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Abstract

The aim of the study was to characterize Maillard reactions in meat under different cooking treatments. Considered temperature-time combinations included raw samples (control), 58, 80, 98 and 160° C for 72 min, 118° C for 8 min and 58° C for 17 hours. Furosine, a marker for heat treatment, was detected in all groups with roasting having a 4-fold increase over the control. Sous-vide treatment at 80°C, boiling and autoclaving also contribute to a significant increase in furosine. Nɛ-carboxymethyllysine, an indicator for advanced glycation end products, showed negligible amount in control, but increased with cooking temperature, with oven samples showing the highest values. A similar increasing trend was observed in lanthionine, covalently bonded protein crosslinks, which arises due to severe thermal regimes. Simultaneously, glycation and deamidation formation were tracked in meat proteins through peptidomics to highlight residue level changes that might affect nutrient value in processed muscle based foods.

Keywords	Furosine; lanthionine; protein crosslinks; carboxymethyllysine; advanced glycation end products; Maillard reaction; cooked meat; residue level modifications
Taxonomy	Agriculture, Biological Sciences
Corresponding Author	Jorge Ruiz-Carrascal
Corresponding Author's Institution	University of Copenhagnen
Order of Authors	Bhaskar Mitra, René Lametsch, Ines Greco, Jorge Ruiz-Carrascal
Suggested reviewers	shiyuan dong, Deborah Markowicz Bastos, Jose Manuel Lorenzo Rodriguez

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Advanced glycation end products, protein crosslinks and post translational modifications in pork subjected to different heat treatments

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Corresponding author's name:

Jorge Ruiz-Carrascal <u>Mailing address</u>: Department of Food Science Food Design and Consumer Behaviour University of Copenhagen Rolighedsvej 30, 3rd floor 1958 Frederiksberg C Phone:45 35 33 32 22 E-mail: jorgeruiz@food.ku.dk

This paper deals with the effect of an assortment of heat treatments, reflecting those most used for heat processed meat products, on the levels of Maillard reactions markers and on the consequent protein modifications of pork proteins, including formation of furosine, carboxymethyllysine and lanthionine. Protein residue level modification was also addressed through proteomics.

Both cooking time and cooking temperature showed a clear effect on most of these parameters, indicating that the type of heat process for meat products leads to different extent of Maillard reactions and derived protein modifications that might eventually influence the nutritional quality and the protein bio-accessibility. Peptide modifications, such as formation of carboxymethlylysine or pyroglutamic acid or deamidation were also detected at residue level. Interestingly, studied proteins showed a different level of modifications.

The information obtained provides with knowledge about the extent of protein structural modifications under specific cooking conditions, and may be useful in the optimization of heat processing for meat products aiming for optimized protein nutritional features.

HIGHLIGHTS

- Maillard reactions in pork under different heat treatments were studied.

- Early stage Maillard reactions and AGEs increased with higher cooking temperature and time

- Glycation and deamidation were tracked in meat proteins through peptidomics

- Proteins showed a different extent of modification due to Maillard reactions at the residue level

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4 5	1	Advanced glycation end products, protein crosslinks and post translational modifications in pork
6 7	2	subjected to different heat treatments.
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10 11	4	Authors: Bhaskar Mitra, Rene Lametsch, Ines Greco, Jorge Ruiz-Carrascal*
12 13	5	Address: Department of Food Science, Faculty of Science, University of Copenhagen,
14 15	6	Rolighedsvej 30, DK-1958 Frederiksberg C, Denmark
16 17	7	
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21	10	* Author to whom the correspondence should be sent:
23 24	11	Jorge Ruiz Carrascal, Department of Food Science, Faculty of Science, University of Copenhagen,
25 26	12	Rolighedsvej 30, DK-1958 Frederiksberg C, Denmark
28	13	Phone: +45 23810623
29 30	14	E-mail: jorgeruiz@food.ku.dk
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Abstract

The aim of the study was to characterize Maillard reactions in meat under different cooking treatments. Considered temperature-time combinations included raw samples (control), 58, 80, 98 and 160° C for 72 min, 118° C for 8 min and 58° C for 17 hours. Furosine, a marker for heat treatment, was detected in all groups with roasting having a 4-fold increase over the control. Sous-vide treatment at 80°C, boiling and autoclaving also contribute to a significant increase in furosine. N^{ε} -carboxymethyllysine, an indicator for advanced glycation end products, showed negligible amount in control, but increased with cooking temperature, with oven samples showing the highest values. A similar increasing trend was observed in lanthionine, covalently bonded protein crosslinks, which arises due to severe thermal regimes. Simultaneously, glycation and deamidation formation were tracked in meat proteins through peptidomics to highlight residue level changes that might affect nutrient value in processed muscle based foods.

Keywords: Furosine; lanthionine; protein crosslinks; carboxymethyllysine; advanced glycation end products; Maillard reaction; cooked meat; residue level modifications

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1. Introduction

124 33 Cooking does not only make meat microbiologically safer, but also enhances its aroma, colour and 125 126 34 palatability (Lund & Ray, 2017). However, undesired and unintentional outcomes such as loss of 127 128 35 essential amino acids and generation of hazardous compounds occur under the influence of 129 ¹³⁰ 36 thermal processing, which has a detrimental effect on meat nutritive quality and safety (Trevisan, 131 132 37 De Almeida Lima, Sampaio, Soares, & Markowicz Bastos, 2016). With cooking operations 133 134 38 intermediate Amadori compounds are formed, following different chemical pathways that produce 135 136 39 aroma, flavour and browning, important for consumer acceptance. However, heat treatment of food 137 also results in development of advanced glycation end products (AGEs) that are potentially toxic 138 40 139 and decrease the nutritional value of protein (Henle, 2009). 140 41

During the early stage of Maillard reactions (MRs), furosine acts as an indicator of the extent of 142 42 143 damage in food items (Pompei, Spagnolello, & Alimentari, 1997) and on their slow degradation, 144 43 145 146 44 partial AGEs are formed (Li, Liu, Meng, & Wang, 2017). Out of many reactions during non-147 enzymatic browning, when lysine reacts with reducing sugars, fructosylysine (FL) is formed, and ₁₄₈ 45 149 46 further oxidized to N^e-carboxymethyl lysine (CML), a frequently used marker of dietary AGEs 150 151 (Račkauskiene et al., 2015; Roldan et al., 2015). As much chemical methods determine formation 47 152 153 48 of CML, such glycation modifications could also be tracked via proteomics which provides a well-154 155 established analytical platform. The fact that AGE formation was higher in frying and roasting 49 156 157 50 rather than boiling could be confirmed through redox proteomics as mentioned by Hu et al. (2017). 158 159 51 Heat and alkali treatments during food processing also result in the formation of dehydro- and 160 161 cross-linked amino acids, such as lysinoalanine (LAL), histidinoalanine and lanthionine (LAN) in 52 162 ¹⁶³ 53 proteins (Friedman, 1999). With a proton from cystine abstracted and persulfide elimination in the 164 ¹⁶⁵ 54 β position, dehydroalanine (DHA) is yielded which then attacks the nucleophilic side of amino acids 166 167 resulting in the above mentioned cross-links. These DHA-derived compounds and covalent cross-55 168 169 56 links (LAN and LAL), apart from decreasing protein digestibility and texture also impact tertiary 170 171 57 protein structure with an increase in molecular weight (Wada, 2014).

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The intake of MRPs from processed foods has a possible correlation with serum AGE levels in humans with the possibility that it might promote oxidative damage, aging, diabetes, obesity and cardiovascular diseases (Trevisan et al., 2016). Some studies suggest that dietary AGEs are potential indicators of oxidative stress and inflammation (Chen & Scott Smith, 2015). Furthermore, no association of dietary AGEs was found with protein bound AGEs in human body, while ¹⁹¹ 63 significantly increasing free CML levels in plasma and urine (Scheijen et al., 2017). However, the 193 64 risk effects of dietary AGEs on human health are still contentious (Sun et al., 2015).

195 65 Typically, the amount of formed AGEs is dependent upon several parameters, like cooking method, temperature, time or protein and fat content (Scheijen et al., 2016). There is however very 197 66 little information about the extent of MRs and the consequent formation of MRPs, including AGEs, 199 67 201 68 in different types of meat products. While cooked meat has been considered as a main source of AGEs in diets (Goldberg et al., 2004), such information was based on enzymatic assays, which 203 69 have been demonstrated totally inaccurate for food matrixes (Poulsen et al., 2013).

Therefore, our work aimed to get a deeper knowledge on how thermal treatments of pork, with different combinations of time and temperature that mimic those most commonly used for meat processing, could induce Maillard and cross-link modifications in pork. Early and late stage MRPs were tracked chemically, opening the possibility of use them as markers for thermal treatment in cooked meat products. Assessment of AGEs content through detection of CML in cooked meat samples so that guidelines could be developed for evaluating associated risks with dietary AGE consumption in the future. Furthermore, impact of protein glycation was also investigated on amino acid residues via a peptidomic approach to gain a deeper understanding about residue level ²²² 79 modifications.

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2. Materials and methods

2.1. Chemicals (Analytical grade)

244 Reagents used in this experiment are enlisted below: Iodoacetamide (IAA), Phosphate buffered 82 245 246 83 saline (PBS), Perfluoropentanoic Acid (CF₂)₃COOH) and DL-lanthionine were brought from 248 84 Sigma Aldrich, Missouri, USA. Other chemicals like Sodium dodecyl sulphate (SDS) and 1, 4-249 250 85 Dithio-DL-Threit (ol) (DTT) were obtained from AppliChem GmbH, Darmstadt, Germany. Urea 252 86 (CH_4N_2O) , Sodium Acetate and Hydrochloric Acid (HCl) were purchased from Merck KGaA, 254 Darmstadt, Germany. Buffers including Acetonitrile (CH₃CN) and Formic Acid (FA) were 87 255 outsourced from VWR International, Søborg, Denmark. External and internal standards included 256 88 N^s-carboxymethyl-L-Lysine (CML), Furosine dihydrochloride and deuterated lysine (L-Lysine-4, 4, 258 89 90 5, 5 -d4 hydrochloride) and they were from Polypeptide Group (Strasbourg, France). Millipore-Milli-260 262 91 Q system (Milli-Q Plus, Bedford, MA) treated water was used for buffer preparation.

2.2. Processing Design

Seven female pigs weighing in the range of 83 - 86 kg were collected from Danish Crown (Supplier 93 266 94 No. 77752, Denmark). Animals were CO₂ stunned and killed by exsanguination. pH values ranged 268 from 5.5-5.6 and the proportion of carcass lean ranged 59 – 63 %. Carcasses were stored for 24h 95 270 96 at 4°C. Longissimus lumborum muscles from both sides of the carcass were selected. Steaks of 2 97 cm thickness were chopped, labelled and packed in vacuum bags (LogiCon EM-628824 -98 Vacuumpose 200 x 270 x 0,090 mm³, Kolding, Denmark) and kept at -80° C. Study design 276 99 included 7 pigs x 7 cooking methods x 3 steaks, for a total of 147 steaks. Sample replicates were ²⁷⁹100 then thawed and cooked.

²⁸¹ 101 2.3. Cooking treatments

²⁸³ 102 Pork chops were cooked in various ways, trying to reflect the most common heat treatments and 284 ²⁸⁵ 103 cooking methods for meat. Treatments were RAW (control), OV16072 (roasted in convective oven 286 287 104 at 160 °C for 72 min), B9872 (braised vacuum packaged in simmering water at 98 °C for 72 min), 288 289 105 SV5872 (sous vide treatment at 58 °C for 72 min in a thermostatized water bath), SV5817 (sous 290 291 106 vide treatment at 58 °C for 17 hours, in the same water bath), SV8072 (sous vide treatment at 80

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²⁹⁹107 °C for 72 min, also in the same water bath) and AC1188 (autoclave treatment at 118 °C for 8 min, 300 301 108 with an F-value = 2.56). Those chops to be cooked under 100° C, were coded and vacuum-packed 302 ³⁰³109 in Cryovac CN 300 bags (Sealed Air Corporation, North Carolina, USA); those aiming for cooking 304 ³⁰⁵110 at 118 °C were put in LogiCon vacuum bags (EM-62890, Kolding, Denmark) while oven samples 306 ³⁰⁷111 were roasted unpackaged. A Type T external probe (fitted to a Testo 176 T4 data logger) was 308 ³⁰⁹112 attached to a dummy sample in each batch to track the time-temperature profile of the meat core 310 311 113 and surface. After cooking, samples were submerged under ice cold water at 4 °C. Replicates 312 313114 were then packed again, coded and stored at -80 °C. 314

315 115 2.4. Protein determination

Protein determination of steak samples was performed after they were measured at a wavelength
of 280 nm following a procedure previously described by (Mitra, Lametsch, Akcan, & RuizCarrascal, 2018).

323119 2.5. Tracking Furosine

₃₂₅ 120 Furosine content was determined in meat samples as described by Jansson et al. (2014) with 326 ₃₂₇ 121 major adaptations. 2.5 g of frozen meat was homogenized by Ultra Turrax T25 for 30 sec with 328 ₃₂₉122 20,500 rpm in 20 mL of PBS (0.01 M, pH 7.4). Acid hydrolysis was made by mixing 1 mL of meat 330 123 homogenate, 3 mL of 10 M HCl was added in a screw cap glass tube and nitrogen (2 atmosphere 331 332 333 124 pressure) was bubbled through the mixture for 2 min to make it homogenous and prevent it from 335[→]125 334 coming in contact with oxygen. The tubes were sealed and placed in the oven at 110° C for 18 ³³⁶ 337 126 hours. After heating, samples were cooled in a fume hood and cooled mixture was filtered through ³³⁸127 a filter paper (Syrevasket foldefilter 3FF-15 cm, 20 µm, Frisenette ApS, Knebel, Denmark). 1 mL of 339 ³⁴⁰128 the filtrate was pipetted out by a 3-piece single-use syringe (Omnifix-F, B. Braun Melsungen AG, 341 ³⁴²129 Germany) and was subjected to pass through a 0.45 μ m disposable filter (Minisart NML Plus, 343 ³⁴⁴ 130 Sartorius Stedim Biotech GmbH, Goettingen, Germany). The sample was diluted 5 times in 3M 345 ³⁴⁶131 HCl and 300 µL was transferred into HPLC Vials (Phenomenex, Danaher Corporation, USA). 347 Detection of furosine was performed on a HPLC System (Agilent 1100 series, USA) with a Diode 348 132 349 350 133 Array Detector (DAD, Gilson, USA), using a Supelco Supercoil LC-8 Column (Sigma-Aldrich Inc.)

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³⁵⁸ 359 **13**4 and was triggered onto the autosampler prior analysis. With a flow rate of 1 mL/ min, 0.06 M ³⁶⁰ 135 sodium acetate buffer solution was operated as the mobile phase in an isocratic mode. The 361 ³⁶²136 injection volume was 10 µL, and the DAD detection (UV) was set at 280 nm. The temperature of 363 ³⁶⁴ 137 the column was kept steady at 25 °C by a chilling-heating system in a column oven (Jones 365 ³⁶⁶138 Chromatography 7955, SpectraLab Scientific Inc., Canada). Quantification was performed by using 367 368 139 external calibration with furosine dihydrochloride. Furosine concentration was expressed in mg/100 369 370 140 g protein. All the analyses were carried out in triplicates.

372 141 2.6. AGEs and protein crosslinks

374 142 Acidic hydrolysis of meat samples was performed in order to quantify AGEs and protein cross-links 375 via LC-MS/MS. Modifications and major adaptations were done to the protocol as proposed by 376143 377 378 144 Roldan et al. (2015). Briefly, 50 mg of meat were homogenized with 1 mL 6 M HCl and incubated 379 for 24 hours at 110 °C. Thereafter, HCl was evaporated by gentle nitrogen flow. Dry samples were 380 145 381 dissolved in 1 mL water, sonicated for 5 minutes at room temperature and centrifuged at 19,000 382 146 383 ₃₈₄ 147 rpm at 4° C. Supernatants were diluted 1:20 (v/v) in water containing 1 µg/mL deuterated lysine 385 ₃₈₆ 148 (internal standard for LC-MS/MS quantification). Following a second centrifugation step (19,000 387 ₃₈₈149 rpm at 4°C), 10 µL of supernatant were injected for LC-MS/MS analysis.

389 390¹⁵⁰ Simultaneous determination of CML and LAN was performed by reverse-phase UHPLC coupled 391 392¹⁵¹ with mass spectrometer (ThermoScientific Q-Exactive Orbitrap, USA), using electrospray ionization ³⁹³ 394 **152** in positive mode. Source parameters were optimized by auto-tuning the mass spectrometer via ³⁹⁵ 396</sub>153 direct injection of standard solutions in the ionization chamber. The method was designed for a ³⁹⁷154 two-step separation of analytes of interest: 100% aqueous buffer (5 mM perfluoropentanoic acid in 398 ³⁹⁹ 155 water, buffer A) from 0 to 5 minutes for detection of LAN, followed by a 0 to 50% organic mobile 400 ⁴⁰¹ 156 phase gradient (5 mM perfluoropentanoic acid in 100% acetonitrile, buffer B) from 5 to 15 minutes, 402 ⁴⁰³157 when detection of CML was achieved. Flow was then as follow: 50 to 100 % B (15 to 17 minutes); 404 ⁴⁰⁵158 100% B (17 to 22 minutes); 100 to 0% B (22 to 24 minutes) and 100 % A (24 to 27 minutes). 406 407 159 Identification of peaks was performed by monitoring the typical m/z ratio for each analyte and two 408 409 160 of the most abundant derived fragments, using ThermoScientific Xcalibur software. With a

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417 161 retention time of 10.4 min and 12.3 min and with m/z ratio of 205.1 and 151.1, CML and deuterated 418 419 420 **162** lysine were detected. Two daughter fragments were identified which were 84.1 and 130.1 for CML ⁴²¹ 163 and 88.1 and 134.1 for deuterated lysine. Simultaneously, LAN was detected with a retention time 422 ⁴²³164 of 3 min and m/z ratio of 209.1, and the most abundant derived daughter ion was identified as 120. 424 ⁴²⁵ 165 Quantification was performed based on a previously derived external calibration curve in which the 426 427 166 peak area ratios of pure analytes compared to the areas of the internal standard detected in each 428 429 167 run were calculated. Standard concentrations ranged from 5 to 10,000 ng/mL. The resulting 430 431 168 concentrations in meat samples were then referred to the known protein content of each sample 432 433 169 and expressed as mg/100 g protein.

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2.7. Peptidomic approach to trace modifications

Samples were first hydrolysed by using trypsin following the method previously described by Mitra 437 171 438 439 172 et al. (2018). After acidification, peptide modification of samples were analysed by a Dionex 3000 440 441 **173** RSLC UHPLC system (Thermo Fisher Scientific, Hvidovre, Denmark) coupled with a Q Exactive 442 ₄₄₃174 mass spectrometer (Thermo Fisher Scientific, Hvidovre, Denmark) following the conditions 444 ₄₄₅ 175 previously described (Mitra et al., 2018). Tracked site specific modifications taken from Deb-446 ₄₄₇ 176 Choudhury et al. (2014) are enlisted in Table 1. Carbamidomethylation was added as static 448 449⁻¹⁷⁷ modification and rest all modifications uploaded was dynamic. Different amino acid residue targets 450 were set in accordance to the modification type and their mass shift were recorded. In addition to it, 178 451 452 453 **179** a separate database search was also conducted to check susceptibility of lysine via participation in 454 455 **180** AGEs formation in myosin and actin for the salt soluble fraction and in β -enolase and myoglobin for ⁴⁵⁶ 181 water soluble fraction. Apart from this, one the most important post-translational modifications, 457 ⁴⁵⁸ 182 referred to as deamidation was also tracked in myoglobin in our experiments as literature suggests 459 ⁴⁶⁰ 183 that amount of this modification can play a crucial role in protein unfolding and utility (Cañete, 461 ⁴⁶² 184 Mora, & Toldrá, 2017). Total abundance of selected proteins (myosin, actin, beta-enolase and 463 ⁴⁶⁴ 185 myoglobin) and calculation of the modification ratio were calculated as explained in Mitra et al. 465 466 186 (2018), using equation 1. 467 468 187 Equation 1: Modification Ratio = (peptide abundance (sample) / protein abundance (sample)).

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476	2.8.	Statistical Analysis	
⁴⁷⁷ 478	One-wav A	ANOVA was used with cooking treatment as the independent variable, using the Gene	eral
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481		der (GLM) procedure (SPSS 22.0, IBM, OSA). Descriptive statistics and takey's test w	ere
⁴⁸² 191 483	performed	to determine variations among the mean values. When the effect was significant (F	D <
⁴⁸⁴ 192 485	0.05), Tuk	ey's test was used at 5% level to make pair wise comparisons between sample mea	ns.
⁴⁸⁶ 193 487	All values i	represented are shown as mean with standard error bar.	
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3. Results and discussion

3.1. Furosine

⁵³⁹ 197 Furosine often referred to as $(\epsilon$ -N-(furoylmethyl)-, lysine), is considered to be an indirect indicator 540 ⁵⁴¹ 198 for Amadori products and often times related to early stage Maillard reaction products (Henle, 542 ⁵⁴³199 2009). Fig. 1 details the amount of furosine formation induced by cooking treatments. Such 544 545 200 reactions could also be influenced by the availability of reducing sugars like glucose and ribose 546 547 201 that react with ε-amino groups of lysine (Roldan et al., 2015). No increase in furosine was 548 observed between RAW and SV5872 groups, probably owing to the fact that the extent of 549 202 550 formation of this type of compounds is likely to occur at higher temperatures. But at this same 551 203 552 temperature and with longer time (17 h) a significant increase was traced from RAW group, 553204 554 555205 possibly because longer time might positively influence the formation of indirect Amadori 556 557 206 compounds. However, there was no increase in furosine content in samples cooked at 58°C from 558 559 **207** 72 min to 17 h. With increase in temperature, SV8072, B9872 and AC1188 groups had significantly 560 ₅₆₁ 208 higher values than RAW and 58°C sous vide groups. This is a very similar trend observed by 562 ₅₆₃209 Pompei and Spagnolello (1997), who showed that the higher formation of furosine in cooked hams 564 ₅₆₅210 was directly linked to increasing heating temperature. To support the above statement, our 566 ₅₆₇211 interpretation is strengthened by the observation that when we compare AC1188 group with 569²¹² 568 SV5817 samples, furosine formation is higher at 118 °C than 58 °C irrespective of the duration of 570 571**213** the treatment. Additionally, OV16072 samples had a 4-fold increase in furosine concentration from ⁵⁷²214 the RAW ones, suggesting increased reaction between lysine residues and reducing sugars 573 ⁵⁷⁴215 probably due to the same reason as mentioned above. On top of that, oven samples were the only 575 ⁵⁷⁶216 unpackaged ones, which lead to a strong dehydration of the surface during the process, and due to 577 ⁵⁷⁸217 that, probably to a marked decrease in water activity. It is well known that low water activity 579 ⁵⁸⁰218 enhances the rate of MRs, which might also contribute to the much higher levels found in oven 581 ⁵⁸²219 cooked samples.

584 220 However, for B9872, SV8072 and AC1188 sample groups, there was no difference in furosine 585 586221 content, even though there was a marked elevation in temperature. This might be due to the fact

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⁵⁹⁴_222 that, even if furosine production was high, some of these compounds might get degraded as MR 595 ⁵⁹⁶ 597**223** progressed, in the process generating intermediate and end products (Trevisan et al., 2016). With ⁵⁹⁸224 such modifications as instigated by MR, lysine loses its biological value with 40 percent of the 599 ⁶⁰⁰225 Amadori product getting transformed into furosine (Rufián-Henares, Delgado-Andrade, Jiménez-601 ⁶⁰²226 Pérez, & Morales, 2007; Schmidt, Boitz, & Mayer, 2017). Therefore, these results point out to an 603 ⁶⁰⁴227 important decrease in nutritional values of meat proteins as cooking temperature increases. 605

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Tracing CML as an AGE marker

608229 CML, being an important indicator for AGEs, was measured in all the sample groups as illustrated 609 in Fig. 2. In the RAW and SV5872 samples, CML values were guite similar indicating to those from 610230 611 samples cooked at lower temperature CML formation was limited. A further confirmation of CML 612231 613 614232 limitation was also observed in SV5817 group when samples had same values with the previous 615 treatments even though the heat treatment took 17 hours. Samples that were braised at 98° C and 616233 617 ₆₁₈234 autoclaved at 118° C did have a significant difference with raw samples, but were similar to 619 ₆₂₀235 SV8072 group, suggesting that CML formation had quite a similar trend with furosine formation. 621 ₆₂₂236 One of the possible reasons for the autoclaved samples to have no increase in CML values was 623 ₆₂₄237 possibly because at this temperature N^ε-carboxyethyl Lysine (CEL) formation is highly favoured 625 626²³⁸ and preferred more than CML generation; chemistry behind such observation may be due to the 628²³⁹ 627 faster reaction rate of methylglyoxal with lysine, rather than the reaction of glyoxal with lysine, at 629 630**240** pasteurization temperatures (Yu et al., 2016). Alternately, another possible way of describing ⁶³¹ 632</sub>241 limited formation of CML can be presence of carnosine as an anti-glycating agent that inhibits ⁶³³242 crosslink and protein glycation induced by reducing sugars and reactive aldehydes (Roldan et al., 634 ⁶³⁵243 2015).

Interestingly when AC1188 and SV5872 groups were compared it could be noticed that
temperature had a role to play in the formation of CML. As reported by Račkauskiene et al. (2015),
CML formation could be based upon two pathways; firstly via oxidative cleavage, the enediol form
of N^ε-fructosyllysine may give rise to CML formation; secondly via the Namiki pathway where the
amino group of lysine can react with GO. In fact, even at a holding time of 8 min, values were

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⁶⁵³249 higher in samples cooked at 118°C than in those cooked at 58 °C for 72 min. In addition to it, 654 ⁶⁵⁵ 656</sub>250 OV16072 samples, had a high significant increase in CML values than all the treatment groups ⁶⁵⁷251 658 which was approximately a 3.5 fold increase from B9872, AC1188 and SV8072 samples, following ⁶⁵⁹252 a similar trend to that reported by Chen & Scott Smith et al. (2015). Such elevated rise in CML 660 ⁶⁶¹253 formation can be attributed to the fact that carbonyls from lipid oxidation might contribute to the 662 ⁶⁶³254 formation of CML via the MR route (Yu et al., 2016). Moreover, upon dehydration caused by 664 665255 roasting, water soluble precursors would be transferred to the meat surface with a higher degree of 666 exposure, and at a lower water activity, hence AGEs formation was accordingly influenced (Chen & 667 256 668 Scott Smith, 2015). The CML results reported by Roldan et al. (2015) were in fact not in agreement 669257 670 with the ones reported here in our study, possibly because their core temperature was kept at 73° 671258 672 C, while in our case the internal temperature in oven samples reached 135 °C. Hence, it seems 673**259** 674 675**260** clear that AGEs generated from the core also regulated the total glycation pool other than the 676 677**261** surface. At any rate, these results confirm that temperature plays a pivotal role in the formation of 678 ₆₇₉262 AGEs.

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Covalent protein cross-links

682 ₆₈₃264 Formation of crosslinks like LAN occurs as a consequence of cooking treatments, as depicted in 684 ₆₈₅265 Fig 3. When food proteins are exposed to heat, alkali and oxidative treatments, inter and 686 687²⁶⁶ intramolecular crosslinking occur. LAN is formed from an early dehydration of cysteine residue to ⁶⁸⁸ 689</sub>267 form dehydroalanine, which then reacts with thiol groups of cysteine to form a crosslinked ⁶⁹⁰268 derivative (Clerens, Plowman, & Dyer, 2012; Singh, 1991). According to Yu et al., (2016), reports 691 ⁶⁹²269 suggest that formation of LAN were much below the level of detection and in some cases after 693 ⁶⁹⁴270 prolonged boiling no traces were found as detected by HPLC. However, with our mass 695 ⁶⁹⁶271 spectrometry method, we were able to detect LAN as a protein covalent crosslink in heated meat 697 ⁶⁹⁸272 products after acidic hydrolysis, possibly due to the higher sensitivity of the mass spectrometry-699 700273 based determination method. Even though formation of LAN is known to occur under alkaline 701 702274 conditions, the formation of LAL by heating in the acidic and neutral pH regions has also been 703

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reported (Friedman, 1999), and so has been its presence in heated meat (Hasegawa, Mukai, 714 276
 Gotoh, Honjo, & Matoba, 1987).

The presence of low levels of LAN in RAW samples is surprising and difficult to ascribe to any controlled factor. Levels of LAN did not significantly increase for SV5872, SV5817 and SV8072 groups as compared to RAW. Reports have also suggested that significant amount of LAN were also traced in keratin polypeptides that were derived from bovine skin (Friedman, 1999), suggesting that the LAN found in the RAW pork could also be naturally present.

A significantly increasing trend could be observed when meat steaks were subjected at a braising temperature of 98° C and at an autoclaving temperature of 118° C thereby confirming that higher temperature might have a role to play in formation of crosslinks. In spite of having no significant differences in LAN values among B9872, AC1188 and OV16072, when we compare RAW to OV16072, we did see a 3-fold increment in this crosslinking process. Owing to which, cross linking ₇₃₆287 formation might influence protein aggregation, due to which protein digestibility could be impaired with reduced enzymatic proteolysis as stated by Wada et al., (2014). On the other hand, Hendriks ₇₄₀289 et al., (2002) stated that LAN had no significant correlation to amino acid digestibility. ₇₄₂290 Nevertheless, although there are inconsistencies in formation of LAN under different heating regimes, our results might direct us to come to a conclusion that temperature might be an 746²⁹² imperative factor in influencing crosslink formation.

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Qualitative Overview of residue level changes 3.4.

3.4.1. Heat induced and other modifications

⁷⁷⁵296 Residue level modifications which are induced thermally are documented in Table 2. Heat induced 776 ⁷⁷⁷ 297 modifications like CML and CEL could be successfully detected in the LCMS analysis. 778 ⁷⁷⁹298 Deamidation, dehydration, di-dehydro and pyroglutamate formation have been tracked and 780 781 299 mapped along with their site specific positions. With myosin being the most abundant protein, it 782 783 300 was more susceptible towards these types of modifications. Surprisingly, no CML and CEL were 784 785 301 tracked in myoglobin and actin. The reason for absence of CML in both actin and myoglobin could 786 be attributed to the fact that they exhibited much more heat stability even after autoclaving meat 787 302 788 samples (Yu, Morton, Clerens, & Dyer, 2016). Nevertheless, deamidation was seen to occur quite 789303 790 791 304 extensively in all the meat fractions but with limited amount in myoglobin.

The ratio of lysine modification was quantified in myosin and beta-enolase as shown in Fig 4A and 793 305 794 795 306 4B respectively. In myosin, some modifications were traced in RAW samples possibly due to 796 ₇₉₇307 sampling, packaging, mincing or postmortem handling prior the freeze thaw process (Yu, Morton, 798 ₇₉₉ 308 Clerens, & Dyer, 2015a) or via formation of actomyosin bridge formation (Yu et al., 2016). In 800 ₈₀₁ 309 SV5872, SV8072, AC1188 and SV5817 groups, an increase in mean value of lysine modification 802 803 310 ratio was observed suggesting that heating might have exposed these hydrophobic amino acids as 804 805³¹¹ protein unfolded (Sun, Zhou, Zhao, Yang, & Cui, 2011). With respect to B9872 and OV16072 806 807</sub>312 groups, mean values were quite high compared to RAW ones and other groups indicating that ⁸⁰⁸ 809</sub>313 such strict treatments might have had a faster effect on lysine modification to CML. Such elevated ⁸¹⁰314 increase in CML could be explained by three theories, firstly, by interaction of carbonyls with lipid 811 ⁸¹²315 peroxidation products (Hu et al., 2017), secondly by a possible faster kinetic reaction between 813 ⁸¹⁴316 radicals and reducing sugars forming more stable products (Utrera et al., 2014) and thirdly with 815 ⁸¹⁶317 dehydration, an increase in pro-oxidant concentration that might contribute to advanced MR 817 ⁸¹⁸318 (Utrera & Estévez, 2013). In beta enclase, a slightly different trend could be seen. While RAW and 819 820319 SV5872 group had negligible CML modification, SV8072 and SV5817 samples had higher mean 821 822320 ratios directing us to hypothesize that higher temperature and longer time did have an influence in 823

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⁸³⁰, 321 glycation modification reactions. A similar scenario for B9872 group in myosin and beta enolase 831 832 was noted. For AC1188, mean ratio was a bit lower possibly due to a holding time of 8 min. 833 ⁸³⁴323 Surprisingly, for the oven samples, lower mean ratio values can be attributed to the fact that such 835 ⁸³⁶324 glycation based compounds might have participated onto further advanced reactions or perhaps 837 ⁸³⁸325 have been aggregated (Yu, Morton, Clerens, & Dyer, 2015b) due to which proteomic detection was 839 ⁸⁴⁰326 difficult.

842327 Pyro-glutamic formation could also be seen on almost all the meat proteins except myoglobin. 843 Such formations not only take place at higher temperatures but are also possible at relatively 844 328 845 milder conditions. In fact pyro-glutamic acid formation is not caused by glycation or oxidation but it 846329 847 is believed to occur due to non-enzymatic heating that result in cyclization reactions where a free 848330 849 850331 amino group from glutamine or glutamic acid gets converted into a lactam (Deb-Choudhury et al., 851 852332 2014). According to Yu et al., (2016), the conversion of glutamic acid (Glu, E) to pyro-Glu is at a 853 854333 much slower rate than that of Glutamine (Gln, Q). This is guite in accordance with our results 855 where we identified only 10 modified peptides for E and 16 modified peptides for Q in myosin. ₈₅₆334 857 ₈₅₈ 335 Even for actin, the only modified pyro-Glu formation was for O as represented by 859 860³³⁶ QEYDEAGPSIVHR. Although, protein crosslinking was identified chemically in our aforesaid 861 862³³⁷ mentioned results, through proteomics, there was no detection of dehydroalanine in any of the 863 864³³⁸ proteins, in accordance with previous reported heat modification of meat proteins (Deb-Choudhury 865 866 339 et al., 2014). Among other modifications, di-dehydro conversion was also noticed only in actin in a 867 868 340 serine residue. The possibility of such a transformation exists as was also confirmed by Yu et al., ⁸⁶⁹341 (2015) where di-dehydro of a threonine residue was spotted. In this case either serine or threonine 870 ⁸⁷¹ 342 could participate, as both of them have hydroxyl groups in their amino acid side chains. 872 ⁸⁷³343 Dehydration modifications could also be observed quite a lot in serine and threonine residues in 874 ⁸⁷⁵344 myosin rather than the other proteins.

3.4.2. Deamidation

Modification of amino acids play quite an important role in influencing flavour, taste properties and meat chemistry. Deamidations could be tracked in nearly all the proteins, and more specifically, in meat chemistry. Deamidations could be tracked in nearly all the proteins, and more specifically, in

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⁸⁸⁹348 the four selected ones (Fig 2). One of the key factors explaining the extent of deamidation is the 890 ⁸⁹¹349 availability of asparagine, which is deamidated at much higher rates than glutamine, possibly 892 ⁸⁹³350 because of the side chain amide group from the peptide nitrogen (Robinson & Robinson, 2001). 894 ⁸⁹⁵351 This holds true for our case as well, in which we see from Table 2 that number of asparagine 896 ⁸⁹⁷352 residues deamidated are more than glutamine residues, be it in myosin, actin, beta-enolase or 898 ⁸⁹⁹353 myoglobin. Additionally, the peptide sequence, HGNTVLTALGGILK, derived from myoglobin, with 900 901 354 the letter N highlights the possibility of asparagine getting deamidated more than glutamine. Lastly, 902 903355 for deamidation to occur, it is preferred that N and O residues are always present at the extreme 904 end of the peptide chain rather than being situated in central positions where susceptibility might 905356 906 be low (Cañete et al., 2017). 907357

909358 Fig 4C illustrates the deamidation ratio in myoglobin. From our qualitative data, we do observe 910 conversion of glutamine and asparagine to glutamic acid and aspartic acid respectively indicating 911359 912 913**360** possible deamidation. The chemistry behind it could be described as removal of ammonia from the 914 ₉₁₅361 peptide chain via hydrolysis of the amide groups where glutamine or asparagine residue is 916 ₉₁₇362 transformed into its carboxylic form (Cañete et al., 2017). According to Cañete et al., (2017), 918 ₉₁₉363 temperature, pH and salting conditions are the main drivers behind deamidation, and such 920 921³⁶⁴ deamidations could also be responsible for protein unfolding and protein hydrolysis. Deamidation 922 _____365 in RAW group was present, possibly due to sample handling, including freeze-thaw process. 924 925**366** Values in in SV5872, SV5817 and SV8072 groups were not very different to RAW, indicating that 926 927**367** sous vide cooking methods at moderate temperature had not much to contribute to this ⁹²⁸368 modification. For high temperature groups like B9872, OV16072 and AC1188, deamidation rates 929 ⁹³⁰369 increased up to many fold times, probably due to increased thermal impact. This is in accordance 931 ⁹³²370 with Izzo et al., (1993), who reported a positive correlation between high temperature and the 933 ⁹³⁴371 increase of deamidation ratio.

Deamidation ratio is somehow connected to protein functionality. Thus, Cañete et al., (2017)
suggested that a deamidation of 2-6 % might be beneficial for improving nutritional quality.
However, excessive deamidation rates might impair protein quality as well, due to higher

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 975 possibilities of protein aggregation via interaction by hydrophobic and electrostatic forces (Lei,
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 376 Zhao, Selomulya, & Xiong, 2015). Hence temperature has possibly a profound effect on
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 957 deamidation.

4. Conclusion

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⁹⁵⁶379 This experimental study elucidates the progressive stages of MR from formation of furosine to 957 958 380 generation of AGEs and protein crosslink indicators in the form of LAN. Oven cooked samples 959 960381 showed the highest levels for all these indicators, followed by meat cooked in the autoclave and 961 962382 braised, pointing out to a clear effect of temperature on the development of MR in meat. On the 963 other hand, low temperature cooking methods seems to generate not much of furosine, AGEs or 964383 965 LAN. Thus, compared to roasting and autoclaving, meat cooked at lower temperature will 966384 967 968385 contribute very little to MRP generation and might be a decisive strategy for reducing dietary 969 AGEs. Determination of post-translational modifications at peptide level like deamidation and pyro-970386 971 972**387** glutamate conversion has provided an insight of the susceptibility of amino acid residues to 973 974 **388** chemical modifications likely to occur in the most abundant meat proteins. Through proteomics, we 975 ₉₇₆ 389 also identified lysine modifications and losses that might impair meat eating quality and nutrient 977 978³⁹⁰ uptake. Therefore, such advanced techniques deployed in this study will provide a fundamental 979 980³⁹¹ platform in order to choose optimum cooking treatments that perhaps will have less effect on the 981 982 392 nutritional quality of meat proteins. Concomitantly, emphasis should be given onto how such 983 984</sub>393 glycation and other modifications could regulate nutrient utilization and enzymatic hydrolysis which ⁹⁸⁵ 986</sub>394 in turn could influence digestibility behaviour and biological value of essential quality nutrients.

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1008	daily laboratory activities is undeniable. Lastly, Cristian De Gobba, Post-Doctoral researcher is also)
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1010402	thanked for running our samples in the mass spectrometer.	
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101 403	The authors declare no conflict of interest.	
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1335 1336 30	changes and amino acid residue-level modification in cooked lamb longissimus thoracis et
1337 5 31 1338	lumborum: The effect of roasting. <i>Meat Science</i> , 119, 80–88.
¹³³⁹ 5 32 1340	http://doi.org/10.1016/j.meatsci.2016.04.024
¹³⁴ 533 1342	
¹³⁴³ 34 1344	
1345 1346	
1347 1348	
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¹³⁶¹ 535 Table 1. List of heat induced and other modifications of amino acid residues under the influence of 5**36** 1364 cooking. ¹³⁶538 Table 2. Overview of Maillard induced and other modifications in peptide sequences at amino acid residue level with positions. **341** Figure 1. Effect of processing on the formation of furosine (mg /100 g protein) as an early stage Maillard reaction product. Data shown is represented as mean with standard error bars. Different letters were ascribed for spotting significant differences (P < 0.05). Figure 2. Determination of CML (mg /100 g protein) content as an indicator for AGEs. Data shown is represented as mean with standard error bars. Significant differences (P < 0.05) were **546** denoted by different letters. **549** Figure 3. Effect of cooking treatments on the formation of LAN (mg/100 g protein) as protein cross-link. Data shown is represented as mean with standard error bars. Different letters were 1393**551** ascribed for spotting significant differences (P < 0.05). 1395**52** 553 1397 Figure 4. Ratio highlighting susceptibility to Maillard and other modifications - (A) Lysine 554 1399 modification in Myosin. (B) Lysine modification in beta-enolase. (C) Deamidation ratio in ¹⁴⁰⁰555 Myoglobin. Only mean values have been shown for a gualitative overview.









Table 1. List of heat induced and other modifications of amino acid residues under the influence of cooking.

Slno	Modification	Amino Acid Residue	Position	Formula	Mass Shift (Da)
1	Hex (2)	KR	any	C(12) H(20) O(10)	324.10
2	Carboxymethylation (CML)	KUW	any	C(2) H(2) O(2)	58.01
3	Carboxyethylation (CEL)	HK	any	C(3) H(4) O(2)	72.02
5	Deamidation	NQR	any	H(-1) N(-1) O(1)	00.98
6	Dehydration	DSTY	any	H(-2) O(-1)	-18.01
7	Didehydro	STY	any	H(-2)	-02.01
8	Dehydroalanine (Tyr to Dha)	Y	any	H(-6) C(-6) O(-1)	-94.04
8	Acetyl	HKSTY	any	C(2) H(2) O	42.01
9	Pyro-glu	Q	N-terminal	H(-2) O(-1)	-17.02
10	Pyro-glu	Е	N-terminal	H(-3) N(-1)	-18.01

Ductoin	S	Amina Arid	D::4:	M- difi ti
Protein	Sequence	Amino Acid	Position	Modification
Myosın	EALV <u>S</u> QL <u>S</u> R	Serine	S5; S8	2xAcetyl
	VAAWMIVTVSGI ECVTVNPVKWI PVVNAEVVTAVR	Tyrosine/Threonine/Lysine/Serine	Y/T/K/S (any)	1xAcetyl
		Thraonina	т7	1x A gotyl
	QLDEKD <u>I</u> LVSQLSK	Infeonine	1 /	TXACetyl
	ALQEA <u>H</u> QQALDDLQAEED <u>K</u> VNTLTK	Histidine; Lysine	H6; K19	2xCEL
	OLEAEKLELOSALEEAEASLEHEEGK	Lysine	K6	1xCEL
		<u>,</u>		
	OI EAEKI ELOSALEEAEASI EUEECK	Lucino	V6	
	OLDEVEAL VGOLGD		K0 V.	
	QLDE <u>K</u> EALVSQLSK	Lysine	K5	IXCML
	IAE <u>k</u> deeidqlk	Lysine	K4	1xCML
	TKLEQQVDDLEGSLEQEKK	Lysine	K2	1xCML
	VKNAYEESLDOLETLKR	Lysine	K2	1xCML
	TKEDIAK	Lysine	к2	1xCMI
	TEVETDAIOD	Lysine	K2 V2	
		Lysine	KZ K2	
	T <u>K</u> LEQQVDDLEGSLEQEK	Lysine	K2	IXCML
	LAQESTMDIENDKQQLDE <u>K</u>	Lysine	K13	1xCML
	V <u>K</u> NAYEESLDQLETLK	Lysine	K2	1xCML
	LETDISOIOGEMEDIIOEAR	Glutamine	07.09	2xDeamidated
		Clutamine	Q^{\prime}, Q^{\prime}	2xDeamidated
		Glutanine	Q_2, Q_1	2xDeannualed
	KKLEIDIS <u>Q</u> IQGEMEDII <u>Q</u> EAR	Glutamine	QII; Q (any)	2xDeamidated
	KLETDIS QIQ GEMEDII Q EA <u>R</u>	Glutamine/Arginine	Q/R (any)	2xDeamidated
	QAEEAEEQSNVNLSK	Asparagine	N10; N12	2xDeamidated
	ELTYOTEEDR	Glutamine	05	1xDeamidated
	KI OHEI EEAEER	Glutamine	Õ3	1xDeamidated
		Chutamina	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	
		Giutamine	Q2	ixDeamidated
	\mathbf{Q} LDEKEALVSQLSR	Glutamine	QI	IxDeamidated
	\mathbf{Q} LDEKDTLVSQLSR	Glutamine	Q1	1xDeamidated
	KKLETDIS QIQ GEMEDIV O EAR	Glutamine	0	1xDeamidated
	ALOFAHOOTL DDI OAFFDK VNTI TK	Glutamine/Asparagine	O/N (anv)	1xDeamidated
		Clutamine/Asparagine	Q/N(any)	1xDeamidated
	ENKILOUEISDLIEUIAEOOK	Glutannine/Asparagine	Q/IN (ally)	TxDeamidated
	<u>N</u> AYEESLD <u>Q</u> LETLK	Glutamine/Asparagine	Q/N (any)	1xDeamidated
	<u>N</u> LQQEISDLTEQIAEGGK <u>R</u>	Glutamine/Asparagine/Arginine	Q/N/R (any)	1xDeamidated
	ADIAESOVNKLR	Asparagine	N9	1xDeamidated
	AAVLOGINSADLIK	Asnaragine	N8	1xDeamidated
	ELENEVENEOK		NA	1-Deamidated
	ELE <u>N</u> EVENEQK	Asparagine	IN4	TxDeamidated
	VK <u>N</u> AYEESLDQLETLK	Asparagine	N3	1xDeamidated
	LI <u>N</u> ELSAQK	Asparagine	N3	1xDeamidated
	VKNAYEESLDOLETLKR	Asparagine	N3	1xDeamidated
		Asnaragine	N3	1xDeamidated
	ANSEVAOUD	Asparagina	NO	1xDeamidated
	A <u>N</u> SEVAQWK	Asparagine	INZ	TxDeamidated
	AEAHFSLIHYAGI VDY <u>N</u> I I GWLDK	Asparagine	NI/	IxDeamidated
	HADSVAELGEQID <u>N</u> LQR	Asparagine	N14	1xDeamidated
	NTQGVLK	Asparagine	N1	1xDeamidated
	NAYEESLOOLETLKR	Asparagine	N1	1xDeamidated
	VOLUHTONTSUNTKK	Asparagina	N (any)	1xDeamidated
	OATEA IDNI D		N(any)	
	QATEAI <u>RN</u> L <u>R</u>	Asparagine/Arginine	N/K (any)	TxDeamidated
	SR <u>n</u> dai <u>r</u>	Asparagine/Arginine	N/R (any)	1xDeamidated
	<u>N</u> L <u>RN</u> TQGVLK	Asparagine/Arginine/Glutamine	N/R/Q (any)	1xDeamidated
	ELENEVENEOKR	Asparagine/Glutamine	N/O (any)	1xDeamidated
	NLOOFISDI TEOLAEGGK	Asparagine/Glutamine	N/O (any)	1xDeamidated
		A spara gina/Clutamina	N/Q (any)	1yDeamidated
	VALEALEVON VILOK	Asparagine/Olutanine	N/Q (ally)	
	VQLLHIQNISLINIK	Asparagine/Glutamine	IN/Q (any)	ixDeamidated
	ADIAES <u>Q</u> V <u>N</u> K	Asparagine/Glutamine	N/Q (any)	1xDeamidated
	I Q LEL <u>NQ</u> VK	Asparagine/Glutamine	N/Q (any)	1xDeamidated
	LODAEEHVEAVNAK	Asparagine/Glutamine	N/Q (anv)	1xDeamidated
	VRELENEVENEOKR	Asparagine/Glutamine/Arginine	N/O/R (any)	1xDeamidated
	SNAACAALDKK	Asparagine	N2	1vDeamidated
		Asparagina	112 NO	
	U <u>N</u> UVLEUIK	Asparagine	1N2	ixDeanndated
	EQ <u>Y</u> EEEQEAK	Tyrosine	Y3	1xDehydrated
	QLEEE <u>T</u> K	Threonine	T6	1xDehydrated
	OAFTOOIEELKR	Threonine	T4	1xDehydrated
	<u>OATEAIR</u>	Threonine	Т3	1xDehvdrated
		Throoning	T (arrel)	1xDabudratad
		Threonine	I (any)	IxDenydrated
	EL <u>TY</u> QTEEDRK	Threonine/Tyrosine	T/Y (any)	IxDehydrated
	<u>DT</u> QLHL <u>DD</u> AIR	Threonine/Aspartic Acid	T/D (any)	1xDehydrated
	EQDTSAHLER	Threonine/Aspartic Acid/Serine	T/D/S (any)	1xDehydrated
	ELEGEVESEOKR	Serine	S8	1xDehydrated
	ELEEISER	Serine	<u>\$6</u>	1xDehvdrated
	EALVSOLSD	Sorino	85	1xDabudratad
		Scille	55	TxDenydrated
	SELQAALEEAEA <u>S</u> LEHEEGK	Serine	S13	IxDehydrated
	TKYET D AIQR	Aspartic Acid	D6	1xDehydrated
	KLEGDIK	Aspartic Acid	D5	1xDehydrated
	LDEAFOIALK	Aspartic Acid	D2	1xDehvdrated
		Sorino	\$2	1xDahudratad
			52 D2	
	HDCDLLK	Aspartic Acid	D2	IxDehydrated
	EKSELK	Glutamic Acid	E(any), N-Term	1xGlu->pyro-Glu
	EALVSOLSR	Glutamic Acid	E(anv) N-Term	1xGlu->pyro-Glu
	ELEGEVESEORD	Glutamic Acid	E(any) N Tame	lyGlu Spyro Chy
			Equity), IN-Term	1 Cl
	<u>elenevene</u> qk	Giutamic Acid	E(any), N-Term	1xGlu->pyro-Glu

Myosin ELTYQTEEDRK Glutamic Acid E(any), N-Term IxGlu->pyro-Ghu (Continued) EQDTSAHLER Glutamic Acid E(any), N-Term IxGlu->pyro-Ghu EQDESALER Glutamic Acid E(any), N-Term IxGlu->pyro-Ghu ELEEJSER Glutamic Acid E(any), N-Term IxGlu->pyro-Ghu ØSNEGGTKK Glutamic Acid E(any), N-Term IxGlu->pyro-Ghu ØSNEGGTKK Glutamine Q(any), N-Term IxGlu->pyro-Ghu ØAFTOQUEELK Glutamine Q(any), N-Term IxGlu->pyro-Ghu ØAFTOQUEELK Glutamine Q(any), N-Term IxGlu->pyro-Ghu ØAFTOQUEELK Glutamine Q(any), N-Term IxGlu->pyro-Ghu ØAFEAEEQSNVILSK Glutamine Q(any), N-Term IxGlu->pyro-Ghu ØAFEAEEQAEPDGTFEVADK Glutamine Q(any), N-Term IxGlu->pyro-Ghu ØAFEAEEQAEPDGTFEVADK Glutamine Q(any), N-Term IxGlu->pyro-Ghu ØAFEAEEQAENTNLSK Glutamine Q(any), N-Term IxGlu->pyro-Ghu ØAFEAEEQAENDCUALEEAEASLEHEEGK Glutamine Q(any), N-Term IxGlu->		<u>ELENEVE</u> NEQKR	Glutamic Acid	E(any), N-Term	1xGlu->pyro-Glu
(Continued) EQDTENATILER Glutamic Acid E(any), N-Term IxGlu->pyro-Glu EVYEEEQEAK Glutamic Acid E(any), N-Term IxGlu->pyro-Glu ELEEJSER Glutamic Acid E(any), N-Term IxGlu->pyro-Glu QSSEEGGTKK Glutamic Acid E(any), N-Term IxGlu->pyro-Glu QSSEEGGTKK Glutamic Acid Q(any), N-Term IxGlu->pyro-Glu QSSEEGGTKK Glutamic Q(any), N-Term IxGlu->pyro-Glu QAFEAEEQSNVLSK Glutamine Q(any), N-Term IxGlu->pyro-Glu QAFEAEEQSNVLSK Glutamine Q(any), N-Term IxGlu->pyro-Glu QAFEAEEQSNVLSK Glutamine Q(any), N-Term IxGlu->pyro-Glu QAFEAEEQALPDGTFVADK Glutamine Q(any), N-Term IxGlu->pyro-Glu QVEQEKEQALEEAEASILEHEEGK Glutamine Q(any), N-Term IxGlu->pyro-Glu QVEQEKEQALEEAEASILEHEEGK Glutamine Q(any), N-Term IxGlu->pyro-Glu QVEQEKEQALEEAEASILEHEEGK Glutamine Q(any), N-Term IxGlu->pyro-Glu QLEAKLELQSALEEAEASILEHEEGK Glutamine Q(any), N-Term Ix	Myosin	<u>E</u> LTYQT <u>EE</u> DRK	Glutamic Acid	E(any), N-Term	1xGlu->pyro-Glu
EOYDEEDCEAKGlutamic AcidE(am), N-TemIxGlu->pyro-GluELEEISERGlutamic AcidE(am), N-TemIxGlu->pyro-GluESIFCIQYNIRGlutamic AcidE(any), N-TemIxGlu->pyro-GluQSEEGGTKKGlutamineQ(any), N-TemIxGln->pyro-GluQSEEGGTKKGlutamineQ(any), N-TemIxGln->pyro-GluQAFEDAEDSNVNLSKGlutamineQ(any), N-TemIxGln->pyro-GluQAFEDAEDSNVNLSKGlutamineQ(any), N-TemIxGln->pyro-GluQAFEDAEDSNVNLSKGlutamineQ(any), N-TemIxGln->pyro-GluQAFEDAEDSNVNLSKGlutamineQ(any), N-TemIxGln->pyro-GluQAFEDAEDSNVNLSKGlutamineQ(any), N-TemIxGln->pyro-GluQVEDEXDEDGTEVADKGlutamineQ(any), N-TemIxGln->pyro-GluQVEDEXDEDGTEVADKGlutamineQ(any), N-TemIxGln->pyro-GluQVEDEKDTLVSQLSRGlutamineQ(any), N-TemIxGln->pyro-GluQLEEARLELEASALEHEEGKGlutamineQ(any), N-TemIxGln->pyro-GluQUEQEKGlutamineQ(any), N-TemIxGln->pyro-GluQUEQEKGlutamineQ(any), N-TemIxGln->pyro-GluQUEQEKGlutamineQ(any), N-TemIxGln->pyro-GluQUEQEKGlutamineQ(any), N-TemIxGln->pyro-GluQUEQEKGlutamineQ(any), N-TemIxGln->pyro-GluQUEQEKGlutamineQ(any), N-TemIxGln->pyro-GluQUEQEKGlutamineQ(any), N-TemIxGln->pyro-GluQUEQEKGlutamineQ(any), N-TemIxGln->pyro	(Continued)	EQDTSAHLER	Glutamic Acid	E(any), N-Term	1xGlu->pyro-Glu
ELESTER Glutamic Acid E(any), N-Term 1xGlu->pyro-Glu SIFECIOYNIR Glutamic Acid E(any), N-Term 1xGlu->pyro-Glu SIEEGGTKK Glutamine Q(any), N-Term 1xGln->pyro-Glu SSEEGGTKK Glutamine Q(any), N-Term 1xGln->pyro-Glu QAEEAEEQSNVNLSK Glutamine Q(any), N-Term 1xGln->pyro-Glu QVEQEKEQALEEAEASLEHEEGK Glutamine Q(any), N-Term 1xGln->pyro-Glu QLEAEKLEQALEEAEASLEHEEGK Glutamine Q(any), N-Term 1xGln->pyro-Glu QVEQEK Glutamine		EQYEEEQEAK	Glutamic Acid	E(any), N-Term	1xGlu->pyro-Glu
ESIFCIQYNIR Glutamic Acid Eany, N-Term IxGlu->pyro-Glu 0E0EXSELQAALEEAEASLEHEEGK Glutamine Q(any), N-Term IxGln->pyro-Glu 0SSEEGGTK Glutamine Q(any), N-Term IxGln->pyro-Glu 0AFE0AEEQSNVNLSK Glutamine Q(any), N-Term IxGln->pyro-Glu 0AFE0AEEQSNVNLSK Glutamine Q(any), N-Term IxGln->pyro-Glu 0AFE0AEEQSNVNLSK Glutamine Q(any), N-Term IxGln->pyro-Glu 0AFE0AEDOTEVADK Glutamine Q(any), N-Term IxGln->pyro-Glu 0AFE0AEDOTEVADK Glutamine Q(any), N-Term IxGln->pyro-Glu 0FYEETHAELEASQ Glutamine Q(any), N-Term IxGln->pyro-Glu 0LEARKLELEASALEHEEGK Glutamine Q(any), N-Term IxGln->pyro-Glu 0LEARKLELEASALEHEEGK Glutamine Q(any), N-Term IxGln->pyro-Glu 0LEARKLELEASALEHEEGK Glutamine Q(any), N-Term IxGln->pyro-Glu 0LEARKLELASALE Glutamine Q(any), N-Term IxGln->pyro-Glu 0LEARKLELASALE Glutamine Q(any), N-Term IxGln->pyro-Glu		ELEEISER	Glutamic Acid	E(any), N-Term	1xGlu->pyro-Glu
Action Difference O(may) N-Term LsGin>pyro-Glu QSSEEGGTKK Glutamine O(any) N-Term LsGin>pyro-Glu QSSEEGGTK Glutamine O(any) N-Term LsGin>pyro-Glu QAFEAEQSNVNLSK Glutamine O(any) N-Term LsGin>pyro-Glu QAFEAEQSNVNLSK Glutamine Q(any) N-Term LsGin>pyro-Glu QAFEAEQSNVNLSK Glutamine Q(any) N-Term LsGin>pyro-Glu QAFEAESQALEEAEASLEHEEGK Glutamine Q(any) N-Term LsGin>pyro-Glu QVFQEKSEQAALEEAEASLEHEEGK Glutamine Q(any) N-Term LsGin>pyro-Glu QLEAAELQSALEAEASLEHEEGK Glutamine Q(any) N-Term LsGin>pyro-Glu QLEAAELQSALEAEASLEHEEGK Glutamine Q(any) N-Term LsGin>pyro-Glu QLEAAELQSALEAEASLEHEEGK Glutamine Q(any) N-Term LsGin>pyro-Glu QVFQEK Glutamine Q(any) N-Term LsGin>pyro-Glu QVFQEK Glutamine Q(any) N-Term LsGin		ESIFCIOYNIR	Glutamic Acid	E(any), N-Term	1xGlu->pyro-Glu
9JEG2EXSELQAALEEAEASLEHEEGKGlutamineQ(any), N-Term1sGln->pyro-GluQSSEEGGTKKGlutamineQ(any), N-Term1sGln->pyro-GluQAFT2QJEELKGlutamineQ(any), N-Term1sGln->pyro-GluQAEEAEEQSNVLSKGlutamineQ(any), N-Term1sGln->pyro-GluQAEEAEEQSNVLSKGlutamineQ(any), N-Term1sGln->pyro-GluQAEEAEEQSNVLSKGlutamineQ(any), N-Term1sGln->pyro-GluQXEEQAEPDGTEVADKGlutamineQ(any), N-Term1sGln->pyro-GluQVEQEKSEQAALEEAEASLEHEEGKGlutamineQ(any), N-Term1sGln->pyro-GluQVEQEKSEQAALEEAEASLEHEEGKGlutamineQ(any), N-Term1sGln->pyro-GluQLEAEKLELQSALEEAEASLEHEEGKGlutamineQ(any), N-Term1sGln->pyro-GluQLEAEKLELQSALEEAEASLEHEEGKGlutamineQ(any), N-Term1sGln->pyro-GluQLEQENGlutamineQ(any), N-Term1sGln->pyro-GluQLFQEKGlutamineQ(any), N-Term1sGln->pyro-GluQLFQEKGlutamineQ(any), N-Term1sGln->pyro-GluQLFQEKGlutamineQ(any), N-Term1sGln->pyro-GluQLFQEKGlutamineQ(any), N-Term1sGln->pyro-GluQLFQEKGlutamineQ(any), N-Term1sGln->pyro-GluQLFQEKGlutamineQ(any), N-Term1sGln->pyro-GluQLFQCUEGAPSIVHRAsparagineN141sDeanidatedSYELPDGQVTI[GNERSerine/Tyrosine/ThreonineSY/T (any)1sAcetylFRCPETLPQPSFIGMESAGIHETTYNSMCDIDIRSerineS271sDiddydro <td< td=""><td></td><td>- `</td><td></td><td></td><td>15</td></td<>		- `			15
QSSEEGGTKK Glutamine Q(any), N-Term IxGin->pyro-Glu QAFTQQIEELK Glutamine Q(any), N-Term IxGin->pyro-Glu QAEEAEEQSNVNLSK Glutamine Q(any), N-Term IxGin->pyro-Glu QAEEAEEQSNVNLSK Glutamine Q(any), N-Term IxGin->pyro-Glu QAEEAEEQSNVNLSK Glutamine Q(any), N-Term IxGin->pyro-Glu QVEQEKSEQAALEEAEASLEHEEGK Glutamine Q(any), N-Term IxGin->pyro-Glu QVEQEKSEQAALEEAEASLEHEEGK Glutamine Q(any), N-Term IxGin->pyro-Glu QLDEKDTUSQLSR Glutamine Q(any), N-Term IxGin->pyro-Glu QLDEKDTUSQLSR Glutamine Q(any), N-Term IxGin->pyro-Glu QLDEKDTUSQLSR Glutamine Q(any), N-Term IxGin->pyro-Glu QAFEAEEQANTNLSK Glutamine Q(any), N-Term IxGin->pyro-Glu QA		$\underline{\mathbf{O}}$ IE $\underline{\mathbf{O}}$ EKSEL $\underline{\mathbf{O}}$ AALEEAEASLEHEEGK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QSSEEGGTKGlutamineQ(any), N-TermIxGln->pyro-GluQAFEQQUEELKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQSNTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQSNTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQNEEQAEPDGTEVADKGlutamineQ(any), N-TermIxGln->pyro-GluQVEQEKSEQAALEEAEASLEHEEGKGlutamineQ(any), N-TermIxGln->pyro-GluQLDEKDTLVSQLSRGlutamineQ(any), N-TermIxGln->pyro-GluQLDEKDTLVSQLSRGlutamineQ(any), N-TermIxGln->pyro-GluQLEAEKLEQSALEEAEASLEHEEGKGlutamineQ(any), N-TermIxGln->pyro-GluQLEAEKLEQSALEAEASLEHEEGKGlutamineQ(any), N-TermIxGln->pyro-GluQLEAEKLEQSALEAEASLEHEEGKGlutamineQ(any), N-TermIxGln->pyro-GluQLEAEKLEQSALEAEASLEHEEGKGlutamineQ(any), N-TermIxGln->pyro-GluQLEAEKLEQANTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQANTNLSKGlutamine		Q SSEEGGTKK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QAFTQOIEELK Glutamine Q(any), N-Term lxGin>pyro-Glu QAEEAEEQSNVNLSK Glutamine Q(any), N-Term lxGin>pyro-Glu QAEEAEEQSNVNLSK Glutamine Q(any), N-Term lxGin>pyro-Glu QREEQAEPDGTEVADK Glutamine Q(any), N-Term lxGin>pyro-Glu QVEQEKSEIQAALEEAEASLEHEEGK Glutamine Q(any), N-Term lxGin>pyro-Glu QLDEKDTU-SQLSR Glutamine Q(any), N-Term lxGin>pyro-Glu QFEQEK Glutamine Q(any), N-Term lxGin>pyro-Glu QAFEAEEQANTNLSK Glutamine Q(any), N-Term		Q SSEEGGTK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QAEEAEEQSNINLSKGlutamineQ(any), N-TermlxGin->pyro-GluQREEQAEPDGTEVADKGlutamineQ(any), N-TermlxGin->pyro-GluQVEQEKSEIQAALEEAEASLEHEEGKGlutamineQ(any), N-TermlxGin->pyro-GluQLEAEKLEQSNINLSKGlutamineQ(any), N-TermlxGin->pyro-GluQLEAEKLEQSLEAEASLEHEEGKGlutamineQ(any), N-TermlxGin->pyro-GluQLEAEKLEQSALEEAEASLEHEEGKGlutamineQ(any), N-TermlxGin->pyro-GluQLEAEKLEQSALEEAEASLEHEEGKGlutamineQ(any), N-TermlxGin->pyro-GluQAFTQQIEELKRGlutamineQ(any), N-TermlxGin->pyro-GluQAFTQQIEELKRGlutamineQ(any), N-TermlxGin->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermlxGin->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermlxGin->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermlxGin->pyro-GluQATEAIRGlutamineQ(any), N-TermlxGin->pyro-GluQATEAIRGlutamineQ(any), N-TermlxGin->pyro-GluQATEAIRSYELPDGQVITIGNERSystemicTyrosineSYT (any)lxAectylNHHTFYYEIRAsparagineN14lxDeamidatedSYELPDGQVITIGNERAsparagineN14lxDeamidatedSYELPDGQVITIGNERGlutamineQ(any), N-TermlxGin->pyro-GluQEYDEAGPSIVHRGlutamineQ(any), N-TermlxGin->pyro-GluQEYDEAGPSIVHRSystemicTyrosineSYT (any)lxAectylHADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN14lxDeamid		Q AFT QQ IEELK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
AcEAQuary, N-TermIxGin>pyro-GluQREQAQREQAGlutamineQ(any), N-TermIxGin>pyro-GluQVEQEKSEIQAALEEAEASLEHEEGKGlutamineQ(any), N-TermIxGin>pyro-GluQLDEXDITVSQLSRGlutamineQ(any), N-TermIxGin>pyro-GluQLDEXDITVSQLSRGlutamineQ(any), N-TermIxGin>pyro-GluQAFTQOIEELKRGlutamineQ(any), N-TermIxGin>pyro-GluQAFTQOIEELKRGlutamineQ(any), N-TermIxGin>pyro-GluQVEQEKGlutamineQ(any), N-TermIxGin>pyro-GluQVEQEKGlutamineQ(any), N-TermIxGin>pyro-GluQAEAAEEQANTNLSKGlutamineQ(any), N-TermIxGin>pyro-GluQATEAIRGlutamineQ(any), N-TermIxGin>pyro-GluQATEAIRGlutamineQ(any), N-TermIxGin>pyro-GluQATEAIRGlutamineQ(any), N-TermIxGin>pyro-GluActinYELPDGQVITIGNERAsparagineN14IxDeamidatedYELPDGQVITIGNERAsparagineN14IxDeamidatedYELPDGQVITIGNERAspartic Acid/Serine/TyrosineD/S/Y (any)IxDehydratedOEYDEAGPSIVHRHistidineH1IxAcetylHACCPETLEPGSIVHRLysineK30IxCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN14IxDeamidatedNGKYDLDFKLysineK17IxCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN1IxDeamidatedNGKYDLDFKLysineK17IxCMLHADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagine <td></td> <td>\mathbf{Q}AEEAEE\mathbf{Q}SNVNLSK</td> <td>Glutamine</td> <td>Q(any), N-Term</td> <td>1xGln->pyro-Glu</td>		\mathbf{Q} AEEAEE \mathbf{Q} SNVNLSK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QREEQ.AEPOGTEVADKGlutamineQ(any), N-TermIxGln->pyro-GluQVEQEKSEIQAALEEAEASLEHEEGKGlutamineQ(any), N-TermIxGln->pyro-GluQLEAEKLEIQSALEEAEASLEHEEGKGlutamineQ(any), N-TermIxGln->pyro-GluQLEAEKLEIQSALEEAEASLEHEEGKGlutamineQ(any), N-TermIxGln->pyro-GluQVEQEKGlutamineQ(any), N-TermIxGln->pyro-GluQVEQEKGlutamineQ(any), N-TermIxGln->pyro-GluQVEQEKGlutamineQ(any), N-TermIxGln->pyro-GluQVEQEKGlutamineQ(any), N-TermIxGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermIxGln->pyro-GluQATEAIRGlutamineQ(any), N-TermIxGln->pyro-GluQATEAIRGlutamineQ(any), N-TermIxGln->pyro-GluActin <u>Y</u> ELPDGQVITIGNERGlutamineQ(any), N-TermIxGln->pyro-GluActin <u>Y</u> ELPDGQVITIGNERAsparagineN14IxDeanidatedSYELPDGQVITIGNERAsparagineN14IxDeanidatedSYELPDGQVITIGNERAsparagineN14IxDeanidatedYELPDGQVITIGNERAsparagineN14IxDehydratedPEVDEAGPSIVHRGlutamineQ(any), N-TermIxCln->pyro-GluBeta-enolase <u>H</u> TGEKHistidineH1IxCetylHADLAGRPDLVLPVPAFNVINGGSHAGNKAsparagineN1IxCethHADLAGRPDLVLPVPAFNVINGGSHAGNKAsparagineN1IxDeanidatedNGKYDLDFKLysineK3IxCMLHADLAGRPDLVLPVPAFNVINGGSHAGNKAsparagine		\mathbf{Q} AEEAEE \mathbf{Q} SNTNLSK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
PVEQEXSEQAALEEAESLEHEEGKGlutamineQ(any), N-TermIxGln>pyro-GluQKYEETHAELEASQKGlutamineQ(any), N-TermIxGln>pyro-GluQLDEKDTLVSQLSRGlutamineQ(any), N-TermIxGln>pyro-GluQAFTQQIEELKRGlutamineQ(any), N-TermIxGln>pyro-GluQVEQEKGlutamineQ(any), N-TermIxGln>pyro-GluQVEQEKGlutamineQ(any), N-TermIxGln>pyro-GluQVEQEKGlutamineQ(any), N-TermIxGln>pyro-GluQAFEAEEQANTNLSKGlutamineQ(any), N-TermIxGln>pyro-GluQATEAIRGlutamineQ(any), N-TermIxGln>pyro-GluActinSELPDGQVITIGNERSerine/Tyrosin/ThreonineSY/T (any)IxAcetylWHHTYYDELRAsparagineN14IxDeamidatedSYELPDGQVITIGNERAsparagineN14IxDeamidatedSYELPDGQVITIGNERAsparagineN14IxAcetylWHHTYYDELRGlutamineQ(any), N-TermIxGln>pyro-GluQEYDEAGPSIVHRAsparagineN14IxDeamidatedVELPDGQVITIGNERAsparagineN14IxDeamidatedVELPDGQVITIGNERGlutamineQ(any), N-TermIxGln>pyro-GluVEVEAGPSIVHRGlutamineQ(any), N-TermIxGln>pyro-GluVEVEAGPSIVHRAspartic Acid/Serine/TyrosineS27IxDehydratedVEVEAGPSIVHRGlutamineQ(any), N-TermIxGln>pyro-GluVIGMDVAASEFYRNGKYDLDFKLysineK3IxCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN1IxDeamidated <t< td=""><td></td><td>\mathbf{Q}REE\mathbf{Q}AEPDGTEVADK</td><td>Glutamine</td><td>Q(any), N-Term</td><td>1xGln->pyro-Glu</td></t<>		\mathbf{Q} REE \mathbf{Q} AEPDGTEVADK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QKYEETHAELEASQK Glutamine Q(any), N-Term lxGln->pyro-Glu QLEAEKLELQSALEEAEASLEHEEGK Glutamine Q(any), N-Term lxGln->pyro-Glu QAFTQQIEELKR Glutamine Q(any), N-Term lxGln->pyro-Glu QVEQEK Glutamine Q(any), N-Term lxGln->pyro-Glu QFQEK Glutamine Q(any), N-Term lxGln->pyro-Glu QAEEAEQANTNLSK Glutamine Q(any), N-Term lxGln->pyro-Glu QATETAIR Glutamine Q(any), N-Term lxGln->pyro-Glu QATEAREQANTNLSK Glutamine Q(any), N-Term lxGln->pyro-Glu QATEAREQANTNLSK Glutamine Q(any), N-Term lxGln->pyro-Glu QATEAR QATEAREQANTNLSK Glutamine Q(any), N-Term lxGln->pyro-Glu QATEAR QATEAREQANTNLSK Glutamine Q(any), N-Term lxGln->pyro-Glu Actin SYELPDGQVITIGNER Asparagine N14 lxDeamidated SYELPDGQVITIGNER Asparagine N14 lxDeamidated SYELPDGQVITIGNER Asparatic Acid/Serine/Tyrosine S(27) lxDidehydro QEYDEAGPSIVHR Glutamine Q(any), N-Term		\mathbf{Q} VE \mathbf{Q} EKSEI \mathbf{Q} AALEEAEASLEHEEGK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QLDEKDTLVSQLSRGlutamineQ(any), N-TermIxGIn->pyro-GluQLAFEUELQSALEEAEASLEHEEGKGlutamineQ(any), N-TermIxGIn->pyro-GluQAFTQQIEELKRGlutamineQ(any), N-TermIxGIn->pyro-GluQVEQEKGlutamineQ(any), N-TermIxGIn->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermIxGIn->pyro-GluQATEAIRGlutamineQ(any), N-TermIxGIn->pyro-GluQATEAIRGlutamineQ(any), N-TermIxGIn->pyro-GluQATEAIRGlutamineQ(any), N-TermIxGIn->pyro-GluActinSYELPDQVITIGNERSerine/Tyrosine/ThreonineN/Y/T (any)IxAeetylNWHITFYNELRAsparagineN8IxDeamidatedSYELPDGQVITIGNERAsparagineN14IxDenmidatedSYELPDGQVITIGNERAsparaic AcidD6IxDehydratedQEYDEAGPSIVHRAspartic AcidD6IxDehydratedPECAEPSIGMESAGIHETTYNSIMKCDIDIRSerineS27IxDichydroBeta-enolaseHITGEKHistidineH1IxAcetylHIALGNPDLVLPVAFNVINGGSHAGNKLysineK30IxCMLNGKYDLDFKLysineK30IxCMLVIGMDVAASEFYRNGKYDLDFKLysineK17IxCMLNGKYDLDFKAsparagineN1IxDeamidatedNGKYDLDFKAsparagineN1IxDeamidatedNGKYDLDFKAsparagineN1IxDeamidatedNGKYDLDFKAsparagineN1IxDeamidatedNGKYDLDFKAsparagineN1IxDeamidatedNGKY		Q KYEETHAELEAS Q K	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QLEAEKLELQŠALEEAEASLEHEEGKGlutamineQ(any), N-TermIxGin->pyro-GluQAFTQQIEELKRGlutamineQ(any), N-TermIxGin->pyro-GluQVEQEKGlutamineQ(any), N-TermIxGin->pyro-GluQAELAEEQANTNLSKGlutamineQ(any), N-TermIxGin->pyro-GluQATEAAEQANTNLSKGlutamineQ(any), N-TermIxGin->pyro-GluQATEAAEQANTNLSKGlutamineQ(any), N-TermIxGin->pyro-GluQATEAARGlutamineQ(any), N-TermIxGin->pyro-GluQATEAARGlutamineQ(any), N-TermIxGin->pyro-GluActinSYELPDGQVITIGNERSerine/Tyrosine/ThreonineS'Y/T (any)IxAcetylNHHTTYNELRAsparagineN14IxDeamidatedSYELPDGQVITIGNERAspartic Acid/Serine/TyrosineD6IxDehydratedSYELPDGQVITIGNERAspartic Acid/Serine/TyrosineD/S'Y (any)IxDehydratedFRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIRGlutamineQ(any), N-TermIxGin->pyro-GluBeta-enolaseHITOEKHistidineH1IxAcetylHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK30IxCMLNGKYDLDFKLysineK17IxCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN14IxDeamidatedNGKYDLDFKLysineK17IxCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11IxDeamidatedMGKYDLDFKAsparagineN11IxDeamidatedMGKYDLDFKAsparagineN11IxDeamidatedMGKYDLDFKAsparagineN (any)I		Q LDEKDTLVS Q LSR	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QAFTQQIEELKRGlutamineQ(any), N-Term1xGln->pyro-GluQVEQEKGlutamineQ(any), N-Term1xGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-Term1xGln->pyro-GluQATEARGlutamineQ(any), N-Term1xGln->pyro-GluQATEARGlutamineQ(any), N-Term1xGln->pyro-GluMattineSYELPDGQVITIGNERSerine/Tyrosine/ThreonineS/YT (any)1xAcetylIWHHTFYNELRSerine/Tyrosine/ThreonineS/YT (any)1xAcetylSYELPDGQVITIGNERAsparagineN141xDeamidatedSYELPDGQVITIGNERAsparagineN141xDehydratedGEYDEAGPSIVHRAspartic Acid/Serine/TyrosineD/S/Y (any)1xDehydratedGEYDEAGPSIVHRGlutamineQ(any), N-Term1xGln->pyro-GluDEYDEAGPSIVHRGlutamineQ(any), N-Term1xGln->pyro-GluBeta-enolaseHITGEKHistidineH11xAcetylHALGSNOWGVMVSHRTyptophanW71xCMLHALGANPDL/VLPVPAFNVINGGSHAGNKLysineK171xCMLNGKYDLDFKLysineK171xCMLHALGANPDL/VLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedNGKYDLDFKMineneQ41xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKAsparagineN11xDeamidated		QLEAEKLELQSALEEAEASLEHEEGK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QVEQEKGlutamineQany), N-TermlxGln->pyro-GluQIEQEKGlutamineQ(any), N-TermlxGln->pyro-GluQAEEAEEQANTNLSKGlutamineQ(any), N-TermlxGln->pyro-GluQATEAIRGlutamineQ(any), N-TermlxGln->pyro-GluQATEAIRGlutamineQ(any), N-TermlxGln->pyro-GluActinYELPDGQVTIGNERSerine/Tyrosine/ThreonineSY/T (any)lxAcetylIWHHTFYNELRAsparagineN14lxDeamidatedSYELPDGQVTIGNERAsparagineN14lxDeamidatedSYELPDGQVTIGNERAsparagineD/S/Y (any)lxDehydratedQEYDEAGPSIVHRAsparatic Acid/Serine/TyrosineD/S/Y (any)lxDehydratedGEYDEAGPSIVHRGlutamineQ(any), N-TermlxGln->pyro-GluBeta-enolaseHITGEKHistidineH1lxAcetylHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK30lxCMLNGKYDLDFKLysineK30lxCMLNGKYDLDFKLysineK17lxCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN1lxDeamidatedNGKYDLDFKLysineN1lxDeamidatedNGKYDLDFKAsparagineN1lxDeamidatedNGKYDLDFKAsparagineN1lxDeamidatedNGKYDLDFKAsparagineN1lxDeamidatedNGKYDLDFKAsparagineN1lxDeamidatedNGKYDLDFKAsparagineN1lxDeamidatedNGKYDLDFKAsparagineN1lxDeamidatedNGKYDLDFKAsparagine <td< td=""><td></td><td>QAFTQQIEELKR</td><td>Glutamine</td><td>Q(any), N-Term</td><td>1xGln->pyro-Glu</td></td<>		Q AFT QQ IEELKR	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QIEQEKGlutamineQany, N-Term1xGln->pyro-GluQATEAREQANTNLSKGlutamineQ(any), N-Term1xGln->pyro-GluQATEAIRGlutamineQ(any), N-Term1xGln->pyro-GluActin YELPDGQVITIGNER Serine/Tyrosine/ThreonineS/Y1 (any)1xActinSYELPDGQVITIGNERAsparagineN81xDeamidatedSYELPDGQVITIGNERAsparagineN141xDeamidatedQEYDEAGPSIVHRAspartic AcidD61xDehydratedQEYDEAGPSIVHRAspartic Acid/Serine/TyrosineD/S/Y (any)1xDehydratedQEYDEAGPSIVHRGlutamineQ(any), N-Term1xGln->pyro-GluDEta-enolase HITGEK HistidineH11xAcetylHADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedVVIGMDVAASEFYRNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedNGYDLDFGGFAPNILENNEALELLKAsparagineN (any)1xDeamidatedNPVVSIEDPFDQDDWKA		QVEQEK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QAĒEAEEQANTNLSKGlutamineQ(any), N-Term1xGin->pyro-GluQATEAIRGlutamineQ(any), N-Term1xGin->pyro-GluActinYELPDGQVITIGNERSerine/Tyrosine/ThreonineS/Y (any)1xAcetylIWHHTFYNELRAsparagineN81xDeamidatedSYELPDGQVITIGNERAsparagineN141xDeamidatedSYELPDGQVITIGNERAspartic AcidD61xDehydratedGEYDEAGPSIVHRAspartic Acid/Serine/TyrosineD/S/Y (any)1xDehydratedFRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIRSerineS271xDiehydratedGEYDEAGPSIVHRGlutamineQ(any), N-Term1xGin->pyro-GluBeta-enolaseHITGEKHistidineH11xAcetylLAQSNGWGVMVSHRTryptophanW71xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN12; N292xDeamidatedMGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidated<		QIEQEK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
QATEAIRGlutamineQ(any), N-Term1xGln->pyro-GluActinSYELPDGQVITIGNERSerine/Tyrosine/ThreonineSYY/T (any)1xAcetylIWHHTFYNELRAsparagineN81xDeamidatedSYELPDGQVITIGNERAsparagineN141xDeamidatedSYELPDGQVITIGNERAsparagineN141xDeamidatedQEYDEAGPSIVHRAspartic Acid/Serine/TyrosineD/S/Y (any)1xDehydratedQEYDEAGPSIVHRGlutamineQ(any), N-Term1xGln->pyro-GluBeta-enolaseHITGEKHistidineH11xAcetylIAQSNGWGVWSHRTryptophanW71xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN12; N292xDeamidatedMGYDLDFKGlutamineQ41xDeamidatedMGYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKKAsparagineN11xDeamidatedMGKYDLDFKSAsparagineN11xDeamidatedMGKYDLDFKSAsparagineN11xDeamidatedMGKYDLDFKKAsparagineN11xDeamidatedMGKYDLDFKKAsparagineN11xDeamidatedMGKYDLDFKSAsparagineN11xDeamidated <tr<< td=""><td></td><td>QAEEAEEQANTNLSK</td><td>Glutamine</td><td>Q(any), N-Term</td><td>1xGln->pyro-Glu</td></tr<<>		QAEEAEEQANTNLSK	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
ActinSYELPDGQVITIGNERSerine/Tyrosine/ThreonineS/Y/T (any)1xAcetylIWHHTFYNELRAsparagineN81xDeamidatedSYELPDGQVITIGNERAsparagineN141xDeamidatedSYELPDGQVITIGNERAspartic AcidD61xDehydratedQEYDEAGPSIVHRAspartic Acid/Serine/TyrosineD/S/Y (any)1xDehydratedPCPDEAGPSIVHRAspartic Acid/Serine/TyrosineD/S/Y (any)1xDehydratedDESTDEAGPSIVHRGlutamineQ(any), N-Term1xGln->pyro-GluBeta-enolaseHITGEKHistidineH11xAcetylLAQSNGWGVMVSHRTryptophanW71xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLVVIGMDVAASEFYRNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedMGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKSPDDPSRAsparagineN11xDeamidatedMJVGDEGGFAPMLENNEALELLKAsparagineN (any)1xDeamidatedMAUGOSLAVCKAsparagineN (any)1xDeamidatedNYPVVSIEDPFDQDWKAsparagineN (any)1xDeamidatedMAUGOSLAFPRMILENKALELLKAsparagineN (any)1xDeamidatedMOTORDFNUNGSHAGNKAsparag		QATEAIR	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
IWHHTFYNELR Asparagine N8 1xDeamidated SYELPDGQVITIGNER Asparagine N14 1xDeamidated SYELPDGQVITIGNER Aspartic Acid D6 1xDehydrated QEWDEAGPSIVHR Aspartic Acid/Serine/Tyrosine D/S/Y (any) 1xDehydrated FRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIR Serine S27 1xDidehydro QEYDEAGPSIVHR Glutamine Q(any), N-Term 1xGln->pyro-Glu Beta-enolase HITGEK Histdine H1 1xAccetyl IAQSNGWGVMVSHR Tryptophan W7 1xCML HADLAGNPDLVLPVPAFNVINGGSHAGNK Lysine K30 1xCML VVIGMDVAASEFYRNGKYDLDFK Lysine K17 1xCML HIADLAGNPDLVLPVPAFNVINGGSHAGNK Asparagine N2; N29 2xDeamidated MGKYDLDFK Lysine K17 1xCML HIADLAGNPDLVLPVPAFNVINGGSHAGNK Asparagine N1 1xDeamidated MGKYDLDFK Asparagine N1 1xDeamidated	Actin	SYELPDGQVITIGNER	Serine/Tyrosine/Threonine	S/Y/T (any)	lxAcetyl
SYELPDGQVITIGNERAsparagineN141xDeamidatedSYELPDGQVITIGNERAspartic AcidD61xDehydratedQEYDEAGPSIVHRAspartic Acid/Serine/TyrosineD/S/Y (any)1xDehydratedFRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIRSerineS271xDidehydroQEYDEAGPSIVHRGlutamineQ(any), N-Term1xGn->pyro-GluBeta-enolaseHITGEKHistidineH11xAcetylILAQSNGWGVMVSHRTryptophanW71xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLVVIGMDVAASEFYRNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedMGKYDLDFKGlutamineQ41xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedMGKYDLDFKSPDDPSRAsparagineN (any)1xDeamidatedMATWGDEGGFAPNILENNEALELLKAsparagineN (any)1xDeamidatedMATWGDEGGFAPNILENNEALELLKAsparagineN41xDeamidatedMATUGTUREMATUGVSLAVCKAsparagineN41xDeam		IWHHTFYNELR	Asparagine	N8	1xDeamidated
SYELPDGQVITIGNERAspartic AcidD61xDehydratedQEYDEAGPSIVHRAspartic Acid/Serine/TyrosineD/S/Y (any)1xDehydratedFRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIRSerineS271xDidehydroQEYDEAGPSIVHRGlutamineQ(any), N-Term1xGh->pyro-GluBeta-enolaseHITGEKHistidineH11xAcetylIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLNGKYDLDFKLysineK31xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKSPDDPSRAsparagineN11xDeamidatedDATNVGDEGGFAPNILENNEALELLKAsparagineN (any)1xDeamidatedMATNVGDEGGFAPNILENNEALELLKAsparagineN41xDeamidatedMATNVEVSIEDPFDQDDWKAsparagineN41xDeamidatedMANDMANDMADEAMidedMADIMMADEAMidedMANDMADEAMILENNEALELLKAsparagineN41xDeamidatedMANDMADIMMADEAMIDATENNEALELLKMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIMMADIM <td></td> <td>SYELPDGQVITIGNER</td> <td>Asparagine</td> <td>N14</td> <td>1xDeamidated</td>		SYELPDGQVITIGNER	Asparagine	N14	1xDeamidated
QEYDEAGPSIVHR FRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIR FRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIR QEYDEAGPSIVHRAspartic Acid/Serine/Tyrosine SerineD/S/Y (any)1xDehydratedBeta-enolaseHITGEK LAQSNGWGVMVSHRHistidineH11xAcetylHADLAGNPDLVLPVPAFNVINGGSHAGNK VVIGMDVAASEFYRNGKYDLDFKHysineK301xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNK VVIGMDVAASEFYRNGKYDLDFKLysineK31xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNK VVIGMDVAASEFYRGlutamineQ41xDeamidatedAGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNK HIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNK NGKYDLDFKAsparagineN (any)1xDeamidatedMATNVGDEGGFAPNILENNEALELLK NANLGVSLAVCKAsparagineN (any)1xDeamidatedNYPVVSIEDPFDQDDWKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparagineN41xDeamidatedNYPVYSIEDPFDQDDWKAsparagineN41xDeamidatedNYPVYSIEDPFDQDDWKAsparagineN41xDeamidatedNYPVYSIEDPFDQDDWKAsparagineN41xDehydrated <td></td> <td>SYELPDGQVITIGNER</td> <td>Aspartic Acid</td> <td>D6</td> <td>1xDehydrated</td>		SYELPDGQVITIGNER	Aspartic Acid	D6	1xDehydrated
FRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIR QEYDEAGPSIVHRSerineS271xDidehydroBeta-enolaseHITGEK LAQSNGWGVMVSHRHistidineH11xAcetylIAQSNGWGVMVSHRTryptophanW71xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLVVIGMDVAASEFYRNGKYDLDFKLysineK31xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedMGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMGKYDLDFKSPDDPSRAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedMIADLAGNPDLVLPVAFNVINGGSHAGNK <td< td=""><td></td><td>QEYDEAGPSIVHR</td><td>Aspartic Acid/Serine/Tyrosine</td><td>D/S/Y (any)</td><td>1xDehydrated</td></td<>		QEYDEAGPSIVHR	Aspartic Acid/Serine/Tyrosine	D/S/Y (any)	1xDehydrated
QEYDEAGPSIVHRGlutamineQ(any), N-Term1xGln->pyro-GluBeta-enolaseHITGEKHistidineH11xAcetylLAQSNGWGVMVSHRTryptophanW71xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLNGKYDLDFKLysineK31xCMLVVIGMDVAASEFYRNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedMGKYDLDFKGlutamineQ41xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedMIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedMATNVGDEGGFAPNILENNEALELLKAsparagineN (any)1xDeamidatedMYPVVSIEDPFDQDDWKAsparagineN41xDeamidatedMUDOTNYPVVSIEDPFDQDDWKAsparagineN41xDeamidated		FRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIR	Serine	S27	1xDidehydro
Beta-enolaseHITGEKHistidineH1IxAcetylLAQSNGWGVMVSHRTryptophanW7IxCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK30IxCMLNGKYDLDFKLysineK3IxCMLVVIGMDVAASEFYRNGKYDLDFKLysineK17IxCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedAIQAAGYPDKVVIGMDVAASEFYRGlutamineQ4IxDeamidatedMGKYDLDFKAsparagineN1IxDeamidatedMGKYDLDFKAsparagineN1IxDeamidatedDATNVGDEGGFAPNILENNEALELLKAsparagineN (any)IxDeamidatedFGANAILGVSLAVCKAsparagineN (any)IxDeamidatedNYPVVSIEDPFDQDDWKAsparagineN4IxDeamidatedDATNVGDEGGFAPNILENNEALELLKAsparagineN4IxDeamidatedMCDOLOGAsparagineN4IxDeamidatedMCDOLOGAsparagineN4IxDeamidatedASPARAGINEAsparagineN4IxDeamidatedMATNVGDEGGFAPNILENNEALELLKAsparagineN4IxDeamidatedMCDOLOGMATLGVSLAVCKAsparagineN4IxDeamidatedMCDOLOGMCDOLOGAsparagineN4IxDeamidatedMCDOLOGMCDOLOGAsparagineN4IxDeamidatedMCDOLOGMCDOLOGAsparagineN4IxDeAMIDATEMCDOLOGMCDOLOGMCDOLOGMCDOLOGMCDOLOGMCDOLOGMCDOLOGMCDOLOGMCDOLOGMCDOLOGMCDOLOGMCDOLOG <td></td> <td>QEYDEAGPSIVHR</td> <td>Glutamine</td> <td>Q(any), N-Term</td> <td>1xGln->pyro-Glu</td>		QEYDEAGPSIVHR	Glutamine	Q(any), N-Term	1xGln->pyro-Glu
LAQSNGWGVMVSHRTryptophanW71xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLNGKYDLDFKLysineK31xCMLVVIGMDVAASEFYRNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedTAIQAAGYPDKVVIGMDVAASEFYRGlutamineQ41xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKSPDDPSRAsparagineN11xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLPVAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNATIGVSLAVCKAsparagineN (any)1xDeamidatedHIADLAGNATIGNKAsparagineN (any) </td <td>Beta-enolase</td> <td>HITGEK</td> <td>Histidine</td> <td>H1</td> <td>1xAcetyl</td>	Beta-enolase	HITGEK	Histidine	H1	1xAcetyl
HIADLAGNPDLVLPVPAFNVINGGSHAGNKLysineK301xCMLNGKYDLDFKLysineK31xCMLVVIGMDVAASEFYRNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedTAIQAAGYPDKVVIGMDVAASEFYRGlutamineQ41xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKAsparagineN11xDeamidatedMGKYDLDFKSPDDPSRAsparagineN11xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN11xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLVVSEGSHAGNKAsparagineN (any)1xDeamidatedHIADLAGNPDLVLVVVSEQGFAPNILENNEALELLKAsparagineN (any)1xDeamidatedMYPVVSIEDPFDQDDWKAsparagineN41xDeamidatedMYPVVSIEDPFDQDDWKAsparagineN41xDehydratedNYPVVSIEDPFDQDDWKAsparagineN41xDehydrated		LAQSNGWGVMVSHR	Tryptophan	W7	1xCML
NGKYDLDFKLysineK31xCMLVVIGMDVAASEFYRNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedTAIQAAGYPDKVVIGMDVAASEFYRGlutamineQ41xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedDATNVGDEGGFAPNILENNEALELLKAsparagineN (any)1xDeamidatedFGANAILGVSLAVCKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparagineD/S1xDehydrated		HIADLAGNPDLVLPVPAFNVINGGSHAGNK	Lysine	K30	1xCML
VVIGMDVAASEFYRNGKYDLDFKLysineK171xCMLHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedTAIQAAGYPDKVVIGMDVAASEFYRGlutamineQ41xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN(any)1xDeamidatedDATNVGDEGGFAPNILENNEALELLKAsparagineN (any)1xDeamidatedFGANAILGVSLAVCKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparagineN41xDeamidated		NGKYDLDFK	Lysine	K3	1xCML
HIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN22; N292xDeamidatedTAIQAAGYPDKVVIGMDVAASEFYRGlutamineQ41xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedDATNVGDEGGFAPNILENNEALELLKAsparagineN (any)1xDeamidatedFGANAILGVSLAVCKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparagineD/S1xDehydrated		VVIGMDVAASEFYRNG K YDLDFK	Lysine	K17	1xCML
TAIQAAGYPDKVVIGMDVAASEFYRGlutamineQ41xDeamidatedNGKYDLDFKAsparagineN11xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1xDeamidatedDATNVGDEGGFAPNILENNEALELLKAsparagineN (any)1xDeamidatedFGANAILGVSLAVCKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparagineN41xDeamidatedNYPVVSIEDPFDQDDWKAsparatic Acid/SerineD/S1xDehydrated		HIADLAGNPDLVLPVPAFNVINGGSHAGNK	Asparagine	N22; N29	2xDeamidated
NGKYDLDFKAsparagineN11 xDeamidatedNGKYDLDFKSPDDPSRAsparagineN11 xDeamidatedHIADLAGNPDLVLPVPAFNVINGGSHAGNKAsparagineN (any)1 xDeamidatedDATNVGDEGGFAPNILENNEALELLKAsparagineN (any)1 xDeamidatedFGANAILGVSLAVCKAsparagineN41 xDeamidatedNYPVVSIEDPFDQDDWKAsparatic Acid/SerineD/S1 xDehydrated		TAIQAAGYPDKVVIGMDVAASEFYR	Glutamine	04	1xDeamidated
NGKYDLDFKSPDDPSR Asparagine N1 1xDeamidated HIADLAGNPDLVLPVPAFNVINGGSHAGNK Asparagine N (any) 1xDeamidated DATNVGDEGGFAPNILENNEALELLK Asparagine N (any) 1xDeamidated FGANAILGVSLAVCK Asparagine N4 1xDeamidated NYPVVSIEDPFDQDDWK Asparatic Acid/Serine D/S 1xDehydrated		NGKYDLDFK	Asparagine	N1	1xDeamidated
HIADLAG NPDLVLPVPAF NVINGGSHAGNK Asparagine N (any) 1xDeamidated DAT NVGDEGGFAP NILE NEALELLK Asparagine N (any) 1xDeamidated FGA NAILGVSLAVCK Asparagine N4 1xDeamidated NYPVVSIED PFDQDD WK Asparatic Acid/Serine D/S 1xDehydrated		NGKYDLDFKSPDDPSR	Asparagine	N1	1xDeamidated
DATNVGDEGGFAPNILENNEALELLK Asparagine N (any) 1xDeamidated FGANAILGVSLAVCK Asparagine N4 1xDeamidated NYPVVSIEDPFDQDDWK Aspartic Acid/Serine D/S 1xDehydrated		HIADLAGNPDLVLPVPAFNVINGGSHAGNK	Asparagine	N (any)	1xDeamidated
FGAMAILGVSLAVCK Asparagine N4 1xDeamidated NYPVVSIEDPFDQDDWK Aspartic Acid/Serine D/S 1xDehydrated		DATNVGDEGGFAPNILENNEALELLK	Asparagine	N (any)	1xDeamidated
NYPVVSIEDPFDQDDWK Aspartic Acid/Serine D/S 1xDehydrated		FGANAILGVSLAVCK	Asparagine	N4	1xDeamidated
		NYPVVSIEDPFDODDWK	Aspartic Acid/Serine	D/S	1xDehvdrated
EILDSR Glutamic Acid E(anv). N-Term IxGlu->pyro-Glu		EILDSR	Glutamic Acid	E(any), N-Term	1xGlu->pvro-Glu
Myoglobin HGNTVLTALGGILK Asparagine N3 IxDeamidated	Mvoglobin	HGNTVLTALGGILK	Asparagine	N3	1xDeamidated