+08	7	7	7	23,7	50,16	25,65	25,1994	26,1007	6	3	3	0,205268	-0,901311	B8NP77	B8NP77	1	AFLA_128600	2-oxoisovalerate dehydrogenase complex alpha subunit, putative
NaN	24,4573	24,9282	24,4863	25,1596	NaN		4,82E-17	3,98E+08	5	5	5	21,8	35,37	24,7578	24,6928	24,8229	4	2	2	0,781353	-0,130176	B8NP80	B8NP80	1	AFLA_128630	Ubiquinone biosynthesis methlytransferase Coq5, putative
27,7674	27,7094	27,4423	27,5221	27,651	27,7319		3,54E-66	2,13E+09	15	15	15	22,4	114,45	27,6373	27,6397	27,635	6	3	3	0,97006	0,0046832	B8NP92	B8NP92	1	AFLA_128750	Assimilatory sulfite reductase
26,4882	26,3993	26,216	25,7634	25,9386	26,0258	+	6,46E-14	7,27E+08	5	5	5	23	24,979	26,1386	26,3678	25,9093	6	3	3	0,014596	0,458584	B8NP93	B8NP93	1	AFLA_128760	Uncharacterized protein
30,0933	29,6986	29,3477	29,6209	29,6718	29,8066		0	8,64E+09	12	12	12	66,7	28,249	29,7065	29,7132	29,6997	6	3	3	0,954538	0,0134894	B8NP97	B8NP97	1	AFLA_128800	Proteasome subunit alpha type (EC 3.4.25.1)
NaN	24,856	24,7965	24,7645	24,1609	24,8268		2,90E-05	2,89E+08	2	2	2	3,6	100,95	24,681	24,8263	24,5841	5	2	3	0,443334	0,242206	B8NPA0	B8NPA0	1	AFLA_128830	PHD finger domain protein, putative
28,8247	28,9164	29,4037	29,1743	28,9176	28,9905		5,78E-150	4,28E+09	14	14	14	51,3	44,491	29,0378	29,0482	29,0274	6	3	3	0,920277	0,0208022	B8NPA7	B8NPA7	1	AFLA_128900	3'(2'),5'-bisphosphate nucleotidase
25,4596	25,4183	25,6439	25,24	25,5361	25,2769		1,33E-17	3,48E+08	2	2	2	19,7	16,916	25,4291	25,5073	25,351	6	3	3	0,249557	0,156301	B8NPB6	B8NPB6	1	AFLA_128990	Ubiquitin conjugating enzyme Ubc8, putative
25,4348	24,911	24,8142	24,5094	NaN	NaN		4,76E-13	3,05E+08	4	4	4	15,5	60,648	24,9173	25,0533	24,5094	4	3	1	1	0,543979	B8NNK3	B8NNK3	1	AFLA_129040	Metallopeptidase family M24, putative
29,1939	29,4061	29,4413	29,3159	29,2842	29,4009		7,15E-138	6,06E+09	15	15	15	28,8	75,166	29,3404	29,3471	29,3337	6	3	3	0,881973	0,0134099	B8NNN2	B8NNN2	1	AFLA_129330	Uncharacterized protein
25,7943	25,9649	25,8013	25,6526	25,4928	25,8735		9,18E-17	6,08E+08	4	4	4	17,9	31,527	25,7632	25,8535	25,673	6	3	3	0,218	0,180533	B8NNN4	B8NNN4	1	AFLA_129350	Uncharacterized protein
30,8772	30,3271	29,9978	30,1283	30,1989	30,3849		0	1,33E+10	16	16	16	38,8	58,683	30,3191	30,4007	30,2374	6	3	3	0,574774	0,163317	B8NNP3	B8NNP3	1	AFLA_129440	1,3-beta-glucanosyltransferase (EC 2.4.1.-)
25,778	25,1983	27,4832	26,9596	26,3179	26,5276		1,89E-35	1,18E+09	11	11	11	51	36,986	26,3774	26,1532	26,6017	6	3	3	0,562535	-0,448528	B8NNR3	B8NNR3	1	AFLA_129640	Deoxyhypusine hydroxylase (DOHH) (EC 1.14.99.29) (Deoxyhypusine dioxygenase) (Deoxyhypusine monooxygenase)
25,1757	NaN	24,8866	24,9966	NaN	NaN		9,87E-39	2,56E+08	4	4	4	8,1	89,01	25,0196	25,0311	24,9966	3	2	1	1	0,0345688	B8NNR8	B8NNR8	1	AFLA_129690	Cell division control protein (Cdc5), putative
24,0944	23,5603	NaN	23,9964	23,7642	24,0706		8,79E-06	1,58E+08	4	4	4	15,6	37,519	23,8973	23,8274	23,9437	5	2	3	0,65053	-0,116333	B8NNS2	B8NNS2	1	AFLA_129730	mRNA decapping hydrolase, putative
28,1826	28,015	27,808	28,1509	28,1354	28,3162		1,13E-62	3,23E+09	11	11	11	48,8	27,327	28,1014	28,0019	28,2008	6	3	3	0,180584	-0,198941	B8NNS3	B8NNS3	1	AFLA_129740	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)
26,3467	26,1694	25,7215	25,1646	25,5647	25,0919	+	3,05E-25	5,47E+08	6	6	6	6,3	129,33	25,6765	26,0792	25,2737	6	3	3	0,027344	0,805493	B8NNS5	B8NNS5	1	AFLA_129760	RNA binding protein Jsn1, putative
28,8481	28,6364	28,6923	28,6452	28,7142	28,7381		4,82E-175	4,65E+09	16	16	16	34,3	69,117	28,7124	28,7256	28,6992	6	3	3	0,722172	0,0264047	B8NNT0	B8NNT0	1	AFLA_129810	Cytoplasmic asparaginyl-tRNA synthetase, putative
25,2307	24,8948	24,6655	24,2355	24,5258	24,4539	+	6,25E-20	3,16E+08	5	5	5	9,3	88,502	24,6677	24,9304	24,405	6	3	3	0,047542	0,525314	B8NNT1	B8NNT1	1	AFLA_129820	Differentiation regulator (Nrd1), putative
27,3062	27,2211	26,9567	27,1164	27,2307	27,3629		4,75E-87	1,7E+09	5	5	5	36,1	25,396	27,199	27,1613	27,2367	6	3	3	0,58504	-0,0753536	B8NNT5	B8NNT5	1	AFLA_129860	Uncharacterized protein
27,116	26,8253	26,5985	26,861	26,7046	26,8818		5,71E-45	1,25E+09	13	13	13	25,7	83,22	26,8312	26,8466	26,8158	6	3	3	0,85669	0,0307865	B8NPC5	B8NPC5	1	AFLA_129970	IdgA domain protein
26,3817	26,2692	25,9051	26,2218	26,6034	26,2925		3,29E-34	8,62E+08	5	5	5	41,9	21,753	26,2789	26,1853	26,3726	6	3	3	0,369983	-0,187246	B8NPC7	B8NPC7	1	AFLA_129990	Riboflavin kinase, putative
32,1582	31,9084	31,6759	32,0916	32,037	32,1397		0	4,12E+10	27	27	27	65,9	54,147	32,0018	31,9142	32,0895	6	3	3	0,285724	-0,175284	B8NPD5	B8NPD5	1	AFLA_130070	Hexokinase (EC 2.7.1.1)
26,5581	26,5408	26,6218	25,8284	25,8569	25,6881	+	6,86E-64	7,8E+08	2	2	2	28,6	13,678	26,1824	26,5736	25,7911	6	3	3	0,000171	0,782435	B8NPD8	B8NPD8	1	AFLA_130100	SnRNP and snoRNP protein (Snu13), putative
26,3225	25,6232	25,1327	24,899	25,5212	26,1757		9,48E-12	5,29E+08	3	3	3	37,2	13,168	25,6124	25,6928	25,532	6	3	3	0,766046	0,160839	B8NPD9	B8NPD9	1	AFLA_130110	Uncharacterized protein
NaN	25,4083	26,2006	26,205	26,4801	25,9173		6,50E-55	1,1E+09	12	12	12	20,5	90,96	26,0423	25,8044	26,2008	5	2	3	0,353813	-0,396372	B8NPE3	B8NPE3	1	AFLA_130150	NAD+ dependent glutamate dehydrogenase, putative
27,4849	26,9548	26,7918	26,3337	26,4398	26,5828	+	2,97E-77	1,19E+09	8	8	8	33,9	48,828	26,7646	27,0772	26,4521	6	3	3	0,04761	0,625093	B8NPF1	B8NPF1	1	AFLA_130230	Heterogeneous nuclear ribonucleoprotein HRP1

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
26,91	26,7023	26,4182	26,6909	26,9519	27,0071		1,14E-45	1,41E+09	9	9	9	26,7	53,615	26,7801	26,6768	26,8833	6	3	3	0,29791	-0,206489	B8NPF4	B8NPF4	1	AFLA_130260	Chromatin remodeling and histone acetyltransferase complexes subunit
32,2872	31,9449	31,471	31,6405	31,7157	31,8341		0	4,99E+10	28	28	28	62,5	56,397	31,8156	31,901	31,7301	6	3	3	0,520937	0,170941	B8NPF9	B8NPF9	1	AFLA_130310	Protein disulfide-isomerase (EC 5.3.4.1)
25,7783	26,2814	26,4021	26,1147	26,6583	26,55		9,95E-33	9,01E+08	5	5	5	26,3	26,124	26,2975	26,1539	26,441	6	3	3	0,320158	-0,287039	B8NPG7	B8NPG7	1	AFLA_130390	Glutamine amidotransferase:cyclase
26,57	26,1909	25,6824	25,6469	25,6844	26,0824		9,95E-11	6,7E+08	3	3	3	9,9	42,125	25,9762	26,1478	25,8046	6	3	3	0,305696	0,343192	B8NPH6	B8NPH6	1	AFLA_130480	Replication protein A 70 kDa DNA-binding subunit
25,3501	25,151	NaN	24,7553	25,5957	25,3815		1,50E-50	1,08E+09	10	10	10	25,1	73,215	25,2467	25,2505	25,2441	5	2	3	0,98589	0,0064084	B8NPH7	B8NPH7	1	AFLA_130490	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)
26,2923	26,5714	26,5652	24,6066	24,8468	NaN	+	6,27E-88	5,95E+08	7	7	7	45,3	27,389	25,7765	26,4763	24,7267	5	3	2	0,001321	1,74962	B8NFL4	B8NFL4	1	AFLA_131050	Uncharacterized protein
NaN	22,9375	22,624	NaN	22,277	NaN		0,00013	88960000	2	2	2	5,5	47,754	22,6128	22,7807	22,277	3	2	1	1	0,503738	B8NFL5	B8NFL5	1	AFLA_131060	14-alpha sterol demethylase Cyp51B
28,0342	27,7724	27,25	27,6905	27,7309	27,8604		1,53E-139	2,15E+09	17	17	17	14,4	160,35	27,723	27,6855	27,7606	6	3	3	0,766631	-0,0750167	B8NFM7	B8NFM7	1	AFLA_131280	Actin cortical patch assembly protein Pan1, putative
28,8124	29,3844	29,5525	29,2977	29,0265	28,9572		0	6,79E+09	10	10	10	33,7	50,769	29,1718	29,2498	29,0938	6	3	3	0,561959	0,155959	B8NFY0	B8NFY0	1	AFLA_131410	Eukaryotic translation initiation factor 3 subunit M (eIF3m)
29,3405	29,1631	28,9811	29,2834	29,2017	29,3053		8,26E-124	5,43E+09	9	9	9	48,4	23,642	29,2125	29,1616	29,2635	6	3	3	0,400661	-0,101883	B8NFY1	B8NFY1	1	AFLA_131420	Uridylate kinase (UK) (EC 2.7.4.14) (ATP:UMP phosphotransferase) (Deoxycytidylate kinase) (Uridine monophosphate kinase)
30,9681	30,85	30,5577	30,4349	30,602	30,669		0	1,66E+10	25	25	25	56,4	64,887	30,6803	30,7919	30,5686	6	3	3	0,18697	0,223321	B8NFY6	B8NFY6	1	AFLA_131470	Eukaryotic translation initiation factor 3 subunit D (eIF3d)
27,8282	28,3502	28,2592	28,4897	28,0893	28,2083		2,81E-140	2,85E+09	18	18	18	40,2	72,33	28,2041	28,1459	28,2624	6	3	3	0,591394	-0,11655	B8NG06	B8NG06	1	AFLA_131670	Oxidoreductase, putative
23,9386	24,1878	23,6001	23,546	23,247	23,1442	+	1,16E-10	3,28E+08	3	3	3	11,2	47,213	23,6106	23,9089	23,3124	6	3	3	0,045989	0,59643	B8NG30	B8NG30	1	AFLA_131910	Uncharacterized protein
26,6988	26,3677	26,235	26,5657	26,4013	26,5715		3,85E-30	9,76E+08	9	9	9	54,3	28,929	26,4734	26,4339	26,5128	6	3	3	0,623593	-0,0789789	B8NG46	B8NG46	1	AFLA_132070	Uncharacterized protein
27,0341	27,1637	26,5167	24,9593	26,1149	25,0284	+	5,42E-31	8,97E+08	9	9	9	58,6	28,548	26,1362	26,9048	25,3676	6	3	3	0,022109	1,53727	B8NG47	B8NG47	1	AFLA_132080	Small nuclear ribonucleoprotein U2, A
26,9707	26,8937	26,6267	27,0774	27,0002	26,9743		2,49E-66	1,54E+09	9	9	9	42	37,926	26,9239	26,8304	27,0173	6	3	3	0,160602	-0,186975	B8NG53	B8NG53	1	AFLA_132140	Pantoate--beta-alanine ligase
27,0615	26,4929	26,6246	26,3595	26,84	26,9184		2,63E-50	9,06E+08	13	11	11	34,9	54,821	26,7162	26,7263	26,706	6	3	3	0,937835	0,0203412	B8NG57	B8NG57	1	AFLA_132180	Aldehyde dehydrogenase ALDH
26,4452	26,3823	25,7371	25,7499	25,8343	26,0267		1,01E-18	7,28E+08	4	4	4	15,5	36,36	26,0293	26,1882	25,8703	6	3	3	0,257015	0,317889	B8NG67	B8NG67	1	AFLA_132280	Thiamin pyrophosphokinase-related protein
28,6185	28,2905	28,1627	28,5262	28,4839	28,4904		1,57E-68	3,61E+09	7	7	7	62,7	16,274	28,4287	28,3572	28,5002	6	3	3	0,353624	-0,142951	B8NH12	B8NH12	1	AFLA_132360	Glial factor naturation factor, putative
27,9567	27,7653	27,6342	27,9201	28,0002	27,9735		5,68E-140	2,19E+09	9	9	9	55,7	36,758	27,875	27,7854	27,9646	6	3	3	0,136994	-0,179225	B8NH13	B8NH13	1	AFLA_132370	Molybdopterin binding domain protein
29,2511	29,1733	29,2094	29,5111	29,2293	29,3786		9,65E-188	6,24E+09	11	11	10	35	33,833	29,2921	29,2113	29,373	6	3	3	0,127988	-0,161762	B8NH15	B8NH15	1	AFLA_132390	Oxidoreductase, short chain dehydrogenase/reductase family
31,3042	30,9727	30,7508	30,7831	30,6371	30,7958		0	2,07E+10	6	6	6	65,5	12,024	30,8739	31,0092	30,7387	6	3	3	0,183889	0,270582	B8NH30	B8NH30	1	AFLA_132540	Thioredoxin
29,9241	29,5076	29,4449	30,3042	30,1561	30,1796	+	3,65E-201	1,1E+10	10	10	10	64	22,19	29,9194	29,6255	30,2133	6	3	3	0,020155	-0,587762	B8NH38	B8NH38	1	AFLA_132620	Rho-gdp dissociation inhibitor
NaN	24,9371	25,3131	25,9565	25,2117	25,0619		3,28E-13	3,77E+08	5	5	5	15,7	52,026	25,2961	25,1251	25,41	5	2	3	0,511448	-0,284988	B8NH39	B8NH39	1	AFLA_132630	APSES transcription factor, putative
26,1106	25,8688	25,5877	25,3405	25,7635	25,6784		4,16E-27	5,58E+08	4	4	4	11,3	58,551	25,7249	25,8557	25,5942	6	3	3	0,258672	0,261517	B8NH40	B8NH40	1	AFLA_132640	mRNA cleavage and polyadenylation factor CLP1
28,2907	28,0612	27,9553	28,052	28,1371	28,2666		1,14E-70	2,52E+09	11	11	11	49,4	35,675	28,1271	28,1024	28,1519	6	3	3	0,69423	-0,0494703	B8NH43	B8NH43	1	AFLA_132670	Quinone oxidoreductase, putative
25,1929	25,0399	NaN	24,3449	25,3307	25,6756		0,000131	4,61E+08	2	2	2	2,9	94,875	25,1168	25,1164	25,1171	5	2	3	0,999068	-0,0006568	B8NH48	B8NH48	1	AFLA_132720	MYB DNA binding protein (Tbf1), putative
28,1427	27,0036	25,9984	23,9081	25,0428	25,2307	+	9,31E-35	5,54E+08	9	9	9	25,1	58,984	25,8877	27,0482	24,7272	6	3	3	0,035616	2,32103	B8NH51	B8NH51	1	AFLA_132750	Uncharacterized protein
27,3932	27,774	27,5665	25,4835	25,2721	24,8319	+	1,14E-47	1,29E+09	14	14	14	41,6	46,429	26,3869	27,5779	25,1958	6	3	3	0,000422	2,3821	B8NH55	B8NH55	1	AFLA_132790	37S ribosomal protein S5
26,0453	25,8844	NaN	NaN	24,9609	NaN		9,23E-17	3,34E+08	5	5	5	14,3	58,708	25,6302	25,9648	24,9609	3	2	1	1	1,00391	B8NH56	B8NH56	1	AFLA_132800	tRNA(M5U54)methyltransferase
27,6497	28,5263	28,9082	28,9663	28,8762	28,8535		9,88E-287	5,44E+09	17	17	17	61,4	47,205	28,63	28,3614	28,8986	6	3	3	0,224352	-0,537233	B8NH60	B8NH60	1	AFLA_132840	Arp2/3 complex subunit (Arp3), putative
26,6013	26,7349	26,6602	26,7505	26,2551	26,2482		5,83E-57	1,2E+09	12	12	12	22,1	94,631	26,5417	26,6655	26,4179	6	3	3	0,220664	0,247553	B8NH66	B8NH66	1	AFLA_132900	Protein methyltransferase RmtC
24,6072	24,9451	25,0787	NaN	NaN	NaN		1,38E-12	1,94E+08	5	5	5	8	87,029	24,877	24,877	NaN	3	3	0	1	NaN	B8NH67	B8NH67	1	AFLA_132910	Pre-mRNA splicing factor RNA helicase (Prp43), putative
25,5321	25,1216	NaN	25,1515	25,0012	25,151		1,44E-16	4,62E+08	2	2	2	15,8	23,454	25,1915	25,3268	25,1012	5	2	3	0,267465	0,225609	B8NH69	B8NH69	1	AFLA_132930	Secretory pathway protein Ssp120, putative
24,7696	24,5169	24,2895	24,0439	24,402	24,4852		6,12E-12	2,26E+08	8	8	8	4,8	233,83	24,4178	24,5253	24,3104	6	3	3	0,329556	0,214954	B8NH76	B8NH76	1	AFLA_133000	Pre-mRNA splicing factor (Prp8), putative
NaN	24,2667	25,7913	27,4071	23,9408	NaN		4,88E-58	9,47E+08	2	2	2	17	20,117	25,3515	25,029	25,674	4	2	2	0,765826	-0,644972	B8NH79	B8NH79	1	AFLA_133030	Cytochrome c subunit Vb, putative
26,7819	25,6843	NaN	25,5733	25,7734	25,8647		2,60E-26	5,89E+08	6	5	5	15,3	34,294	25,9355	26,2331	25,7371	5	2	3	0,326469	0,495972	B8NH86	B8NH86	1	AFLA_133100	Aldehyde reductase, putative
30,1087	30,0109	29,7583	29,7294	29,7648	29,8821		0	1E+10	15	15	15	63	38,309	29,8757	29,9593	29,7921	6	3	3	0,216753	0,167217	B8NFQ0	B8NFQ0	1	AFLA_133290	KH domain RNA-binding protein
29,1548	29,3356	29,9761	30,3734	29,5958	29,2777		0	8,71E+09	24	24	24	51,7	62,104	29,6189	29,4888	29,749	6	3	3	0,560106	-0,260139	B8NFS0	B8NFS0	1	AFLA_133490	Aspartyl-tRNA synthetase Dps1, putative
27,5417	27,2415	27,2956	27,2745	27,3802	27,4841		1,08E-52	1,47E+09	10	10	10	39,1	44,755	27,3696	27,3596	27,3796	6	3	3	0,864961	-0,0200195	B8NFS1	B8NFS1	1	AFLA_133500	HAD superfamily hydrolase, putative
28,1703	27,5884	27,0132	26,6786	27,5203	27,6608		4,22E-55	1,44E+09	12	12	12	19,6	100,68	27,4386	27,5906	27,2866	6	3	3	0,539282	0,304037	B8NFS3	B8NFS3	1	AFLA_133520	Coatomer subunit gamma
NaN	24,4487	24,2162	24,399	NaN	24,3588		8,50E-11	2,44E+08	4	4	4	22,9	28,045	24,3557	24,3324	24,3789	4	2	2	0,731761	-0,0464706	B8NFS4	B8NFS4	1	AFLA_133530	Phosducin family protein
26,9728	27,0179	26,873	26,4349	26,8342	26,7085		1,62E-27	1,1E+09	8	8	8	22,6	45,817	26,8069	26,9546	26,6592	6	3	3	0,078079	0,295363	B8NFS9	B8NFS9	1	AFLA_133580	Casein kinase I, putative
24,4651	23,9504	24,3412	24,1019	24,1273	NaN		7,39E-08	1,1E+08	5	5	5	5	164,13	24,1972	24,2522	24,1146	5	3	2	0,541646	0,137645	B8NFT0	B8NFT0	1	AFLA_133590	Cell polarity protein (Tea1), putative
24,1197	24,6168	25,6305	24,4754	NaN	23,9989		5,06E-24	4,54E+08	6	6	6	24,6	38,508	24,5683	24,789	24,2372	5	3	2	0,426045	0,551836	B8NFV4	B8NFV4	1	AFLA_133830	Alcohol dehydrogenase, putative
25,0124	25,3641	25,6145	26,3288	26,0849	25,479		2,05E-14	4,91E+08	5	5	5	16,9	59,92	25,6473	25,3303	25,9642	6	3	3	0,107933	-0,633928	B8NFV7	B8NFV7	1	AFLA_133860	Uncharacterized protein
32,7143	32,4942	32,3446	32,6607	32,6887	32,7963		0	6,06E+10	10	10	10	78,3	15,607	32,6165	32,5177	32,7152	6	3	3	0,161058	-0,197538	B8NFW3	B8NFW3	1	AFLA_133920	Acyl CoA binding protein family
27,4241	27,745	29,3345	28,9615	29,3863	28,622		0	4,01E+09	10	10	10	64,8	17,23	28,5789	28,1678	28,9899	6	3	3	0,262351	-0,8221	B8NFW5	B8NFW5	1	AFLA_133940	Uncharacterized protein
26,2259	25,6614	25,8242	25,7938	26,3856	26,3131		5,28E-34	5,5E+08	4	4	4	21,1	30,397	26,034	25,9038	26,1642	6	3	3	0,357818	-0,26033	B8NFW6	B8NFW6	1	AFLA_133950	Triosephosphate isomerase
31,9121	31,9773	31,8157	32,1808	32,1571	32,2236	+	0	4,46E+10	31	31	31	79	52,207	32,0444	31,9017	32,1872	6	3	3	0,004934	-0,285517	B8NFX0	B8NFX0	1	AFLA_133990	Secretory pathway gdp dissociation inhibitor
26,3534	27,036	27,471	27,3535	27,3375	26,9504		1,26E-57	1,72E+09	15	15	15	27,4	83,676	27,0886	26,9535	27,2138	6	3	3	0,499421	-0,260321	B8NG70	B8NG70	1	AFLA_134090	3-isopropylmalate dehydratase (EC 4.2.1.33) (Alpha-IPM isomerase) (Isopropylmalate isomerase)
29,8171	29,3303	28,9638	29,3975	29,553	29,5542		4,02E-282	7,7E+09	14	14	14	57,4	26,541	29,436	29,3704	29,5016	6	3	3	0,630852	-0,131209	B8NG73	B8NG73	1	AFLA_134120	Orotate phosphoribosyltransferase
28,4488	28,5726	27,9508	28,1636	28,7944	28,8175		4,35E-111	3,4E+09	15	15	15	34,6	69,076	28,4579	28,3241	28,5918	6	3	3	0,402738	-0,267741	B8NG74	B8NG74	1	AFLA_134130	Methylenetetrahydrofolate reductase (EC 1.5.1.20)
26,4722	26,4242	24,4344	NaN	NaN	NaN		2,98E-12	5,04E+08	3	3	3	17,6	22,928	25,7769	25,7769	NaN	3	3	0	1	NaN	B8NG77	B8NG77	1	AFLA_134160	V-type ATPase F subunit, putative
30,6656	30,3509	29,9352	30,1881	30,2473	30,3814		0	1,31E+10	14	14	14	72	26,998	30,2948	30,3172	30,2723	6	3	3	0,847449	0,0449562	B8NG89	B8NG89	1	AFLA_134290	Proteasome subunit alpha type (EC 3.4.25.1)
NaN	26,149	27,157	27,5769	26,1871	25,5462		3,98E-117	9,58E+08	8	8	8	35,4	33,553	26,5232	26,653	26,4367	5	2	3	0,817718	0,216268	B8NG94	B8NG94	1	AFLA_134340	BAR domain protein
27,3432	27,1729	27,2306	27,5455	27,5172	27,6079	+	1,07E-43	1,91E+09	14	14	14	52,2	43,447	27,4029	27,2489	27,5569	6	3	3	0,005587	-0,307952	B8NGA5	B8NGA5	1	AFLA_134450	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)
26,2265	26,0391	25,7822	26,264	26,8178	26,8664		5,72E-26	9,45E+08	9	9	9	67,6	25,538	26,3327	26,016	26,6494	6	3	3	0,052548	-0,633443	B8NGB5	B8NGB5	1	AFLA_134550	HD family hydrolase, putative
25,5471	25,0015	24,5487	24,3297	24,8152	25,2732		5,34E-11	2,7E+08	5	5	5	6,6	104,9	24,9193	25,0325	24,8061	6	3	3	0,598868	0,2264	B8NGC3	B8NGC3	1	AFLA_134630	Signal transduction protein BroA, putative
25,9017	26,5572	26,8207	25,9754	25,5553	26,0332		2,71E-197	6,86E+08	4	4	4	24,7	19,411	26,1406	26,4265	25,8546	6	3	3	0,14072	0,571868	B8NGD0	B8NGD0	1	AFLA_134700	Small nuclear ribonucleoprotein (LSM1), putative
27,879	27,8004	30,6177	28,3519	27,6727	27,6765		0	3,05E+09	20	20	20	43,6	44,346	28,333	28,7657	27,9004	6	3	3	0,415416	0,865323	B8NGD4	B8NGD4	1	AFLA_134740	60S ribosomal protein L3
30,6569	30,7753	30,6653	30,8866	30,72	30,7106		0	1,85E+10	30	30	30	61,6	54,349	30,7358	30,6992	30,7724	6	3	3	0,346756	-0,0732085	B8NGE1	B8NGE1	1	AFLA_134810	Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)
25,8096	25,5235	25,3227	24,1945	24,9445	24,1804	+	1,12E-19	3,75E+08	3	3	3	31,4	13,537	24,9959	25,5519	24,4398	6	3	3	0,018382	1,11212	B8NGE7	B8NGE7	1	AFLA_134870	U6 snRNA-associated Sm-like protein LSM4, putative
25,7827	25,5641	25,4524	25,2622	25,3866	25,4842		3,25E-07	4,49E+08	4	4	4	13,7	58,589	25,4887	25,5997	25,3777	6	3	3	0,128932	0,222057	B8NGE8	B8NGE8	1	AFLA_134880	Histone acetyltransferase type b catalytic subunit, putative
28,3068	28,315	28,0776	28,155	28,2352	28,3823		1,23E-89	3,25E+09	5	5	5	63,4	12,036	28,2453	28,2331	28,2575	6	3	3	0,823476	-0,0243785	B8NH98	B8NH98	1	AFLA_135030	Mitochondrial intermembrane space translocase subunit Tim13, putative
26,6303	26,5828	26,4648	26,7107	26,8107	26,4764		2,22E-22	1,2E+09	8	8	8	22,9	44,083	26,6126	26,5593	26,6659	6	3	3	0,389677	-0,106614	B8NH99	B8NH99	1	AFLA_135040	cAMP-dependent protein kinase catalytic subunit PkaC1
30,0162	29,6453	29,2313	29,6658	29,8066	29,8637		0	8,73E+09	32	32	32	62,2	72,633	29,7048	29,6309	29,7787	6	3	3	0,562336	-0,147778	B8NHB9	B8NHB9	1	AFLA_135240	Carnitine acetyl transferase
26,883	26,7446	25,7436	26,0088	26,261	26,1041		5,76E-22	8,08E+08	7	7	7	19,5	44,23	26,2908	26,4571	26,1246	6	3	3	0,415595	0,332418	B8NHC9	B8NHC9	1	AFLA_135340	Acetylornithine aminotransferase
NaN	23,9591	24,1571	24,8638	23,8149	23,5942		3,59E-08	2,14E+08	3	3	3	20,8	27,961	24,0778	24,0581	24,091	5	2	3	0,952722	-0,032891	B8NHD1	B8NHD1	1	AFLA_135360	Hydroxymethylglutaryl-CoA lyase
24,5621	23,5852	NaN	26,0592	27,4958	27,7217	+	2,94E-76	4,9E+08	9	9	9	37,4	42,347	25,8848	24,0737	27,0922	5	2	3	0,028963	-3,01856	B8NHE1	B8NHE1	1	AFLA_135460	Uncharacterized protein
27,3694	28,0192	28,1197	27,2947	28,0613	27,945		1,97E-119	2,75E+09	20	20	20	28,8	117,83	27,8016	27,8361	27,767	6	3	3	0,846646	0,0690893	B8NHE8	B8NHE8	1	AFLA_135530	Uncharacterized protein
27,9182	28,7468	28,8329	28,9137	28,9438	28,997		3,24E-88	4,95E+09	10	10	10	47,3	24,181	28,7254	28,4993	28,9515	6	3	3	0,197191	-0,452164	B8NHE9	B8NHE9	1	AFLA_135540	ATP synthase oligomycin sensitivity conferral protein, putative
23,9881	23,7918	24,5579	24,1158	23,8397	23,9647		7,18E-14	3,76E+08	4	4	4	8,2	44,239	24,043	24,1126	23,9734	6	3	3	0,597806	0,139169	B8NHG2	B8NHG2	1	AFLA_135670	Translocation protein Sec62, putative
25,5218	24,4671	24,3033	24,0465	24,3728	24,2799		4,78E-08	2,69E+08	4	4	4	6,9	59,379	24,4985	24,764	24,2331	6	3	3	0,248991	0,530979	B8NHG6	B8NHG6	1	AFLA_135710	NADPH:adrenodoxin oxidoreductase, mitochondrial (EC 1.18.1.6)
25,4648	25,9907	26,0137	25,4504	25,8753	25,5782		3,78E-48	1,09E+09	10	10	10	49,7	33,105	25,7289	25,8231	25,6346	6	3	3	0,438163	0,188421	B8NHH4	B8NHH4	1	AFLA_135790	Vesicular-fusion protein sec17
NaN	26,0676	26,0108	26,0158	24,8104	24,6846		3,04E-18	5,05E+08	5	5	5	14,7	67,705	25,5178	26,0392	25,1703	5	2	3	0,211109	0,868954	B8NHH5	B8NHH5	1	AFLA_135800	Pre-rRNA processing protein Tsr1, putative
28,0289	28,5186	28,4885	28,9339	28,7568	28,72		1,85E-82	4,35E+09	12	12	12	59,4	29,275	28,5745	28,3453	28,8036	6	3	3	0,055828	-0,458256	B8NHH7	B8NHH7	1	AFLA_135820	Urease accessory protein UreG, putative
28,6419	28,3121	27,6462	27,7388	28,5065	28,474		3,01E-286	3,96E+09	18	18	18	24,7	135,79	28,2199	28,2001	28,2398	6	3	3	0,922887	-0,0397193	B8NGG2	B8NGG2	1	AFLA_135890	Protein transport protein (SEC31), putative

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

A. Total data

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	t-test Difference	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
25,6284	26,3329	25,7872	24,6025	24,3853	24,2224	+	3,09E-08	5,13E+08	3	3	3	29,3	10,958	25,1598	25,9162	24,4034	6	3	3	0,003242	1,51276	B8NGG5	B8NGG5	1	AFLA_135920	Cytochrome c oxidase polypeptide vib
24,4638	24,2991	24,207	25,4169	25,3645	24,7353	+	1,91E-10	2,77E+08	3	3	3	24,5	17,865	24,7478	24,3233	25,1722	6	3	3	0,021448	-0,848916	B8NGG8	B8NGG8	1	AFLA_135950	Nudix/MutT family protein
25,084	25,4094	25,6609	25,8333	25,8358	25,8418		2,33E-28	4,43E+08	4	4	4	19,4	32,89	25,6109	25,3848	25,837	6	3	3	0,053686	-0,452181	B8NGH4	B8NGH4	1	AFLA_136010	Pyrimidine 5'-nucleotidase, putative
25,2236	25,1242	24,953	25,05	24,8133	24,6892		5,54E-21	2,77E+08	4	4	4	11,2	49,272	24,9755	25,1003	24,8508	6	3	3	0,132019	0,249445	B8NGI3	B8NGI3	1	AFLA_136100	GATA transcription factor (AreB), putative
25,0513	24,1358	24,5419	24,1539	24,4618	24,6004		3,80E-13	2,2E+08	3	3	3	6,4	57,774	24,4909	24,5763	24,4054	6	3	3	0,594412	0,170946	B8NGK6	B8NGK6	1	AFLA_136330	Exoenzymes regulatory protein aepA, putative
23,1724	23,8179	24,5234	24,7694	23,9748	23,7419		3,67E-20	1,87E+08	5	5	5	13	52,197	24	23,8379	24,162	6	3	3	0,55132	-0,324149	B8NGK7	B8NGK7	1	AFLA_136340	Aminotransferase family protein (LolT), putative
26,689	26,7512	26,3499	26,8023	26,6688	26,7054		3,63E-27	1,13E+09	9	9	9	6,5	160,85	26,6611	26,5967	26,7255	6	3	3	0,380805	-0,128805	B8NGK9	B8NGK9	1	AFLA_136360	GYF domain protein
29,3131	29,3292	29,5011	29,4774	29,6353	29,6011		0	7,8E+09	24	24	21	51	77,75	29,4762	29,3811	29,5713	6	3	3	0,068825	-0,190144	B8NGL5;B8	B8NGL5	2	AFLA_136420	Bifunctional tryptophan synthase TRPB
25,1109	26,6838	27,1063	26,2864	26,7392	26,1462		1,12E-84	1,79E+09	14	14	14	41,9	56,675	26,3455	26,3003	26,3906	6	3	3	0,89345	-0,0902964	B8NGL6	B8NGL6	1	AFLA_136430	V-type ATPase, B subunit, putative
24,2724	23,9539	23,894	NaN	NaN	24,2325		0,000195	1,74E+08	2	2	2	8	37,374	24,0882	24,0401	24,2325	4	3	1	1	-0,192373	B8NGM2	B8NGM2	1	AFLA_136490	NAD dependent epimerase/dehydratase, putative
29,8981	29,7663	29,0698	29,6098	29,6609	29,689		3,71E-57	8,67E+09	8	8	8	47,3	12,139	29,6156	29,5781	29,6532	6	3	3	0,785309	-0,0751502	B8NGN0	B8NGN0	1	AFLA_136570	Cytochrome c
NaN	NaN	NaN	25,3139	26,244	NaN		8,48E-12	4,81E+08	5	5	5	14,1	58,327	25,7789	NaN	25,7789	2	0	2	1	NaN	B8NGN2	B8NGN2	1	AFLA_136590	Phenylalanyl-tRNA synthetase alpha subunit (PodG), putative
26,9191	27,8969	28,4759	28,881	28,4281	28,2088		3,62E-164	2,68E+09	11	11	11	44,9	28,09	28,135	27,764	28,5059	6	3	3	0,208664	-0,741966	B8NGN3	B8NGN3	1	AFLA_136600	GrpE protein homolog
34,6175	34,5527	34,5236	34,727	34,552	34,5872		0	2,7E+11	59	59	58	68,2	94,226	34,5933	34,5646	34,622	6	3	3	0,394287	-0,057443	B8NGN7	B8NGN7	1	AFLA_136640	Translation elongation factor EF-2 subunit, putative
29,4524	29,6669	29,86	29,4907	29,4165	29,0557		3,93E-245	7,4E+09	15	15	15	70,4	34,384	29,4904	29,6598	29,321	6	3	3	0,130675	0,338819	B8NGP4	B8NGP4	1	AFLA_136710	Uncharacterized protein
NaN	NaN	NaN	NaN	24,2863	23,8987		5,20E-14	1,91E+08	6	6	6	17,3	58,227	24,0925	NaN	24,0925	2	0	2	1	NaN	B8NHI5	B8NHI5	1	AFLA_136790	Thiamine pyrophosphate enzyme, putative
28,7642	28,9348	28,6839	28,1415	28,3232	28,2072	+	2,49E-175	3,96E+09	14	14	14	52,7	58,402	28,5091	28,7943	28,224	6	3	3	0,003319	0,570358	B8NHI9	B8NHI9	1	AFLA_136830	Aromatic aminotransferase Aro8, putative
24,6472	24,1572	23,7888	NaN	24,4426	24,5254		5,58E-06	1,37E+08	2	2	2	16,6	18,162	24,3122	24,1977	24,484	5	3	2	0,44006	-0,286274	B8NHK6	B8NHK6	1	AFLA_137000	Ubiquitin conjugating enzyme, putative
26,7208	25,723	26,1737	26,2577	25,8604	26,7016		4,44E-50	9,47E+08	7	7	7	22,2	32,652	26,2395	26,2058	26,2732	6	3	3	0,866907	-0,0673726	B8NHP7	B8NHP7	1	AFLA_137410	SAP domain protein, putative
26,9461	27,0686	25,4553	27,9557	28,2755	27,7531	+	1,85E-83	1,12E+09	6	6	6	70,1	18,158	27,2424	26,49	27,9948	6	3	3	0,049587	-1,50474	B8NHS0	B8NHS0	1	AFLA_137640	Uncharacterized protein
24,6354	25,2275	25,3472	26,0954	26,4485	26,1633	+	4,30E-126	1,22E+09	10	10	10	24,8	49,624	25,6529	25,07	26,2358	6	3	3	0,008944	-1,16573	B8NGR8	B8NGR8	1	AFLA_137860	Uncharacterized protein
29,785	29,9056	29,7944	29,9905	29,8062	29,9482		0	1,16E+10	28	28	28	69,9	59,793	29,8717	29,8283	29,915	6	3	3	0,270671	-0,0866547	B8NGS7	B8NGS7	1	AFLA_137950	GMP synthase
30,6778	30,5124	30,1722	30,4541	30,4547	30,5457		0	1,6E+10	41	41	41	64,3	79,759	30,4695	30,4542	30,4848	6	3	3	0,849782	-0,0306842	B8NGS8	B8NGS8	1	AFLA_137960	Arginyl-tRNA synthetase
25,8782	25,5421	25,2543	NaN	25,7585	NaN		8,75E-36	7,85E+08	5	5	5	25,3	31,925	25,6083	25,5582	25,7585	4	3	1	1	-0,200334	B8NGT0	B8NGT0	1	AFLA_137980	NADH-cytochrome b5 reductase (EC 1.6.2.2)
25,8154	26,2022	26,4444	26,2241	26,3825	26,1927		1,77E-32	7,77E+08	8	8	8	52,9	26,124	26,2102	26,154	26,2664	6	3	3	0,590349	-0,112406	B8NGT1	B8NGT1	1	AFLA_137990	Uncharacterized protein
28,013	27,5555	26,0788	26,4923	26,6824	27,1067		9,76E-30	2,33E+09	4	4	4	14,1	70,487	26,9881	27,2158	26,7605	6	3	3	0,497745	0,455273	B8NGY8	B8NGY8	1	AFLA_138570	Protease S8 tripeptidyl peptidase I, putative
NaN	NaN	NaN	23,7701	NaN	24,0625		1,58E-05	68467000	2	2	2	19,4	12,311	23,9163	NaN	23,9163	2	0	2	1	NaN	B8NHV1	B8NHV1	1	AFLA_138870	Uncharacterized protein
26,4562	26,1392	26,1391	26,0914	26,2201	26,2375		1,26E-14	6,77E+08	5	5	5	31,4	30,934	26,2139	26,2448	26,183	6	3	3	0,620293	0,0618051	B8NHW6	B8NHW6	1	AFLA_139020	Uncharacterized protein
27,4819	27,1004	27,5034	26,7919	27,7564	27,8306		0	1,07E+10	14	14	14	40,9	50,794	27,4108	27,3619	27,4596	6	3	3	0,799023	-0,0977434	B8NI10	B8NI10	1	AFLA_139470	Beta-cyclopiazonate dehydrogenase (EC 1.21.99.1) (Beta-Cyclopiazonate oxidocyclase) (FAD-dependent oxidoreductase cpaO)
NaN	25,375	26,2025	NaN	25,6191	25,7765		1,29E-303	6,15E+09	11	11	11	35	49,232	25,7433	25,7887	25,6978	4	2	2	0,849133	0,0909014	B8NI11	B8NI11	1	AFLA_139480	Dimethylallyl tryptophan synthase, putative
24,8269	25,07	24,9229	NaN	24,3244	NaN		5,56E-13	1,99E+08	4	4	4	10,5	48,761	24,786	24,9399	24,3244	4	3	1	1	0,615558	H9CNZ7	H9CNZ7	1	AFLA_m0250	Ribosomal protein S5

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

B. Quantitative and qualitative results

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2 Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	Log2(t-test Difference)	Fold Change	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
31,0839	30,3486	30,067	29,1636	29,5708	29,7497	+	0	7,72E+09	14	14	14	34	66,878	29,9973	30,4998	29,4947	6	3	3	0,045103	1,00511	2,007096525	B8NTV3	B8NTV3	1	AFLA_101240	Vacuolar carboxypeptidase Cps1, putative
26,9594	26,6196	26,126	25,6693	25,2932	25,6965	+	3,61E-110	7,07E+08	7	7	7	23,6	47,87	26,0607	26,5683	25,553	6	3	3	0,020912	1,01529	2,021309161	B8NIN1	B8NIN1	1	AFLA_068180	Ethanolamine kinase, putative
25,9221	25,5111	26,569	24,6678	25,0753	25,1869	+	2,77E-21	3,64E+08	7	7	7	9,8	117,64	25,4887	26,0008	24,9767	6	3	3	0,041561	1,02407	2,033648017	B8NLC2	B8NLC2	1	AFLA_090490	Alpha,alpha-trehalose glucohydrolase TreA/Ath1
25,1881	25,7921	24,7573	23,9946	24,1597	24,4006	+	5,21E-13	3,71E+08	5	5	5	10,9	64,216	24,7154	25,2458	24,185	6	3	3	0,030215	1,06081	2,086102434	B8MZ71	B8MZ71	1	AFLA_083600	RNA splicing factor (Pad-1), putative
28,6053	28,0431	28,0829	27,1183	27,1388	27,2818	+	7,33E-105	1,64E+09	16	16	14	27,5	89,135	27,7117	28,2438	27,1796	6	3	3	0,004829	1,06414	2,090923095	B8NLD2	B8NLD2	1	AFLA_090590	Alpha-1,2-mannosidase, putative subfamily
28,0544	27,5733	27,1719	26,1577	26,6132	26,8018	+	1,23E-74	9,43E+08	7	7	7	17,8	62,965	27,062	27,5998	26,5242	6	3	3	0,027938	1,07561	2,107613024	B8MW63	B8MW63	1	AFLA_074100	Gamma-glutamyltranspeptidase
31,9513	32,1439	32,1406	31,2945	30,8648	30,7891	+	7,10E-271	3,38E+10	8	8	8	95,4	11,087	31,5307	32,0786	30,9828	6	3	3	0,002966	1,09576	2,137256409	B8NB77	B8NB77	1	AFLA_044520	60S acidic ribosomal protein P2/allergen Asp F 8
25,8096	25,5235	25,3227	24,1945	24,9445	24,1804	+	1,12E-19	3,75E+08	3	3	3	31,4	13,537	24,9959	25,5519	24,4398	6	3	3	0,018382	1,11212	2,161630596	B8NGE7	B8NGE7	1	AFLA_134870	U6 snRNA-associated Sm-like protein LSM4, putative
26,0032	25,8031	25,2907	24,5498	24,5185	24,6825	+	3,05E-10	4,05E+08	3	3	3	34,7	11,23	25,1413	25,699	24,5836	6	3	3	0,006908	1,11544	2,166610774	B8N5Y8	B8N5Y8	1	AFLA_015720	Small nuclear ribonucleoprotein (LSM2), putative
30,941	30,3806	30,6761	28,9999	29,7498	29,8324	+	0	1,03E+10	13	13	13	72,4	27,369	30,0967	30,6659	29,5274	6	3	3	0,021419	1,13856	2,201611636	B8N226	B8N226	1	AFLA_034200	2-heptaprenyl-1,4-naphthoquinone methyltransferase, putative
27,518	27,342	26,8867	25,9822	26,2654	26,0739	+	2,67E-30	1,25E+09	4	4	4	39,8	10,067	26,678	27,2489	26,1072	6	3	3	0,005161	1,1417	2,206408623	B8N6N8	B8N6N8	1	AFLA_015510	Small nuclear ribonucleoprotein F (snRNP-F) (Sm protein F)
29,8676	29,52	29,6738	28,1225	28,6653	28,6684	+	6,77E-158	4,75E+09	20	19	19	44,4	78,235	29,0863	29,6872	28,4854	6	3	3	0,004414	1,20175	2,30018516	B8MVZ8	B8MVZ8	1	AFLA_073450	Amine oxidase
29,795	29,112	29,1525	27,7735	28,2348	28,4026	+	4,67E-251	3,59E+09	11	11	11	34,8	45,012	28,7451	29,3532	28,1369	6	3	3	0,013823	1,21625	2,323420047	B8NAS6	B8NAS6	1	AFLA_043010	Formamidase FmdS
31,7271	31,0988	31,0474	29,8645	30,0048	30,2584	+	0	1,41E+10	20	20	20	58,4	49,457	30,6668	31,2911	30,0426	6	3	3	0,007213	1,24853	2,375992035	B8NAS7	B8NAS7	1	AFLA_043020	Fructosyl amine:oxygen oxidoreductase
27,6051	27,6491	27,4452	26,2362	26,5395	26,1732	+	6,53E-94	1,41E+09	3	3	3	45,5	13,43	26,9414	27,5665	26,3163	6	3	3	0,000633	1,25018	2,378710995	B8N488	B8N488	1	AFLA_035010	Small nuclear ribonucleoprotein SmD1, putative
26,6341	26,4183	26,1295	24,9647	25,2437	NaN	+	1,65E-58	6,32E+08	4	4	4	64,1	11,564	25,8781	26,3939	25,1042	5	3	2	0,009335	1,28971	2,444789072	B8NEM0	B8NEM0	1	AFLA_062180	37S ribosomal protein S16
31,2696	30,7442	30,2784	29,358	29,3359	29,6638	+	0	1,12E+10	18	18	18	25,2	105,17	30,1083	30,7641	29,4526	6	3	3	0,01268	1,31152	2,482029048	B8NEE0	B8NEE0	1	AFLA_060490	Pyridine nucleotide-disulphide oxidoreductase family protein
26,3849	26,3853	25,0397	24,5244	24,4591	24,7901	+	4,08E-25	3,29E+08	3	3	3	9	48,41	25,2639	25,9366	24,5912	6	3	3	0,042965	1,34544	2,541076837	B8N429	B8N429	1	AFLA_033520	Ubiquitin-like protein DskB, putative
28,8337	29,55	29,0813	27,5395	27,8819	27,9697	+	1,54E-195	4,51E+09	21	21	20	34	71,973	28,476	29,155	27,797	6	3	3	0,005387	1,35797	2,563242547	B8N9S2	B8N9S2	1	AFLA_112180	ATP dependent RNA helicase (Dbp1), putative
NaN	25,8932	26,5679	25,3502	24,7942	24,4546	+	7,41E-82	7,1E+08	11	10	10	31,9	50,409	25,412	26,2305	24,8663	5	2	3	0,047686	1,36421	2,574353193	B8N6T0	B8N6T0	1	AFLA_016830	Tubulin subunit TubB
33,6746	33,4854	33,317	32,2475	31,9621	32,1464	+	0	1,02E+11	11	11	11	73,9	17,009	32,8055	33,4924	32,1187	6	3	3	0,000493	1,37371	2,591360982	B8NQF0	B8NQF0	1	AFLA_006300	Nucleoside diphosphate kinase (EC 2.7.4.6)
27,1212	27,2078	27,0494	25,5732	25,825	25,6162	+	1,36E-176	1,47E+09	6	6	6	40,9	27,781	26,3988	27,1261	25,6714	6	3	3	8,66E-05	1,45467	2,74093858	B8NM09	B8NM09	1	AFLA_094650	60S acidic ribosomal protein P0, putative
29,1856	28,6991	28,565	27,0618	27,5958	27,4143	+	1,67E-68	2,7E+09	8	8	8	30,4	32,116	28,0869	28,8166	27,3573	6	3	3	0,003998	1,45931	2,749768186	B8N7K8	B8N7K8	1	AFLA_104510	Methyltransferase family protein
31,8229	32,0133	31,9106	30,7668	30,238	30,3273	+	0	2,4E+10	10	10	10	48,9	33,441	31,1798	31,9156	30,444	6	3	3	0,001035	1,47159	2,773273689	B8N1E9	B8N1E9	1	AFLA_030140	60S ribosomal protein P0
26,9801	27,2405	26,6433	25,3008	25,7383	25,3957	+	6,11E-47	1,49E+09	7	7	7	46	21,415	26,2165	26,9547	25,4783	6	3	3	0,002482	1,4764	2,782535319	B8N1B1	B8N1B1	1	AFLA_029760	Small monomeric GTPase SarA, putative
25,6284	26,3329	25,7872	24,6025	24,3853	24,2224	+	3,09E-08	5,13E+08	3	3	3	29,3	10,958	25,1598	25,9162	24,4034	6	3	3	0,003242	1,51276	2,853554268	B8NGG5	B8NGG5	1	AFLA_135920	Cytochrome c oxidase polypeptide vib
28,3924	28,0101	27,4117	26,0774	26,6422	26,5513	+	6,47E-11	1,52E+09	3	3	3	16,3	11,278	27,1809	27,9381	26,4237	6	3	3	0,010635	1,5144	2,856799923	B8NS34	B8NS34	1	AFLA_052650	Uncharacterized protein
30,4844	30,5277	30,4712	29,2864	28,74	28,8897	+	1,23E-47	8,01E+09	5	5	5	35,8	17,937	29,7332	30,4944	28,972	6	3	3	0,000747	1,52239	2,872665476	B8MY77	B8MY77	1	AFLA_080140	60S ribosomal protein L12
25,7202	25,4898	25,813	NaN	24,1901	24,1029	+	4,78E-07	1,77E+08	2	2	2	8,1	37,827	25,0632	25,6743	24,1465	5	3	2	0,001271	1,52779	2,883437997	B8MZL2	B8MZL2	1	AFLA_085020	Class II aldolase/adducin domain protein
27,0341	27,1637	26,5167	24,9593	26,1149	25,0284	+	5,42E-31	8,97E+08	9	9	9	58,6	28,548	26,1362	26,9048	25,3676	6	3	3	0,022109	1,53727	2,902447557	B8NG47	B8NG47	1	AFLA_132080	Small nuclear ribonucleoprotein U2, A
27,358	27,9344	27,5985	26,1587	26,2463	25,8464	+	6,65E-107	1,17E+09	12	12	12	37,9	44,308	26,8571	27,6303	26,0838	6	3	3	0,001702	1,54649	2,921055966	B8NRZ7	B8NRZ7	1	AFLA_052280	Uncharacterized protein
26,991	27,2145	27,4383	25,596	25,8747	25,5202	+	7,62E-21	1,64E+09	8	8	8	22,4	55,064	26,4391	27,2146	25,6636	6	3	3	0,000769	1,55096	2,930120508	B8MW24	B8MW24	1	AFLA_073710	Mitochondrial ribosomal protein DAP3, putative
27,68	27,3944	28,9959	26,5979	26,343	26,4452	+	1,47E-39	1,33E+09	5	5	5	29,4	18,491	27,2427	28,0234	26,462	6	3	3	0,035148	1,5614	2,951401103	B8N0D5	B8N0D5	1	AFLA_087760	40S ribosomal protein S11
28,3727	27,9593	27,1425	26,3009	26,4615	26,0184	+	3,73E-15	1,53E+09	4	4	4	36,2	12,867	27,0425	27,8248	26,2603	6	3	3	0,015161	1,56453	2,957811268	B8N0U1	B8N0U1	1	AFLA_026260	Small nuclear ribonucleoprotein SmD3, putative
26,3248	26,5591	25,5442	24,7399	25,0755	23,8537	+	3,30E-21	5,29E+08	9	9	9	21,7	48,134	25,3495	26,1427	24,5564	6	3	3	0,029112	1,58634	3,002865797	B8NLT8	B8NLT8	1	AFLA_093940	Mitochondrial large ribosomal subunit YmL35, putative
28,0893	27,5951	27,4665	25,8266	26,3498	26,2066	+	1,36E-60	1,45E+09	14	14	14	27,7	78,204	26,9223	27,717	26,1277	6	3	3	0,002945	1,58932	3,009074863	B8MXD8	B8MXD8	1	AFLA_077250	Acyl-coenzyme A oxidase
25,9946	26,1703	25,9359	24,6189	24,2005	NaN	+	4,82E-24	4,43E+08	4	4	4	19,2	33,102	25,3841	26,0336	24,4097	5	3	2	0,002899	1,62391	3,082092157	B8N9A8	B8N9A8	1	AFLA_110540	Uncharacterized protein
27,2515	27,4169	27,5856	24,8292	26,5341	25,9757	+	5,04E-41	7,17E+08	8	8	8	21,4	61,89	26,5988	27,418	25,7797	6	3	3	0,032711	1,63836	3,113117435	B8NYW3	B8NYW3	1	AFLA_114750	Glutamyl-tRNA(Gln) amidotransferase subunit A, putative
26,2117	26,1625	25,7806	23,8974	24,396	24,9421	+	5,46E-11	4,87E+08	4	4	4	50,5	10,64	25,2317	26,0516	24,4118	6	3	3	0,007741	1,63978	3,116183088	B8MXA7	B8MXA7	1	AFLA_076940	Small nuclear ribonucleoprotein SmE, putative
27,9075	27,6179	27,5312	25,6869	26,5304	25,7127	+	1,56E-64	1,32E+09	5	5	5	35,5	19,836	26,8311	27,6855	25,9767	6	3	3	0,00466	1,70888	3,269069389	B8N9R2	B8N9R2	1	AFLA_112080	Small nuclear ribonucleoprotein SmB, putative
31,6763	31,3276	31,1972	29,2447	29,7845	30,0068	+	0	1,23E+10	27	27	26	66,8	75,372	30,5395	31,4003	29,6786	6	3	3	0,003005	1,7217	3,298248272	B8N268	B8N268	1	AFLA_034620	Amine oxidase
30,7568	30,84	30,705	29,4784	28,8326	28,8116	+	2,21E-42	8,56E+09	6	6	6	46	14,147	29,9041	30,7673	29,0409	6	3	3	0,001483	1,72639	3,308987863	B8MY51	B8MY51	1	AFLA_079880	60S ribosomal protein L22, putative
26,2923	26,5714	26,5652	24,6066	24,8468	NaN	+	6,27E-88	5,95E+08	7	7	7	45,3	27,389	25,7765	26,4763	24,7267	5	3	2	0,001321	1,74962	3,362699823	B8NFL4	B8NFL4	1	AFLA_131050	Uncharacterized protein
31,5319	31,0917	30,8204	29,2128	29,306	29,4598	+	0	1,37E+10	9	9	9	29,7	43,181	30,2371	31,148	29,3262	6	3	3	0,00115	1,82181	3,535244509	B8NE68	B8NE68	1	AFLA_057990	Purine nucleoside permease, putative
25,8966	25,6782	26,5028	23,2843	24,6635	24,4795	+	1,65E-12	4,8E+08	5	5	5	28	28,345	25,0842	26,0259	24,1424	6	3	3	0,019371	1,88343	3,689511979	B8NI48	B8NI48	1	AFLA_064530	Glutathione S-transferase GliG-like, putative
27,391	27,2011	26,5929	24,86	25,1521	25,5167	+	2,77E-48	9,75E+08	5	5	5	21,7	36,186	26,119	27,0617	25,1763	6	3	3	0,003548	1,8854	3,694553449	B8NEL6	B8NEL6	1	AFLA_062140	RNA binding protein, putative
25,3948	24,7556	24,8642	22,855	23,3669	23,1142	+	2,68E-05	1,55E+08	2	2	2	3,9	65,705	24,0584	25,0049	23,112	6	3	3	0,001551	1,89284	3,713655529	B8NMX2	B8NMX2	1	AFLA_123160	Laccase, putative
26,1371	26,6486	26,1072	24,4544	24,6195	24,1401	+	3,80E-25	5,2E+08	3	3	3	42,6	13,05	25,3511	26,2976	24,4046	6	3	3	0,001093	1,89297	3,713990178	B8NKX6	B8NKX6	1	AFLA_093800	Small nuclear ribonucleoprotein SmD2, putative
27,0614	27,2948	27,0051	24,894	25,9488	24,7398	+	4,41E-63	5,53E+08	11	11	11	14,4	115,12	26,1573	27,1204	25,1942	6	3	3	0,007832	1,92623	3,800607391	B8N6J8	B8N6J8	1	AFLA_015110	Uncharacterized protein
24,9074	25,0935	NaN	23,3612	NaN	22,746	+	6,60E-17	2,32E+08	4	4	4	9,8	64,728	24,027	25,0005	23,0536	4	2	2	0,026181	1,94689	3,855425258	B8NWT6	B8NWT6	1	AFLA_121230	L-amino acid oxidase LaoA
26,4842	26,523	26,4493	24,5883	24,6968	24,2798	+	1,23E-16	4,5E+08	4	4	4	13,3	35,184	25,5035	26,4855	24,5216	6	3	3	0,000101	1,96384	3,900989189	B8N1X2	B8N1X2	1	AFLA_032760	Pre-RNA splicing factor Srp2, putative
32,9401	32,5188	33,711	31,0613	31,0406	31,1508	+	0	5,77E+10	27	27	27	52,7	80,383	32,0704	33,0566	31,0842	6	3	3	0,004914	1,9724	3,924203885	B8NBM3	B8NBM3	1	AFLA_045980	Probable dipeptidyl-peptidase 5 (EC 3.4.14.-) (Dipeptidyl-peptidase V) (DPP V) (DppV)
27,4245	26,3567	27,0415	24,5807	24,9304	25,2521	+	4,11E-22	4,39E+08	8	8	8	22	54,086	25,931	26,9409	24,9211	6	3	3	0,005348	2,0198	4,0552757	B8NC44	B8NC44	1	AFLA_038390	Sarcosine oxidase, putative
26,288	26,2291	25,8768	24,1274	23,8704	24,28	+	3,99E-28	2,51E+08	7	7	7	16,1	74,805	25,112	26,1313	24,0926	6	3	3	0,000313	2,03871	4,108779758	B8N3Z9	B8N3Z9	1	AFLA_033220	Amidase family protein
28,1391	28,259	27,7888	25,6613	26,3241	NaN	+	8,31E-75	1,78E+09	2	2	2	10,8	25,563	27,2345	28,0623	25,9927	5	3	2	0,006658	2,06956	4,197586339	B8NC17	B8NC17	1	AFLA_047420	Uncharacterized protein
26,1584	26,2865	26,178	24,0663	24,0835	NaN	+	3,27E-28	3,86E+08	5	5	5	17,8	52,303	25,3545	26,2076	24,0749	5	3	2	3,16E-05	2,13272	4,385435141	B8NNE9	B8NNE9	1	AFLA_127600	40S ribosomal protein S2, putative
27,8932	27,911	27,3422	25,4256	25,7199	25,4279	+	9,71E-45	1,58E+09	7	7	7	50	33,532	26,62	27,7155	25,5245	6	3	3	0,000483	2,19103	4,566313781	B8MWC5	B8MWC5	1	AFLA_088150	Fe superoxide dismutase, putative
24,861	26,1242	25,7298	23,3385	23,3838	23,1413	+	7,97E-19	2,88E+08	4	4	4	13	55,58	24,4298	25,5717	23,2879	6	3	3	0,003877	2,28382	4,869656467	B8NCZ6	B8NCZ6	1	AFLA_054670	Tryptophanyl-tRNA synthetase, putative
26,5223	26,8495	25,9997	24,1572	24,2282	24,0797	+	3,36E-73	6,58E+08	5	5	5	27,6	24,22	25,3061	26,4572	24,155	6	3	3	0,000786	2,30213	4,931853687	B8N208	B8N208	1	AFLA_034020	Uncharacterized protein
28,1427	27,0036	25,9984	23,9081	25,0428	25,2307	+	9,31E-35	5,54E+08	9	9	9	25,1	58,984	25,8877	27,0482	24,7272	6	3	3	0,035616	2,32103	4,996888409	B8NH51	B8NH51	1	AFLA_132750	Uncharacterized protein
26,6098	26,814	26,2816	24,2622	24,2739	24,0779	+	6,08E-44	5,42E+08	7	7	7	32,2	34,813	25,3866	26,5685	24,2047	6	3	3	0,000147	2,36378	5,147172025	B8NDQ5	B8NDQ5	1	AFLA_055460	37S ribosomal protein S9
27,3932	27,774	27,5665	25,4835	25,2721	24,8319	+	1,14E-47	1,29E+09	14	14	14	41,6	46,429	26,3869	27,5779	25,1958	6	3	3	0,000422	2,3821	5,212949919	B8NH55	B8NH55	1	AFLA_132790	37S ribosomal protein S5
28,1488	29,5291	30,38	27,485	26,6826	26,7169	+	2,17E-105	5,04E+09	8	8	8	47,4	15,612	28,1571	29,3526	26,9615	6	3	3	0,026987	2,39116	5,245789801	B8NMV9	B8NMV9	1	AFLA_127220	60S ribosomal protein L27
27,4766	27,6662	27,39	25,2561	25,3826	24,6681	+	7,93E-57	1,24E+09	10	10	10	35,8	44,771	26,3066	27,5109	25,1022	6	3	3	0,000509	2,4087	5,309956344	B8NEM2	B8NEM2	1	AFLA_062200	Uncharacterized protein
28,498	28,5127	28,0301	25,8226	26,0485	25,8662	+	3,13E-49	1,83E+09	10	10	10	42,5	35,332	27,1297	28,3469	25,9125	6	3	3	0,000148	2,43446	5,405619633	B8MWP8	B8MWP8	1	AFLA_075060	Transformer-SR ribonucleoprotein, putative
27,1434	27,5683	27,4071	25,1086	25,1061	24,4081	+	8,72E-38	7,92E+08	10	10	10	29,7	51,166	26,1236	27,3729	24,8743	6	3	3	0,000694	2,49867	5,651641679	B8NB59	B8NB59	1	AFLA_044340	Uncharacterized protein
27,5903	28,9126	26,6158	25,6323	24,9213	24,8968	+	2,41E-95	1,51E+09	15	15	15	41,8	54,862	26,4282	27,7062	25,1501	6	3	3	0,022541	2,55609	5,881116217	B8NSF7	B8NSF7	1	AFLA_048200	Pseudouridylate synthase family protein
25,996	26,418	25,8418	23,4718	23,4541	23,4886	+	1,09E-14	4,96E+08	5	5	5	27	34,242	24,7784	26,0852	23,4715	6	3	3	0,000111	2,61371	6,120756606	B8N514	B8N514	1	AFLA_020520	30S ribosomal protein S15
26,1613	26,3705	26,1261	NaN	23,9914	23,2131	+	1,84E-16	4,33E+08	6	6	6	54,7	18,499	25,1725	26,2193	23,6022	5	3	2	0,003368	2,61707	6,135028305	B8MWA9	B8MWA9	1	AFLA_087990	40S ribosomal protein S8
26,8105	26,3249	25,8094	23,6535	23,4816	23,8801	+	2,19E-35	2,71E+08	5	5	5	15	52,932	24,9933	26,315	23,6717	6	3	3	0,001054	2,64323	6,247287828	B8NAC3	B8NAC3	1	AFLA_039680	Uncharacterized protein
25,243	25,8815	25,3651	23,2826	22,8335	22,3956	+	4,08E-24	2,87E+08	8	8	8	27	51,308	24,1669	25,4965	22,8373	6	3	3	0,001177	2,65927	6,317133233	B8N570	B8N570	1	AFLA_021980	30S ribosomal subunit S4, putative
26,8359	26,2061	NaN	24,2495	23,5217	23,7787	+	1,65E-25	5,04E+08	8	8	8	16,2	63,696	24,9184	26,521	23,8499	5	2	3	0,005131	2,67109	6,369102103	B8NX59	B8NX59	1	AFLA_122470	CobW domain protein
30,7709	30,189	31,0186	28,0018	27,757	27,7172	+	0	7,67E+09	11	11	11	38,8	28,509	29,2424	30,6595	27,8253	6	3	3	0,000411	2,83412	7,131077089	B8N180	B8N180	1	AFLA_029450	Ribosomal L18ae protein family
29,6276	30,276	31,2166	28,2164	26,978	27,3119	+	0	7,27E+09	13	13	13	59	29,018	28,9377	30,3734	27,5021	6	3	3	0,008302	2,8713	7,317242136	B8NCT6	B8NCT6	1	AFLA_041710	60S ribosomal protein L7
30,4242	30,9908	31,5229	28,1911	27,3704	27,7701	+	1,66E-190	9,17E+09	8	8	8	49,7	16,827	29,3783	30,9793	27,7772	6	3	3	0,00127	3,20212	9,203100607	B8NV82	B8NV82	1	AFLA_103770	60S ribosomal protein L27a, putative
30,2361	29,9794	28,9112	26,154	26,7371	26,4545	+	7,56E-218	4,87E+09	11	11	11	26,9	57,28	28,0787	29,7089	26,4485	6	3	3	0,001758	3,26038	9,582353257	B8NVT9	B8NVT9	1	AFLA_117760	Phytase, putative
25,1296	25,199	NaN	NaN	21,9163	21,556	+	4,12E-11	2,05E+08	2	2	2	9,8	28,186	23,4502	25,1643	21,7362	4	2	2	0,002852	3,42808	10,76353451	B8NTI7	B8NTI7	1	AFLA_098270	RNase III domain protein
30,5965	30,6596	30,9785	27,4041	26,9891	27,5533	+	3,41E-219	1,26E+10	12	12	12	51,2	24,222	29,0302	30,7449	27,3155	6	3	3	7,64E-05	3,42934	10,77293911	B8NIL3	B8NIL3	1	AFLA_068000	Ribosomal protein

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

B. Quantitative and qualitative results

LFQ intensity AF_$CaCl_2$ PgAFP_1	LFQ intensity AF_$CaCl_2$ PgAFP_2	LFQ intensity AF_$CaCl_2$ PgAFP_3	LFQ intensity AF_$CaCl_2$ Control_1	LFQ intensity AF_$CaCl_2$ Control_2	LFQ intensity AF_$CaCl_2$ Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_$CaCl_2$ PgAFP	Mean AF_$CaCl_2$ Control	Valid values	Valid values AF_$CaCl_2$ PgAFP	Valid values AF_$CaCl_2$ Control	t-test p value	Log2(t-test Difference)	Fold Change	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
30,6685	31,0742	30,9058	28,5294	26,7783	27,0226	+	6,41E-114	1,53E+10	8	8	8	37	16,959	29,1631	30,8828	27,4434	6	3	3	0,003564	3,43939	10,8482468	B8NSF1	B8NSF1	1	AFLA_048140	60S ribosomal protein L23
29,2772	29,8472	30,2209	26,9979	25,9408	26,0707	+	4,91E-22	4,39E+09	5	5	5	39	11,978	28,0591	29,7818	26,3365	6	3	3	0,001332	3,44532	10,89292879	B8N9U3	B8N9U3	1	AFLA_112390	60S ribosomal protein L36
31,5775	32,1415	32,8978	29,1156	27,988	28,5129	+	0	2,31E+10	24	24	24	71	40,245	30,3722	32,2056	28,5388	6	3	3	0,001874	3,6668	12,70038213	B8NR98	B8NR98	1	AFLA_005730	60S ribosomal protein L4, putative
30,4012	30,9258	31,5159	27,7354	26,4745	26,7871	+	0	9,39E+09	15	15	15	47,3	25,677	28,9733	30,9476	26,999	6	3	3	0,001363	3,94864	15,44041902	B8NYZ9	B8NYZ9	1	AFLA_115110	60S ribosomal protein L13
29,9897	30,5897	30,6484	26,9519	25,7414	26,2005	+	5,21E-111	7,09E+09	7	7	7	22,4	33,628	28,3536	30,4093	26,298	6	3	3	0,00056	4,11131	17,28333833	B8N3M3	B8N3M3	1	AFLA_029260	Ribosomal protein L15
27,4661	27,9398	29,1133	24,337	23,8529	23,8823	+	1,50E-36	1,43E+09	7	7	7	33,1	14,625	26,0986	28,1731	24,0241	6	3	3	0,00128	4,14898	17,74056436	B8NJV8	B8NJV8	1	AFLA_069180	60S ribosomal protein L35
30,9771	31,3758	31,0232	27,5222	26,535	26,7988	+	0	1,46E+10	16	16	16	46,6	29,318	29,0387	31,1254	26,952	6	3	3	0,000202	4,17335	18,04278327	B8N204	B8N204	1	AFLA_033980	Cytosolic large ribosomal subunit protein L7A
29,6524	30,1015	30,4015	25,8646	24,8516	25,4759	+	2,13E-67	5,19E+09	6	6	6	37,5	20,782	27,7246	30,0518	25,3974	6	3	3	0,000222	4,65445	25,1842524	B8NC19	B8NC19	1	AFLA_047440	60S ribosomal protein L18
29,3796	28,6452	28,5507	24,08	NaN	24,1284	+	5,88E-146	1,28E+09	9	9	9	24	74,712	26,9568	28,8585	24,1042	5	3	2	0,000783	4,75426	26,98825887	B8NMK6	B8NMK6	1	AFLA_124420	Amine oxidase, putative
29,7651	29,9713	29,8813	25,1314	24,9765	24,5285	+	0	6,55E+09	11	11	11	21,3	55,822	27,3757	29,8726	24,8788	6	3	3	1,25E-05	4,99378	31,86233297	B8NTS2	B8NTS2	1	AFLA_100030	Nucleolin protein Nsr1, putative
30,2294	29,1182	30,6719	NaN	24,4705	24,9859	+	1,13E-163	2,83E+09	10	10	10	39,9	39,669	27,8952	30,0065	24,7282	5	3	2	0,003514	5,2783	38,80847937	B8MYC9	B8MYC9	1	AFLA_080660	L-asparaginase
29,3324	27,7717	29,8263	22,8134	NaN	23,6589	+	7,76E-200	1,68E+09	12	12	12	34,4	68,812	26,6805	28,9768	23,2362	5	3	2	0,006839	5,74064	53,46934134	B8N0I7;B8	B8N0I7	2	AFLA_024300	Amidase, putative
24,7894	23,8782	23,1912	NaN	NaN	NaN		3,65E-09	1,16E+08	3	3	3	9,7	45,489	23,9529	23,9529	NaN	3	3	0	1	NaN	Detected in treated only	B8NR26	B8NR26	1	AFLA_004100	Transesterase (LovD), putative
NaN	25,496	25,2161	NaN	NaN	NaN		1,19E-26	4,18E+08	4	4	4	30,4	17,901	25,3561	25,3561	NaN	2	2	0	1	NaN	Detected in treated only	B8NQA4	B8NQA4	1	AFLA_004950	Cytochrome c oxidase subunit Va, putative
23,9111	22,9263	NaN	NaN	NaN	NaN		3,40E-05	36316000	2	2	2	3,5	62,125	23,4187	23,4187	NaN	2	2	0	1	NaN	Detected in treated only	B8NR85	B8NR85	1	AFLA_005600	SNARE domain protein
25,2682	24,0655	23,3112	NaN	NaN	NaN		1,61E-09	1,65E+09	5	5	5	13,5	65,179	24,215	24,215	NaN	3	3	0	1	NaN	Detected in treated only	B8NR95	B8NR95	1	AFLA_005700	Aromatic amino acid aminotransferase, putative
24,1517	23,5019	26,3569	NaN	NaN	NaN		2,41E-16	1,65E+08	5	5	5	12,6	54,048	24,6702	24,6702	NaN	3	3	0	1	NaN	Detected in treated only	B8NY90	B8NY90	1	AFLA_010600	Siderophore biosynthesis acetylase AceI, putative
NaN	24,6347	24,0037	NaN	NaN	NaN		2,93E-10	1,49E+08	2	2	2	4,2	87,437	24,3192	24,3192	NaN	2	2	0	1	NaN	Detected in treated only	B8N5Z4	B8N5Z4	1	AFLA_015780	Small oligopeptide transporter, OPT family
23,3543	NaN	23,2887	NaN	NaN	NaN		1,06E-06	83990000	3	3	3	4,4	95,857	23,3215	23,3215	NaN	2	2	0	1	NaN	Detected in treated only	B8N5A2	B8N5A2	1	AFLA_022300	Chromosome segregation protein (SepB), putative
NaN	23,7726	24,1818	NaN	NaN	NaN		1,58E-12	2,3E+08	4	4	4	19,8	40,882	23,9772	23,9772	NaN	2	2	0	1	NaN	Detected in treated only	B8N0P2	B8N0P2	1	AFLA_024850	Deoxyhypusine synthase, putative
NaN	24,59	24,9343	NaN	NaN	NaN		1,37E-08	1,63E+08	4	4	4	26,6	26,433	24,7622	24,7622	NaN	2	2	0	1	NaN	Detected in treated only	B8N3G8	B8N3G8	1	AFLA_028710	Short chain type dehydrogenase, putative
25,5719	24,6714	NaN	NaN	NaN	NaN		9,65E-08	1,15E+08	4	4	4	19,8	46,735	25,1216	25,1216	NaN	2	2	0	1	NaN	Detected in treated only	B8N3Q7	B8N3Q7	1	AFLA_031410	Ribonuclease T2 family, putative
23,4636	23,8317	NaN	NaN	NaN	NaN		1,01E-21	4,58E+08	3	3	3	26,3	15,049	23,6477	23,6477	NaN	2	2	0	1	NaN	Detected in treated only	B8N418	B8N418	1	AFLA_033410	Uncharacterized protein
25,0694	23,5346	NaN	NaN	NaN	NaN		8,84E-07	47980000	2	2	2	12	38,961	24,302	24,302	NaN	2	2	0	1	NaN	Detected in treated only	B8NBY8	B8NBY8	1	AFLA_047130	Uncharacterized protein
27,6971	27,1201	26,7562	NaN	NaN	NaN		4,28E-09	9,42E+08	2	2	2	17,6	19,894	27,1911	27,1911	NaN	3	3	0	1	NaN	Detected in treated only	B8NS36	B8NS36	1	AFLA_052670	RNA recognition motif (Rrm) domain containing protein, putative
NaN	27,2454	26,7823	NaN	NaN	NaN		0,00016	3,57E+08	2	2	2	10,3	38,792	27,0138	27,0138	NaN	2	2	0	1	NaN	Detected in treated only	B8NDS7	B8NDS7	1	AFLA_055680	Esterase, putative
NaN	24,5913	24,8918	NaN	NaN	NaN		1,56E-08	2,67E+08	2	2	2	20,7	16,051	24,7416	24,7416	NaN	2	2	0	1	NaN	Detected in treated only	B8NEW9	B8NEW9	1	AFLA_058330	Mitochondrial intermembrane space translocase subunit Tim9, putative
NaN	25,2471	24,7419	NaN	NaN	NaN		6,80E-09	2,65E+08	2	2	2	17,4	21,01	24,9945	24,9945	NaN	2	2	0	1	NaN	Detected in treated only	B8NEE9	B8NEE9	1	AFLA_060580	NEDD8 conjugating enzyme (UbcL), putative
23,6373	23,9637	23,7981	NaN	NaN	NaN		8,49E-21	2,93E+08	5	5	5	15,6	53,058	23,7997	23,7997	NaN	3	3	0	1	NaN	Detected in treated only	B8NFA6	B8NFA6	1	AFLA_061500	Squalene monooxygenase Erg1
NaN	25,8149	26,7776	NaN	NaN	NaN		0,000171	2,15E+08	2	2	2	11,5	25,038	26,2962	26,2962	NaN	2	2	0	1	NaN	Detected in treated only	B8MX33	B8MX33	1	AFLA_076200	HAD superfamily hydrolase, putative
24,7904	NaN	23,0477	NaN	NaN	NaN		1,08E-06	1,03E+08	2	2	2	4	68,226	23,9191	23,9191	NaN	2	2	0	1	NaN	Detected in treated only	B8MXU4	B8MXU4	1	AFLA_078810	Oxidoreductin
23,2484	23,4539	23,0619	NaN	NaN	NaN		2,05E-09	1,54E+08	4	4	4	10,9	37,363	23,2547	23,2547	NaN	3	3	0	1	NaN	Detected in treated only	B8MXX9	B8MXX9	1	AFLA_079160	Ribosome biogenesis protein, putative
NaN	22,9565	23,6506	NaN	NaN	NaN		6,07E-27	2,91E+08	3	3	3	7,6	58,844	23,3036	23,3036	NaN	2	2	0	1	NaN	Detected in treated only	B8MZN7	B8MZN7	1	AFLA_085270	T-complex protein 1, zeta subunit, putative
24,0109	23,4908	NaN	NaN	NaN	NaN		2,14E-05	74033000	2	2	2	4,1	77,122	23,7509	23,7509	NaN	2	2	0	1	NaN	Detected in treated only	B8MWT6	B8MWT6	1	AFLA_088860	Acetyltransferase, putative
NaN	24,5129	24,5236	NaN	NaN	NaN		1,74E-14	2,91E+08	5	5	5	9,5	80,72	24,5183	24,5183	NaN	2	2	0	1	NaN	Detected in treated only	B8NKL5	B8NKL5	1	AFLA_091810	Uncharacterized protein
NaN	23,3384	23,9758	NaN	NaN	NaN		3,74E-08	1,7E+08	4	4	4	15,6	41,918	23,6571	23,6571	NaN	2	2	0	1	NaN	Detected in treated only	B8N8G5	B8N8G5	1	AFLA_107590	3-methyl-2-oxobutanoate dehydrogenase, putative
23,8482	NaN	25,589	NaN	NaN	NaN		5,58E-12	57945000	5	5	5	19,3	41,531	24,7186	24,7186	NaN	2	2	0	1	NaN	Detected in treated only	B8N950	B8N950	1	AFLA_109960	Uncharacterized protein
24,9965	25,2946	24,9387	NaN	NaN	NaN		2,92E-57	2,03E+08	8	8	8	34,1	30,478	25,0766	25,0766	NaN	3	3	0	1	NaN	Detected in treated only	B8N9W4	B8N9W4	1	AFLA_112600	37S ribosomal protein S25, mitochondrial
24,8045	24,375	NaN	NaN	NaN	NaN		7,79E-15	1,95E+08	5	5	5	7,7	81,936	24,5898	24,5898	NaN	2	2	0	1	NaN	Detected in treated only	B8NA76	B8NA76	1	AFLA_113720	Ribosome biogenesis (Nop4), putative
23,7553	NaN	28,4655	NaN	NaN	NaN		3,78E-64	9,46E+08	5	5	5	39,1	20,206	26,1104	26,1104	NaN	2	2	0	1	NaN	Detected in treated only	B8NVQ0	B8NVQ0	1	AFLA_117370	Uncharacterized protein
24,175	NaN	25,0388	NaN	NaN	NaN		5,12E-69	8,92E+08	3	3	3	22,5	30,301	24,6069	24,6069	NaN	2	2	0	1	NaN	Detected in treated only	B8NWE1	B8NWE1	1	AFLA_119780	Neutral protease 2 homolog AFLA_119780 (EC 3.4.24.39) (Deuterolysin AFLA_119780)
23,6358	NaN	22,959	NaN	NaN	NaN		5,25E-06	76535000	2	2	2	5,4	51,017	23,2974	23,2974	NaN	2	2	0	1	NaN	Detected in treated only	B8NX26;B8	B8NX26;B8	2	AFLA_122130	Mannan endo-1,6-alpha-mannosidase DCW1, putative
24,1106	NaN	25,0047	NaN	NaN	NaN		1,99E-09	1,62E+08	3	3	3	4,9	83,122	24,5576	24,5576	NaN	2	2	0	1	NaN	Detected in treated only	B8NX31	B8NX31	1	AFLA_122180	Uncharacterized protein
24,9916	25,4149	NaN	NaN	NaN	NaN		3,80E-05	3,07E+08	2	2	2	3,5	80,926	25,2033	25,2033	NaN	2	2	0	1	NaN	Detected in treated only	B8NP31	B8NP31	1	AFLA_128140	Sister chromatid separation protein (Src1), putative
24,6072	24,9451	25,0787	NaN	NaN	NaN		1,38E-12	1,94E+08	5	5	5	8	87,029	24,877	24,877	NaN	3	3	0	1	NaN	Detected in treated only	B8NH67	B8NH67	1	AFLA_132910	Pre-mRNA splicing factor RNA helicase (Prp43), putative
26,4722	26,4242	24,4344	NaN	NaN	NaN		2,98E-12	5,04E+08	3	3	3	17,6	22,928	25,7769	25,7769	NaN	3	3	0	1	NaN	Detected in treated only	B8NG77	B8NG77	1	AFLA_134160	V-type ATPase F subunit, putative
23,4702	NaN	27,1883	NaN	NaN	NaN		1,45E-49	6,84E+08	9	9	9	20,6	69,301	25,3293	25,3293	NaN	2	2	0	1	NaN	Detected in treated only	B8NC58	B8NC58	1	AFLA_038530	Extracellular metalloproteinase mep (EC 3.4.24.-) (Elastinolytic metalloproteinase mep) (Fungalysin mep)
22,7042	21,4608	NaN	31,4209	31,5292	31,6738	+	0	3,1E+10	25	25	25	57,4	52,758	27,7578	22,0825	31,5413	5	2	3	0,000273	-9,45874	-703,6625879	B8N5M5	B8N5M5	1	AFLA_013680	Phosphatidylglycerol specific phospholipase C, putative
22,4239	22,0115	21,7122	29,7705	30,0022	30,2119	+	0	8,35E+09	18	18	18	48,1	69,417	26,022	22,0492	29,9949	6	3	3	5,17E-06	-7,94565	-246,5352278	B8MZ53	B8MZ53	1	AFLA_083420	Non-hemolytic phospholipase C, putative
27,2886	26,0026	24,9291	31,2714	32,0032	32,0819	+	0	1,79E+10	15	15	15	45,7	55,696	28,9295	26,0735	31,7855	6	3	3	0,001434	-5,71204	-52,41980203	B8NYI6	B8NYI6	1	AFLA_011560	Phosphatidylglycerol specific phospholipase, putative
24,1174	23,075	23,478	28,5781	28,6952	28,7459	+	0	3,59E+09	8	8	8	48	31,217	26,1149	23,5568	28,673	6	3	3	7,65E-05	-5,11626	-34,68548133	B8N1G5	B8N1G5	1	AFLA_030300	Uncharacterized protein
27,1748	26,5578	26,1767	31,1604	31,2486	31,369	+	3,00E-277	2,05E+10	8	8	8	27,3	46,686	28,9479	26,6365	31,2593	6	3	3	9,95E-05	-4,62288	-24,63914006	B8NCF7	B8NCF7	1	AFLA_041320	Acid phosphatase, putative
27,1688	26,1288	24,8564	30,3821	30,5189	30,7118	+	5,34E-125	1,05E+10	5	5	5	15,1	49,097	28,2945	26,0514	30,5376	6	3	3	0,002668	-4,48622	-22,41231858	B8NRS0	B8NRS0	1	AFLA_050610	Acid phosphatase PHOa
NaN	25,3462	24,8921	29,4939	29,6535	28,1187	+	1,57E-16	2,26E+09	3	3	3	29,3	14,092	27,5009	25,1192	29,0887	5	2	3	0,008874	-3,96953	-15,6656204	B8NVA8;B8	B8NVA8	2	AFLA_104030	Histone H2A
NaN	24,4029	24,4384	28,0252	28,3331	27,1151	+	9,92E-95	1,71E+09	11	11	11	31,6	57,045	26,4629	24,4206	27,8245	5	2	3	0,005506	-3,4038	-10,58390418	B8N4G1	B8N4G1	1	AFLA_036640	PH domain protein
24,5621	23,5852	NaN	26,0592	27,4958	27,7217	+	2,94E-76	4,9E+08	9	9	9	37,4	42,347	25,8848	24,0737	27,0922	5	2	3	0,028963	-3,01856	-8,103583355	B8NHE1	B8NHE1	1	AFLA_135460	Uncharacterized protein
25,0394	26,6436	25,6593	28,991	29,555	27,6582	+	1,11E-42	3,48E+09	6	6	1	51,5	11,356	27,2578	25,7808	28,7347	6	3	3	0,015592	-2,95395	-7,74867696	B8N4Q3	B8N4Q3	1	AFLA_017620	Histone H4
25,5834	25,2197	25,1219	27,4858	28,069	28,3951	+	6,16E-154	3,27E+09	12	12	12	51,7	29,585	26,6458	25,3084	27,9833	6	3	3	0,000883	-2,67492	-6,386032964	B8NWI5	B8NWI5	1	AFLA_120220	Uncharacterized protein
24,9033	24,775	26,4225	27,6445	28,1505	28,0507	+	7,36E-77	2,36E+09	10	10	10	37,1	45,706	26,6578	25,3669	27,9486	6	3	3	0,009424	-2,58163	-5,986156514	B8NJ90	B8NJ90	1	AFLA_065230	Glycerophosphoryl diester phosphodiesterase family protein
26,3918	27,9108	27,3845	29,9385	30,0177	29,1827	+	1,24E-134	4,14E+09	5	5	5	31,9	14,972	28,471	27,229	29,713	6	3	3	0,008725	-2,48392	-5,594154117	B8NVA9	B8NVA9	1	AFLA_104040	Histone H2B
23,9076	23,8574	22,5438	25,3155	25,8902	26,013	+	4,64E-25	2,52E+08	6	6	6	17,8	59,924	24,5879	23,4363	25,7396	6	3	3	0,009673	-2,30329	-4,935820742	B8MXJ8	B8MXJ8	1	AFLA_077850	Phenylalanine ammonia-lyase (EC 4.3.1.24)
25,5507	25,7206	NaN	27,7446	27,9553	28,0361	+	9,14E-136	1,9E+09	13	13	13	45,8	51,072	27,0015	25,6356	27,912	5	2	3	0,000395	-2,27635	-4,844507478	B8N8U9	B8N8U9	1	AFLA_108950	Histidine acid phosphatase, putative
24,6153	25,2839	25,5642	27,2808	27,5638	27,3517	+	1,59E-28	8,89E+08	11	11	11	22,9	72,59	26,2766	25,1545	27,3988	6	3	3	0,001582	-2,24434	-4,738202968	B8NJ06	B8NJ06	1	AFLA_071230	AIF-like mitochondrial oxidoreductase (Nfrl), putative
24,8302	23,9889	NaN	25,8991	26,3248	26,5989	+	8,17E-30	3,15E+08	2	2	2	8,8	23,433	25,5284	24,4095	26,2743	5	2	3	0,019797	-1,86471	-3,641947183	B8NTJ8	B8NTJ8	1	AFLA_098380	Conidial hydrophobin RodA/RolA
27,1593	27,0339	25,5066	28,2344	28,4499	28,5881	+	6,92E-114	2,68E+09	3	3	3	38,6	13,55	27,4954	26,5666	28,4241	6	3	3	0,02647	-1,85752	-3,623841862	B8NIT4	B8NIT4	1	AFLA_069620	Uncharacterized protein
23,1196	23,1786	23,2721	25,7325	24,4701	24,5863	+	1,27E-13	2,12E+08	5	5	5	13,3	66,502	24,0599	23,1901	24,9296	6	3	3	0,012721	-1,73956	-3,339333077	B8NTU3	B8NTU3	1	AFLA_100240	Glucose dehydrogenase, putative
27,4075	26,8201	26,4688	28,3054	28,6848	28,6901	+	5,84E-71	2,56E+09	7	7	7	25	34,953	27,7294	26,8988	28,5601	6	3	3	0,005326	-1,6613	-3,163014128	B8MZ00	B8MZ00	1	AFLA_082890	Ribonuclease T2, putative
26,1216	26,0942	27,1876	27,8534	28,3388	28,1102	+	4,74E-149	2,85E+09	20	20	20	32,9	95,766	27,2843	26,4678	28,1008	6	3	3	0,013403	-1,63296	-3,10148633	B8N6M3	B8N6M3	1	AFLA_015360	N-methyltransferase, putative
23,7744	24,9905	25,15	26,1952	26,3511	26,2122	+	1,16E-33	4,71E+08	6	6	6	20,2	45,89	25,4456	24,6383	26,2529	6	3	3	0,020965	-1,61451	-3,062075808	B8NSR2	B8NSR2	1	AFLA_050130	Uncharacterized protein
26,154	24,7076	24,6158	26,3338	26,6088	27,1175	+	1,04E-26	5,55E+08	11	11	11	39,7	34,644	25,9229	25,1591	26,6867	6	3	3	0,049561	-1,52756	-2,882978344	B8NIR6	B8NIR6	1	AFLA_069440	Pyridoxal reductase (AKR8), putative
26,9461	27,0686	25,4553	27,9557	28,2755	27,7531	+	1,85E-83	1,12E+09	6	6	6	70,1	18,158	27,2424	26,49	27,9948	6	3	3	0,049587	-1,50474	-2,837735255	B8NHS0	B8NHS0	1	AFLA_137640	Uncharacterized protein
29,7937	29,3306	29,1088	30,9832	30,765	30,7766	+	0	1,48E+10	19	17	17	61,3	43,173	30,1263	29,411	30,8416	6	3	3	0,002598	-1,43056	-2,695513248	B8NWM6	B8NWM6	1	AFLA_120630	Glyoxylate/hydroxypyruvate reductase, putative
25,2673	25,4799	25,1486	26,9574	26,6569	26,368	+	3,07E-24	4,62E+08	6	6	6	37,8	25,614	25,9797	25,2986	26,6608	6	3	3	0,002243	-1,36218	-2,570733396	B8N2C2	B8N2C2	1	AFLA_036070	Maleylacetoacetate isomerase MaiA
31,5192	31,0407	30,5129	32,3898	32,2883	32,3916	+	0	4,87E+10	22	22	20	72,3	40,145	31,6904	31,0243	32,3566	6	3	3	0,010392	-1,33232	-2,518072811	B8ND35	B8ND35	1	AFLA_055060	NAD-dependent formate dehydrogenase AciA/Fdh
29,6768	29,7969	29,6173	30,6462	31,2973	31,1403	+	0	1,28E+10	27	27	27	65,2	66,547	30,3625	29,697	31,028	6	3	3	0,002807	-1,33096	-2,515700193	B8N2F2	B8N2F2	1	AFLA_036370	Phosphoenolpyruvate carboxykinase AcuF
27,2273	28,5195	28,285	29,1538	29,444	29,2296	+	3,92E-148	5,5E+09	18	18	18	33,6	67,874	28,6432	28,0106	29,2758	6	3	3	0,035884	-1,26518	-2,403571966	B8MXQ5	B8MXQ5	1	AFLA_078420	Fumarate reductase Osm1, putative
24,6354	25,2275	25,3472	26,0954	26,4485	26,1633	+	4,30E-126	1,22E+09	10	10	10	24,8	49,624	25,6529	25,07	26,2358	6	3	3	0,008944	-1,16573	-2,243467057	B8NGR8	B8NGR8	1	AFLA_137860	Uncharacterized protein

Supplementary Table S2. Data on proteins obtained from label-free proteomics from *Aspergillus flavus* grown in presence of 0.1 M $CaCl_2$ treated with 10 µg/ml PgAFP and untreated control.

B. Quantitative and qualitative results

LFQ intensity AF_CaCl2 PgAFP_1	LFQ intensity AF_CaCl2 PgAFP_2	LFQ intensity AF_CaCl2 PgAFP_3	LFQ intensity AF_CaCl2 Control_1	LFQ intensity AF_CaCl2 Control_2	LFQ intensity AF_CaCl2 Control_3	t-test Significant	PEP	Intensity	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Mol. weight [kDa]	Mean	Mean AF_CaCl2 PgAFP	Mean AF_CaCl2_ Control	Valid values	Valid values AF_CaCl2 PgAFP	Valid values AF_CaCl2 Control	t-test p value	Log2(t-test Difference)	Fold Change	Protein IDs	Majority protein IDs	Proteins	Gene Names	Protein names
27,3946	27,3644	27,4069	28,7295	28,5466	28,2777	+	3,70E-274	2,53E+09	13	13	13	37,1	55,616	27,9533	27,3886	28,518	6	3	3	0,001019	-1,12931	-2,187540914	B8NS30	B8NS30	1	AFLA_052610	Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5)
30,6311	30,8276	31,5586	32,4185	32,0477	31,8304	+	0	3,89E+10	31	31	31	66,9	58,086	31,5523	31,0058	32,0988	6	3	3	0,029671	-1,09306	-2,13326028	B8MWA0	B8MWA0	1	AFLA_087900	Pyruvate kinase (EC 2.7.1.40)
NaN	NaN	NaN	NaN	23,5699	23,5492		3,31E-26	2,66E+08	4	4	4	17,4	47,811	23,5595	NaN	23,5595	2	0	2	1	NaN	Detected in control only	B8NQZ7	B8NQZ7	1	AFLA_003810	Endonuclease/exonuclease/phosphatase family protein
NaN	NaN	NaN	26,2119	26,2701	26,5487		3,45E-43	8,27E+08	6	6	6	17,5	57,585	26,3436	NaN	26,3436	3	0	3	1	NaN	Detected in control only	B8NXS3	B8NXS3	1	AFLA_008930	Purple acid phosphatase (EC 3.1.3.2)
NaN	NaN	NaN	24,2323	24,5589	24,6255		2,64E-07	1,78E+08	2	2	2	9,3	18,627	24,4722	NaN	24,4722	3	0	3	1	NaN	Detected in control only	B8NYQ2	B8NYQ2	1	AFLA_012220	Cyclin-dependent kinases regulatory subunit, putative
NaN	NaN	NaN	23,2952	23,9189	23,3138		2,45E-29	3,74E+08	5	5	5	31	23,258	23,5093	NaN	23,5093	3	0	3	1	NaN	Detected in control only	B8N5H5	B8N5H5	1	AFLA_013180	Williams-beuren syndrome chromosome region, putative
NaN	NaN	NaN	22,7949	22,4155	22,3787		7,60E-94	1,73E+09	6	6	6	27,6	32,989	22,5297	NaN	22,5297	3	0	3	1	NaN	Detected in control only	B8N5N1	B8N5N1	1	AFLA_013740	Acid phosphatase, putative
NaN	NaN	NaN	26,6009	27,3877	NaN		2,72E-12	5,37E+08	3	3	3	16,9	15,333	26,9943	NaN	26,9943	2	0	2	1	NaN	Detected in control only	B8N4Q2	B8N4Q2	1	AFLA_017610	Histone H3
NaN	NaN	NaN	24,1966	24,3803	NaN		2,12E-12	1,52E+08	4	4	4	5,3	90,123	24,2885	NaN	24,2885	2	0	2	1	NaN	Detected in control only	B8N5B4	B8N5B4	1	AFLA_022420	Microtubule binding protein HOOK3, putative
NaN	NaN	NaN	NaN	24,5609	24,3599		6,37E-06	2,14E+08	3	3	3	20,4	21,449	24,4604	NaN	24,4604	2	0	2	1	NaN	Detected in control only	B8N1K7	B8N1K7	1	AFLA_030720	RNA exonuclease Rex2, putative
NaN	NaN	NaN	NaN	24,4917	24,301		1,56E-16	2,42E+08	5	5	5	7,1	108,52	24,3964	NaN	24,3964	2	0	2	1	NaN	Detected in control only	B8N3S6	B8N3S6	1	AFLA_031600	SNARE-dependent exocytosis protein (Sro7), putative
NaN	NaN	NaN	25,5384	26,0352	25,8052		6,39E-08	2,85E+08	2	2	2	5,9	50,604	25,7929	NaN	25,7929	3	0	3	1	NaN	Detected in control only	B8NCN0	B8NCN0	1	AFLA_039370	Acid phosphatase, putative
NaN	NaN	NaN	NaN	24,1963	23,4775		6,84E-16	1,78E+08	4	4	4	8,8	75,098	23,8369	NaN	23,8369	2	0	2	1	NaN	Detected in control only	B8NB18	B8NB18	1	AFLA_043930	MFS phosphate transporter, putative
NaN	NaN	NaN	24,7185	25,3773	25,6684		5,14E-10	4,09E+08	5	5	5	11	74,691	25,2547	NaN	25,2547	3	0	3	1	NaN	Detected in control only	B8NBF0	B8NBF0	1	AFLA_045250	Biotin apo-protein ligase, putative
NaN	NaN	NaN	24,0118	24,413	NaN		5,62E-08	1,58E+08	4	4	4	9,4	65,081	24,2124	NaN	24,2124	2	0	2	1	NaN	Detected in control only	B8NSJ9	B8NSJ9	1	AFLA_048620	Histone acetyltransferase, putative
NaN	NaN	NaN	27,5088	27,4891	27,6653		1,06E-42	1,57E+09	4	4	4	32,2	19,57	27,5544	NaN	27,5544	3	0	3	1	NaN	Detected in control only	B8NDN7	B8NDN7	1	AFLA_059760	Uncharacterized protein
NaN	NaN	NaN	27,2497	27,6974	27,6582		7,84E-34	1,07E+09	9	9	9	20	74,118	27,5351	NaN	27,5351	3	0	3	1	NaN	Detected in control only	B8NEP7	B8NEP7	1	AFLA_062450	Sphingomyelin phosphodiesterase
NaN	NaN	NaN	25,3229	25,2405	25,716		1,14E-11	4,08E+08	2	2	2	12	26,52	25,4264	NaN	25,4264	3	0	3	1	NaN	Detected in control only	B8NFD0	B8NFD0	1	AFLA_062640	Uncharacterized protein
NaN	NaN	NaN	26,6398	26,5628	26,7352		4,15E-67	1,19E+09	5	5	5	22,3	39,792	26,6459	NaN	26,6459	3	0	3	1	NaN	Detected in control only	B8NJU9	B8NJU9	1	AFLA_069090	GPI anchored protein, putative
NaN	NaN	NaN	23,9876	NaN	22,4329		1,30E-10	1,28E+08	4	4	4	21,3	28,879	23,2103	NaN	23,2103	2	0	2	1	NaN	Detected in control only	B8NJ29	B8NJ29	1	AFLA_071460	Uncharacterized protein
NaN	NaN	NaN	25,4028	25,778	NaN		7,40E-07	1,55E+08	3	3	3	22,3	22,33	25,5904	NaN	25,5904	2	0	2	1	NaN	Detected in control only	B8MXS2	B8MXS2	1	AFLA_078590	Extracellular matrix protein, putative
NaN	NaN	NaN	26,123	27,431	27,535		1,35E-58	8,57E+08	6	6	6	21,6	50,64	27,0297	NaN	27,0297	3	0	3	1	NaN	Detected in control only	B8MZU5	B8MZU5	1	AFLA_085850	Uncharacterized protein
NaN	NaN	NaN	25,1091	25,1069	24,5207		2,82E-08	1,92E+08	5	5	5	22,6	27,235	24,9123	NaN	24,9123	3	0	3	1	NaN	Detected in control only	B8NM17	B8NM17	1	AFLA_094730	Exosome complex subunit Csl4, putative
NaN	NaN	NaN	24,3513	25,0113	24,9895		8,71E-16	1,67E+08	3	3	3	12,8	40,381	24,784	NaN	24,784	3	0	3	1	NaN	Detected in control only	B8NUG2	B8NUG2	1	AFLA_099240	D-arabinitol dehydrogenase ArbD, putative
NaN	NaN	NaN	24,9468	24,8329	24,2013		1,04E-20	4,42E+08	3	3	3	27	26,851	24,6603	NaN	24,6603	3	0	3	1	NaN	Detected in control only	B8NUN1	B8NUN1	1	AFLA_100840	Pyridoxamine phosphate oxidase, putative
NaN	NaN	NaN	28,1967	28,514	28,7807		0	6,87E+09	12	12	12	45,2	54,633	28,4971	NaN	28,4971	3	0	3	1	NaN	Detected in control only	B8N7N3	B8N7N3	1	AFLA_104760	Purple acid phosphatase (EC 3.1.3.2)
NaN	NaN	NaN	NaN	23,1509	23,2382		9,47E-07	55611000	2	2	2	10,6	33,212	23,1945	NaN	23,1945	2	0	2	1	NaN	Detected in control only	B8N8F1	B8N8F1	1	AFLA_107450	Pirin, putative
NaN	NaN	NaN	25,3324	24,9761			9,07E-77	2,12E+08	4	4	4	11,4	75,17	25,1543	NaN	25,1543	2	0	2	1	NaN	Detected in control only	B8N8P3	B8N8P3	1	AFLA_108370	Tyrosinase, putative
NaN	NaN	NaN	25,6679	26,0469	26,1643		5,28E-12	4,69E+08	4	4	4	17,7	37,584	25,9597	NaN	25,9597	3	0	3	1	NaN	Detected in control only	B8N9K7	B8N9K7	1	AFLA_111530	Zinc-containing alcohol dehydrogenase, putative
NaN	NaN	NaN	24,4964	24,4219	NaN		1,41E-24	3,39E+08	8	8	8	11,7	97,024	24,4592	NaN	24,4592	2	0	2	1	NaN	Detected in control only	B8NAA2	B8NAA2	1	AFLA_113980	Cyclin dependent kinase inhibitor Pho81, putative
NaN	NaN	NaN	23,7777	NaN	24,6947		8,11E-07	1,28E+08	3	3	3	18,6	35,485	24,2362	NaN	24,2362	2	0	2	1	NaN	Detected in control only	B8NYT7	B8NYT7	1	AFLA_114490	Histidinol-phosphatase
NaN	NaN	NaN	24,508	24,7829	NaN		7,14E-09	3,55E+08	4	4	4	7,7	78,476	24,6454	NaN	24,6454	2	0	2	1	NaN	Detected in control only	B8NW15	B8NW15	1	AFLA_119430	Sec1 family superfamily
NaN	NaN	NaN	27,3167	28,3767	28,4127		3,55E-141	2,03E+09	12	12	12	25,9	85,243	28,0353	NaN	28,0353	3	0	3	1	NaN	Detected in control only	B8NWD3	B8NWD3	1	AFLA_119700	Alpha-1,2-mannosidase family protein
NaN	NaN	NaN	NaN	26,0367	25,9783		5,20E-32	4,36E+08	5	5	5	31,5	34,269	26,0075	NaN	26,0075	2	0	2	1	NaN	Detected in control only	B8NN48;R	B8NN48	2	AFLA_124820	Uncharacterized protein
NaN	NaN	NaN	NaN	27,5362	27,6342		3,18E-09	8,43E+08	3	3	3	14,1	31,401	27,5852	NaN	27,5852	2	0	2	1	NaN	Detected in control only	B8NNE2	B8NNE2	1	AFLA_127530	BCAS2 family protein
NaN	NaN	NaN	25,3139	26,244	NaN		8,48E-12	4,81E+08	5	5	5	14,1	58,327	25,7789	NaN	25,7789	2	0	2	1	NaN	Detected in control only	B8NGN2	B8NGN2	1	AFLA_136590	Phenylalanyl-tRNA synthetase alpha subunit (PodG), putative
NaN	NaN	NaN	NaN	24,2863	23,8987		5,20E-14	1,91E+08	6	6	6	17,3	58,227	24,0925	NaN	24,0925	2	0	2	1	NaN	Detected in control only	B8NHI5	B8NHI5	1	AFLA_136790	Thiamine pyrophosphate enzyme, putative
NaN	NaN	NaN	23,7701	NaN	24,0625		1,58E-05	68467000	2	2	2	19,4	12,311	23,9163	NaN	23,9163	2	0	2	1	NaN	Detected in control only	B8NHV1	B8NHV1	1	AFLA_138870	Uncharacterized protein
NaN	NaN	NaN	24,2299	26,2617	25,5851		7,42E-14	2,96E+08	7	7	7	22,7	44,372	25,3589	NaN	25,3589	3	0	3	1	NaN	Detected in control only	B8N151	B8N151	1	AFLA_028260	Probable glucan 1,3-beta-glucosidase A (EC 3.2.1.58) (Exo-1,3-beta-glucanase 1) (Exo-1,3-beta-glucanase A)
NaN	NaN	NaN	NaN	24,0153	24,0315		2,75E-08	1,26E+08	3	3	3	7,2	62,91	24,0234	NaN	24,0234	2	0	2	1	NaN	Detected in control only	B8NTI4	B8NTI4	1	AFLA_098240	Probable D-xylulose kinase A (Xylulokinase A) (EC 2.7.1.17)

V. DISCUSIÓN

V.1. Espectro de actividad antimicrobiana de PgAFP *in vitro*

La proteína PgAFP había mostrado su capacidad para reducir el desarrollo de algunos mohos toxigénicos como *Penicillium expansum*, *P. commune* y *A. niger* (Acosta et al. 2009), aunque no se había establecido el grado de susceptibilidad de otros microorganismos que se encuentran habitualmente en alimentos de humedad intermedia. PgAFP no mostró actividad inhibidora frente a ninguna bacteria o levadura en los ensayos realizados. La falta de actividad frente a bacterias y levaduras es común en este tipo de proteínas pequeñas y básicas producidas por mohos (Marx 2004) y solo la proteína Anafp, producida por *A. niger*, muestra cierta actividad frente a algunas levaduras como *Candida albicans*, *Saccharomyces cerevisiae* o *Trichosporon beigelii* (Gun Lee et al. 1999). Esta falta de sensibilidad de bacterias y levaduras puede considerarse una ventaja, dado que algunos de estos microorganismos juegan un papel fundamental en el desarrollo del aroma característico durante la maduración de los derivados cárnicos curado-madurados (Andrade et al. 2010; Ruiz-Moyano et al. 2011; Cano-García et al. 2014). Por otra parte, este hecho puede permitir la utilización conjunta de la proteína PgAFP con levaduras y bacterias para combatir el desarrollo de mohos toxigénicos en productos madurados.

En el grupo de mohos estudiados se observaron diferentes niveles de sensibilidad frente a PgAFP. Entre los mohos cuyo crecimiento se ve reducido se encuentran especies frecuentes en alimentos curado-madurados con gran potencial toxigénico. Así se observaron diferentes grados de inhibición de mohos productores de ocratoxina A (*A. carbonarius*, *A. ochraceus*, *P. nordicum* y *P. verrucosum*), de aflatoxinas (*A. flavus* y *A. parasiticus*), esterigmatocistina (*A. versicolor*) y patulina (*P. expansum* y *P. griseofulvum*).

Por lo tanto, dada la problemática que supone la producción de micotoxinas en alimentos madurados de humedad intermedia (Núñez et al. 2007; Rodríguez et al. 2012d), PgAFP podría ser útil dentro de una estrategia de biocontrol de mohos toxigénicos en este tipo de alimentos. Sin embargo, algunas de las cepas estudiadas se mostraron resistentes incluso a la concentración mayor de PgAFP ensayada (312,7 µg/ml), incluyendo a la cepa de *P. chrysogenum* productora de PgAFP, *P. polonicum* y *Rhizopus oryzae*. Aunque ninguna de estas especies ha sido relacionada con micotoxicosis alimentarias (Richard 2007), el hecho de existir cepas resistentes puede suponer una limitación para el uso de esta proteína como agente protector.

V.2. Aplicación de PgAFP en alimentos

Para evaluar de forma más precisa su potencial para el control de mohos toxigénicos en alimentos madurados, la capacidad antifúngica de PgAFP se probó en salchichón y queso. En estos alimentos es posible que se produzcan interacciones con la matriz, más compleja que un medio de cultivo, que puedan limitar el efecto antifúngico de la proteína. En los ensayos realizados se observaron resultados dispares dependiendo del alimento.

Sobre salchichón, PgAFP fue capaz de reducir el crecimiento de *A. flavus* y *P. restrictum* tras una incubación de 5 días (Delgado et al. 2015a), por lo que podría descartarse que las interacciones de la proteína con los componentes del embutido anulen su actividad antifúngica, lo que permitiría su aplicación en este tipo de productos. Sin embargo, considerando que esta proteína no muestra una actividad fungicida, sino fungistática, no es esperable que el efecto protector frente a mohos toxigénicos pueda extenderse durante el procesado completo de los embutidos. En este sentido, a pesar de que durante las primeras 24 h tras el tratamiento con PgAFP se produce una disminución en las proteínas relacionadas con la ruta biosintética de aflatoxinas en *A. flavus* (Delgado et al. 2015b), al no producirse una inhibición total del crecimiento de mohos toxigénicos, a más largo plazo puede provocar un estímulo de la producción de aflatoxinas al inducir un estrés oxidativo en el moho productor (Delgado et al. 2015b). En consecuencia, a pesar de que la aplicación de PgAFP puede ser útil para el control del peligro que supone el desarrollo de mohos toxigénicos en este tipo de alimentos, es preciso plantearse su utilización como una medida complementaria junto a otras estrategias de biocontrol, como puede ser la utilización de cultivos iniciadores.

Por otra parte, en un ensayo similar realizado sobre queso, PgAFP fue incapaz de inhibir el crecimiento de *A. flavus* utilizando concentraciones que habían sido eficaces en medios de cultivo y en el salchichón. Dado que la concentración de PgAFP, las condiciones de temperatura, actividad de agua, humedad relativa, fueron similares en ambos experimentos, y que la concentración de NaCl y el pH entre 1 y 12 no afectan a la actividad antifúngica (Delgado et al. 2015a), la diferencia en cuanto a eficacia del tratamiento antifúngico debe residir en compuestos que estén presentes en queso y no en salchichón. Entre los compuestos presentes en queso susceptibles de disminuir la eficiencia de PgAFP se encuentran diferentes cationes, especialmente el calcio (Chekri et al. 2012). Los cationes pueden jugar un papel fundamental en la reducción de la eficacia de proteínas antifúngicas (Galgóczy et al. 2013; Kaiserer et al. 2003; Theis et al. 2003; Thevissen et al. 1999, 1996) y al encontrarse en concentraciones relativamente altas en queso, podrían ser los responsables de la pérdida de actividad de PgAFP en este alimento. Para evaluar su efecto sobre la actividad antifúngica, *A. flavus* se trató con PgAFP en

medios enriquecidos con $CaCl_2$, $MgCl_2$ y KCl. Las sales que aportaron iones divalentes redujeron drásticamente la eficiencia de PgAFP siendo el más notable el caso de Ca^{2+}, mientras que el K^+ no tuvo un efecto reseñable sobre la actividad antifúngica de PgAFP (Delgado et al. 2015d). El papel del calcio en los mecanismos de resistencia de *A. flavus* frente a PgAFP se discutirá más adelante.

La falta de actividad de PgAFP en queso y probablemente en otros alimentos ricos en calcio, junto con la limitación de que puede no ser suficiente para evitar el crecimiento de mohos toxigénicos durante un período prolongado y el hecho de que algunos mohos toxigénicos de interés en alimentos, como *A. parasiticus*, sean poco susceptibles a PgAFP (Delgado et al. 2015a) obligan a diseñar estrategias que permitan aumentar la eficacia de PgAFP asegurando el control de la producción de micotoxinas. Como se ha indicado anteriormente, el uso de bacterias y levaduras que no se vean inhibidas por PgAFP abriría una nueva vía para su uso combinado con PgAFP, incrementado su efecto antifúngico. Como un paso previo para la utilización de esta estrategia se probaron en medio de cultivo con y sin adición de calcio diferentes combinaciones de PgAFP, *D. hansenii* y *P. acidilactici*, microorganismos habitualmente presentes en alimentos madurados. Las cepas de *D. hansenii* Dh253 (Andrade et al. 2014; Núñez et al. 2015) y *P. acidilactici* fargo 35 fueron seleccionadas por su capacidad antifúngica.

Dependiendo del sustrato se obtuvieron resultados distintos. *P. acidilactici* fue el agente que mostró mayor efecto inibidor en medio de cultivo, de modo que provocaba la mayor reducción de micotoxinas tanto cuando se inoculaba de forma aislada como en diferentes combinaciones con PgAFP o *D. hansenii* Dh253. Se asume que *P. acidilactici* produce una bacteriocina que es eficaz en el control de *Listeria monocytogenes* (Montiel et al. 2013), sin embargo se desconoceen qué condiciones se produce esta bacteriocina, así como su efecto frente a mohos. Por otra parte, se ha descrito la liberación de sustancias de carácter peptídico y bajo peso molecular al medio por bacterias lácticas, que sin inhibir el crecimiento de mohos son capaces de reducir la producción de toxinas (Chang and Kim 2007; Gourama and Bullerman 1995). En cuanto al efecto de PgAFP, en medio de cultivo al que no se le añadió $CaCl_2$, provocó un aumento de producción de micotoxinas por parte de *A. parasiticus*. Este hecho podría estar relacionado con la capacidad de PgAFP de inducir ROS, que contribuyen al inicio de la síntesis de micotoxinas (Jayashree and Subramanyan 2000; Reverberi et al. 2012). Sin embargo, el incremento de la biosíntesis de micotoxinas debido al estrés oxidativo puede descartarse observando los valores de expresión del gen *foxA*, íntimamente ligado a la biosíntesis de aflatoxinas (Reverberi et al. 2012). Por tanto, el estrés oxidativo por sí solo no parece explicar el aumento en la producción de micotoxinas. Además, el papel de las ROS en la producción de

aflatoxinas es controvertido. Recientemente se ha demostrado que durante la producción de aflatoxinas se producen ROS, que a su vez aumentan la tolerancia de las nuevas esporas al estrés oxidativo (Roze et al. 2015). Por otra parte, el aumento en la producción de micotoxinas no se observó en el mismo medio de cultivo cuando contenía calcio, donde tampoco se produjo efecto fungistático. La no estimulación de producción de micotoxinas por parte de PgAFP en presencia de calcio parece ser debida al efecto de la calcineurina y la gamma glutamiltranspeptidasa aumentadas, que limitarían los estímulos estresantes como se discutirá después.

Teniendo en cuenta los resultados obtenidos en medios de cultivo, en alimentos se probaron las combinaciones PgAFP + Dh253 y PgAFP + Dh253 + Pa fargo 35. En salchichón y queso el efecto conjunto de PgAFP y *D. hansenii* disminuyó drásticamente tanto los recuentos como la producción de aflatoxinas por *A. parasiticus*, durante al menos 15 días en un rango amplio de valores de a_w, sin que *P. acidilactici* aportase ningún efecto antifúngico adicional. El efecto conjunto de PgAFP y *D. hansenii* permite maximizar el efecto antifúngico de ambos, ya que la acción aislada de PgAFP se ve limitada en el tiempo (Delgado et al. 2015a) y no es eficaz en alimentos ricos en calcio (Delgado et al. 2015d), y *D. hansenii* no muestra actividad antifúngica a valores de a_w de alrededor de 0.84 (Andrade et al. 2014). De modo que esta combinación muestra un efecto antifúngico duradero y extrapolable a las condiciones físico-químicas de maduración de productos cárnicos crudo-curados y queso. Y por tanto podría incluirse en el sistema de Análisis de Peligros y Puntos de Control Crítico, utilizándose estos agentes bioprotectores tanto como una medida preventiva para evitar el desarrollo de mohos toxigénicos, así como medida correctora, tras eliminar la población fúngica de riesgo. Sorprendentemente, el efecto conjunto de estos dos agentes que carecen de acción por separado en las condiciones probadas ofrece una inhibición de mohos satisfactoria. Este hecho podría explicarse por la acción conjunta de los diferentes mecanismos de acción propuestos para cada uno de estos agentes. De modo que esta cepa de *D. hansenii* compite por el sustrato y el espacio además de producir compuestos volátiles que inhiben el desarrollo de mohos (Núñez et al. 2015), mientras que PgAFP permeabiliza las membranas e induce ROS y apoptosis (Delgado et al. 2015b). Por tanto, este efecto conjunto permitiría desestabilizar la fisiología del moho toxigénico, dando lugar a un efecto inhibidor potenciado.

V.3. Mecanismo de acción de PgAFP

Se analizó la respuesta de una cepa aflatoxigénica sensible de *A. flavus* con y sin la adición de calcio en el medio de cultivo, ya que existen evidencias de que la presencia de estos iones reduce la actividad de proteínas antifúngicas (Galgóczy et al., 2013; Kaiserer et al., 2003; Theis et al., 2003; Thevissen et al., 1999, 1996). Por otra parte, se estudió la respuesta que

permite no ser inhibidos por PgAFP a dos mohos resistentes: la propia cepa de *P. chrysogenum* productora de PgAFP y *P. polonicum*.

En primer lugar se observaron diferencias claras en cuanto al lugar de unión de PgAFP marcada con FITC. En *A. flavus* PgAFP apareció tanto unida en la superficie externa como en el interior celular (Delgado et al. 2015b). Por tanto, el patrón seguido por esta proteína en cuanto a su localización en el moho sensible se asemeja a AFP (Oberparleiter et al. 2003). En este caso las pruebas realizadas no permiten discernir si la localización intracelular es necesaria para que la proteína complete su actividad antifúngica o se produce como consecuencia de esta actividad, y debido al aumento de la permeabilidad celular que se discutirá más adelante. En cuanto a los mohos resistentes se observó una unión de PgAFP en la cubierta externa de *P. polonicum* y de *A. flavus* cultivado en presencia de calcio, mientras que no se unió a la cepa productora *P. chrysogenum* CECT 20922.

Por otra parte, PgAFP no provocó cambios morfológicos en ninguno de los ensayos, tanto en la cepa sensible como en las resistentes, por lo que PgAFP puede catalogarse como proteína no morfogénica, de forma análoga a lo propuesto por (Terras et al. 1992; Osborn et al. 1995) para defensinas de plantas.

Para el estudio de los mecanismos de acción de PgAFP tanto en cepas sensibles como resistentes se evaluaron los cambios en el proteoma utilizando dos técnicas de proteómica comparativa: 2D-PAGE y Label-Free Comparative Proteomics (LFP), ya que cada una de ellas ofrecía ventajas e inconvenientes.

A partir de las alteraciones observadas en la abundancia relativa de proteínas tras el tratamiento con PgAFP, se realizaron diferentes pruebas para comprobar el efecto y el alcance de dichos cambios sobre el metabolismo y la viabilidad de los mohos tratados.

Cada uno de los tres ensayos realizados mostró un número considerable de proteínas cuya concentración relativa se vio alterada por efecto de PgAFP. Fue común en todos los mohos tratados un incremento en el grupo de proteínas ribosomales y del espliceosoma, que además constituyen los grupos más numerosos en los que se observaron diferencias por el tratamiento (Delgado et al. 2015b; Delgado et al. 2015c; Delgado et al. 2015d). Por tanto, esta parece ser una respuesta común de mohos sensibles y resistentes frente a PgAFP, y que no sirve por sí sola para explicar los fenómenos de sensibilidad y resistencia.

Los principales cambios en el proteoma de *A. flavus* tratado con PgAFP radicaron en proteínas relacionadas con el metabolismo energético, la respuesta al estrés y el metabolismo del glutatión, la integridad de la pared celular y la síntesis de aflatoxinas (Delgado et al. 2015b).

De entre esos grupos, las proteínas que se consideran clave para el efecto de PgAFP son la subunidad beta de la proteína G CpcB y la Rho GTPasa Rho1 (Tabla V1), ambas detectadas en menor cantidad en los cultivos tratados. La proteína G se ha relacionado con la señalización de apoptosis en *Aspergillus nidulans* (Binder et al. 2010) por la acción de la proteína antifúngica PAF. En *A. flavus*, una menor cantidad de la subunidad beta provocada por la acción de PgAFP podría desencadenar fenómenos de apoptosis y necrosis (Fig V1). Este extremo se confirmó tras las tinciones realizadas con AO/EB y Anexina-FITC/yoduro de propidio (Delgado et al. 2015b). Rho1 es una proteína clave para la integridad de la pared celular y está relacionada con la biosíntesis de quitina (Levin 2005). Su disminución en *A. flavus* tratado podría relacionarse con la cantidad de quitina depuesta en la pared celular (Fig V1) de *A. flavus* tratado observada tras la tinción realizada con clacoflúor y un incremento de la permeabilidad del moho al SYTOX Green (Delgado et al. 2015b). El aumento de la permeabilidad podría ser la causa de la localización de PgAFP en el interior celular, como se ha comentado anteriormente y también se ha descrito dentro de los mecanismos de acción de otras proteínas antifúngicas como AFP y varias defensinas (Thevissen et al. 1999; Moreno et al. 2006). Los cambios observados en proteínas implicadas en el metabolismo del glutatión pueden ser indicios de una respuesta a un presunto estrés oxidativo desencadenado como consecuencia de la actividad de PgAFP, tal como se ha señalado para PAF y NFAP (Leiter et al. 2005; Galgóczy et al. 2013). Sin embargo, este incremento parece ser insuficiente para contrarrestar los mayores niveles de ROS provocados por PgAFP (Delgado et al. 2015b), que también podrían influir en la puesta en marcha de los fenómenos de apoptosis observados. Además, la inhibición observada también debe estar relacionada con una menor disponibilidad de energía, a raíz de los datos ofrecidos por los análisis de proteómica comparativa. PgAFP produjo un descenso en varias proteínas pertenecientes a las rutas metabólicas de glucólisis/gluconeogénesis, que se tradujo en una menor actividad metabólica en *A. flavus* observada mediante la tinción con FUN-1 (Delgado et al. 2015b). Por último, cabe destacar la menor cantidad de proteínas relacionadas con la biosíntesis de aflatoxinas. Este efecto es prometedor para el control de estos metabolitos en alimentos. Sin embargo, hay que tener en cuenta que PgAFP desencadena estrés oxidativo, y que este hecho podría estimular la síntesis de micotoxinas (Jayashree and Subramanyan 2000; Reverberi et al. 2012). Por lo tanto, es necesario estudiar la cantidad de estas proteínas en incubaciones más prolongadas y que permitan evaluar de una forma más precisa el efecto de PgAFP sobre la síntesis de aflatoxinas.

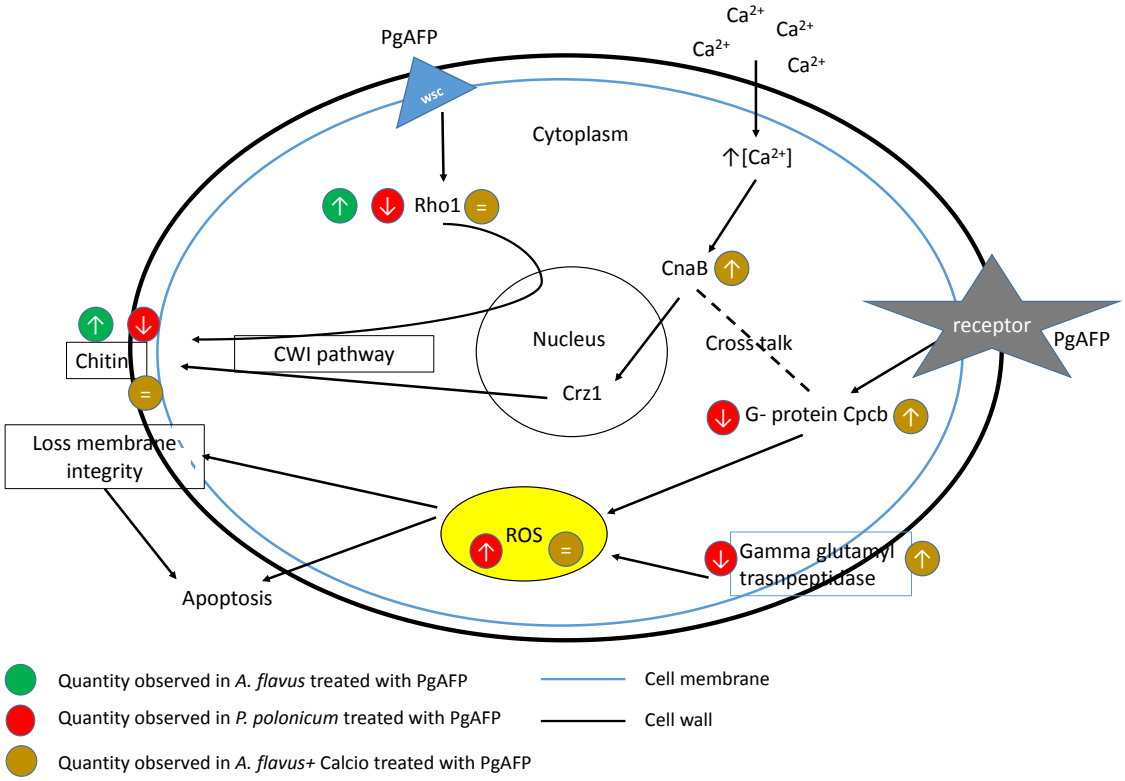

Figura V1. Modelo tentativo para el mecanismo de acción de PgAFP en *A. flavus, P. polonicum* y *A. flavus* en presencia de calcio.

V.4. Mecanismos de resistencia a PgAFP

Los ensayos realizados para estudiar los mecanismos de resistencia en *P. polonicum, A. flavus* y *P. chrysogenum* son unas de las primeras aportaciones al estudio de la resistencia frente a proteínas antifúngicas de mohos. Hasta el momento, la resistencia a estas proteínas se ha estudiado de forma colateral a los fenómenos de sensibilidad, a través de manipulación genética de mohos sensibles para tratar de discernir entre rutas metabólicas que impiden o permiten el mecanismo de acción(Binder et al. 2010). Sólo se han estudiado de forma directa los fenómenos de resistencia en *Sacharomyces cerevisiae* a través de técnicas de manipulación genética (Ouedraogo et al. 2011). Sin embargo, estas manipulaciones pueden alterar la fisiología del organismo manipulado y limitan las rutas metabólicas que se pueden estudiar a aquellas cuya desactivación no comprometa la viabilidad del microorganismo manipulado. Sin embargo la metodología llevada a cabo en el presente trabajo ha permitido estudiar los fenómenos que previenen el efecto inhibitorio de PgAFP sin manipular las condiciones fisiológicas del moho tratado.

De los estudios realizados pueden deducirse diferentes mecanismos de resistencia en mohos como respuesta al tratamiento con PgAFP, según se trate del moho productor de la

proteína, de mohos resistentes de forma natural, como *P. polonicum* o de la resistencia inducida en *A. flavus* por la presencia de calcio.

La resistencia del moho productor de PgAFP, *P. chrysogenum* CETC 20922, parece estar relacionada con la ausencia de receptores para esta proteína en la capa externa celular, dado que no se observa la presencia de PgAFP marcada con FITC en ninguna estructura ni extra ni intracelular (Delgado et al. 2015b). Por lo tanto PgAFP no interacciona con *P. chrysogenum* CETC 20922 y consecuentemente no produce ningún efecto inhibidor. Este hecho se vio corroborado por la ausencia de cambios en los ensayos metabólicos o de viabilidad realizados.

Tampoco los ensayos metabólicos y de viabilidad mostraron cambios en *P. polonicum* tratado con PgAFP. Sin embargo, en este caso sí se observó una unión de PgAFP en la cubierta externa del moho (Delgado et al. 2015c). Como consecuencia de esta unión el proteoma de *P. polonicum* se vio afectado, lo que permite descartar que la carencia de interacción entre PgAFP y el moho sea la causa de la resistencia, sino más bien diferentes mecanismos que *P. polonicum* pone en marcha para contrarrestar el efecto de PgAFP. La mayor cantidad de la proteína Rho GTPasa Rho1 detectada en las muestras tratadas con PgAFP parece ser fundamental para la mayor deposición de quitina observada en el moho con respecto al control no tratado (Fig V1). Este hecho explica parcialmente la disminución de permeabilidad al SYTOX Green en las hifas tratadas con PgAFP, contribuyendo todo ello a la protección frente a PgAFP. Dada la localización de PgAFP, exclusivamente en la cubierta externa de este moho, y que la síntesis de quitina está relacionada con la resistencia, podría pensarse que la proteína antifúngica podría unirse específicamente a la quitina, como se ha observado para AFP (Liu et al. 2002). Sin embargo, PgAFP no tiene capacidad de unirse a quitina regenerada (Delgado et al. 2015c). Por otra parte, *P. polonicum* fue relativamente sensible al tratamiento conjunto con quitinasa y PgAFP. Por lo tanto, la cantidad de quitina depuesta, mediada por Rho1, juega un papel clave en la sensibilidad o resistencia de los mohos a PgAFP. La resistencia en *P. polonicum* va acompañada de un aumento de la quitina, mientras que la sensibilidad de *A. flavus* va ligada a una disminución de quitina (Delgado et al. 2015b) (Fig V1). En consecuencia, puede proponerse la utilización conjunta con quitinasa para aumentar el espectro de inhibición de mohos de PgAFP y por lo tanto la eficiencia del tratamiento antifúngico.

V.4.1. Influencia del calcio en la actividad inhibidora de PgAFP

Como se ha indicado anteriormente, *A. flavus* deja de ser sensible al tratamiento con PgAFP en presencia de calcio, observándose un crecimiento normal y una respuesta a los diferentes ensayos metabólicos y de viabilidad idéntica a la del moho sin tratar. La resistencia

de los mohos a proteínas antifúngicas en presencia de cationes, en el caso de AFP se ha atribuido a que éstos impiden la unión de específica de la proteína al moho porque bloquean por saturación los receptores específicos (Marx 2004). Sin embargo, esta hipótesis puede descartarse en el caso de *A. flavus* tratado con PgAFP en medio enriquecido en calcio, dado que por una parte se observó una unión de la proteína en el exterior del moho y por otra, que se detectaron alteraciones en su proteoma. Estos cambios en el proteoma parecen estar relacionados con una respuesta satisfactoria de *A. flavus* para contrarrestar el efecto de PgAFP gracias a la presencia de calcio, como por ejemplo el aumento de la gamma glutamiltranspeptidasa. La presencia de calcio, tanto en *A. flavus* tratado como sin tratar con PgAFP, provoca un aumento de la subunidad reguladora de la calcineurina que se une al Ca^{2+} Calcineurina CnaB (Delgado et al. 2015d). Dado que la ruta de la calcineurina está implicada en la adaptación al estrés (Juvvadi et al. 2003), este aumento en la señalización ayudaría a contrarrestar los efectos de PgAFP. Por otra parte, también se observó una mayor cantidad de CpcB, cuya importancia en el mecanismo de inhibición se ha descrito anteriormente, siendo mayor en *A. flavus* tratado con PgAFP en presencia de calcio que sin adición de este catión (Tabla V1), lo que puede relacionarse con la ausencia de ROS y de señales apoptóticas. Todo parece indicar, que gracias a los mayores niveles de calcineurina que provoca el calcio *per se, A. flavus* consigue mantener el balance redox en las primeras horas de exposición a PgAFP. Esto puede explicar que se mantengan los niveles de Rho1 y la cantidad de quitina depuesta. Por tanto, limitaría el acceso de PgAFP al citoplasma, permitiendo al moho poner en marcha mecanismos para contrarrestar las ROS, como mayores niveles de gamma glutamiltranspeptidasa, resultando en un balance antioxidante positivo (Fig V1).

El estudio del proteoma de *A. flavus* cultivado en cuatro diferentes combinaciones de ausencia/presencia de PgAFP y 0/0.1M $CaCl_2$, realizando un agrupamiento jerárquico y *heat map*, ha permitido obtener las diferencias que se muestran en la Fig. V2. Los perfiles de los dos cultivos de *A. flavus* en ausencia de calcio, tratado y no tratado con PgAFP, son los que se encuentran más alejados el uno del otro, como puede observarse en el agrupamiento jerárquico realizado a partir de los proteomas obtenidos. Por el contrario, los dos proteomas más parecidos son los pertenecientes a *A. flavus* tratado con PgAFP y sin tratar cultivados con 0.1M de $CaCl_2$. Este hecho parece deberse a que el efecto del calcio *per se* induce cambios en *A. flavus* que le permiten contrarrestar el efecto de PgAFP.

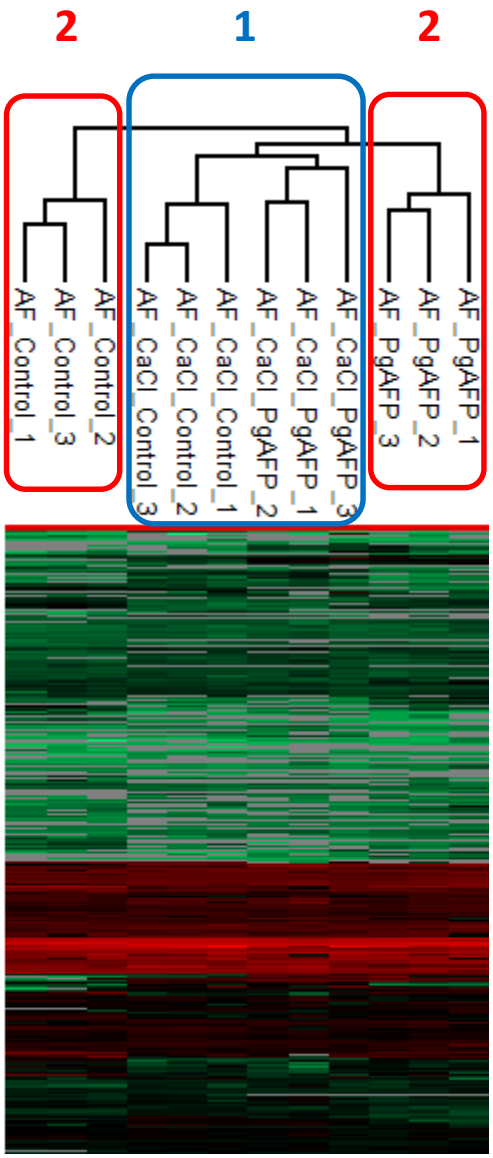

Figura V2. *Heat map* demostrando el agrupamiento jerárquico del análisis comparativo por LFP. Este análisis demuestra que *A. flavus* cultivado en medio rico en $CaCl_2$ exhibe menos variabilidad cuando es tratado con PgAFP (1), que en ausencia de $CaCl_2$ (2).

De todo ello se desprende que existen rutas metabólicas comunes para los fenómenos de sensibilidad y resistencia, y que una mayor o menor cantidad de algunas proteínas claves pertenecientes a estas rutas parecen modular la señalización que acaba conduciendo a la supervivencia o muerte de los mohos (Fig V1). Entre estas proteínas cabe destacar la CpcB, la Rho GTPase Rho1 y otras pertenecientes a la ruta del glutatión (Tabla V1). Sin embargo, no siempre están todas implicadas en los mecanismos de sensibilidad/resistencia que se han evaluado en este trabajo, sino que de forma aislada pueden actuar modulando las respuestas que marcan la diferencia entre supervivencia o muerte de los mohos (Fig V1).

Tabla V1. Aumento (↑) o disminución (↓) relativa en la cantidad de proteínas implicadas en los fenómenos de resistencia/sensibilidad frente a PgAFP.

Nombre de la proteína	*Aspergillus flavus*	*Aspergillus flavus* 0.1 M $CaCl_2$	*Penicillium polonicum*
G protein complex beta subunit CpcB	↓	↑	-
Rho GTPase Rho1	↓	-	↑
Gamma-glutamyltranspeptidase	↓	↑	-
Glutathione S-transferase	↓	-	-
Cys-Gly metallodipeptidase Dug1	↑	-	-
Glutathione synthetase	↑	-	-
Glutathione S-transferase GliG-like	↑	↑	-
Glutathione-S-transferase theta, GST	↑	-	-
Cell wall biogenesis protein glutathione transferase (Gto1)	-	-	↑

Por todo lo anteriormente expuesto, se puede considerar que las proteínas antifúngicas producidas por mohos comparten similitudes en cuanto a sus mecanismos de acción, pero no son exactamente iguales para todas las proteínas. En particular, la resistencia y sensibilidad frente a PgAFP está modulada a través de dos vías, relacionadas con la deposición de quitina y aumento/disminución de ROS mediadas respectivamente por Rho1 y CpcB (Fig. V1), donde las cantidades de estas dos proteínas juegan un papel fundamental en la supervivencia del moho. Además, algunas de las proteínas implicadas en la ruta metabólica del glutatión contribuyen a una respuesta satisfactoria o insatisfactoria frente a las ROS inducidas por PgAFP. En particular, la gamma glutamiltranspeptidasa parece que juega un papel fundamental contrarrestando las ROS, mientras las demás no ofrecen una respuesta de supervivencia satisfactoria (Tabla V1 y Fig. V2). Estos cambios parecen estar relacionados con los altos niveles de calcineurina provocados por una alta concentración de calcio extracelular.

Este trabajo se ha orientado al desarrollo de estrategias para controlar mohos toxigénicos en alimentos. Se ha estudiado el mecanismo de acción y el de resistencia frente a la proteína antifúngica PgAFP, habiéndose diseñado sistemas complementarios para maximizar el efecto de PgAFP. Dado el resultado satisfactorio de la combinación de PgAFP y *D. hansenii* para controlar mohos toxigénicos, se propone su uso como cultivo protector para alimentos madurados de humedad intermedia. De este modo se podría mejorar la seguridad alimentaria para este tipo de alimentos y se reduciría el riesgo para la salud del consumidor.

VI. CONCLUSIONS

PgAFP inhibits a wide range of unwanted moulds in culture media, including the main mycotoxin-producing species. The mechanism of action involves lower relative quantity of Rho1 and G-protein subunit β CpcB and leads to apoptotic and necrotic events triggered by reduced metabolic activity, altered cell wall integrity and increased oxidative stress.

PgAFP increases aflatoxin production by *Aspergillus parasiticus* in culture medium, being not related to changes in peroxisomal β-oxidation.

Intrinsic resistance to PgAFP is due to an activated cell wall integrity pathway through increased Rho1 levels leading to higher chitin deposition in *P. polonicum* or the lack of specific receptors in the outer layer of the PgAFP-producer *P. chrysogenum*.

Calcium abolishes PgAFP inhibition of *A. parasiticus* in culture medium but efficiently decreases aflatoxin production, keeping cell wall integrity and redox balance where increased calcineurin and γ-glutamyltranspeptidase levels play a key role. Similarly, PgAFP displays valuable antifungal ability on dry-fermented sausage but not on ripened cheese, which is also attributed to the high calcium content of the latter.

Pediococcus acidilactici dramatically lowers aflatoxin production by *A. parasiticus* in culture media, even with a high calcium content, but does not enhance the antifungal activity accomplished by the other biopreservative agents on intermediate moisture foods.

The combined treatment of *Debaryomyces hansenii* and PgAFP overcomes the limitations of their individual use, efficiently lowering both aflatoxigenic mould load and aflatoxin production in dry-fermented sausage and ripened cheese.

Appropriate combinations of PgAFP with other biopreservative agents would improve intermediate moisture foods safety by efficiently lowering toxigenic molds counts and mycotoxin production.

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VIII. ABSTRACT

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Moulds growing on foods with intermediate moisture, such as cheeses or dry-cured meats, can contribute to the final sensory characteristics in these products. However, these moulds can produce mycotoxins that are potentially hazardous for consumers. To control the mycotoxin occurrence through food processing, the prevention of toxigenic mould growth is a key issue. One of the best strategies is those based on the use of antifungal proteins and their combination with bioprotective microorganisms to enhance their potential inhibition. To maximize the antifungal effect of these proteins is necessary to know the mechanism of action as well as the survival response of resistant moulds. The main objective of this work was to study the antifungal effect and the mechanism of action of PgAFP protein produced by *Penicillium chrysogenum* against common toxigenic moulds. The combined action of PgAFP with *Debaryomyces* hansenii and *Pediococcus acidilactici* has been also evaluated. For that, comparative proteomics, metabolic, and viability tests and gene expression methods have been used.

The antifungal protein PgAFP exhibited an efficient fungistatic effect against toxigenic moulds usually present in dry-cured foods both in culture medium and on dry-fermented sausage, but not on cheese. On the other hand, PgAFP increased aflatoxin production in culture media, but this fact seems not to be consequence of oxidative stress, given that the unaltered expression of *foxA*, a marker for fatty acid oxidation linked to aflatoxin production. In culture media, *Pediococcus acidilatici* alone or combined with PgAFP and/or *D. hansenii* dramatically reduced aflatoxin production. Nevertheless, on dry-fermented sausage as well as on cheese PgAFP and *D. hansenii* reduced significantly mould counts and aflatoxin production, whilst *P. acidilactici* did not enhance the inhibitory activity of this efficient combination. Therefore, the combined use of PgAFP and *D. hansenii* can be proposed as a preventive action or corrective measure to control unwanted moulds in critical stages of dry-cured products to enhance the food safety.

PgAFP is located both inside and bound to the outer layer on treated sensitive *A. flavus*. Comparative proteomic analyses revealed that the mechanism of action of PgAFP on the sensitive *Aspergillus flavus* seems to be multifactorial. Lower relative amounts of Rho1 and G-protein subunit β CpcB play a key role triggering apoptosis or necrosis through increasing cell permeability, reducing chitin content in cell wall, and increasing reactive oxygen species (ROS). A decrease of proteins involved in aflatoxin biosynthesis was also noticed.

PgAFP neither bound nor penetrated in the resistant PgAFP-producer *P. chrysogenum*. Then, the resistance of this mould should be due to the absence of receptors in its outer layer. However, PgAFP bound to the outer layer of resistant *P. polonicum*, provoking an increase of G-protein subunit β CpcB and Rho1. Thus, the absence or block of receptors in this mould can be ruled out, and the successful response of the resistant mould seems to be based on the higher abundance of protein Rho1 that would lead to the increased chitin deposition via cell wall integrity (CWI) signaling pathway. Indeed, a combined treatment with PgAFP and chitinase provoked *P. polonicum* inhibition, showing synergistic effect. Thus, this can be a strategy to exploit to enhance the PgAFP range of inhibition.

The addition of calcium to substrate provokes a loss of inhibitory activity of PgAFP against the sensitive *A. flavus*. In medium with 0.1 M $CaCl_2$, PgAFP bound to the outer layer of *A. flavus*, but it was not able to penetrate into the cytoplasm. Moreover, PgAFP did not alter metabolic capability, chitin deposition, intracellular ROS levels, and hyphae viability. *A. flavus* resistance to PgAFP in 0.1 M $CaCl_2$ seems to be mediated by calcineurin, G-protein, and γ-glutamyltranspeptidase that combat oxidative stress and impede apoptosis.

The results obtained in this work could serve to design new strategies to improve the bicontrol of toxigenic moulds in dry-cured foods using PgAFP combined with *D. hansenii* and *P. acidilactici*.