Understanding collagen degradation patterns in parchment, leather, and commercial collagen using proteomics

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Abstract

The study of ancient proteins provides invaluable insight into past cultures and societies. Proteins undergo various degradation processes which make their lifespan highly variable. Collagen, the main protein in hide materials, is a particularly useful protein to study due to its stability and long survival. Understanding the degradation patterns of collagen is an important step to understand the use and conservation history of archaeological and historical objects made from animal skins such as parchment and leather which can be further applied to the leather and food industries. This thesis aims to explore available tools in palaeoproteomics to assess (a) changes in proteins present in hide materials caused by manufacturing processes and use history, and (b) the relevance and application of palaeoproteomics methods to the modern-day processing of collagen in the food industry.

This thesis demonstrates two novel uses of the ZooMS methodology: (1) as a tool for the preliminary identification of proteins from milk, egg, and wheat origin alongside species identification and (2) when compared to current methods, as a faster and more accurate method of quality control in the processing of collagen in the food industry. Additionally, the development and application of a targeted method for the determination of piscine gelatine, aided by data derived from palaeoproteomics studies, which aims to support enforcement in food safety, is presented. Finally, this thesis analyses the degradation patterns of collagen based on the deamidation of glutamine on a variety of hide materials processed in varying pH environments. The results highlight the need for studies on the kinetics of deamidation under varied conditions to further our understanding of the forces behind protein degradation and damage. Together, the results of this thesis evidence the importance of the correlation of palaeoproteomics studies to commonly used methods in associated fields for the preservation of cultural heritage.

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Author's Declaration

I declare that this thesis is a presentation of original work and I am the sole author. This work has not previously been presented for an award at this, or any other, University. All sources are acknowledged as References.

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Chapter Contributions

All chapters which are not explicitly mentioned below are the sole work of Carla Soto Quintana (CSQ).

Chapter 3: Using ZooMS as a screening tool for the preliminary identification of proteins of interest in parchment

- Sampling, protein extraction, data processing, analysis and interpretation, and write up were completed by CSQ.
- Nikifor Haralampiev (NH) contributed samples

Chapter 4: Collagen degradation patterns in hide materials

- Sampling, protein extraction, data processing, analysis and interpretation, and write up were completed by CSQ
- Matthew Collins (MC) contributed to data interpretation and discussion.
- Gordon Paul (GP) contributed samples from Devro plc; NH contributed parchment samples; Anne Lama, Andrea Pataki, and Lianne Jordan contributed leather samples

Chapter 5: ZooMS as a fast and effective method to measure deamidation levels in commercial collagen samples

- Sampling, protein extraction, data processing, analysis and interpretation, and write up were done by CSQ
- GP provided data and samples from Devro plc
- MC and GP helped with data interpretation

Chapter 6: A qualitative peptide biomarker approach to identify piscine gelatine to support food security

- CSQ performed sampling, protein extraction, data processing, analysis and interpretation during method development, optimisation, and testing.
- Manuscript preparation by Helen Grundy (HG) and CSQ, with input from Kristine Richter (KKR) and the rest of the authors.
- KKR, HG, and CSQ prepared collagen database
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- HG and Antony Lloyd contributed to sample extraction and preparation for HRAM MS.
- James Donarski (JD) and HG secured funding. JD had overall responsibility of the project and HG acted as project manager.

Chapter 1: Research Framework and Aims

1.1 Research context and significance

This PhD is part of the TEMPERA (Teaching Emerging Methods in Palaeoproteomics for the European Research Area) European Training Network (ETN). TEMPERA is a Marie Skłodowska-Curie European Training Network (ETN) aiming at providing international, intersectoral and interdisciplinary state-of-the-art doctoral training to prepare the next generation of specialists in **mass spectrometry-based ancient protein residues analysis** for **biomolecular diagnostics** and **conservation of cultural heritage material.**

The study of ancient proteins provides invaluable insight into past cultures and societies. Proteins undergo physical, chemical and biological degradation processes which make their lifespan highly variable. Collagen, the most common protein in vertebrates, is a particularly useful protein to study due to its stability and long survival. Thus, understanding the degradation patterns of collagen is an important step to understand the use and conservation history of archaeological and historical objects made from hide materials such as parchment and leather and can be further applied to the modern leather and food industries, both of which continue to make goods from collagen based materials.

This thesis explores the available tools for analysis of collagen degradation and damage assessment and their application to hide materials from modern and historical sources.

1.2 Aims and objectives

This thesis aims to use the available tools in the field of palaeoproteomics to assess:

A. changes in proteins present in hide materials caused by their manufacturing processes and use history, and

B. the relevance and application of palaeoproteomics methods to modern-day processing of collagen in the food industry.

To achieve these aims this thesis will:

- Assess the suitability of ZooMS as a screening method for proteins, other than collagen, arising from the manufacturing process of parchment (Chapter 3).
- Analyse the post-translational modifications that affect collagen to assess the processing and use history of ancient and modern hide materials (Chapter 4).
- Demonstrate the suitability of ZooMS as a quality control and assurance method in the modern collagen industry (Chapter 5)
- Develop and demonstrate the use of proteomics methods to determine piscine gelatine in order to support food safety (Chapter 6)

1.3 Thesis Structure and Outline

This PhD is structured in the form of an introduction (Chapter 2), followed by four discrete research articles (Chapters Chapter 3, Chapter 4, Chapter 5 and Chapter 6), and a discussion section (Chapter 7). This approach was chosen as it enables aspects of this research to be prepared for publication as journal articles. For chapters which have already been submitted for publication the formatting, structure and bibliographic style have been altered from the submitted version to give consistency to the thesis as a whole.

1.3.1 Chapter Outline

Chapter 2 introduces the key elements of the thesis, starting with an overview of proteins and post-translational modifications, and goes on to discuss the analytical methods used in this thesis and their context in previous studies.

Chapter 3: Using ZooMS as a screening tool for the preliminary identification of proteins of interest in parchment proposes the use of peptide mass fingerprinting for the screening of proteins other than collagen.

Abstract: Historical manuscripts written on parchment are a great reservoir of information on past societies and cultures. Parchments hold a large amount of biological information that can be interrogated using biomolecular techniques such as palaeoproteomics. Biocodicology utilises the biological information stored in parchment to inform about a variety of topics such as livestock economies and breed diversification, handling, conservation, and the historic use of the object, as well as craft and technology. Furthermore, the variability in the quality of parchment can be assessed and then referred to the methods of production. This study analyses 'additions' made to the parchment production process, aimed at making the final product softer and/or smoother. Using ZooMS, twenty two peptide markers were identified for the preliminary identification of proteins from milk, egg and wheat origin. These proteins are associated to treatments applied to parchment that are of interest when analysing the production and use history of an object. These methods can be further applied to the analysis of other hide materials, such as leather, or be used as a quality control measure in the modern food industry.

Chapter 4: Collagen degradation patterns in hide materials focuses on the analysis of degradation patterns found in collagen from modern and historical hide materials.

Abstract: Proteins undergo physical, chemical and biological degradation processes which make their lifespan highly variable. Understanding the degradation patterns of collagen is an important step to understand the use and conservation history of archaeological and historical objects made from hide materials such as parchment and leather and can be further applied to the modern leather and food industries, both of which continue to make goods from collagen based materials. This work shows the available methods for assessing the level of deamidation of a sample and emphasises the importance of further studies of glutamine deamidation kinetics and mechanisms to

better estimate damage to the collagen molecule. This is highlighted by the difference in the deamidation patterns, rates of reaction and reaction pathways of samples that have been subjected to acidic conditions (leather) when compared to those processed in an alkaline environment (parchment), where glutamine deamidation is faster than that of asparagine in samples aged under acidic conditions.

Chapter 5: ZooMS as a fast and effective method to measure deamidation levels in commercial collagen samples demonstrates the use of ZooMS as a quality control method suitable for the collagen food industry.

Abstract: The development and improvement of scientific and technological innovations is a critical step towards more sustainable patterns of production of goods and services. Collagen-rich by-products from the slaughter of livestock, like skin and bones, generate opportunities to minimise waste and produce high-value derivatives from slaughtered animals and are widely used in the food and beverage industries. Particular protein modifications, like deamidation, which result from external chemical, physical or biological processes acting on the proteins can be detected by mass spectrometry and used to assess the damage and overall degradation state of a protein. This study shows the use of deamidation level measurements (PQI) designed for the analysis of ancient proteins applied to the food industry as a quality control method. Using ZooMS and PQI measurements we were able to reduce the analysis time by 66% and achieved better sample separation when compared to the in-house method. Implementing ZooMS and PQI measurements for quality control and assurance would enable the measurement of slight variations in deamidation levels which can then be correlated to the physicochemical and mechanical properties of edible collagen films and casings and inform the continuous improvement and development of new and existing products.

Chapter 6: A qualitative peptide biomarker approach to identify piscine gelatine to support food security discusses the application of proteomics methods for determination of piscine gelatine by identification of piscine collagen peptide markers and its importance in food safety and security.

Abstract: Pressure for commercial gelatine suppliers to provide gelatines of known species origin is driven by due diligence, requiring certification, inspection and audit. Following the Europewide adulteration of processed foods with horse meat in 2013, the 2014 Elliott Review into the Integrity and Assurance of Food Supply Networks highlighted the requirement for analytical surveillance methods to support due diligence. Additionally, for piscine gelatine, there is a food labelling requirement regarding the inclusion of fish-derived ingredients on a food label due to concerns over elicitation of an allergic response. We present a targeted peptide biomarker approach by liquid chromatography-mass spectrometry, suitable to the type of instrumentation available to food enforcement officers, to determine the presence of piscine gelatine. The method was successfully applied to gelatine granules, capsules and composite retail food products. The obtained data indicates the method is reproducible between replicates of sub-samples with a limit of detection of 0.1% (w/w).

Chapter 7 Outlines how the aims of the thesis have been achieves and concludes the thesis with a discussion of the challenges faced during this PhD and considerations for future work to expand on this research.

Chapter 2: Introduction

This chapter introduces the methodological approaches of this thesis and the current state of ancient protein research. Protein chemistry (2.1) and the major proteins found in Cultural Heritage (CH) objects will be introduced (2.2), with a focus on collagen and its most common post-translational modifications (PTMs) (2.3) – the understanding of which forms the basis of this PhD. Lastly, the methods for palaeoproteomics and their development will be introduced (2.4).

2.1 Protein Chemistry

Proteins are linear chains made up of 20 different building blocks called amino acids (Table 1). Amino acids have a common general structure featuring a central carbon (α-carbon), a carboxylic group (COOH), an amino group (NH_2), a hydrogen atom and an R group which is unique to each amino acid. Amino acids are joined together by peptide linkages between the carboxyl and amino groups of adjacent blocks to create chains of amino acids called peptides. The end of the chain with the free carboxyl group is called the C-terminus and the side with a free amino group is referred to as the N-terminus.

Proteins are organised into several structural levels. The sequence of amino acids determines the primary structure; the secondary structure is the local conformation of the polypeptide backbone, determined by the pattern of hydrogen bonds between peptide groups; the tertiary structure corresponds to the three-dimensional structure of the protein molecule and determines protein function and the quaternary structure is the aggregation of multiple tertiary structures. Furthermore, proteins can be classified according to their structure in two main categories: (i) fibrous proteins: linear polypeptide chains which are usually water-insoluble, and (ii) globular proteins: water-soluble proteins with a round or spherical tertiary structure.

Table 1. List of the 20 amino acids, their letter abbreviations, their monoisotopic and average mass and occurrence in proteins (%) (L. *et al.*, 2005)

Amino Acid	Three Letter Code	One Letter Code	Monoisotopic mass	Average mass	Occurrence in proteins (%)
Alanine	Ala	A	71.03712	71.079	7.8
Arginine	Arg	R	156.10112	156.188	5.1
Asparagine	Asn	N	114.04293	114.104	4.3
Aspartic Acid	Asp	D	115.02695	115.089	5.3
Cysteine	Cys	C	103.00919	103.144	1.9
Glutamic Acid	Glu	E	129.0426	129.116	6.3
Glutamine	Gln	Q	128.05858	128.131	4.2
Glycine	Gly	G	57.02147	57.052	7.2
Histidine	His	H	137.05891	137.142	2.3
Isoleucine	Ile	I	113.08407	113.16	5.3
Leucine	Leu	L	113.08407	113.16	9.1
Lysine	Lys	K	128.09497	128.174	5.9
Methionine	Met	M	131.04049	131.198	2.3
Phenylalanine	Phe	F	147.06842	147.177	3.9
Proline	Pro	P	97.05277	97.117	5.2
Serine	Ser	S	87.03203	87.078	6.8
Threonine	Thr	T	101.04768	101.105	5.9
Tryptophan	Try	W	186.07932	186.213	1.4
Tyrosine	Tyr	Y	163.06333	163.17	3.2
Valine	Val	V	99.06842	99.133	6.6

2.2 Proteins in Cultural Heritage

The study of ancient proteins refers to the retrieval of peptide sequences that are identified from cultural heritage (CH) objects and objects in the archaeological record (Cappellini, Collins and Gilbert, 2014). Proteins can be found in archaeological and cultural heritage objects such as fossils, archaeological bones, skin, parchment, leather, teeth, tools, textiles, ceramics, and in artworks as binding media and adhesives. Identification of proteins can be used to understand the history of the objects being

analysed, providing critical information to reconstruct ancient societies, understand materials' sources, selections and trades, manufacturing processes, dietary habits, authenticity and deterioration mechanisms. Additionally, the chemical changes which occur to amino acids after protein synthesis, called post-translational modifications (PTMs) can be detected and used to evaluate protein authenticity and unveil the object's history (Mackie *et al.*, 2018). In cultural heritage samples, these modifications can arise from exposure to light, oxygen, and water in either storage or display environments, as well as from reactions with other organic and inorganic materials present in the object under investigation. In general, protein-based archaeological materials survive where the burial environment has low temperature, and low exposure to light, water, and oxygen, although they are prone to microbial attacks. Good preservation is also found in frozen and waterlogged environments, such as peat-bogs, where microbial activity is suppressed (Brandt *et al.*, 2014). Mineralised tissues (e.g. hydroxyapatite) protect collagen and other proteins from degradation (Collins *et al.*, 2002).

2.2.1 Structural proteins

Structural proteins are fibrous proteins, which provide protection, structure and support to cells and organisms. They form protein filaments shaped like rods or wires and are water-insoluble. This class of proteins include collagens, keratins, and fibroins.

2.2.1.1 Collagens

Collagens are the most abundant proteins in mammals. Currently, 28 collagens have been identified (Henriksen and Karsdal, 2019). Type I collagen is the most abundant collagen and is the key structural composition of skin, teeth, and bones; and the most commonly found protein in archaeological and cultural heritage objects. As such, it is the main protein of interest in this thesis and is referred to as collagen, throughout, unless otherwise specified. The major amino acids of this protein are glycine and proline and it has an atypical triple helix structure, unlike the more common secondary

structures found in other structural proteins like keratin and fibroin. A more detailed overview of this protein can be seen in 2.2.3.

2.2.1.2 Keratin

Natural fibres (e.g. fur, hair, wool, etc.) and other organic materials such as skin, hooves, horns, scales, beaks, baleens, quills, and feathers (O'Connor, Solazzo and Collins, 2015) consist mainly of keratin, a sulfur-rich protein formed primarily of α-helical domains and rich in glycine (G, Gly), alanine (A, Ala), and cysteine (C, Cys) residues. These chemical and structural properties make keratinous fibres relatively resistant to biodegradation (Lange, Huang and Busk, 2016), to the point that they have been found preserved in frozen (Rasmussen *et al.*, 2010), dry (Wilson *et al.*, 2013), and waterlogged environments (Frei *et al.*, 2015).

Using mass spectrometry (MS) based techniques, it is possible to identify the biological origin of many keratinous materials (Hollemeyer, Altmeyer and Heinzle, 2002) down to the genus level for mammals (Solazzo, Wadsley, *et al.*, 2013a; Solazzo, Rogers, *et al.*, 2014; Solazzo, 2019; Azémard *et al.*, 2021) and whale baleen (Solazzo *et al.*, 2017). Keratins from sheep, cattle, goat, and red deer have been detected on the coat, shoes, and clothing of Oetzi, the Tyrolean Iceman (Hollemeyer *et al.*, 2008, 2012), and dog hair and sheep wool in textiles from the Pacific Northwest (Solazzo *et al.*, 2011).

2.2.1.3 Fibroin

Fibroin is the main component of silk, a natural fibre produced by certain insect's larvae. This protein is made primarily of antiparallel β-sheet domains and consists mainly of Gly and Ala residues. Amino acid analysis and MS-based techniques have been used to understand degradation (Becker, Willman and Tuross, 1995; Solazzo, Dyer, Deb-Choudhury, *et al.*, 2012), date silk textiles (Araki and Moini, 2011a), and identify the species of origin in textiles (Chen *et al.*, 2019; Solazzo, 2019), sediment imprints (Gong *et*

al., 2016; Li, Zhu and Xie, 2021) and traces of textiles that have come in contact with metal artefacts (Yu *et al.*, 2017; Zheng *et al.*, 2020).

2.2.2 Globular Proteins

Globular proteins realise several roles in metabolic reactions in living organisms. For example, as catalysts, like enzymes, or transport molecules, like haemoglobin. These proteins have a round or spherical tertiary structure and are, generally, water-soluble. Globular proteins, include proteins commonly present in milk, egg, and blood.

2.2.2.1 Milk proteins

The most common proteins found in mammalian milk are caseins (82%) and whey proteins (18%), of which the main protein is lactoglobulin (50%). Protein analysis is able to identify milk proteins in cultural heritage materials such as mortars and plasters (Kuckova, Hynek and Kodicek, 2009; Krizkova *et al.*, 2014). It has also allowed for the identification of casein in a 4000 year-old vessel (Buckley, Melton and Montgomery, 2013), and milk proteins have been found in dental calculus and ancient food residues, which provide evidence of dairying practices in the past (Hong *et al.*, 2012; Salque *et al.*, 2013; C. Warinner *et al.*, 2014; Hendy, Colonese, *et al.*, 2018; Grillo *et al.*, 2020).

2.2.2.2 Egg proteins

Both egg yolk and egg white contain globular proteins. Ovalbumin (54%), ovotransferrin (12%), ovomucoid (11%), lysozyme (3.4%), and ovomucin (3.5%) are the main proteins in egg white, while egg yolk contains mainly lipovitellins (36%), livetins (38%), phosvitin (8%), and low-density lipoproteins (17%) (Kovacs-Nolan, Phillips and Mine, 2005; Abeyrathne, Lee and Ahn, 2013). Proteomics is able to identify egg proteins commonly used, for example, as binders in artworks (Tokarski *et al.*, 2006; Kuckova, Hynek and Kodicek, 2007), ink (Rasmussen *et al.*, 2012) and mural paintings (Chambery *et al.*, 2009),

and marker peptides from eggshell can distinguish common bird taxa such as chicken, duck and goose (Stewart *et al.*, 2014; Fothergill *et al.*, 2017; Jonuks *et al.*, 2018; Maltby *et al.*, 2018)

2.2.2.3 Blood proteins

The main proteins present in blood plasma are serum albumin (55%), globulins (38%), and fibrinogen (7%) (Anderson and Anderson, 1977). Haemoglobin, the oxygen-transport protein, is carried within red blood cells. Bovine and porcine blood have been identified in historical mortars from the Czech Republic (Krizova *et al.*, 2017) and from Chinese wooden buildings (Rao *et al.*, 2015).

2.2.3 Collagen

Collagen is the most abundant protein in skin, teeth and bones; and the most commonly found protein in archaeological and cultural heritage objects. Its high stability, a result of its fibrillar structure, makes collagen a useful protein in the study of cultural heritage and archaeological objects (Brown, Kozlikin, *et al.*, 2021). Collagen has an atypical structure. It is composed of three chains which coil around each other to form a triple helix. Multiple helices form fibrils and then fibres (Shoulders and Raines, 2009). The structure of the chains that form the triple helix has a repeating pattern of three amino acids, GXY, where every third residue is Gly. This is mandated by the tight packing of the helices within the triple helix, as only the side chain of Gly is small enough to fit into its centre. The amino acids in the X and Y positions are often proline (P, Pro) and hydroxyproline (Hyp), with the most common triplet being GlyProHyp (Ramshaw, Shah and Brodsky, 1998; Shoulders and Raines, 2009).

Collagen studies have been crucial to understanding, for example, the species of origin of the materials being analysed, e.g. bone fragments (Buckley *et al.*, 2010; van Doorn, 2014), in an 18th c. gilt sample (Dallongeville *et al.*, 2011), and the terracotta army of Qin

Shihuang (Yan *et al.*, 2014), and dietary patterns or local ecology (Buckley and Kansa, 2011; Vaiglova *et al.*, 2014; Welker, Soressi, *et al.*, 2015)

Collagen, as the main protein in parchment, leather, and other hide materials, is the main protein of interest in this thesis. Hide materials have been used throughout history for a variety of purposes to this day. Indeed, the modern leather, biomedical, and food industries all use cattle skin and hide for the manufacturing of modern goods such as dietary supplements, and edible casings (Hashim *et al.*, 2015; Irastorza *et al.*, 2021). Historical artefacts made of tanned leather include clothing, shoes, furnishings, and other goods (Ebsen *et al.*, 2019). And parchment, a writing medium made from animal skins, is one of the most abundant resources available for the study of past cultures and societies (Fiddyment *et al.*, 2015).

2.3 Modifications and damage in ancient proteins

The survival of proteins in ancient materials is highly variable due to a myriad of physical, chemical and biological degradation processes. Post-translational modifications - the chemical changes that occur to amino acids after protein synthesis - may be the result of a biological process integral to protein function, usually mediated by enzymes, but they can also occur non-enzymatically both in living organisms and proteinaceous materials. In the context of cultural heritage and archaeology, particular protein modifications which result from external processes acting on the proteins can be detected. These can be used to authenticate old proteins or assess the damage and overall degradation state of a protein. Thus, understanding the patterns of degradation of proteins, and how they can be detected, is crucial for the analysis of ancient proteins. In this section, the origins of PTMs (2.3.1) and the main types of PTMs found in collagen - hydroxylation of proline (2.3.2) and deamidation of asparagine and glutamine (2.3.3) - and the conditions in which they occur will be reviewed.

2.3.1 Origin of post-translational modifications

2.3.1.1 Biological modifications

While ancient protein studies are mostly focused on protein modifications in the context of age and diagenesis, it is important to remember that the first chemical alterations happen in the living organism. Most of them are essential to protein function and - given a certain degree of chemical stability - will persist over a long period of time. Therefore, some biological PTMs can still be detected in palaeoproteomics studies and knowing how they originated is key for being able to explain their occurrence. Three of the most important protein modifications, which are stable and abundant enough to be detected in ancient protein samples, are glycosylation (Ozcan *et al.*, 2014), phosphorylation (Cappellini *et al.*, 2018), and hydroxylation (Ehrlich *et al.*, 2010). Additionally, protein hydrolysis occurs during diagenesis but can also be a biological PTM. The case of proteolysis exemplifies a general challenge for PTM analysis in ancient proteomics: biological modifications can be very similar or sometimes identical to PTMs introduced by the diagenesis and use of proteinaceous materials. Being familiar with many potential causes of protein modification helps drawing the correct conclusions.

2.3.1.2 Modifications related to ageing and diagenesis

Proteins can be studied in archaeological samples dating back to millions of years (Demarchi *et al.*, 2016). In particular, the interaction of proteins with specific elements of the surrounding environment (e.g., minerals and metals) can affect protein preservation (Collins *et al.*, 1995; Bada, Wang and Hamilton, 1999; Demarchi *et al.*, 2016). Nonetheless, the preservation status of proteins is strongly influenced by the environmental conditions in which diagenesis occurs and any changes to these conditions, such as removal from burial sites, changes in display and storage conditions (Wilson and Pollard, 2002; Mills and White, 2012), temperature, humidity, pH, light exposure, microbial activity, exposure to oxygen, and the object's chemical environment (Collins *et al.*, 2000; Ostrom *et al.*, 2006; Dobberstein *et al.*, 2009; Buckley and Collins,

2011) have an influence in protein diagenesis and ageing, and the modifications associated to these processes.

Low temperatures slow down chemical processes and microbial growth, therefore extending the lifespan of intact proteins (Bada, Wang and Hamilton, 1999). Archaeological samples found in low-temperature environments, particularly in permafrost conditions, show very good protein preservation (Nielsen-Marsh *et al.*, 2002; Cappellini *et al.*, 2012).

In contrast, high moisture favours protein hydrolysis and microbial growth. One of the highest risks of environmental moisture is the exchange of substances with the surrounding environment. Water can transport polar compounds both to and from the object, causing loss of material and contamination. Finally, the presence of water can induce molecular rearrangements in the object, such as changes in the mineral structure of bone (Wess *et al.*, 2001), which then affects the interaction with proteins and therefore their preservation (Nielsen-Marsh *et al.*, 2000; Reiche *et al.*, 2003).

Extreme pH conditions also accelerate the hydrolysis of peptide bonds, causing the breakdown of the protein into peptides, and side chain modifications like deamidation. The effect of pH can be mitigated by other factors, such as the presence of a mineral matrix in bones, acting like a pH buffer (Collins *et al.*, 1995, 2002).

Exposure to light can induce cleavage of chemical bonds, structure modifications (Miles *et al.*, 2000) and/or, in combination with oxygen, photo-oxidation reactions (Davies and Truscott, 2001; Davies, 2004; Agon *et al.*, 2006; Kerwin and Remmele, 2007; Dalsgaard and Larsen, 2009; Solazzo, Dyer, Deb-Choudhury, *et al.*, 2012).

Some types of samples have inherent characteristics that allow for good preservation of proteins. A well-known example is collagen in bone (Collins *et al.*, 2002). The triple-helix structure of collagen confers this protein high stability and favours its preservation during diagenesis of ancient materials. Moreover, the size of the pores of the mineral structure of bone slows down the influx of water and oxygen, and prevents penetration of microbes or even enzymes, therefore further preventing biodegradation of the organic matter (Lees, 1989; Collins *et al.*, 1995).

Peculiar qualities of the burial environment, such as low temperature, no light, low exposure to water and oxygen, can create good preserving conditions for proteins (Solazzo, Dyer, *et al.*, 2013). However, proteins can also persist in suboptimal conditions. For example, protein residues extracted from archaeological samples found in peat-bogs show very good preservation status despite the wet conditions, since the low oxygen content in this environment suppresses microbial activity (Painter, 1991; Brandt *et al.*, 2014).

2.3.1.3 Modifications induced by usage, handling and modern sources

Protein degradation and PTMs might start at the processing stage of the objects (Solazzo, 2019), such as the use of lime during parchment and leather production (Reed, 1972), or in some artistic techniques (Leo *et al.*, 2011), which induces oxidation and deamidation, or glue preparation, which involves boiling bones and/or other animal residues and effectively hydrolysing collagen. Day to day usage and handling of objects after manufacture, e.g., cooking pots subjected to temperature changes, the mixing of paints and binders, or washing textiles, are inherent sources of modifications during an object's lifetime. The different components of the material can also have a strong influence on the formation of PTMs, as is the example for pigments and dyes in paints, acting as photosensitisers (Pattison, Rahmanto and Davies, 2012). Other circumstances, such as storage conditions (i.e., exposure to light and relative humidity), and the environment to which a material is subject both before and after diagenesis must also be considered. Similarly, stains and pollution (Li *et al.*, 2015), as well as microbial action can influence the state of the proteins at the time of analysis.

Many of the materials used for restoration of objects can introduce protein modifications. Water and organic solvents are often used to clean the surface of archaeological and artistic materials, possibly extracting part of the protein residues and introducing new chemicals, therefore favouring reactions such as hydrolysis. Saliva and synthetic oral fluid are other common cleaning agents, and their enzymatic content contributes to the introduction of new modifications. Finally, the application of consolidating agents, adhesives, and in general conservation materials is also to be

considered a source of modern modifications, e.g., the use of formaldehyde can cause the formation of protein crosslinks, as well as of contamination (animal glue is often used for consolidation of damaged objects). When studying protein modifications, it has to be taken into account that the presence of modern contaminants introduces materials with low levels of modifications.

2.3.1.4 Modifications arising from sample preparation

During protein extraction from the sample matrix and the preparation for proteomics, the analytes will be exposed to the environment and to chemicals. This will introduce additional chemical modifications, which often cannot be distinguished from age-related PTMs.

The most common PTM introduced by sample handling is oxidation of methionine residues to methionine sulfoxide by oxygen from ambient air. It happens relatively quickly and can hardly be controlled, which is why most database search-engines include this as a potential or 'variable' modification by default. Additionally, oxidation products of the aromatic side chains, especially tryptophan, can often be identified. To minimise oxidation reactions, the samples should be processed in a timely manner and heating steps shortened or avoided.

Another inevitable modification is deamidation, i.e. the hydrolysis of the carboxamide groups in asparagine (N, Asn) or glutamine (Q, Gln) residues. It occurs steadily but slowly, when proteins are in aqueous solution (Geiger and Clarke, 1987). Similar to oxidation, the reaction can be slowed down by keeping the procedures short and avoiding long heating steps.

Besides environmental factors, PTMs can also be introduced by the chemicals used for protein extraction and for the alkylation of free cysteine residues. The popular denaturing agent urea has the disadvantage of forming small amounts of isocyanate, which causes carbamylation of lysine side chains and free N-termini. This can be easily avoided by substituting urea with the less reactive guanidine hydrochloride (Kollipara and Zahedi, 2013). Reagents used for the alkylation of free cysteine residues can also

cause unintended protein modification by reacting with other nucleophilic amino acid side chains. For example, the potent alkylating agent iodoacetamide will likely produce some degree of histidine carbamidomethylation. With the less reactive but more selective chloroacetamide, this side reaction can be almost completely prevented (Jersie-Christensen, Sultan and Olsen, 2016; Müller and Winter, 2017).

Lastly, some modifications will be facilitated through protein digestion. Glutamine and glutamic acid (E, Glu) residues located at the N-terminus of peptides tend to cyclise into a lactam ring called pyroglutamic acid (pyroGlu) (Thiede *et al.*, 2000). Similar to methionine oxidation, this is a quick reaction and cannot be avoided, though only a fraction of all peptides will have N-terminal glutamine or glutamate residues.

To summarise, some PTMs introduced during sample preparation, like oxidation and deamidation, cannot be fully prevented but controlled to some extent by handling samples reproducibly. Others, like carbamylation and carbamidomethylation, can be avoided by choosing the right reagents and protocols. In any case, knowing which modifications can be expected from a certain sample type and preparation technique is crucial for making educated decisions for data analysis and interpretation (Li *et al.*, 2008)

2.3.2 Hydroxylation

Hydroxylation is one of the most important biological protein modifications detected in ancient proteins due to its abundance in collagens (Shoulders and Raines, 2009; Ehrlich *et al.*, 2010). Hydroxylation is an oxidative PTM which influences many biological functions including crosslinking and matrix mineralisation, protein-protein interactions, glycosylation, and protein conformation (Gorres and Raines, 2010; Shi *et al.*, 2015). Proline and lysine (K, Lys) are the two main amino acid residues that undergo hydroxylation. The hydroxylation of proline to 4-hydroxyproline is catalysed by Prolyl 4-Hydroxylase (P4H) in the Y position of the (GXY)n repeats of collagens with Pro being the preferred residue in the X position (Gorres and Raines, 2010; Shi *et al.*, 2015). A review by (Gorres and Raines, 2010) details the putative mechanism behind this reaction.

Hydroxyproline plays a critical role in the thermal stabilisation of the collagen triple helix (Berg and Prockop, 1973; Gorres and Raines, 2010) as demonstrated by the difference in melting temperature between a fully hydroxylated type I collagen (43°C) and the non-hydroxylated form (27°C), which is below physiological temperature in humans (Berg and Prockop, 1973). With an abundance of ~4% among the residues in animal proteins, Hyp is more abundant than seven common amino acids (McCaldon and Argos, 1988; Ramshaw, Shah and Brodsky, 1998; Gorres and Raines, 2010). The hydroxylation of lysine residue is catalysed by lysyl hydroxylase, forming hydroxylysine. Some of the hydroxylysine residues are further modified by the sequential steps of O-linked glycosylation producing galactosyl hydroxylysine and glucosylgalactosyl hydroxylysine in collagens and collagen-like proteins (Yamauchi and Sricholpech, 2012; Shi *et al.*, 2015).

The detection of hydroxyproline is essential to the identification of collagens in bone and animal hides. The bone proteome has been characterised in a 700 thousand year (ka) horse (Orlando *et al.*, 2013), a 43 ka mammoth (Cappellini *et al.*, 2012), a 1 ka Moa (Cleland, Schroeter and Schweitzer, 2015), a 150ka bison (Hill *et al.*, 2015), as well as in medieval human dentine (Christina Warinner *et al.*, 2014). A 2016 study of a *Castoroides ohioensis* skull identified proline hydroxylation as both an in vivo and diagenetic post-translational modification (Cleland *et al.*, 2016).

2.3.3 Deamidation

Deamidation is a protein modification occurring on asparagine (N, Asn) and glutamine (Q, Gln) residues where the amide group is transformed into a carboxylic acid, producing aspartic (D, Asp) and glutamic (E, Glu) acids (Figure 1). The reaction can occur enzymatically in living organisms, but it is also known to occur spontaneously and non-enzymatically over time in all protein-based materials (Mycek and Waelsch, 1960; Imada *et al.*, 1973; Wriston and Yellin, 1973; Curthoys and Watford, 1995). As such, it is the most common diagenetic PTM identified in collagen (Cleland, Schroeter and Schweitzer, 2015; Schroeter and Cleland, 2016). The level of deamidation of proteins in biology has

been connected with the age of the organism, using deamidation as a 'molecular clock' (Robinson, McKerrow and Cary, 1970; McKerrow and Robinson, 1974; Robinson, McKerrow and Legaz, 1974; Robinson *et al.*, 2004).

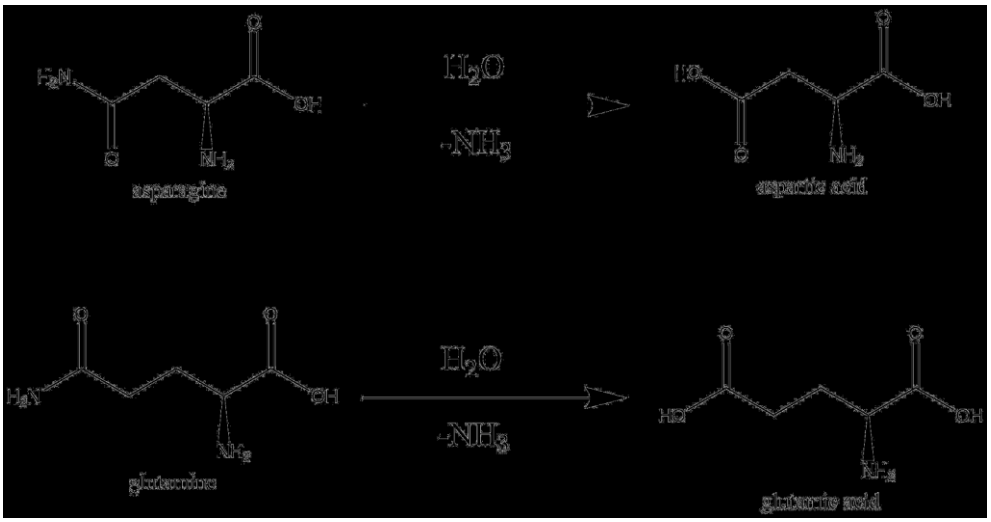

Figure 1. Scheme of the deamidation of the amino acids asparagine and glutamine

Spontaneous deamidation follows, mainly, two mechanisms: the direct hydrolysis of the amide, or the formation of a cyclic amide followed by hydrolysis (Robinson *et al.*, 2004). Both Asn and Gln follow both pathways, and the formation of the cyclical intermediate has an overall faster reaction rate than direct hydrolysis (Sondheimer and Holley, 1957; Capasso, Mazzarella and Sica, 1991; Catak *et al.*, 2009), although deamidation through the formation of a cyclic amide only occurs if the flexibility of the protein is not limited by the protein structure (Geiger and Clarke, 1987; Kosky *et al.*, 1999; Aswad, Paranandi and Schurter, 2000; Radkiewicz *et al.*, 2001; Li *et al.*, 2005). At constant pH, deamidation of Asn and Gln residues follows first-order kinetics (Geiger and Clarke, 1987; Patel and Borchardt, 1990b). In the solid state, deamidation rate is significantly lower than in solution (Oliyai *et al.*, 1994; Lai and Topp, 1999; Song *et al.*, 2001; Li *et al.*, 2005, 2006), which is highly relevant for the study of proteins in cultural heritage samples. The influence of protein structure on deamidation is on average between 50% and 60% based on primary structure (Robinson and Robinson, 2001b; Noah E. Robinson and Robinson, 2004; Robinson *et al.*, 2004). Several factors affect the mechanism and the

rate of deamidation - i.e., pH, ionic strength, temperature, amino acid sequence and structure of the protein, and matrix - and should therefore be considered when studying the kinetics of this reaction.

In acidic conditions (pH < 5) asparagine deamidation (Figure 2) favours direct hydrolysis and the formation of the succinimide (Asu) intermediate is very slow. This reaction is slowest at a pH between 4 and 6 (Robinson *et al.*, 2004). In neutral and alkaline environments the succinimide-intermediate mechanism is prevalent, except in AsnPro sequences, where Asu formation is hindered by the bulk of the Pro side-chain (Patel and Borchardt, 1990b, 1990a; Clarke, 2003). The ionic strength of the solution is likely to have an effect on the rate of the reaction, which is limited by the solvent accessibility of the Asn and Gln residues. Some studies show that the deamidation rate of peptides significantly increases when ionic strength is increased (Scotchler and Robinson, 1974; Capasso, Mazzarella and Zagari, 1991), whereas no influence was observed in other cases (Tyler-Cross and Schirch, 1991). With increasing temperatures, the rate of deamidation for both Asn and Gln residues increases (McKerrow and Robinson, 1974; Yüksel and Gracy, 1986; Geiger and Clarke, 1987; Noah Edward Robinson and Robinson, 2004). Despite the influence on the kinetics of the reaction, temperature does not influence the products obtained from deamidation (Geiger and Clarke, 1987; Noah Edward Robinson and Robinson, 2004).

Under similar conditions as deamidation, hydrolysis of peptide bonds can occur. In acidic pH, the degradation of proteins and peptides preferably occurs C-terminally of Asn and Asp residues through the cleavage of the peptide bond on the C-terminal of Asn (Voorter *et al.*, 1988; Patel and Borchardt, 1990b, 1990a; Oliyai and Borchardt, 1993; Goolcharran *et al.*, 2000).

Glutamine deamidation mechanisms (Figure 3) are not as well studied, but it is likely that direct hydrolysis is responsible for most of the deamidation, except in highly flexible regions or when glutamine is followed by glycine. This is due to the difficulty of forming the glutarimide ring (Joshi *et al.*, 2005; Riggs *et al.*, 2019).

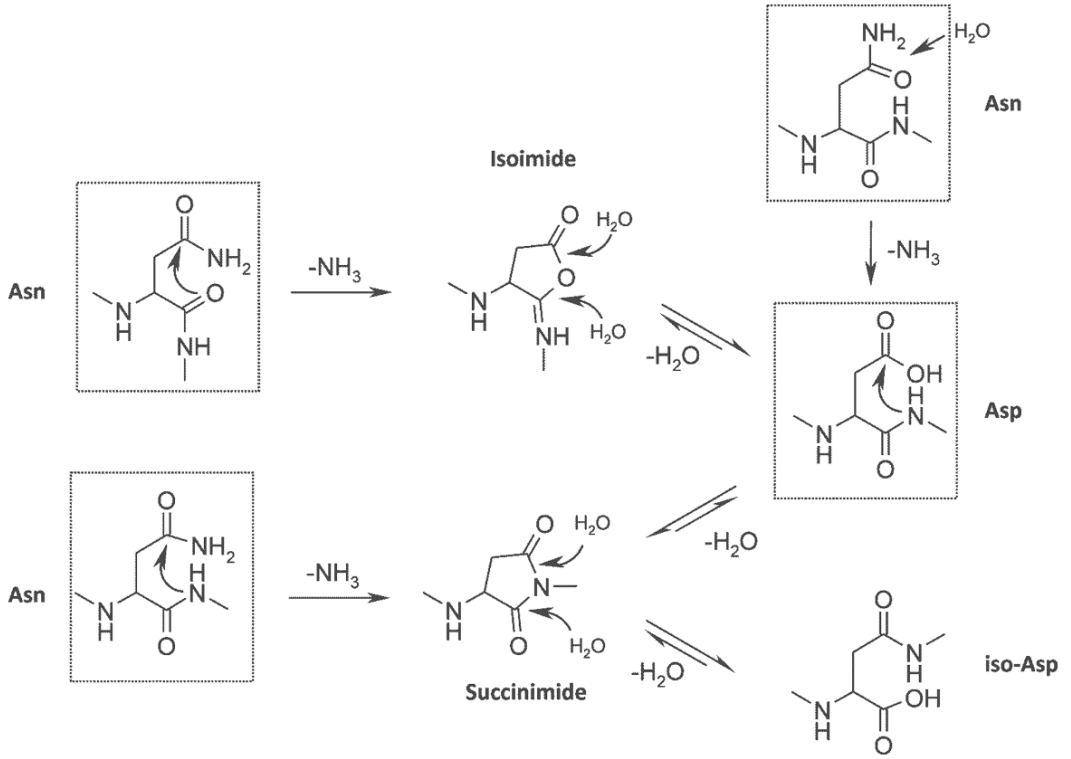

Figure 2. Asparagine and Aspartate degradation pathways. From (Sydow *et al.*, 2014)

Given that asparagine is much more susceptible to deamidation than glutamine (Terwilliger and Clarke, 1981; Daniel, Dines and Petach, 1996; Robinson *et al.*, 2004; Wilson, van Doorn and Collins, 2012), the investigation of the level of deamidation of Gln residues is more suitable for assessing the damage of archaeological and cultural heritage materials (Leo *et al.*, 2011; Van Doorn *et al.*, 2012; Ramsøe *et al.*, 2020; Nair *et al.*, 2022). The rate of deamidation of Asn and Gln at specific locations is heavily influenced by the amino acids found next to them, with AsnGly and GlnGly motifs having the fastest rates, and AsnPro and GlnPro motifs the slowest (Robinson *et al.*, 2004).

The level of deamidation of proteins in biology has been connected with the age of the organism, using deamidation as a 'molecular clock' (Robinson, McKerrow and Cary, 1970; McKerrow and Robinson, 1974; Robinson, McKerrow and Legaz, 1974; Robinson and Robinson, 2001a). However, this principle is not always valid for archaeological and artistic materials because of the influence of environmental factors. Nonetheless, in some cases it can be reasonably assumed that the level of deamidation of two objects is

mostly dependent on how 'old' the objects are. One example is the comparison of keratin deamidation in sheep wool objects stored in controlled museum conditions, in which variation caused by environmental factors is mostly minimised (Araki and Moini, 2011b). However, treated proteinaceous materials (e.g., casein from milk, animal glue) are the most common protein-based compounds in artistic objects. In these cases, it is almost impossible to determine if the measured deamidation level is connected to the preparation treatments of the materials, or to the ageing of the object (Leo *et al.*, 2011; Mackie *et al.*, 2018).

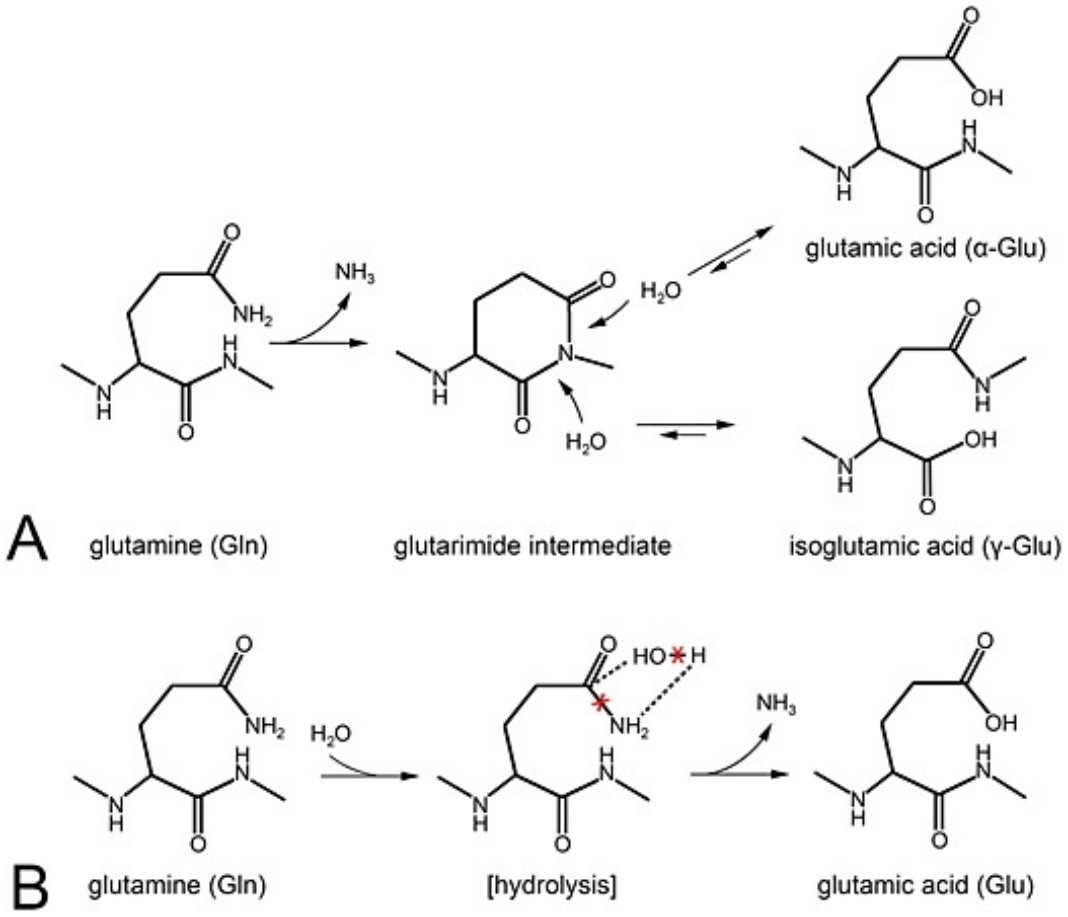

Figure 3. Deamidation of glutamine to glutamic acid via (A) glutarimide intermediate and (B) direct hydrolysis. From: (Schroeter and Cleland, 2016)

In mass spectrometry, deamidation can be identified by its characteristic +0.984 Da mass shift. Bioinformatics tools are available to calculate the overall deamidation of glutamine from ZooMS spectra, the Q2E package (Wilson, van Doorn and Collins, 2012) and the more recent MALDIpqi package (Nair *et al.*, 2022). The Q2E package uses a genetic algorithm to determine the extent of glutamine deamidation by comparing the theoretical and measured distributions of each sample (Wilson, van Doorn and Collins, 2012). MALDIpqi utilises weighted least-squares linear regression, followed by a linear mixed effect model to predict the overall deamidation level of a sample, termed the Parchment Glutamine Index (PQI) (Nair *et al.*, 2022). Similarly, the software tool deamiDATE 1.0 (Ramsøe *et al.*, 2020) assesses the bulk and site-specific deamidation of proteins from LC-MS/MS spectra.

2.4 Methods

During the past decades, several analytical techniques have been developed and optimised for protein identification in samples from cultural heritage objects. Due to the extraordinary value of the objects under study, the methods used to characterise ancient protein residues should ideally be non-invasive, meaning that sampling is not required, and non-destructive, so the sample can be reused.

A detailed overview of the analytical techniques used for protein identification from palaeontological, archaeological and art samples have been widely discussed in the review by Dallongeville *et al.* (2016),the mini-review by Giuffrida, Mazzoli and Pessione (2018) and the palaeoproteomics review by Warinner, Korzow Richter and Collins (2022). This section will discuss the analytical methods involved in the study of ancient proteins in two parts: the methods that existed before mass spectrometry was applied to ancient proteins (2.4.1), and mass spectrometry based proteomics (2.4.2), followed by an overview of basic bioinformatics analysis (2.4.3) and challenges and future perspectives (2.4.4).

2.4.1 Protein analysis prior to mass spectrometry based proteomics

2.4.1.1 Fossil protein analysis

Fossil protein analysis was initially centred on the recovery of amino acids. In 1954, Abelson showed that amino acids in shells were stable over geological time-scales (Abelson, 1954), and detected the L and D isomers of amino acids in fossil shells a decade later (Hare and Abelson, 1968). This formed the basis of amino acid racemization, which has been used to assess the 'age' of archaeological objects (Griffin *et al.*, 2008, 2009; Penkman *et al.*, 2008, 2013; Demarchi *et al.*, 2011; Demarchi and Collins, 2014). Later, immunodetection methods were used to identify epitopes from fossil proteins (de Jong *et al.*, 1974). However, none of these techniques provided protein sequence information.

The first ancient protein sequence – the first 16 residues of osteocalcin – was recovered from a moa bone using Edman degradation (Huq, Tseng and Chapman, 1990). No other ancient protein sequences have ever been obtained by Edman degradation, as it requires a high amount of purified and undamaged protein, a rare occurrence in ancient protein analysis (Cappellini, Prohaska and Racimo, 2018)

2.4.1.2 Detection and Localisation Techniques

Staining

The first experiments on protein identification from samples from works of art were performed by using staining methods based on the application of biological dyes (Ostwald, 1936) for the localisation of proteins in a sample cross-section. But the technique has limited sensitivity, and the presence of pigments can interfere with the identification of the colour of the complex. The first limitation was overcome by the introduction of fluorescent dyes (Wolbers and Landrey, 1987). However, fluorescent stains can also suffer from the auto-fluorescence of some binding media.

Spectroscopic Techniques

Spectroscopic techniques are commonly used in the cultural heritage field to obtain information of both inorganic and organic components as they can be applied non-destructively to very small samples, and portable devices have been introduced making them also non-invasive (Rosi *et al.*, 2013). Infrared spectroscopy (IR) has been used to examine paint cross-sections (Meilunas, Bentsen and Steinberg, 1990; Pilc and White, 1995; Sciutto *et al.*, 2014), enamel, dentin and bones (Lopes *et al.*, 2018), paint binders (Ricciardi *et al.*, 2012; Dooley *et al.*, 2013), and textiles (Delaney *et al.*, 2016). Raman spectroscopy has been applied to the identification of proteinaceous materials in art samples (Vandenabeele *et al.*, 2000; Daher *et al.*, 2010), and archaeological materials (Smith and Clark, 2004) such as ivory (Edwards *et al.*, 2006), teeth (Kirchner *et al.*, 1997), bones (Morris and Mandair, 2011), mummified remains (Edwards *et al.*, 1995), parchment (Edwards *et al.*, 2001) and hair (Wilson *et al.*, 1999). However, while both techniques are able to detect the presence or absence of proteinaceous residues, no information about the protein biological species can be obtained which makes MS techniques more suitable for the work done in this thesis. The application of fluorescence spectroscopy has also been investigated for the study of protein-based materials due to its non-invasive approach.

Time of Flight Secondary Ion Mass Spectrometry

Time-of-flight secondary ion mass spectrometry (TOF-SIMS) is capable of providing, in a single experiment, high-resolution maps of the distribution of various organic and inorganic materials in complex samples which represents a step forward to better understand artists' techniques. Additionally, it's is non-destructive and doesn't require an extraction step. TOF-SIMS has shown some positive results in protein identification in both art and archaeology, such as the identification of an egg-based paint binder in a wall painting sample (Benetti *et al.*, 2015), the detection of animal glue (Sanyova *et al.*, 2011), the detection of markers associated with egg yolk, animal glue, and drying oil in samples from Italian paintings (Voras *et al.*, 2016), the discrimination of collagen and keratin in a human skin remain (Cersoy *et al.*, 2012) and the species identification of

parchment samples (Vilde, Abel and Watts, 2016). However, this technique needs further optimisation since the presence of inorganic compounds, like pigments, can alter the mass spectrum, preventing reliable discrimination among proteinaceous materials (Mazel *et al.*, 2006; Atrei *et al.*, 2014).

2.4.1.3 Immuno-based Techniques

Immunological techniques are based on the antibody/antigen interaction, where the antibody is a protein which is able to bind a region (epitope) of a target protein, the antigen, with high specificity. This category includes several techniques which have been differently applied and developed for the analysis of art and archaeological samples. However, since there are many factors (e.g. inorganic compounds, environment) that can interfere with the protein recognition by the antibody, the application of antibody-based methods to detect ancient proteins remains controversial.

Enzyme-linked immunosorbent assay (ELISA) is one of the most commonly used methods to selectively identify proteins in artistic (Arslanoglu *et al.*, 2010) and archaeological samples (Ulrich *et al.*, 1987). ELISA allows the specific recognition of ovalbumin, mammalian/fish glue, casein, and polysaccharide-based materials. This method has been mostly overcome by proteomic techniques for the analysis of proteins in archaeological/palaeontological samples, but it continues to be of interest in the museum environment since it is simple, low-cost, and specific for certain animal species. However, the presence of other biomolecules and pigments in art samples (Cartechini *et al.*, 2010; Lee *et al.*, 2014), as well as environmental factors for bones (Cattaneo *et al.*, 1995), were determined to catalyse protein modifications which can alter the protein structure and so affect the antibody recognition.

Besides ELISA, there are other immuno-based techniques which have been developed to allow the localisation of the protein of interest in the sample. These include immunofluorescence (IMF), chemiluminescence (CL) and immuno-Surface-Enhanced Raman scattering (immuno-SERS). The application of these micro-imaging immuno-

based techniques to paint cross-sections has been recently summarised in the review by (Sciutto *et al.*, 2017).

Among the less commonly used immuno-based approaches, it is worth mentioning the gel immuno-based, radioimmunoassay (pRIA) and electrochemical immunoassay (Bottari, Oliveri and Ugo, 2014) techniques. The capability to identify the animal species or family from blood residues, allowed to better understand the exploitation of certain animal species by ancient populations (Seeman *et al.*, 2008; Yohe and Bamforth, 2013). pRIA has been mainly applied to the study of archaeological bones and helped to reconstruct the phylogeny of extinct animals (Muyzer *et al.*, 1992).

2.4.2 Mass spectrometry based techniques

The word proteomics describes the study of proteins in terms of identification, quantification and modification. The developments of mass spectrometry in the past two decades led to the introduction of the term palaeoproteomics, now used to describe the application of mass spectrometry-based techniques to the study of ancient proteins (Cappellini, Collins and Gilbert, 2014). The application of palaeoproteomics in the cultural heritage field has increased significantly, and a broad variety of methods based on mass spectrometry have been developed for the analysis of these complex samples (Cleland and Schroeter, 2018) and some standards of practice have been introduced in the field (Hendy, Welker, *et al.*, 2018; Brown, Douka, *et al.*, 2021).Mass spectrometry has now become the go-to tool for ancient protein studies, over the use of immunological approaches (Warinner, Korzow Richter and Collins, 2022).The bottom-up approach, based on the analysis of the peptides released after protein digestion, is the most common strategy employed for the analysis of CH and archaeological samples and, thus, the method used in this thesis. This section will introduce the principles of mass spectrometry, and give an overview of the development of peptide mass fingerprinting (PMF) and peptide sequencing, applied to the analysis of cultural heritage materials.

2.4.2.1 Principles of Mass Spectrometry

Mass spectrometry (MS) is an analytical technique first developed in the late 19th century which has rapidly evolved in the last 30 years (Griffiths, 2008). It has applications in the life and health sciences and, as discussed here, in the context of cultural heritage. Mass spectrometry is based on the separation of molecules according to their mass, since once ionised they have a different behaviour under the influence of electric or magnetic fields. A mass spectrometer consists of three main components: an ion source, a mass analyser, and a detector. In the ion source molecules are converted into ions that are then sorted and separated according to their mass-to-charge ratio (m/z) in the mass analyser before being measured by the detector (Figure 4). The following section will describe the principles involved in mass spectrometry for protein identification.

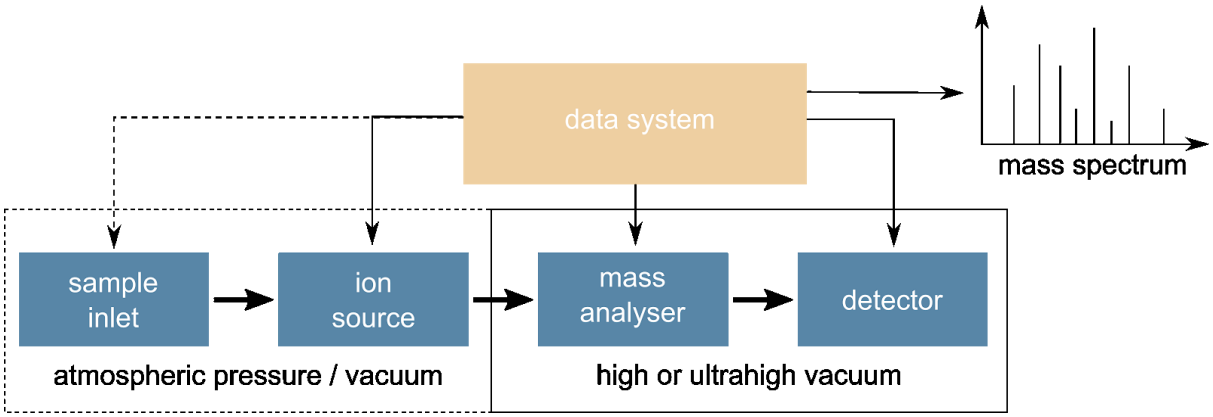

Figure 4. Basic mass spectrometer setup (Adapted from (Gross, 2006))

2.4.2.2 Ionisation

The ion source is responsible for ionising the sample molecules so that they can be sent by electric and/or magnetic fields into the mass analyser. Ionisation techniques are divided into 'hard' and 'soft' depending on the energy imparted to the sample molecules and the degree of fragmentation this produces. Hard ionisation techniques produce a high degree of fragmentation which destroys complex biomolecules. The most common

example of hard ionisation is electron impact (EI). Soft ionisation techniques, such as electrospray ionisation (ESI) and matrix-assisted laser desorption/ionisation (MALDI) are then preferred for the ionisation of molecules such as peptides and nucleotides (Domon and Aebersold, 2006; Lewis, Wei and Siuzdak, 2006; El-Aneed, Cohen and Banoub, 2009). Proteins and peptides are usually detected as positive ions due to the addition of protons (H+) to amine groups, to form ammonium ions.

In MALDI analysis (Hillenkamp *et al.*, 1991) the sample is co-crystallised with a high energy absorbent compound, called matrix, before being bombarded with a laser which both desorbs and ionises the analytes (Lewis, Wei and Siuzdak, 2006).

In electrospray ionisation (ESI) the sample is introduced into the ionisation source via a thin needle. As the sample is sprayed, a high voltage is applied to the needle to create charged droplets (Yamashita and Fenn, 1984; El-Aneed, Cohen and Banoub, 2009). While small molecules of the analyte may be singly charged, ESI is different from MALDI in that most analyte ions are multiply charged.

2.4.2.3 Detection

Once the analyte ions are in the vacuum, they can be moved by electric or magnetic fields and propelled into a mass analyser that can isolate ions based on their m/z values. Different instruments use a variety of systems to separate the ions, but the same principle is applied to all of them where the velocity of the ion is increased and the mass is measured as a function of behaviour after acceleration. The simplest method is the time-of-flight analyser (TOF) where the time it takes for an ion to reach the detection is determined by its mass. The smaller the mass the faster the ion flies. MALDI-TOF-MS is able to analyse proteins down to femtomole quantities very rapidly. Other types of analyser include quadrupole, which involves separating ions as they flux in a field of four electromagnetic rods, or an Orbitrap, in which ions are electrostatically trapped in an orbit around a central electrode. Fourier Transform Ion Cyclotron Resonance (FT-ICR) MS measures mass by detecting the image current produced by ions cyclotroning in the presence of a magnetic field. The mass range, speed and accuracy

vary between detectors but there is always a trade-off between them; the faster detectors (e.g. TOF) are less accurate, while FT-ICR MS is slow but extremely accurate. In peptide sequencing, individual peptides detected by the first mass spectrometer (MS1) can be further fragmented - usually by collision-induced dissociation (CID) - and analysed in a second mass spectrometer (MS2). This approach is called tandem mass spectrometry (MS/MS). Different analysers can be combined together to improve resolution and mass accuracy.

2.4.2.4 Bottom-up Proteomics

Proteomics can be applied in the field of cultural heritage for the identification of proteinaceous materials that can be found in numerous objects such as paint binders and adhesives, parchment manuscripts, leather objects, palaeontological and archaeological remains. Proteins can be very large biomolecules (up to hundreds kDa) and mass spectrometers can only perform rapid and accurate measurements across a narrow range of masses. Typically, in order to detect large proteins, a bottom-up approach is taken. This approach relies on the digestion of the protein into peptides prior to MS analysis. Protein identification is then performed based on peptide mass fingerprinting (PMF) or peptide sequence analysis.

Digestion

Protein digestion has a large influence on the quality of protein identification. The most common method of digestion involves the use of proteases, enzymes which catalyse proteolysis, with different specificities and efficiencies. Trypsin has a high degree of specificity and is the most widely used protease in bottom-up proteomics. Trypsin cleaves peptide bonds C-terminal to lysine and arginine residues, except when followed by a proline residue (Burkhart *et al.*, 2012). Digestion is usually performed at neutral pH in ammonium bicarbonate buffer at 37 °C and is stopped, after the desired digestion time, by the addition of acid. These experimental conditions can be optimised for specific applications (Switzar, Giera and Niessen, 2013). The analysis of tryptic peptides

leads to high-quality MS/MS spectra and reliable identification of proteins in database searches. However, the use of other proteases and/or multi-protease digestion can increase sequence coverage and improve the identification of PTMs, through the analysis of complementary peptides (Tsiatsiani and Heck, 2015; Giansanti *et al.*, 2016).

Interpretation

Once peptide masses have been detected, the resulting spectra need to be compared to reference spectra in order to make meaningful interpretations. Peptide mass fingerprinting (PMF), and database spectral matching from MS/MS spectra of sequenced reference proteins are the most common approaches applied to ancient proteins.

PMF does not involve the direct analysis of the amino acid sequence. Instead, the mass of a peptide from an unknown sample is compared to a reference library of species-diagnostic peptide masses which allows assigning the peptide to a certain species. PMF is most useful for the analysis of samples dominated by a single protein (e.g. bone) and not to a complex sample (e.g. paint binders mixture). The identification of proteins in complex samples can be resolved by MS/MS experiments which imply the peptide sequence reconstruction amino acid by amino acid. Identification is usually achieved by pattern matching between the reconstructed peptide and the theoretical peptides with the same mass, and known biological species, reported in publicly available databases such as NCBI, PRIDE, Global Proteome Machine Database (GPM), PeptideAtlas, etc. (Riffle and Eng, 2009; Schmidt, Forne and Imhof, 2014).

2.4.2.5 Peptide Mass Fingerprinting

Peptide mass fingerprinting applied to the investigation of proteinaceous binders in art (Tokarski *et al.*, 2002) and archaeological/paleontological (Ostrom *et al.*, 2000) samples was first mentioned in the 2000s and it consists of four main steps: (i) protein extraction, (ii) protein digestion, (iii) analysis using MALDI-MS and (iv) match of the

peptide masses from the unknown sample against reference diagnostic peptides for species assignment.

One of the first applications involved the use of a 1% trifluoroacetic acid (TFA) aqueous solution for protein extraction, followed by overnight digestion with trypsin (Tokarski *et al.*, 2002). Later, a much faster procedure based on the direct digestion of the sample for 2 hours without previous extraction was suggested (Hynek *et al.*, 2004; Kuckova *et al.*, 2005). Protein identification was first achieved by manually comparing the results of the unknown sample with lists of peptides characteristic of each protein-based reference material (Kuckova, Hynek and Kodicek, 2007; Kirby *et al.*, 2011). This step was further simplified by the use of chemometrics using principal component analysis (PCA) and soft independent modelling of class analogy (SIMCA) (Fremout *et al.*, 2011).

In the archaeological field, PMF is mainly used for the discrimination of bones from different animal species by analysing collagen sequences. A particular and important application is the distinction, by a single marker, of the morphologically (almost) identical ovid (sheep) and caprid (goat) species (Buckley *et al.*, 2010; Baker, 2018) which has been also used to study the species origin of parchment (Toniolo *et al.*, 2012; Fiddyment *et al.*, 2015; Teasdale *et al.*, 2017).

This collagen-based proteomics is known as Zooarchaeology by mass spectrometry, or ZooMS (Buckley *et al.*, 2010) and it has been used for the analysis of several collagenous materials found in museum objects (Kirby *et al.*, 2013) and archaeological bones and teeth from several contexts from modern samples, to the Neolithic and into the early upper Palaeolithic (Buckley and Kansa, 2011; Tran *et al.*, 2011; Welker, Soressi, *et al.*, 2015; McGrath *et al.*, 2019). ZooMS has also been utilised to distinguish between rodent bones (Buckley *et al.*, 2016), for the identification of fish (Richter *et al.*, 2011b), marine mammals (Buckley *et al.*, 2014), and giant tortoises (Van der Sluis *et al.*, 2014), the identification of biomarkers from a 2000-year-old tumour (Bona *et al.*, 2014), and species identification of eggshell (Stewart *et al.*, 2013; Presslee *et al.*, 2017), antler combs (von Holstein *et al.*, 2014; Brandt, Haase and Collins, 2018), horn, hoof, baleen, tortoiseshell (Solazzo, Wadsley, *et al.*, 2013b; O'Connor, Solazzo and Collins, 2015), and

ivory (Coutu *et al.*, 2016). A comprehensive review on the application of proteomics in the analysis of textiles and clothing has been published by (Solazzo, 2019).

Additionally, ZooMS has also been used in studies on the ageing and extent of degradation of collagen by measuring glutamine deamidation (Araki and Moini, 2011a; Leo *et al.*, 2011; Doorn *et al.*, 2012; Vanden Berghe, 2012; Wilson, van Doorn and Collins, 2012; Solazzo, Wilson, *et al.*, 2014; Welker, Soressi and Roussel, 2017; Brown, Kozlikin, *et al.*, 2021). Brown *et al.* (2016) used ZooMS to screen more than 2000 fragmented bones from the site of Denisova Cave, Russia, to facilitate the discovery of human remains. A single hominin bone was identified and found to carry Neanderthal mitochondrial DNA.

In artworks, PMF and ZooMS have been used to identify the origin of organic colouring in artworks (Kuckova *et al.*, 2005), egg binders in ink (Rasmussen *et al.*, 2012) and murals (Chambery *et al.*, 2009), and even distinguish between the presence of egg yolk or whole egg in paint binders (Tokarski *et al.*, 2006; Kuckova, Hynek and Kodicek, 2007; Tripković *et al.*, 2013). Proteinaceous binding media has also been found in pottery (Yan *et al.*, 2013), mortars and plasters (Kuckova *et al.*, 2009; Kuckova, Hynek and Kodicek, 2009; Krizkova *et al.*, 2014; Krizova *et al.*, 2017), wooden buildings (Rao *et al.*, 2015), and the terracotta army of Emperor Qin Shihuang (Yan *et al.*, 2014).

PMF has also been applied to the study of both proteins and lipids following extraction with organic solvents from the same micro-sample (van der Werf *et al.*, 2012; Calvano *et al.*, 2015). This approach is of considerable relevance in the cultural heritage field where the amount of sample is often limited to a few tens of micrograms and so only one destructive analysis can be performed.

Peptide mass fingerprinting is the simplest and most cost-efficient setup for data acquisition and analysis of PTMs. A single mass spectrum is recorded for a mixture of unmodified and modified peptides and if both forms are present, the modification will be reflected in a mass-shift between the two peaks and can be matched with a library. Due to the lack of peptide fragmentation, the identification of modified peptides is much less reliable than peptide-spectrum matches in tandem-MS and the PTMs cannot be localised to a certain amino acid.

Most commonly, PMF spectra of ancient proteins are analysed manually because conventional software tools (Samuelsson *et al.*, 2004; Murray, 2012) struggle with the high incidence of peptide modifications. This might change in the future with specialised software being developed for peak extraction, mass re-calibration, and peak identification specifically for palaeoproteomics PMF data (Gu and Buckley, 2018; Hickinbotham *et al.*, 2020). However, quantification of modified peptides is not supported yet, which is why manual data interpretation is still the standard. This has for example been done to detect and quantify deamidation (Araki and Moini, 2011a), as a proxy for thermal age and degradation. Deamidation is hard to analyse using PMF data due to the lack of chromatographic separation leading to overlapping isotope envelopes of deamidated and unmodified forms. Hence, quantification requires a software tool for the prediction of the isotope distribution for each peptide (Fernandez-de-Cossio *et al.*, 2004; Wilson, van Doorn and Collins, 2012; Nair *et al.*, 2022).

2.4.2.6 Peptide Sequencing

When using peptide sequencing, the peptides released after protein digestion are isolated, fragmented and detected by tandem mass spectrometry. The peptide sequence is reconstructed amino acid by amino acid and its identification is usually achieved by comparison with theoretical ions generated by the peptides of the same mass present in the database. This bottom-up strategy is therefore ideal for the identification of protein modifications.

The first application of peptide sequencing for the study of proteins in samples from works of art was suggested by (Tokarski *et al.*, 2006). While the protein digestion step is usually the same in all protocols, with trypsin being the enzyme of choice, several extraction methods have been tested such as ammonium bicarbonate buffer (Tripković *et al.*, 2013) assisted by ultrasonic bath (Chambery *et al.*, 2009) and microwave-assisted digestion (Leo *et al.*, 2009). Other steps have also been suggested to improve protein recovery and identification: a deglycosylation step using Peptide-N-Glycosidase F (PNGaseF) before enzymatic digestion, if glycosylated proteins such as egg proteins are present (Vinciguerra *et al.*, 2015), and a clean-up step before sample analysis using

solid-phase extraction (SPE) based on hydrophilic interaction chromatography (HILIC) (Fremout *et al.*, 2010). The same group also proposed a library of MS/MS spectra obtained from reference glues from different animal species (Fremout *et al.*, 2012) in order to overcome the issue of unknown or incomplete sequence of certain proteins. Even if collagens are among the most common proteins found in art samples, attention was also focused on the discrimination of milk origin using 3 specific alpha S1 casein peptides (Chambery *et al.*, 2009). In a recent paper, the distinction of the three most common proteinaceous materials found in artworks (animal glue, egg and milk) was achieved using a targeted proteomics approach based on multiple reaction monitoring (MRM) ion mode (Vinciguerra *et al.*, 2019). Using this strategy, based on the selection of specific proteins for each group, and specific peptides for each protein, the author was able to identify the use of milk as a binder in real samples that gave a negative response when analysed by standard LC-MS/MS peptide sequencing.

Besides the most common application for species identification, an example of the effectiveness of peptide sequencing at studying proteins modifications is illustrated in a recent paper where palaeoproteomics was applied to investigate the conservation layers of a 14th century wall painting, helping the reconstruction of the conservation history of the artwork (Mackie *et al.*, 2018).

As for the application of peptide sequencing in archaeology and palaeontology, proteins have been shown to be more resistant to degradation than DNA, thus making palaeoproteomics an ideal technique to investigate ancient protein-based materials with the most diverse applications: from the study of past human diets (C. Warinner *et al.*, 2014; Hendy, Colonese, *et al.*, 2018; Hendy, Warinner, *et al.*, 2018) to the phylogenetic reconstruction of extant and extinct species (Buckley, Larkin and Collins, 2011; Rybczynski *et al.*, 2013; Welker, Collins, *et al.*, 2015; Cleland *et al.*, 2016; Welker *et al.*, 2016; Cappellini *et al.*, 2018). If compared to art samples, the nature of archaeological and paleontological materials allow the study of proteins mixtures produced not only by single organisms (Cappellini *et al.*, 2012), but also by groups of organisms (metaproteomics) (Jersie-Christensen *et al.*, 2018). The first experiment focused on the study of osteocalcin proteins in bone fossils (Ostrom *et al.*, 2000) but,

following further research which showed the high sensitivity of osteocalcin to degradation (Buckley *et al.*, 2008), attention was then focused on collagen proteins and their degradation to better understand bone diagenesis (Dobberstein *et al.*, 2009; Buckley and Collins, 2011).

Palaeoproteomics can be applied to various substrates, including eggshell (Demarchi *et al.*, 2016), dentin, dental pulp and enamel (Tran *et al.*, 2011; Stewart *et al.*, 2016), dental calculus (Warinner, Speller and Collins, 2015; Jersie-Christensen *et al.*, 2018), keratinous materials from soft and hard tissues (Hollemeyer *et al.*, 2008; Solazzo, Wadsley, *et al.*, 2013a; Brandt *et al.*, 2014; O'Connor, Solazzo and Collins, 2015), food remains (Solazzo *et al.*, 2008; Cappellini *et al.*, 2010; Hong *et al.*, 2012; Buckley, Melton and Montgomery, 2013; Shevchenko *et al.*, 2014; Yang *et al.*, 2014), and residues associated with archaeological vessels (Solazzo *et al.*, 2008; Hong *et al.*, 2012; Buckley, Melton and Montgomery, 2013).

Despite having two more layers of information - retention time and MS2 fragment scans - the analysis of PTMs in data-dependent LC-MS/MS experiments is simple, due to the availability of a wide range of software tools. By default, most common search engines, such as Mascot (Perkins, Pappin and Creasy, 1999), Andromeda (Cox *et al.*, 2011), and Sequest (Eng, McCormack and Yates, 1994) include certain PTMs for database searching. They can be defined as 'fixed', for instance for fully derivatised cysteine residues, or as 'variable', for partial modification, which is the case for most biological and diagenesis-linked PTMs. Fixed modifications will be applied to every peptide containing the respective amino acid, which means that the unmodified form cannot be identified. On the other hand, a peptide with a variable modification site will be searched two times - in the modified and unmodified form. The more variable PTMs are configured and the higher the number of allowed modifications per peptide, the longer the search will take. Consequently, there is a delicate balance between including not enough modifications - and thereby missing peptides with these PTMs - and including too many, which will potentially reduce the number of identifications at a given false-discovery rate. This is because the search space will contain more modified peptide and decoy sequences, increasing the chances of false-positive hits. Unfortunately, there is no easy rule to

determine the ideal number of variable modifications to maximise the number of identified peptides, as these settings depend on the size of the searched data and the database. As a rule of thumb for searching against the full proteome of a mammal, allowing for up to 5 variable PTMs and up to 4 modifications per peptide is a good starting point for further optimisation of the search parameters. The most relevant modifications frequently included in ancient protein data analysis are Deamidation (NQ), Oxidation (M), and Hydroxyproline in collagen-containing samples. These PTMs frequently reach occupancies of over 50% in ancient samples.

2.4.2.7 Non-invasive Protein Extraction

Mass spectrometry-based proteomics provides crucial information about protein-based materials in cultural heritage objects, information that cannot be obtained by the more traditional analytical techniques such as species identification and degradation. However, one of the most critical aspects of this approach is the need of a micro-sample, which can be problematic due to the uniqueness and preciousness of the materials under study. For this reason, new methods for the minimally-invasive extraction of proteins directly from the object have been recently investigated.

A first attempt to perform in-situ protein analysis was suggested in 2009 by means of desorption electrospray ionisation mass spectrometry (DESI-MS). With this method, analytes are desorbed directly from different kinds of surfaces under ambient conditions. The strategy was tested on intact and in-situ tryptic digested proteins applied on the surface of flint flakes or potsherds. The positive results indicated how this strategy would be of great interest to analyse surface residues and food remains in archaeological materials (Heaton *et al.*, 2009).

A completely different approach, based on triboelectric extraction, was introduced in 2015 by Fiddyment et al. for the species identification of the parchment used to manufacture a pocket bible (Fiddyment *et al.*, 2015). Proteins were extracted from the waste material collected after rubbing the parchment surface with a non-abrasive PVC polymer eraser, which is commonly used for parchment cleaning.

Another strategy, based on the use of a functionalised ethyl-vinyl acetate (EVA) film, was first suggested to extract proteins from a manuscript (Zilberstein *et al.*, 2017) and it was further developed with cation/anion exchange and C8 resins for artworks applications (Manfredi *et al.*, 2017). The strip is wetted with distilled water, applied directly on the surface of the material under study and the proteins are then eluted from the film for further digestion. Proteins could be identified from several different supports such as panel and mural paintings, bone and parchment, and it was proved to be efficient also if a varnish layer is present on top of the protein-based material (Barberis *et al.*, 2018). In addition, fungal proteins (hydrophobin) have been employed to create a layer, over a cellulose acetate transparent sheet, which is able to immobilise trypsin and so allow in situ digestion (Cicatiello *et al.*, 2018). The bioactive film showed a good peptide recovery and sequence coverage, comparable to the more traditional digestion protocol (Leo *et al.*, 2009) when tested on paint mock-ups, and it was successfully applied to frescoes and painting linings.

The development of these non-invasive techniques (Fiddyment *et al.*, 2015; Manfredi *et al.*, 2017; Cicatiello *et al.*, 2018; McGrath *et al.*, 2019) has proven a breakthrough technology in biocodicology (Fiddyment *et al.*, 2019), an emerging field dealing with the multidisciplinary analysis of parchment manuscripts, codices, and other historic documents (Toniolo *et al.*, 2012; Fiddyment *et al.*, 2015; Teasdale *et al.*, 2015, 2017; Fiddyment and Collins, 2017; Gordon, 2017; Sommer *et al.*, 2017; Calà *et al.*, 2019; Hickinbotham *et al.*, 2020; Vnouček *et al.*, 2020; Ruffini-Ronzani *et al.*, 2021; S. P. Doherty *et al.*, 2021; Warinner, Korzow Richter and Collins, 2022).

2.4.3 Bioinformatics Analysis

Database searches allow for the quick and accurate identification of large numbers of proteins by matching experimentally generated spectra against spectra theoretically derived *in silico* from protein sequences available in sequence databases (Eng, McCormack and Yates, 1994). The success of database searching depends on the quality of the data, the database, and the search method (Graves and Haystead, 2002). Both

open access and proprietary software, such as MaxQuant (Cox and Mann, 2008), Mascot (Perkins, Pappin and Creasy, 1999), and PEAKS (Ma *et al.*, 2003), are available to perform these searches. A typical database search starts with the *in silico* digestion of protein sequences based on the cleavage patterns of the chosen protease(s). Then, the *in silico* peptides with mass equal to the precursor ion are included in the search (with a pre-defined error). At this stage, peptides containing PTMs where the combined mass matches the precursor ion can also be considered for inclusion. Next, all possible dissociation ions are generated for every *in silico* peptide, and the observed masses are then compared to the masses generated from *in silico* peptides and ranked according to their correspondence.

Typically, the outcome of a proteomics experiment is a list of scored inferences, usually in the form of peptide-spectrum matches (PSMs), peptides, or proteins (The, Tasnim and Käll, 2016). Normally, only inferences with a score above a threshold are of interest. The use of a False Discovery Rate (FDR) - i.e. the expected fraction of results for which the observations are the result of chance - is an easy way to set such a threshold. Identifications are then expressed as a probability of the match and should have a minimum of two supporting peptides. These can be improved by narrowing down the search space (database) by taking into account known information about the nature of the sample (e.g. taxonomic family). Furthermore, analysis should allow for the common PTMs encountered in ancient protein samples, such as methionine and tryptophan oxidation, glutamine and asparagine deamidation, and proline hydroxylation. De-novo sequencing, i.e. building a protein/peptide sequence via analysis of masses of the ion series rather than matching against in silico generate masses, can be used to identify proteins in rare or unusual samples (e.g. extinct species). Finally, database bias must be taken into consideration when performing database searches as databases may have a bias towards pathogenic or commercially relevant species (Graves and Haystead, 2002; The, Tasnim and Käll, 2016; Hendy, Welker, *et al.*, 2018).

2.4.4 Current challenges and future perspectives

Post-translational modifications themselves can be a challenge for ancient protein analysis because they increase spectral complexity and dilute the peptide signals, effectively lowering the overall sensitivity. As of now, there are no methods available to reverse diagenesis-based modifications. Especially in very old proteins, PTMs can accumulate up to a point at which the majority of the detectable peptides are modified. Ignoring them in the analysis of artistic or archaeological samples would significantly decrease the quality of the study.

Replicating protein modifications caused over hundreds to millions of years in a model experiment can hardly be achieved. As a consequence, ancient PTM analyses often rely on few available samples and lack comparable controls. The types of diagenesis-based modifications range from rather quick PTMs, which can often also be introduced during sample preparation, to extremely slow modifications only occurring in million-year-old biomolecules and reaching the limits of organic chemistry theories.

Current data analysis software is capable of identifying a multitude of modifications, but the identified PTMs should not be over-interpreted, for example by using them as linear age markers similar to 14C decay, because the reaction kinetics of all diagenesis-linked PTMs known so far also depend on environmental factors, mainly water content, pH, temperature, and exposure to the atmosphere. Further investigation of the mechanisms of protein modification during sample ageing has the potential to improve proteome coverage and potentially serve as the basis for the discovery of better authenticity and age markers.

Starting with sample preparation, several PTM enrichment methods have been developed to facilitate the detection of low abundant biological modifications, such as phosphorylation (Neville *et al.*, 1997; Oda, Nagasu and Chait, 2001; Pinkse *et al.*, 2004) or acetylation (Kim *et al.*, 2006). In ancient proteomics, this could be used to consistently detect specific PTMs or decrease spectral complexity by selectively sampling only one or few modification types. Alternatively, modified residues with unique chemical

properties can be selectively derivatised to improve or prevent their detection by LC-MS/MS.

During data acquisition and analysis, there is still a lot of room left for optimising the quantification of modified peptides. For instance, the actual stoichiometry of modified to unmodified peptides can be calculated by analysing the same sample type at different states of degradation similar to calculating site occupancies (Olsen *et al.*, 2010) or by absolute quantification through isotope-labelled spike-in standards (Gerber *et al.*, 2003). Moreover, the problem of missing values in larger sample sets can be reduced by multiplexing with isobaric labels, such as iTRAQ or TMT (Jersie-Christensen *et al.*, 2018), however at the cost of losing confidence in detection in each individual sample. Very recently, software tools for the detection, localisation, and quantification of modified peptides by data-independent acquisition have been introduced (Keller *et al.*, 2016; Bekker-Jensen *et al.*, 2019), which has the potential to provide good data completeness, increase the dynamic range, and potentially analyse many more different PTMs in a single search by incorporating them in a merged spectral library.

With increasing knowledge on protein modification in ancient samples, it will become more and more important to develop new standards for sample processing, data acquisition, and analysis methods across the field. Thereby, studies can be kept comparable, transparent and reproducible within an individual and across different laboratories.

Chapter 3: Using ZooMS as a screening tool for the preliminary identification of proteins of interest in parchment

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Relevance: This chapter sees the use of ZooMS as a screening tool for the preliminary identification of proteins, other than collagen, that are of interest when analysing historical hide materials, such as parchment and leather.

Abstract: Historical manuscripts written on parchment are a great reservoir of information on past societies and cultures. Parchments hold a large amount of biological information that can be interrogated using biomolecular techniques such as palaeoproteomics. Biocodicology utilises the biological information stored in parchment to inform about a variety of topics such as livestock economies and breed diversification, handling, conservation, and the historic use of the object, as well as craft and technology. Furthermore, the variability in the quality of parchment can be assessed and then referred to the methods of production. This study analyses 'additions' made to the parchment production process, aimed at making the final product softer and/or smoother. Using ZooMS, twenty two peptide markers were identified for the preliminary identification of proteins from milk, egg and wheat origin. These proteins are associated to treatments applied to parchment that are of interest when analysing the production and use history of an object. These methods can be further applied to the analysis of other hide materials, such as leather, or be used as a quality control measure in the modern food industry.

3.1 Introduction

Historical manuscripts written on parchment, a writing support made of animal skins, are a great reservoir of information on past societies and cultures. Although the origins of parchment are a source of debate (Johnson, 1970; Reed, 1975) the first mention of documents written on skins dates back to the Egyptian 4th Dynasty (c. 2613 to 2494 BCE), and it is known that parchment was widely used until the mass production of paper took over in the 19th century (Ryder, 1964). As such, parchment is found in large volumes and has the advantage of being well dated and provenanced and, in addition to the text, it holds a large amount of biological information that can be interrogated using biocodicology, an emerging field that uses biomolecular techniques such as palaeoproteomics and genomics for the study of biological information stored in manuscripts (Fiddyment *et al.*, 2019).

Using biocodicology, parchment can be interrogated about a variety of topics such as livestock economies and breed diversification, handling, conservation, and the historic use of the object, as well as craft and technology. Furthermore, the variability in the quality of parchment can be assessed and then referred to the methods of production used in its manufacture (Teasdale *et al.*, 2015, 2017; Fiddyment *et al.*, 2019; Demarchi *et al.*, 2020).

3.1.1 Parchment production

Although 'recipes' for the production of parchment and leather are abundant and varied, the basic principles of production of these materials have remained largely unchanged since the eighth century (Ryder, 1964; Reed, 1972; Haines, 1999). During parchment production animal skins (Figure 5) – typically from cow (*Bos taurus*), sheep (O*vis aries*), or goat (C*apra hircus*) - are transformed into a durable sheet suitable for use as a writing medium. The general process of production is as follows; once the skin is removed from the animal it is placed in a highly alkaline solution, typically calcium hydroxide ($Ca(OH)_2$). This process, called liming, serves to:

- facilitate the removal of hair and epidermis by breaking the disulphide bonds in the keratinous tissue (Bienkiewicz, 1983; Covington, 2009);
- remove cutaneous lipids by saponification, making the parchment a lighter colour and improving the absorption of inks (Koppenhoefer, 1938, 1939);
- lower the collagen's iso-electric point by the hydrolysis of amide groups attached to asparagine and glutamine residues, which enables the removal of non-collagenous proteins from the skin (Menderes *et al.*, 1999; Covington, 2009).

After liming, the skin is fleshed to remove the epidermis and fats, leaving the collagen-rich dermis layer. The skin is then delimed in water, stretched, shaved, and dried under tension. After drying, the surface may be pounced to produce a smooth surface (S. Doherty *et al.*, 2021).

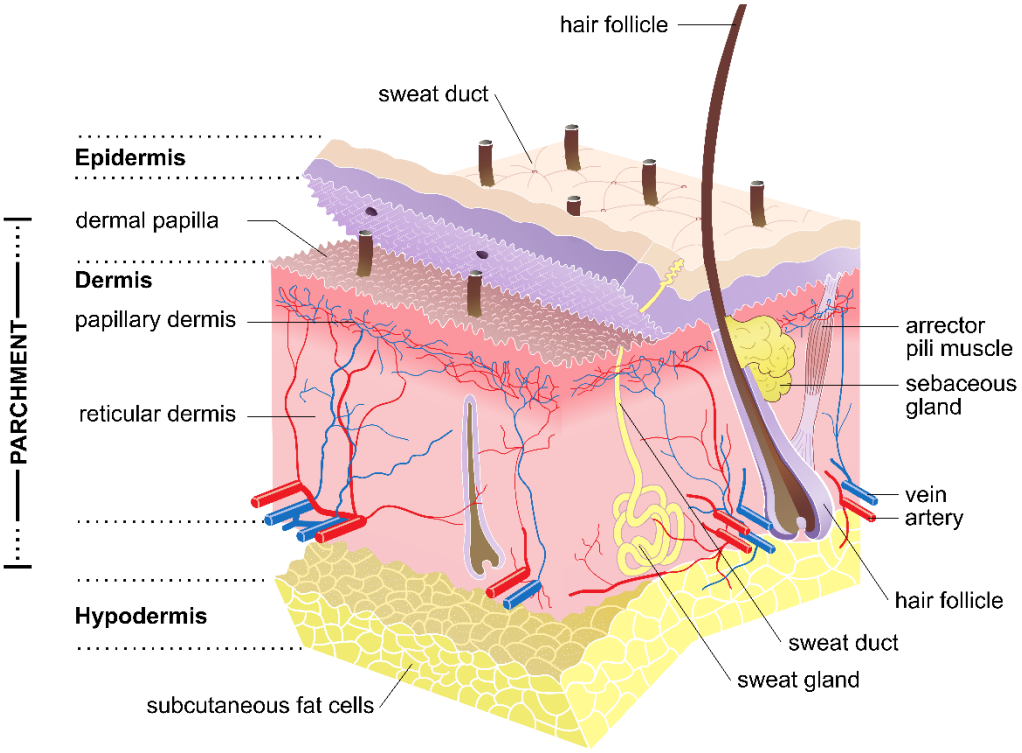

Figure 5. Structure of mammalian skin and the layers typically present in parchment and leather (Sean Doherty, Wikimedia Commons)

3.1.2 Species identification of parchment using ZooMS

Collagen is the most abundant protein found in archaeological and cultural heritage. In structural tissues, like skin, the majority of collagen found is type I (Axelsson *et al.*, 2016). A key interest in ancient proteins lies in the possibility of identifying the species of animal remains due to the phylogenetic and diagenetic information they contain. This has been achieved in recent years with the application of mass spectrometry (MS) based techniques, mainly, matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) and liquid chromatography tandem mass spectrometry (LC-MS/MS). These techniques provide a fast and easy platform for the identification and characterisation of ancient proteins (Ostrom *et al.*, 2000; Brandt, Haase and Collins, 2018).

Species identification by mass spectrometry is based on the detection of sequence variations found in proteins across different taxa, which give rise to differences in the mass and chemical composition of the proteins. The amount of sequence variations between species increases with evolutionary divergence (O'Connor, Solazzo and Collins, 2015). MALDI-TOF MS is a fast and inexpensive soft ionisation technique that allows the detection of peptides and proteins as singly charged ions. Peptide Mass Fingerprinting (PMF) is then used to determine the taxonomic origin of the sample by the identification of specific target peptide masses - also called biomarkers. PMF is most useful for the analysis of samples dominated by a single protein although it is also used for typing microorganisms in clinical settings. When used for archaeological or historical samples, this approach is called Zooarchaeology by Mass Spectrometry (ZooMS) (Buckley *et al.*, 2009). Contrary to single MS (MS1) approaches, tandem MS (MS2) provides data on the primary sequence of the proteins and peptides they detect. This means that PMF studies have some limitations:

- they are able to determine taxonomic origin, but not species, with a few exceptions (Buckley and Collins, 2011);
- although PTMs can be allowed for in analysis, modifications cannot be localised, precluding validation;
- only the most abundant proteins are identified (Cleland and Schroeter, 2018).

Due to these limitations, MALDI-TOF MS has recently been used as a screening tool to identify a small number of samples from large datasets. The samples of interest can then be further analysed by protein sequencing, radiocarbon dating, or other available methods which require more time and resources (Harvey *et al.*, 2016; Welker *et al.*, 2017).

This study analyses 'additions' made to the parchment production process, aimed at making the final product softer and/or smoother. Using ZooMS, peptide markers were identified and subsequently used for the preliminary identification of proteins, other than collagen, associated with these treatments that will aid our understanding of the production and use history of an object.

3.2 Materials and Methods

3.2.1 Parchment samples

Experimental goat's skin parchment samples, prepared according to Armenian recipes from the 17th to 18th centuries were provided for this study and more details about the manufacturing process can be seen in Haralampiev (2012). Besides the traditional steps of parchment making (Saxl, 1954; Reed, 1972, 1975), the Armenian recipes describe additional treatments intended to make the parchment softer and/or smoother. A general diagram of the process can be seen in Figure 6. The softening treatments involve soaking the skins in different solutions like yoghurt and bran water, or rubbing barley flour on the wet skins, whilst the application of surface coatings like glair (egg white) or lime powder (calcium carbonate, $CaCO_3$) is used to make the surface smoother for writing (Haralampiev, 2012). The samples used in this study are described in Table 2 and a diagram of the areas where the described coatings were applied to the skin can be seen in Figure 7. A total of 23 samples were used in the study, where 13 samples (S) were used for peptide marker identification and the remaining 10 samples (T) were used for testing the identified markers. All but two of the samples belong to the sample

set described above. A commercial bovine collagen powder (T1) and an experimental parchment sample from Austria (T2), were added as controls for testing the method.

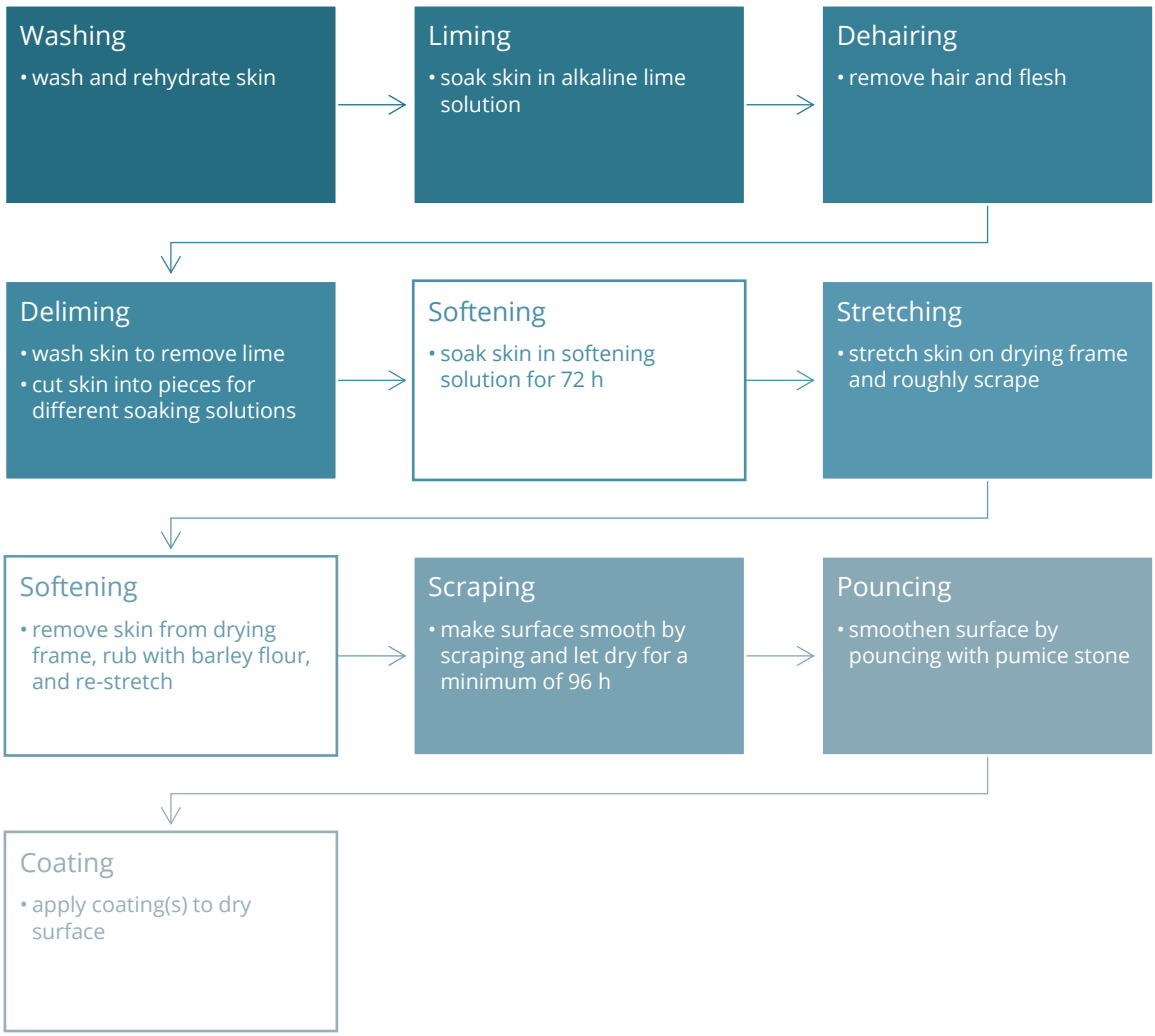

Figure 6. Steps in parchment production. Filled rectangles represent the basic steps in parchment making. Outlined rectangles represent the optional steps found in Armenian recipes from the 17th to 18th centuries.

Table 2. Parchment sample descriptions. ‘S’ samples were used for peptide marker identification. ‘T’ samples were used for testing the results obtained from ‘S’ samples.

Sample	Description
S1	Reference goat’s skin parchment, untreated.
S2	A coating of fish glue was applied to the finished parchment surface.
S3	A coating of flaxseed water extract was applied to the finished parchment surface.
S4	A coating of glair (egg white) was applied to the finished parchment surface.
S5	After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched.
S6	After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched. Once dry, a coating of fish glue was applied to the surface.
S7	After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched. Once dry, a coating of flaxseed water extract was applied to the surface.
S8	After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched. Once dry, a coating of glair was applied to the surface.
S9	After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched.
S10	After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. Once dry, a coating of fish glue was applied to the surface.
S11	After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. Once dry, a coating of flax seed water extract was applied to the surface.
S12	After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. Once dry, a coating of glair was applied to the surface.
S13	After stretching and scraping, while still wet, the skin was removed from its frame and rubbed with barley flour from the grain side. The skin was stretched again and left to dry.
T1	Commercial bovine collagen sample from Devro plc.

Sample	Description
T2	Experimental parchment sample from Austria, untreated.
T3	Goat's skin parchment. After stretching and scraping, while still wet, the skin was removed from its frame and rubbed with barley flour from the grain side. The skin was stretched again and left to dry. Once dry, a coating of glair and flaxseed water was applied to the surface.
T4	Goat's skin parchment. After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched. After smoothening the skin was sprinkled with dried lime powder ($CaCO_3$) and left to dry.
T5	Goat's skin parchment. After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched. Once dry, a coating of flaxseed water was applied to the flesh side of the finished parchment surface.
T6	Goat's skin parchment. After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched. Once dry, a coating of glair and flaxseed water was applied to the surface.
T7	Goat's skin parchment. After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. After smoothening the skin was sprinkled with dried lime powder ($CaCO_3$) and left to dry.
T8	Goat's skin parchment. After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. Once dry, a coating of flaxseed water was applied to the flesh side of the finished parchment surface.
T9	Goat's skin parchment. After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. After stretching and scraping, while still wet, the skin was removed from its frame and rubbed with barley flour from the grain side. The skin was stretched again and left to dry.
T10	Goat's skin parchment. After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. After stretching and scraping, while still wet, the skin was removed from its frame and rubbed with barley flour from the grain side. The skin was stretched again then left to dry. A coating of glair was applied to the finished parchment surface.

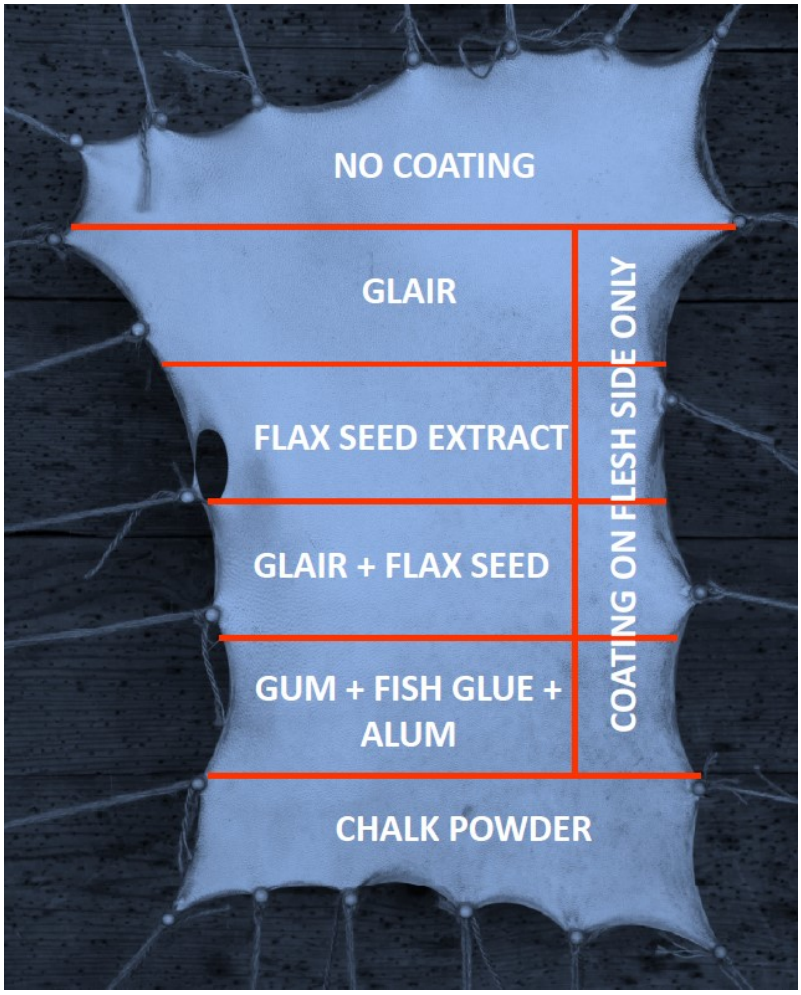

Figure 7. Diagram of coatings application sections in goat skin The coatings were applied to the skin before cutting of each sample (Table 2). Image credit: N. Haralampiev.

3.2.2 Sampling

Sampling was performed according to the protocol developed by (Fiddyment *et al.*, 2015). Here, a Staedtler 'Mars Plastic' eraser was used. The eraser was rubbed against the parchment in one direction and the resulting eraser waste fragments were collected in individual 1.5 mL microcentrifuge tubes. For each sample, a new individual piece of eraser and acid-free paper was used; the eraser and paper were thrown away once

sampling of the parchment was completed to avoid cross-contamination. For sample T1, a small amount (< 2 mg) of collagen powder was put in a microcentrifuge tube. Nitrile gloves were worn throughout the sampling process to avoid keratin (human skin) contamination. All samples were stored at room temperature until required.

3.2.3 MALDI-TOF-MS

ZooMS analysis was performed according to (Fiddyment *et al.*, 2015). Samples were spun down at maximum speed on a benchtop centrifuge for 1 min. Then, 75 µL of 0.05 M ammonium bicarbonate (AmBic) buffer (pH 8) and 1 µL of trypsin (0.4 µg/µL) was added to each sample. The samples were heated at 37 °C for 4 h. After incubation with trypsin, the digests were spun down at maximum speed on a benchtop centrifuge for 1 min and 1 µL of 5% (vol/vol) trifluoroacetic acid (TFA) was added. Samples were desalted and concentrated using C18 resin (Millipore), following the manufacturer's instructions. Peptides were eluted in a final volume of 50 µL of 50% acetonitrile (ACN)/0.1% TFA (vol/vol). One microliter of eluted peptides was mixed on a ground steel plate with 1 µL of α-cyano-4-hydroxycinnamic acid matrix solution [1% in 50% ACN/0.1% TFA (vol/vol/vol)] and air-dried. All samples were spotted in triplicate. Samples were analysed using a calibrated Ultraflex III (NLD1; Bruker Daltonics) MALDI-TOF instrument in reflector mode.

3.2.4 LC-MS/MS

Dried peptide samples were resuspended in 50µl of 80% ACN and 0.1% formic acid (FA). 10µl of each sample was then transferred to a 96 well plate and placed in a vacuum centrifuge at 40ºC until approximately 3 µL of the solution was left. The samples were rehydrated with 10 µL of 0.1% TFA, 5% ACN. Samples were then separated on a 15 cm column (75 µm inner diameter) in-house laser pulled and packed with 1.9 µm C18 beads (Dr. Maisch, Germany) on an EASY-nLC 1000 (Proxeon, Odense, Denmark) connected to a Q-Exactive HF-X (Thermo Scientific, Bremen, Germany) on a 77 min gradient. Buffer A

was milliQ water. The peptides were separated with increasing concentrations of buffer B (80% ACN and 0.1% FA), going from 5% to 30% in 50 min, 30% to 45% in 10 min, 45% to 80% in 2 min, held at 80% for 5 min before dropping back down to 5% in 5 min and held for 5 min. Flow rate was 250 nL/min. The column temperature was maintained at 40°C using an integrated column oven. A wash-blank method using 2 µl 0.1% TFA, 5% ACN was run in between each sample to hinder cross-contamination and column blockage. The Q-Exactive HF-X was operated in data dependent top 10 mode. Spray voltage was 2 kV, S-lens RF level at 50, and heated capillary at 275°C. Full scan mass spectra were recorded at a resolution of 120,000 at m/z 200 over the m/z range 350–1400 with a target value of 3e6 and a maximum injection time of 25 ms. Product ions were recorded at a resolution of 60,000 with a maximum ion injection time set to 118 ms and a target value set to 2e5. Normalised collision energy was set at 28% and the isolation window was 1.2 m/z with the dynamic exclusion set to 20 s.

3.2.5 Protein identification

The raw spectral data was converted to Mascot generic format (mgf) using Proteowizard MSConvert version 3.0.22084 (Chambers *et al.*, 2012) using the 200 most intense peaks in each MS/MS spectrum. MS/MS ion database searching was performed on Mascot (Matrix ScienceTM, version 2.8.0) (Perkins *et al.*, 1999), against a database including goat, sheep, and bovine collagen, fish collagen, wheat, flaxseed, and barley proteins, bovine milk proteins, chicken egg proteins, and contaminants from the Global Proteome Machine's (GPM) common Repository of Adventitious Proteins (cRAP). The parameters are as follows: the peptide tolerance was 10 ppm, MS/MS ion tolerance was 0.07 Da, with a semi-tryptic search strategy with up to two missed cleavages, and a fixed modification of carbamidomethyl (C). Variable modifications included acetyl (protein N-term), deamidation of asparagine and glutamine, methionine oxidation, hydroxylation of proline and lysine, and galactosylation of hydroxylysyl. Searches were performed against a decoy database to estimate protein false discovery rates, which were adjusted to less than 5%. Proteins were identified with a minimum of two different peptides and a default significance threshold of $p<0.05$.

3.2.6 Identification of non-collagen protein markers using mMass

Spectral analysis was performed using the open-source cross-platform software mMass (Strohalm et al. 2010). Raw spectral data was pre-processed and converted to peak lists using the R packages bacollite and MALDIquant (Gibb and Strimmer 2012; Hickinbotham et al. 2020). Peak picking was performed using a signal to noise (S/N) ratio of 3, and peak matching with a tolerance of 0.05 m/z. A semi-manual search for potential markers of the identified proteins was conducted. Markers were included if they occurred in at least two samples and did not overlap any of the matched collagen peptides. The database used to perform peptide searches included mammalian and fish collagen sequences. These were taken into consideration when looking at the overlap in collagen peptides but, due to the great variation in fish collagen sequences and the fact that some sequences are incomplete, no fish collagen markers were identified. The protein matches shown in Appendix A, Table A1 include all the fish and mammalian proteins in the database.

3.3 Results & Discussion

A set of samples (S) of known composition was used for the analysis and identification of peptide markers for proteins, other than collagen, arising from the use of various coatings and softening solutions often present in parchment making recipes. In order for these markers to be of use, they must appear alongside the collagen fingerprint used for species identification in traditional ZooMS analysis. Markers were identified for egg, milk, and wheat proteins and were then tested for validation on a second set of samples (T). LC-MS/MS analysis was performed on discovery samples (S) to confirm protein matches and rule out the presence of laboratory contaminants. Table 3 shows the proteins identified in each sample (S).

Table 3. Summary of proteins of interest identified in treated parchment samples

Species	Protein	Uniprot ID	Samples
Goat	Collagen type I alpha-1 chain	A0A452FHU9	S1 - S13
	Collagen type I alpha-2 chain	A0A452G3V6	S4 - S5, S13
Chicken	Ovalbumin-related protein Y	P01014	S3, S4, S12
	Ovalbumin	P01012	S3, S4, S9 - S13
	Ovotransferrin	P02789	S3, S4, S9, S11, S12
	Ovostatin	P20740	S4, S12
	Lysozyme C	P00698	S4, S8, S12
	Protein TENP	O42273	S4, S8, S12
	Mucin-5B	Q98UI9	S4, S8, S12
	Ovalbumin-related protein X	P01013	S4, S8, S12
	Ovomucoid	P01005	S4, S8, S12
	Avidin	P02701	S4, S8, S12
Cow	Beta-lactoglobulin	P02754	S9
	Alpha-S2-casein	P02663	S9, S11 - S12
	Beta-casein	P02666	S9, S11 - S12
	Alpha-S1-casein	P02662	S9, S11 - S12
Fish	Collagen type I alpha-1 chain	A0A6I9MX97	S10
	Collagen type I alpha-1 chain	A0A1A8K041	S2, S10
	Collagen type I alpha-1 chain	A0A3P9NHJ7	S2, S6, S10
	Collagen type I alpha-1 chain	A0A3P9BC04	S6
	Collagen type I alpha-3 chain	A0A6I9N4J7	S6
	Collagen type I alpha-1 chain	A0A3Q2CSU4	S6
	Collagen type I alpha-2 chain	A0A3B4ZDV7	S6
	Collagen type II alpha-1a chain	Q2I8Y0	S6
Wheat	Histone H3.2	P68428	S5
	Serpin-Z1A	Q41593	S5, S8
	Elongation factor 1-alpha	Q03033	S8
Barley	Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic	P08477	S8

3.3.1 Protein identification

Proteins of milk, egg, and wheat origin were identified in samples soaked in yoghurt or wheat bran, or coated with glair (Table 4) but no barley or flaxseed proteins were identified in the relevant samples (S3, S7, S11, and S13). Egg-origin proteins were identified in samples with a glair coating. Specifically, nine egg-origin proteins were found in samples S4 and S8, and 10 in S12. Additionally, egg-origin proteins were found in some samples without a glair coating. Ovalbumin (OVAL) was identified in samples S3, S4, S8, and S13; ovotransferrin (TRFE) in samples S9 and S11, and ovalbumin-related protein Y (OVALY) in sample S3. Two wheat-origin proteins were identified in each of two of the four samples soaked in wheat bran, S5 and S8. Four milk proteins were identified in S9, and 3 in S11 and S12, but none were found in S10. Due to the great variation in fish collagen sequences, their overlap with mammalian collagen, and the fact our database was not exhaustive, some fish collagen protein matches were treated as contaminants and do not appear in Table 4. A list of all the protein matches made for each sample can be seen in Appendix A (Table A1).

This analysis allowed us to identify proteins of interest for peptide marker screening and rule out the presence of any proteins due to contamination in a laboratory setting. As seen in the results, obtained proteins from milk, egg, or wheat origin were not identified in the reference sample, eliminating the possibility of their presence as a contaminant in the laboratory. The presence of egg-origin proteins in samples where a glair coating was not applied can be explained by cross-contamination that could have occurred during the production process or during sampling of the skins. All the treatments and coatings were applied to the skin before the samples were cut, stored, and then sent for analysis. As seen in Figure 7, the sections where glair was applied are adjacent to sections where other samples relevant to this work were taken from and cross-contamination could have occurred while applying the treatments (i.e. splatter), cutting the samples (if, for example, the cutting tool was not cleaned after each sample was cut) or in the process of storing or packaging them.

Table 4. Proteins of interest identified in treated parchment samples.

Origin	Protein	Uniprot ID	Sequence coverage	Peptide count
S1: goat's skin parchment				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	50.3	1,429
S2: fish glue coating				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	46.5	404
Fish glue (collagen)	Collagen type I alpha-1 chain	A0A3P9NHJ7	9.3	61
	Collagen type I alpha-1 chain	A0A1A8K041	6.6	34
S3: flaxseed water coating				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	47.7	1,143
Egg (chicken)	Ovalbumin	P01012	13.5	28
	Ovotransferrin	P02789	7.0	7
	Ovalbumin-related protein Y	P01014	2.3	2
S4: glair coating				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	56.0	1,786
	Collagen type I alpha-2 chain	A0A452G3V6	43.4	641
Egg (chicken)	Ovalbumin	P01012	45.9	228
	Ovotransferrin	P02789	27.9	163
	Lysozyme C	P00698	25.2	32
	Ovalbumin-related protein Y	P01014	18.8	51

Origin	Protein	Uniprot ID	Sequence coverage	Peptide count
	Protein TENP	O42273	14.3	20
	Mucin-5B	Q98UI9	6.7	20
	Ovostatin	P20740	7.5	17
	Ovalbumin-related protein X	P01013	15.1	20
	Ovomucoid	P01005	4.8	7
S5: soaked in wheat bran				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	55.6	1,664
	Collagen type I alpha-2 chain	A0A452G3V6	40.0	670
Wheat bran	Serpin-Z1A	Q41593	7.8	5
	Histone H3.2	P68428	9.6	4
S6: soaked in wheat bran with fish glue coating				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	44.0	1,039
Fish glue (collagen)	Collagen type I alpha-1 chain	A0A3P9NHJ7	11.2	105
	Collagen type I alpha-1 chain	A0A3P9BC04	4.9	85
	Collagen type I alpha-3 chain	A0A6I9N4J7	4.9	70
	Collagen type I alpha-1 chain	A0A3Q2CSU4	6.2	59
	Collagen type I alpha-2 chain	A0A3B4ZDV7	2.8	30
	Collagen type II alpha-1a chain	Q2I8Y0	3.0	9
S7: soaked in wheat bran with flaxseed water coating				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	48.3	1,105

Origin	Protein	Uniprot ID	Sequence coverage	Peptide count
S8: soaked in wheat bran with glair coating				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	42.8	1,065
Egg (chicken)	Ovotransferrin	P02789	21.4	45
	Lysozyme C	P00698	25.2	18
	Ovalbumin	P01012	19.7	17
	Mucin-5B	Q98UI9	4.0	22
	Protein TENP	O42273	5.5	14
	Ovalbumin-related protein Y	P01014	10.8	8
	Avidin	P02701	13.8	3
	Ovalbumin-related protein X	P01013	2.6	4
	Ovomucoid	P01005	4.8	2
Wheat bran	Serpin-Z1A	Q41593	4.8	6
	Elongation factor 1-alpha	Q03033	4.7	3
Barley flour	Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic	P08477	7.5	2
S9: soaked in yoghurt				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	51.7	1,147
Egg (chicken)	Ovalbumin	P01012	5.7	3
	Ovotransferrin	P02789	2.4	2
Milk (bovine)	Beta-lactoglobulin	P02754	5.1	8
	Alpha-S2-casein	P02663	17.1	12

Origin	Protein	Uniprot ID	Sequence coverage	Peptide count
	Beta-casein	P02666	5.8	3
	Alpha-S1-casein	P02662	10.3	2
S10: soaked in yoghurt with fish glue coating				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	45.5	746
Egg (chicken)	Ovalbumin	P01012	7.8	13
Fish glue (collagen)	Collagen type I alpha-1 chain	A0A1A8K041	8.7	82
	Collagen type I alpha-1 chain	A0A3P9NHJ7	9.3	110
	Collagen type I alpha-1 chain	A0A6I9MX97	3.2	51
S11: soaked in yoghurt with flaxseed water coating				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	55.4	1,489
Egg (chicken)	Ovalbumin	P01012	28.2	32
	Ovotransferrin	P02789	6.5	4
Milk (bovine)	Alpha-S2-casein	P02663	19.8	7
	Alpha-S1-casein	P02662	13.6	3
	Beta-casein	P02666	5.8	10
S12: soaked in yoghurt with glair coating				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	42.8	750
Egg (chicken)	Ovalbumin	P01012	50.8	403
	Ovotransferrin	P02789	36.6	241
	Ovalbumin-related protein Y	P01014	31.4	95

Origin	Protein	Uniprot ID	Sequence coverage	Peptide count
	Lysozyme C	P00698	29.9	30
	Ovalbumin-related protein X	P01013	28.0	38
	Ovostatin	P20740	7.0	31
	Protein TENP	O42273	19.1	14
	Mucin-5B	Q98UI9	3.6	12
	Ovomucoid	P01005	4.8	8
	Avidin	P02701	5.3	3
Milk (bovine)	Alpha-S2-casein	P02663	8.6	12
	Alpha-S1-casein	P02662	23.4	7
	Beta-casein	P02666	12.5	9
S13: rubbed with barley flour				
Parchment (goat collagen)	Collagen type I alpha-1 chain	A0A452FHU9	46.3	664
	Collagen type I alpha-2 chain	A0A452G3V6	31.2	341
Egg (chicken)	Ovalbumin	P01012	7.5	2

3.3.2 Identification of non-collagen protein markers using ZooMS

ZooMS is a cheap and effective technique for species identification of parchment based on collagen markers (Fiddyment *et al.*, 2015). Identifying peptide markers from other proteins can be a useful screening tool when presented with a large sample set and/or where sequencing is limited to a small number of samples due to constraints in time and/or resources. Based on the results from LC-MS/MS analysis of S samples, peptide markers were searched for and identified for commonly found milk, egg, and wheat proteins such as ovalbumin, ovotransferrin, and milk caseins (Table 5). Except for the wheat-origin peptide markers, which only appeared in one sample each, peptides were included where they appeared in two or more samples and did not overlap with any of the matched collagen peptides or known contaminants, like keratins, using a tolerance of ±0.02 Da. The full list of matched peptides can be seen in Appendix A (Table A2).

Table 5. Number of peptide markers found per protein. For each protein, the samples in which they were found using ZooMS and LC-MS/MS are reported.

Protein	Accession	Peptide markers	Samples	
			ZooMS	LC-MS/MS
Chicken's egg (Gallus gallus)				
Mucin-5B	Q98UI9	1	S4, S12	S4, S8, S12
Ovalbumin	P01012	8	S3, S4, S8 - S13	S3, S4, S8 - S13
Ovalbumin-related protein Y	P01014	4	S3, S4, S8, S12	S3, S4, S8, S12
Ovostatin	P20740	1	S4, S12	S4, S12
Ovotransferrin	P02789	4	S3, S4, S8, S12	S3, S4, S8, S9, S11, S12
Cow's milk (Bos taurus)				
Alpha-S2-casein	P02663	2	S9, S11	S9, S11, S12
Wheat (Triticum aestivum)				
Serpin-Z1A	Q41593	2	S5, S8	S5, S8

A total of twenty two markers were identified, eighteen for egg-origin proteins, and two each for cow's milk and wheat proteins. The protein, mass, and samples in which they were identified can be seen in Table 6.

Whilst ovalbumin, ovotransferrin, and milk caseins are common laboratory contaminants, none of the identified markers were present in the reference sample (S1). As seen in Table 5, the markers identified in each sample are consistent with the proteins identified by sequencing. As stated in section 3.2.5, the presence of egg-origin protein markers in samples S3, S9, S11, and S13 could be attributed to cross-contamination during the production process or cutting of the skins.

Table 6. Peptide markers identified for proteins of interest

Protein	Accession	m/z	Sequence	Samples
Chicken's egg (Gallus gallus)				
Mucin-5B	Q98UI9	1677.83	r.IQEIATDPGAEKNYK.v [1xDeamidation]	S4, S12
Ovalbumin	P01012	821.389	r.VTEQESK.p [1xDeamidation]	S9, S10
Ovalbumin	P01012	944.541	r.DILNQITK.p	S4, S9, S12, S13
Ovalbumin	P01012	945.525	r.DILNQITK.p [1xDeamidation]	S3, S9, S11
Ovalbumin	P01012	1345.74	k.HIATNAVLFFGR.c	S4, S8, S12
Ovalbumin	P01012	1514.75	k.PVQMMYQIGLFR.v [2xOxidation]	S3, S10, S13
Ovalbumin	P01012	1858.97	r.ELINSWVESQTNGIIR.n	S4, S8
Ovalbumin	P01012	1859.95	r.ELINSWVESQTNGIIR.n [1xDeamidation]	S8, S12
Ovalbumin	P01012	1804.92	k.HIATNAVLFFGRCVSP. [1xCarbamidomethyl; 1xOxidation]	S3, S9, S12
Ovalbumin-related protein Y	P01014	1412.73	r.YNPTNAILFFGR.y	S4, S8, S12
Ovalbumin-related protein Y	P01014	1007.55	k.TINFDKLR.e [1xDeamidation]	S3, S12
Ovalbumin-related protein Y	P01014	1686.85	k.TFSVLPEYLSCARK.f [1xCarbamidomethyl; 1xOxidation]	S4, S12
Ovalbumin-related protein Y	P01014	3381.73	k.ETNGQIKDLLVSSSIDFGTTMVFINTIYFK.g	S8, S12
Ovostatin	P20740	3167.51	r.VVALDFNFKPVQEMYPLIAVQDPQNNR.i [6xDeamidation; 1xOxidation]	S4, S12
Ovotransferrin	P02789	1534.85	r.SAGWNIPIGTLLHR.g	S4, S8, S12
Ovotransferrin	P02789	1709.86	r.ECNLAEVPTHAVVVR.p [1xCarbamidomethyl; 1xOxidation]	S8, S12

Protein	Accession	m/z	Sequence	Samples
Ovotransferrin	P02789	1710.85	r.ECNLAEVPTHAVVVR.p [1xCarbamidomethyl; 1xDeamidation; 1xOxidation]	S8, S12
Ovotransferrin	P02789	1295.71	r.PASYFAVAVARK.d [1xOxidation]	S3, S9
Cow's milk (Bos taurus)				
Alpha-S2-casein	P02663	1383.77	k.RNAVPITPTLNR.e [2xOxidation]	S9, S11
Alpha-S2-casein	P02663	1385.74	k.RNAVPITPTLNR.e [2xDeamidation; 2xOxidation]	S9, S11
Wheat (Triticum aestivum)				
Serpin-Z1A	Q41593	1643.89	r.IKDILPPGSIDNTTK.l [2xOxidation]	S5
Serpin-Z1A	Q41593	2028.05	.MATTLATDVRLSIAHQTR.f [1xAcetyl; 1xDeamidation]	S8

3.3.3 Testing the peptide markers

A set of ten samples (T) were analysed to validate the results of the peptide marker search. The results can be seen in Table 7. One of the proposed markers for milk-origin proteins was found in samples T7, T8, and T9 but none in T10. One wheat-origin peptide marker was found in T4, T5, and T6. With the exception of sample T10, these results are consistent with the sample descriptions. In contrast, the only samples where egg-proteins should be present are samples T3, T6, and T10, but peptide markers for egg-origin proteins were found in all samples. While this could be due to cross-contamination, these results suggest that the presence of egg proteins needs to be considered more carefully. But, it is worth noting that the markers with masses 1412.7321 (OVALY), 1677.8330 (Mucin-5B), and 1858.9658 (OVAL) were only found in samples with a glair coating in both the peptide marker identification and testing phases. Although out of the scope of this project, future research should aim to conduct a full validation study where the issues of cross-contamination highlighted within this study can be addressed.

Table 7. Protein markers found in test samples.

m/z	Average error	Samples
Alpha-S2-casein		
1383.7703	0.0002	T7, T8, T9
Mucin-5B		
1677.8330	-0.0306	T3
Ovalbumin		
821.3887	-0.0091	T3, T6, T10
945.5251	-0.0495	T9
1345.7375	-0.0172	T3, T6, T8, T10
1514.7494	-0.0113	T3, T4, T5, T6, T7, T8, T9, T10
1804.9163	0.0222	T1
1858.9658	-0.0142	T3, T10
1859.9498	-0.0200	T2, T10

m/z	Average error	Samples
Ovalbumin-related protein Y		
1412.7321	-0.0128	T3, T6, T10
Ovotransferrin		
1709.8639	0.0049	T1
1710.8479	0.0143	T1, T7
Serpin-Z1A		
2028.0543	-0.0021	T4, T5, T6

3.4 Conclusion

The preliminary identification of milk, egg, and wheat proteins present in parchment from their use in the parchment making process was performed using ZooMS. This was done on the basis that MALDI-TOF MS is a fast and low cost analysis when compared to LC-MS/MS that can be used for the screening of samples when there are limited time and/or resources. Usually, ZooMS is used as a species identification tool based on the collagen fingerprint and is not used for the analysis of very complex samples. However, this work identified twenty-two peptide markers that occur alongside the collagen markers used for species identification. This study shows that ZooMS can be used as a fast, cheap, and effective screening tool for the identification of samples of interest in the study of historical hide materials, such as parchment and leather, when protein sequencing is limited due to constraints in time and/or resources. Further to a full validation study, future research should use this study as an example for the identification of protein markers that occur alongside collagen in historical hide materials and/or collagen based materials in the modern leather and food industries. The screening of samples can help decide which samples to analyse further, but can also elucidate the production, use, and conservation history of an object. In the case of modern industries, these methods can contribute to quality control and assurance processes by highlighting contamination issues that can have an impact on the physicochemical properties of the material. The ability to screen samples for these proteins, and other proteins of interest, adds another tool to the biocodicology field.

Chapter 4: Collagen degradation patterns in hide materials

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Relevance: This chapter focuses on the patterns degradation found in collagen from modern and historical hide materials. The focus of this chapter is on deamidation of glutamine and asparagine, and, to some extent, hydroxylation of proline.

Abstract: Proteins undergo physical, chemical and biological degradation processes which make their lifespan highly variable. Understanding the degradation patterns of collagen is an important step to understand the use and conservation history of archaeological and historical objects made from hide materials such as parchment and leather and can be further applied to the modern leather and food industries, both of which continue to make goods from collagen based materials. This work shows the available methods for assessing the level of deamidation of a sample and emphasises the importance of further studies of glutamine deamidation kinetics and mechanisms to better estimate damage to the collagen molecule. This is highlighted by the difference in the deamidation patterns, rates of reaction and reaction pathways of samples that have been subjected to acidic conditions (leather) when compared to those processed in an alkaline environment (parchment), where glutamine deamidation is faster than that of asparagine in samples aged under acidic conditions.

4.1 Introduction

Processed hide materials from cattle, like leather and parchment, have been used throughout history for a variety of purposes. Indeed, the modern leather, biomedical, and food industries all use cattle skin and hide for the manufacturing of modern goods such as dietary supplements, and edible casings (Hashim *et al.*, 2015; Irastorza *et al.*, 2021).

Historical artefacts made of tanned leather include clothing, shoes, furnishings, and other goods (Ebsen *et al.*, 2019). Parchment, a writing medium made from animal skins, is one of the most abundant resources available for the study of past cultures and societies (Fiddyment *et al.*, 2015). Through the application of biomolecular analysis, we can interrogate these materials to explore livestock economies, trade and craft, and explore their production and use history (Fiddyment *et al.*, 2019).

Collagen, the most abundant protein found in vertebrates, is the main protein in parchment, leather, and other hide materials. Its high stability, the result of its fibrillar structure, means it is commonly found in ancient samples (Van Doorn *et al.*, 2012). This makes it a useful protein in the study of historical and archaeological objects (Brown, Kozlikin, *et al.*, 2021). Collagen is composed of three chains which coil around each other to form a triple helix. Multiple helices form fibrils and then fibres (Shoulders and Raines, 2009). The structure of the chains that form the triple helix has a repeating pattern of three amino acids, GXY, where every third residue is glycine (G, Gly). This is mandated by the tight packing of the helices within the triple helix. The amino acids in the X and Y positions are often proline (P, Pro) and hydroxyproline (Hyp), with the most common triplet being GlyProHyp (Ramshaw, Shah and Brodsky, 1998; Shoulders and Raines, 2009).

The survival of proteins in ancient materials is highly variable due to a myriad of physical, chemical and biological degradation processes. Post-translational modifications (PTMs) - the chemical changes that occur to amino acids after protein synthesis - can occur biologically or be introduced by diagenesis, ageing, and other factors, i.e., exposure to oxygen, pollutants, microbes, light, etc. In the context of

cultural heritage and archaeology, particular protein modifications which result from external chemical, physical or biological processes acting on the proteins can be detected. These can be used to authenticate old proteins or assess the damage and overall degradation state of a protein. Thus, understanding the patterns of degradation of proteins, and how they can be detected, is crucial for the analysis of ancient proteins. This work focuses on two PTMs commonly found in collagen: hydroxylation of proline, and deamidation of glutamine and asparagine.

Hydroxylation is one of the most important biological protein modifications detected in ancient proteins due to its abundance in collagens (Shoulders and Raines, 2009; Ehrlich *et al.*, 2010). Hydroxylation is an oxidative PTM which influences many biological functions. The hydroxylation of proline to 4-hydroxyproline (Hyp) is catalysed by P4H in the Y position of the (GXY)n repeats of collagens with Pro being the preferred residue in the X position (Gorres and Raines, 2010; Shi *et al.*, 2015). Hydroxyproline plays a critical role in the thermal stabilisation of the collagen triple helix (Berg and Prockop, 1973; Gorres and Raines, 2010) as demonstrated by the difference in melting temperature between a fully hydroxylated type I collagen (43°C) and the non-hydroxylated form (27°C), which is below physiological temperature in humans (Berg and Prockop, 1973).

Deamidation is a protein modification occurring on asparagine (N, Asn) and glutamine (Q, Gln) residues where the amide group is transformed into a carboxylic acid, producing aspartic (D, Asp) and glutamic (E, Glu) acids (Figure 8). The reaction can occur enzymatically in living organisms, but it is also known to occur spontaneously and non-enzymatically over time in all protein-based materials (Mycek and Waelsch, 1960; Imada *et al.*, 1973; Wriston and Yellin, 1973; Curthoys and Watford, 1995). As such, it is the most common diagenetic PTM identified in collagen (Cleland, Schroeter and Schweitzer, 2015; Schroeter and Cleland, 2016). The level of deamidation of proteins in biology has been connected with the age of the organism, using deamidation as a 'molecular clock' (Robinson, McKerrow and Cary, 1970; McKerrow and Robinson, 1974; Robinson, McKerrow and Legaz, 1974; Robinson *et al.*, 2004).

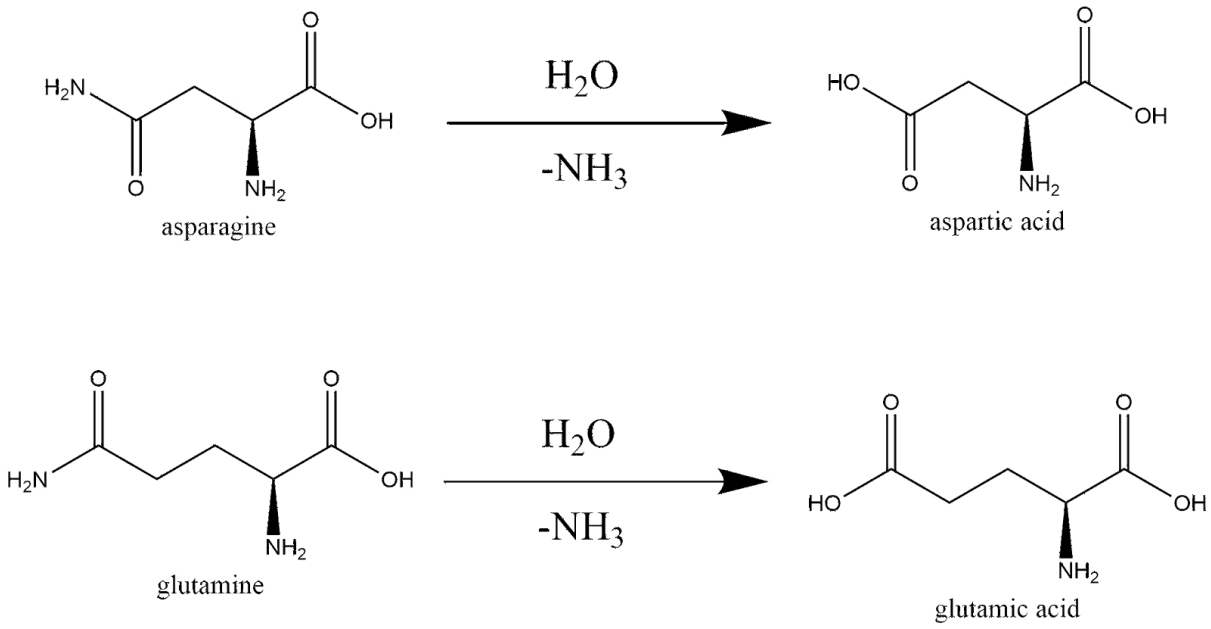


Figure 8. Scheme of the deamidation of the amino acids asparagine and glutamine

Spontaneous deamidation follows, mainly, two mechanisms: the direct hydrolysis of the amide, or the formation of a cyclic amide followed by hydrolysis (Robinson *et al.*, 2004). Both Asn and Gln follow both pathways, and the formation of the cyclical intermediate has an overall faster reaction rate than direct hydrolysis (Sondheimer and Holley, 1957; Capasso, Mazzarella and Sica, 1991; Catak *et al.*, 2009), although deamidation through the formation of a cyclic amide only occurs if the flexibility of the protein is not limited by the protein structure (Geiger and Clarke, 1987; Kosky *et al.*, 1999; Aswad, Paranandi and Schurter, 2000; Radkiewicz *et al.*, 2001; Li *et al.*, 2005). At constant pH, deamidation of Asn and Gln residues follows first-order kinetics (Geiger and Clarke, 1987; Patel and Borchardt, 1990b). In the solid state, deamidation rate is significantly lower than in solution (Oliyai *et al.*, 1994; Lai and Topp, 1999; Song *et al.*, 2001; Li *et al.*, 2005, 2006), which is highly relevant for the study of proteins in cultural heritage samples. The influence of protein structure on deamidation is on average between 50% and 60% based on primary structure, and only for the remaining part on secondary, tertiary, and quaternary structures (Robinson and Robinson, 2001b; Noah E. Robinson and Robinson, 2004; Robinson *et al.*, 2004). Several factors affect the mechanism and the rate of deamidation - i.e., pH, ionic strength, temperature, amino acid sequence and structure

of the protein, and matrix - and should therefore be considered when studying the kinetics of this reaction.

In acidic conditions (pH < 5) asparagine deamidation (Figure 9) favours direct hydrolysis and the formation of the succinimide (Asu) intermediate is very slow. This reaction is slowest at a pH between 4 and 6 (Robinson *et al.*, 2004). In neutral and alkaline environments the succinimide-intermediate mechanism is prevalent, except in AsnPro sequences, where Asu formation is hindered by the bulk of the Pro side-chain (Patel and Borchardt, 1990b, 1990a; Clarke, 2003).

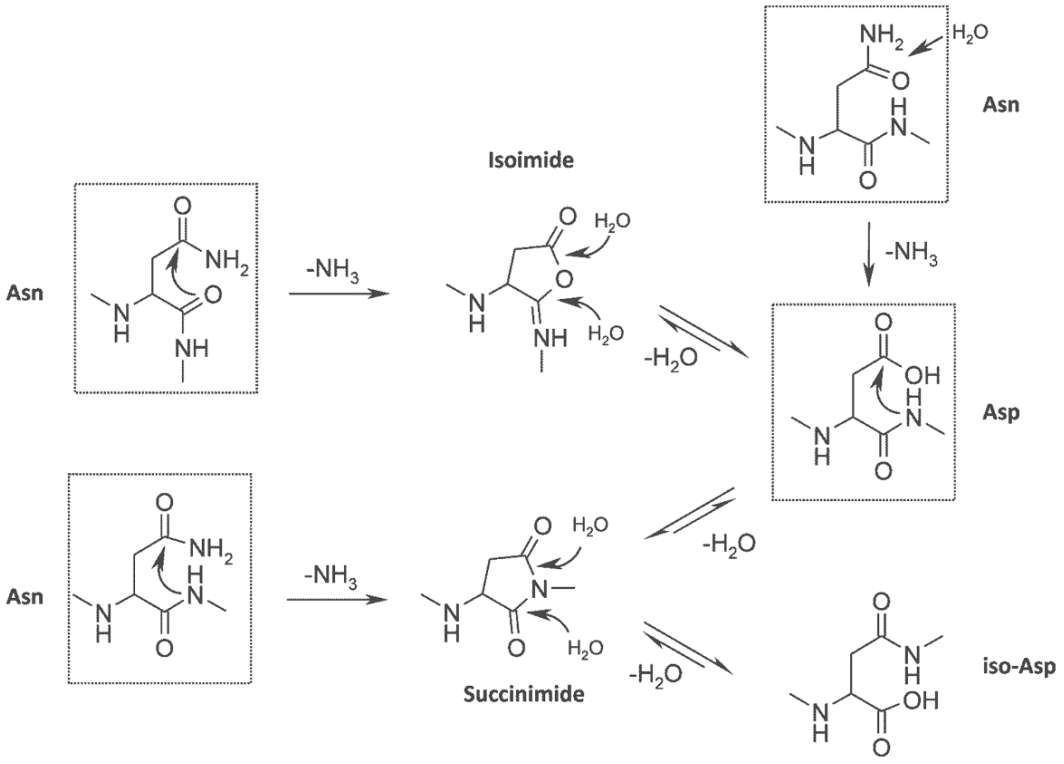


Figure 9. Asparagine and Aspartate degradation pathways. From (Sydow *et al.*, 2014)

Glutamine deamidation mechanisms (Figure 10) are not as well studied, but it is likely that direct hydrolysis is responsible for most of the deamidation, except in highly flexible regions or when glutamine is followed by glycine. This is due to the difficulty of forming the glutarimide ring (Joshi *et al.*, 2005; Riggs *et al.*, 2019).

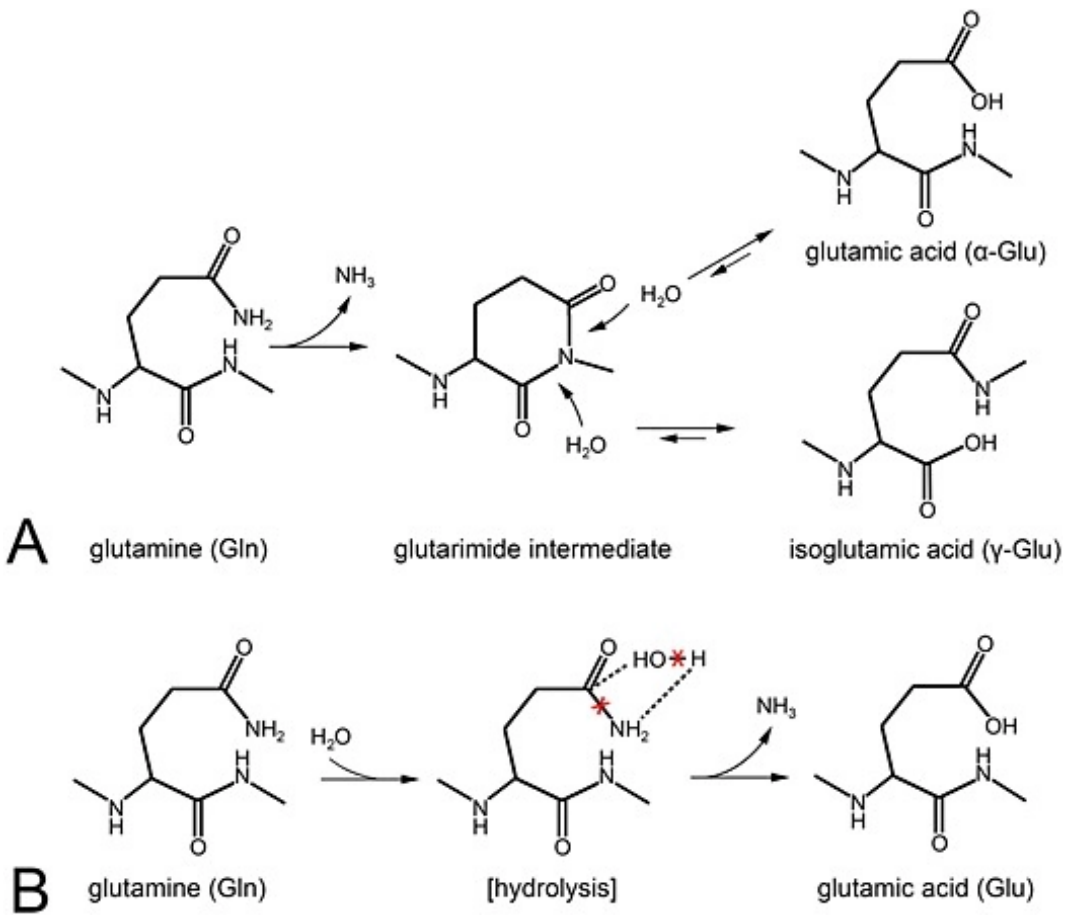


Figure 10. Deamidation of glutamine to glutamic acid via (A) glutarimide intermediate and (B) direct hydrolysis. From: (Schroeter and Cleland, 2016)

Given that asparagine is much more susceptible to deamidation than glutamine (Terwilliger and Clarke, 1981; Daniel, Dines and Petach, 1996; Robinson *et al.*, 2004; Wilson, van Doorn and Collins, 2012), the investigation of the level of deamidation of Gln residues is more suitable for assessing the damage of archaeological and cultural heritage materials (Leo *et al.*, 2011; Van Doorn *et al.*, 2012; Ramsøe *et al.*, 2020; Nair *et al.*, 2022).

The rate of deamidation of Asn and Gln at specific locations is heavily influenced by the amino acids found next to them, with NG and QG motifs having the fastest rates, and NP and QP motifs the slowest (Robinson *et al.*, 2004).

In mass spectrometry deamidation can be identified by its characteristic +0.984 Da mass shift. Bioinformatics tools are available to calculate the overall deamidation of glutamine from ZooMS spectra, the Q2E package (Wilson, van Doorn and Collins, 2012)

and the more recent MALDIpqi package (Nair *et al.*, 2022). The Q2E package uses a genetic algorithm to determine the extent of glutamine deamidation by comparing the theoretical and measured distributions of each sample (Wilson, van Doorn and Collins, 2012). MALDIpqi utilises weighted least-squares linear regression, followed by a linear mixed effect model to predict the overall deamidation level of a sample, termed the Parchment Glutamine Index (PQI) (Nair *et al.*, 2022). Similarly, the software tool deamiDATE 1.0 (Ramsøe *et al.*, 2020) assess the bulk and site-specific deamidation of proteins from LC-MS/MS spectra. The bulk deamidation represents the average remaining N and Q in a given protein and the site-specific deamidation uses the sequence-dependent half-time (the time it takes for a given site to deamidate) estimated by (Robinson *et al.*, 2004) and represents the average remaining portion of N or Q for each three residue combination (X-N-Y and X-Q-Y) per half-time (Ramsøe *et al.*, 2020).

4.2 Materials and Methods

4.2.1 Samples

Experimental and historical parchment and leather and modern collagen samples were chosen for this study. The samples, described in Table 8, are made of different hide materials, have varying manufacturing and use histories, and underwent processing in varying pH environments during production.. Dried and milled collagen powder samples were provided by **Devro plc.** Devro uses bovine hides to make sausage casings and edible collagen films. Goat's skin **parchment** samples, prepared according to Armenian recipes from the 17th to 18th centuries were provided for this study (Haralampiev, 2012). Besides the traditional steps of parchment making (Saxl, 1954; Reed, 1972, 1975), these recipes describe additional treatments intended to make the parchment softer and/or smoother (Haralampiev, 2012). Leather samples that have been artificially **aged** in an ageing chamber under different concentrations of sulphur dioxide (SO_2) and nitrogen dioxide (NO_2) and then left in storage for ten years were

provided by colleagues from the Institute for Creative Leather Technologies (ICLT) at the University of Northampton. A set of six leather samples were obtained from book covers of books stored at the **library of the Palace of Mafra** in Mafra, Portugal. The books range from 1550 to 1826. One of the samples was an unaged reference sample that was kept in the same location. Finally, two leather samples from the **Mary Rose** (Figure 11) a warship from the navy of King Henry VIII, were provided by Lianne Jordan and the Mary Rose Trust. The Mary Rose sank in the strait north of the Isle of Wight in July 1545. The wreck of the Mary Rose was located in 1971 and was raised on 11 October 1982 by the Mary Rose Trust.

Figure 11. Leather fragments from the Mary Rose. Left: leather fragment (MR1); right: leather (shoe sole) (MR2). Image credit: Lianne Jordan

Table 8. Collagen degradation sample references, description and **sample group**

Reference	Description
Devro, commercial collagen	
D1	Bovine collagen. Liming was done in a lime and sulphide solution for 18 h, the hide was then delimed and split, dried and milled.
D2	Bovine collagen. Liming was done in a lime and sulphide solution for 18 h, the hide was then split, and re-limed without the presence of sulphide for a further 24 h, then delimed, dried, and milled.
D3	Bovine collagen. Liming was done in a lime and sulphide solution for 18 h, the hide was then split and re-limed without the presence of sulphide for a further 48 h, then delimed, dried, and milled.

Reference	Description
D4	Bovine collagen. Liming was done in a lime and sulphide solution for 18 h, the hide was then split and re-limed, without temperature control, in a lime pit for an unknown period of time, then delimed, dried, and milled.
D5	Bovine collagen. Liming was done in a lime and sulphide solution for 18 h, the hide was then split and re-limed, without temperature control, in a lime pit for an unknown period of time, then delimed, dried, and milled.
D6	Bovine collagen. Liming was done in a lime and sulphide solution for 18 h, the hide was then split and re-limed, without temperature control, in a lime pit for an unknown period of time, then delimed, dried, and milled.
D7	Bovine collagen. Liming was done in a lime and sulphide solution for 18 h, the hide was then split and re-limed, without temperature control, in a lime pit for an unknown period of time, then delimed, dried, and milled.
Parchment	
P1	Reference goat's skin parchment, untreated.
P2	Goat's skin parchment, a coating of fish glue was applied to the finished parchment surface.
P3	Goat's skin parchment, a coating of flaxseed water extract was applied to the finished parchment surface.
P4	Goat's skin parchment, a coating of glair (egg white) was applied to the finished parchment surface.
P5	Goat's skin parchment. After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched.
P6	Goat's skin parchment. After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched. Once dry, a coating of fish glue was applied to the finished parchment surface.
P7	Goat's skin parchment. After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched. Once dry, a coating of flaxseed water extract was applied to the finished parchment surface.
P8	Goat's skin parchment. After liming and dehairing, the skin was soaked in wheat bran water solution for three days before being washed and stretched. Once dry, a coating of glair was applied to the finished parchment surface.

Reference	Description
P9	Goat's skin parchment. After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched.
P10	Goat's skin parchment. After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. Once dry, a coating of fish glue was applied to the surface.
P11	Goat's skin parchment. After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. Once dry, a coating of flax seed water extract was applied to the finished parchment surface.
P12	Goat's skin parchment. After liming and dehairing, the skin was soaked in cow's milk yoghurt for three days before being washed and stretched. Once dry, a coating of glair was applied to the finished parchment surface.
Aged leather, goat	
AL0	Quebracho-tanned goat leather, unaged control sample.
AL3	Quebracho-tanned goat leather, aged for 3 weeks in the ageing chamber with 40 ppm SO_2 and 20 ppm NO_2
AL6	Quebracho-tanned goat leather, aged for 6 weeks in the ageing chamber with 40 ppm SO_2 and 20 ppm NO_2
AL9	Quebracho-tanned goat leather, aged for 9 weeks in the ageing chamber with 40 ppm SO_2 and 20 ppm NO_2
AL12	Quebracho-tanned goat leather, aged for 12 weeks in the ageing chamber with 40 ppm SO_2 and 20 ppm NO_2
Aged leather, goat (unshaved)	
AG0	Quebracho-tanned goat leather, unshaved, unaged control sample
AG1	Quebracho-tanned goat leather, unshaved, aged for 1 week in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2
AG2	Quebracho-tanned goat leather, unshaved, aged for 2 weeks in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2
AG3	Quebracho-tanned goat leather, unshaved, aged for 3 weeks in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2
AG4	Quebracho-tanned goat leather, unshaved, aged for 4 weeks in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2
AG5	Quebracho-tanned goat leather, unshaved, aged for 5 weeks in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2

Reference	Description
AG6	Quebracho-tanned goat leather, unshaved, aged for 6 weeks in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2
Aged leather, bovine, buffalo (calf)	
AB0	Tanned buffalo calf leather (Tusting) unaged control sample
AB3	Tanned buffalo calf leather (Tusting) aged for 3 weeks in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2
AB6	Tanned buffalo calf leather (Tusting) aged for 6 weeks in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2
Aged leather, bovine, cow (calf)	
AC0	Tanned cow calf leather (Tusting) unaged control sample
AC3	Tanned cow calf leather (Tusting) aged for 3 weeks in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2
AC6	Tanned cow calf leather (Tusting) aged for 6 weeks in the ageing chamber under 80 ppm SO_2 and 40 ppm NO_2
Mafra library leather, historical leather	
MF	Unaged leather reference kept in the library at the Palace of Mafra in Mafra, Portugal.
MF1826	Book (1826) with leather cover from the library at the Palace of Mafra in Mafra, Portugal.
MF1741	Book (1741) with leather cover from the library at the Palace of Mafra in Mafra, Portugal.
MF1664	Book (1664) with leather cover from the library at the Palace of Mafra in Mafra, Portugal.
MF1661	Book (1661) with leather cover from the library at the Palace of Mafra in Mafra, Portugal.
MF1550	Book (1550) with leather cover from the library at the Palace of Mafra in Mafra, Portugal.
Mary Rose leather, historical leather	
MR1	Leather fragment recovered from the Mary Rose, ca. 1545. Sample was waterlogged in a marine environment for 437 years.
MR2	Leather shoe sole fragment recovered from the Mary Rose, ca. 1545. Sample was waterlogged in a marine environment for 437 years.

4.2.2 Sampling

Parchment and leather sampling was performed according to (Fiddyment *et al.*, 2015). Using a Staedtler "Mars Plastic" eraser, rubbing the eraser in one direction and collecting the resulting eraser waste fragments in individual 1.5 mL microcentrifuge tubes. In the case of the collagen powder and Mary Rose leather samples, a small amount (< 2 mg) of dried collagen was put in individual 1.5 mL microcentrifuge tubes.

For each sample, a new individual piece of eraser and acid-free paper was used; the eraser and paper were thrown away once sampling of the folio was completed to avoid cross-contamination. Nitrile gloves were worn throughout the sampling process to avoid keratin (human skin) contamination. All samples were stored at room temperature until required.

4.2.3 MALDI-TOF-MS

ZooMS analysis was performed according to the protocol developed by (Fiddyment *et al.*, 2015). Samples were spun down at maximum speed on a benchtop centrifuge for 1 min. Then, 75 µL of 0.05 M ammonium bicarbonate (AmBic) buffer (pH 8) and 1 µL of trypsin (0.4 µg/µL) was added to each sample. The samples were heated at 37 °C for 4 h. After incubation with trypsin, the digests were spun down at maximum speed on a benchtop centrifuge for 1 min and 1 µL of 5% (vol/vol) trifluoroacetic acid (TFA) was added. Samples were desalted and concentrated using C18 resin (Millipore), following the manufacturer's instructions. Peptides were eluted in a final volume of 50 µL of 50% acetonitrile (ACN)/0.1% TFA (vol/vol). One microliter of eluted peptides was mixed on a ground steel plate with 1 µL of α-cyano-4-hydroxycinnamic acid matrix solution [1% in 50% ACN/0.1% TFA (vol/vol/vol)] and air-dried. All samples were spotted in triplicate. Samples were analysed using a calibrated Ultraflex III (NLD1; Bruker Daltonics) MALDI-TOF instrument in reflector mode.

4.2.4 LC-MS/MS

Commercial collagen samples from Devro, and parchment samples were processed at the University of Copenhagen (CPH), Denmark. Leather samples were analysed at the Centre of Excellence for Mass Spectrometry (CoEMS) at the University of York, UK.

4.2.4.1 LC-MS/MS at CPH

Dried peptide samples were resuspended in 50µl of 80% acetonitrile (ACN) and 0.1% formic acid (FA). 10µl of each sample was then transferred to a 96 well plate and placed in a vacuum centrifuge at 40ºC until approximately 3 µL of the solution was left. The samples were rehydrated with 10 µL of 0.1% trifluoroacetic acid (TFA), 5% ACN. Samples were then separated on a 15 cm column (75 µm inner diameter) in-house laser pulled and packed with 1.9 µm C18 beads (Dr. Maisch, Germany) on an EASY-nLC 1000 (Proxeon, Odense, Denmark) connected to a Q-Exactive HF-X (Thermo Scientific, Bremen, Germany) on a 77 min gradient. Buffer A was milliQ water. The peptides were separated with increasing buffer B (80% ACN and 0.1% FA), going from 5% to 30% in 50 min, 30% to 45% in 10 min, 45% to 80% in 2 min, held at 80% for 5 min before dropping back down to 5% in 5 min and held for 5 min. Flow rate was 250 nL/min. The column temperature was maintained at 40°C using an integrated column oven. A wash-blank method using 2 µl 0.1% TFA, 5% ACN was run in between each sample to hinder cross-contamination and column blockage. The Q-Exactive HF-X was operated in data dependent top 10 mode. Spray voltage was 2 kV, S-lens RF level at 50, and heated capillary at 275°C. Full scan mass spectra were recorded at a resolution of 120,000 at m/z 200 over the m/z range 350–1400 with a target value of 3e6 and a maximum injection time of 25 ms. Product ions were recorded at a resolution of 60,000 with a maximum ion injection time set to 118 ms and a target value set to 2e5. Normalised collision energy was set at 28% and the isolation window was 1.2 m/z with the dynamic exclusion set to 20 s.

4.2.4.2 LC-MS/MS at CoEMS

Peptides were re-suspended in aqueous 0.1% trifluoroacetic acid (v/v) then loaded onto an mClass nanoflow UPLC system (Waters) equipped with a nanoEaze M/Z Symmetry 100 Å C 18 , 5 µm trap column (180 µm x 20 mm, Waters) and a PepMap, 2 µm, 100 Å, C 18 EasyNano nanocapillary column (75 m x 500 mm, Thermo). The trap wash solvent was aqueous 0.05% (v:v) trifluoroacetic acid and the trapping flow rate was 15 µL/min. The trap was washed for 5 min before switching flow to the capillary column. Separation used gradient elution of two solvents: solvent A, aqueous 0.1% (v:v) formic acid; solvent B, acetonitrile containing 0.1% (v:v) formic acid. The flow rate for the capillary column was 300 nL/min and the column temperature was 40°C. The linear multi-step gradient profile was: 3-10% B over 7 min, 10-35% B over 30 min, 35-99% B over 5 min and then proceeded to wash with 99% solvent B for 4 min. The column was returned to initial conditions and re-equilibrated for 15 min before subsequent injections.

The nanoLC system was interfaced with an Orbitrap Fusion Tribrid mass spectrometer (Thermo) with an EasyNano ionisation source (Thermo). Positive ESI-MS and MS2 spectra were acquired using Xcalibur software (version 4.0, Thermo). Instrument source settings were: ion spray voltage, 1,900 V; sweep gas, 0 Arb; ion transfer tube temperature; 275°C. MS1 spectra were acquired in the Orbitrap with: 120,000 resolution, scan range: m/z 375-1,500; AGC target, 4e 5; max fill time, 100 ms. Data dependent acquisition was performed in topN mode using a selecting the 12 most intense precursors with charge states >1. Easy-IC was used for internal calibration. Dynamic exclusion was performed for 50 s post precursor selection and a minimum threshold for fragmentation was set at 5e3. MS2 spectra were acquired in the Orbitrap with: 30,000 resolution, max fill time, 100 ms, HCD; activation energy: 32 NCE.

The York Centre of Excellence in Mass Spectrometry was created thanks to a major capital investment through Science City York, supported by Yorkshire Forward with funds from the Northern Way Initiative, and subsequent support from EPSRC (EP/K039660/1; EP/M028127/1).

4.2.5 Protein identification

Raw files were searched using MaxQuant 1.6.2.6 (Cox and Mann, 2008) against a database containing mammalian and piscine collagens and common contaminants from the common Repository of Adventitious Proteins (cRAP) (Appendix B, File B1). The search was conducted using a non-specific search strategy (i.e. no protease was selected) and a maximum peptide length of 45. The variable modifications included hydroxyproline, deamidation (NQR), glucosylgalactosyl hydroxylysine, glycosylation (K), and oxidation (M). All other parameters were set to MaxQuant's defaults, including a false discovery rate (FDR) of 1%.

4.2.6 Measuring deamidation

Deamidation was measured using three different methods. Deamidation from ZooMS spectra was measured using the Q2E package (Wilson, van Doorn and Collins, 2012) and the MALDIpqi package (Nair *et al.*, 2022). For these calculations, all samples were submitted in triplicate and default parameters were used unless stated otherwise. Bulk and site-specific deamidation from LC-MS/MS data was obtained using the software tool deamiDATE 1.0 (Ramsøe *et al.*, 2020).

Q2E uses a genetic algorithm to determine the extent of glutamine deamidation by comparing the theoretical and measured distributions of each sample. A Q2E value of 1 indicates no deamidation and a value of 0 indicates complete deamidation (Wilson, van Doorn and Collins, 2012). The peptides used for this analysis can be seen in Table 9.

The MALDIpqi package utilises weighted least-squares linear regression, followed by a linear mixed effect model to predict the overall deamidation level of a sample, termed the Parchment Glutamine Index (PQI, (Nair *et al.*, 2022). A half-window size of 3 was used for smoothening with the Savitzky-Golay filter (Savitzky and Golay, 1964). The peptide markers reported by (Nair *et al.*, 2022) were used in this analysis (Table 9).

Table 9. List of peptides used for Q2E and PQI calculations From: (Nair *et al.*, 2022)

Peptide	m/z	nQ	Sequence
COL1α1 508-519	1105.58	1	GVQGPPGPAGPR (1 Hyp)
COL1α1 270-291	2019.95	1	GEPGPTGIQGPPGPAGEEGKR (2 Hyp)
COL1α1 375-396	2040.97	1	TGPPGPAGQDGRPGPPGPPGAR (3 Hyp)
COL1α1 934-963	2689.25	2	GFSGLQGPPGPPGSPGEQGPSGASGPAGPR (2 Hyp)
COL1α2 756-789	3033.5	1	GPSGEPGTAGPPGTPGPQGLLGAPGFLGLPGSR (5 Hyp)
COL1α2 535-567	3093.48	1	GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR (5 Hyp)
COL1α1 9-42	3084.42	2	GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR (5 Hyp)
COL1α1 9-42	3116.4	2	GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR (7 Hyp?)

deamiDATE 1.0 was designed as a method for the authentication of ancient proteins by measuring site-specific deamidation rates (Ramsøe *et al.*, 2020). It uses MaxQuant results output files to determine bulk and site-specific deamidation for each sample (Ramsøe *et al.*, 2020). Bulk deamidation represents the average relative remaining N and Q per protein per sample. Site-specific deamidation uses the sequence-dependent half-time estimated by (Robinson *et al.*, 2004) and represents the average remaining portion of N or Q for each three residue combination (X-N-Y and X-Q-Y) per half-time (Ramsøe *et al.*, 2020).

4.3 Results and discussion

The deamidation levels of each sample were calculated and analysis of the deamidation and hydroxylation patterns was conducted for this study. The results emphasise the importance of future studies on the kinetics of glutamine deamidation.

4.3.1 Deamidation

The relative amount of deamidation in each sample was calculated using three methods. Relative glutamine deamidation was measured from ZooMS spectra using the Q2E package (Wilson, van Doorn and Collins, 2012) and the MALDIpqi package (Nair *et al.*, 2022). Bulk and site-specific deamidation from LC-MS/MS data was obtained using the software tool deamiDATE 1.0 (Ramsøe *et al.*, 2020). Additionally, the position of each deamidated asparagine and glutamine, and hydroxyproline were recorded for analysis.

4.3.1.1 Glutamine deamidation from ZooMS spectra

The glutamine deamidation level for each sample was calculated using the R (R Core Team, 2021) packages Q2E and MALDIpqi (Wilson, van Doorn and Collins, 2012; Nair *et al.*, 2022). In the method reported by (Wilson, van Doorn and Collins, 2012) deamidation values have a range of 0 to 1, where 1 indicates no deamidation and 0 full deamidation. Nair *et al.*, (2022) argue that, in theory, the PQI values should fall between 0 and 1, but in practice, the noise and baseline corrections applied to the spectra sometimes produce values above 1, which should be interpreted as very low deamidation but cannot be discarded. Additionally, values close to 0 don't occur in parchment or leather objects as this would indicate full gelatinisation (Nair *et al.*, 2022). This contrast in approach means that for samples with very low levels of deamidation the difference between samples' Q2E value might be too subtle to judge once the associated error is accounted for, while the PQI value better highlights small differences in the deamidation levels. This is particularly useful when analysing modern samples with very low levels of glutamine deamidation. This is exemplified by the difference in Q2E and PQI values seen in modern commercial collagen samples (Figure 13). The PQI and Q2E values can be seen in Appendix B (Table B1).

With the exception of a single sample (MF1664) the PQI values are higher than the Q2E and there is a greater range of values, which translates as better distinction between samples. This is because in Q2E all values above 1 are assumed to be 100% and thus capped, while in PQI there is no upper limit and values can often exceed 1, which is

interpreted as little to no deamidation. The Q2E values for three samples were capped at 1 and for twelve samples the calculation could not be computed (Figure 13). The Q2E associated error seems to increase with greater levels of deamidation. Surprisingly, the leather samples from the Mary Rose show very good preservation, as indicated by their low deamidation levels (Figure 13). For samples with known liming times and/or experimental conditions, such as the aged leather samples, we can see the change in deamidation over time (Figure 12). We would expect that samples with longer liming times or exposure to a damaging environment, like the ageing chamber, to have higher deamidation rates. Although both the goat and cow aged leather follow this pattern, the rest of them display differing levels of deamidation. This is likely due to the fact that samples were stored after treatment for about 10 years in an uncontrolled environment which means degradation processes continued without monitoring.

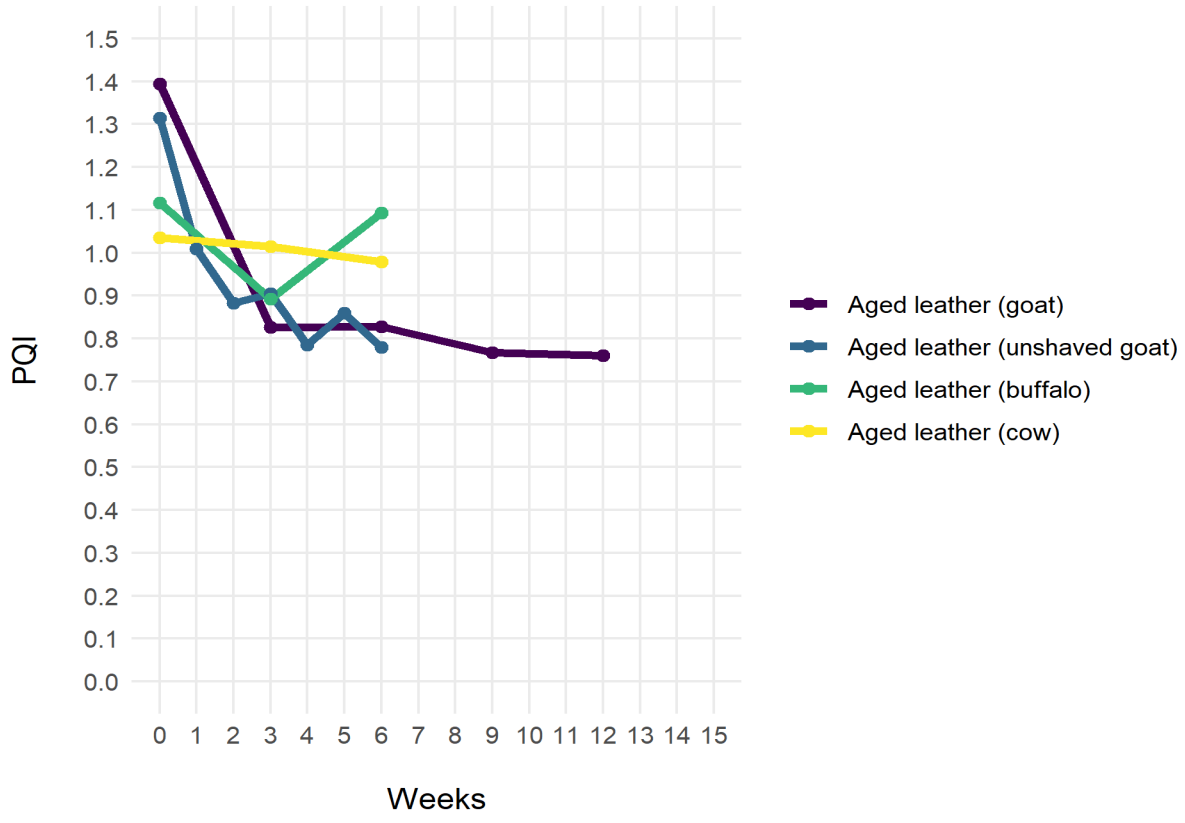


Figure 12. Parchment Glutamine Index over time in weeks for aged leather samples.

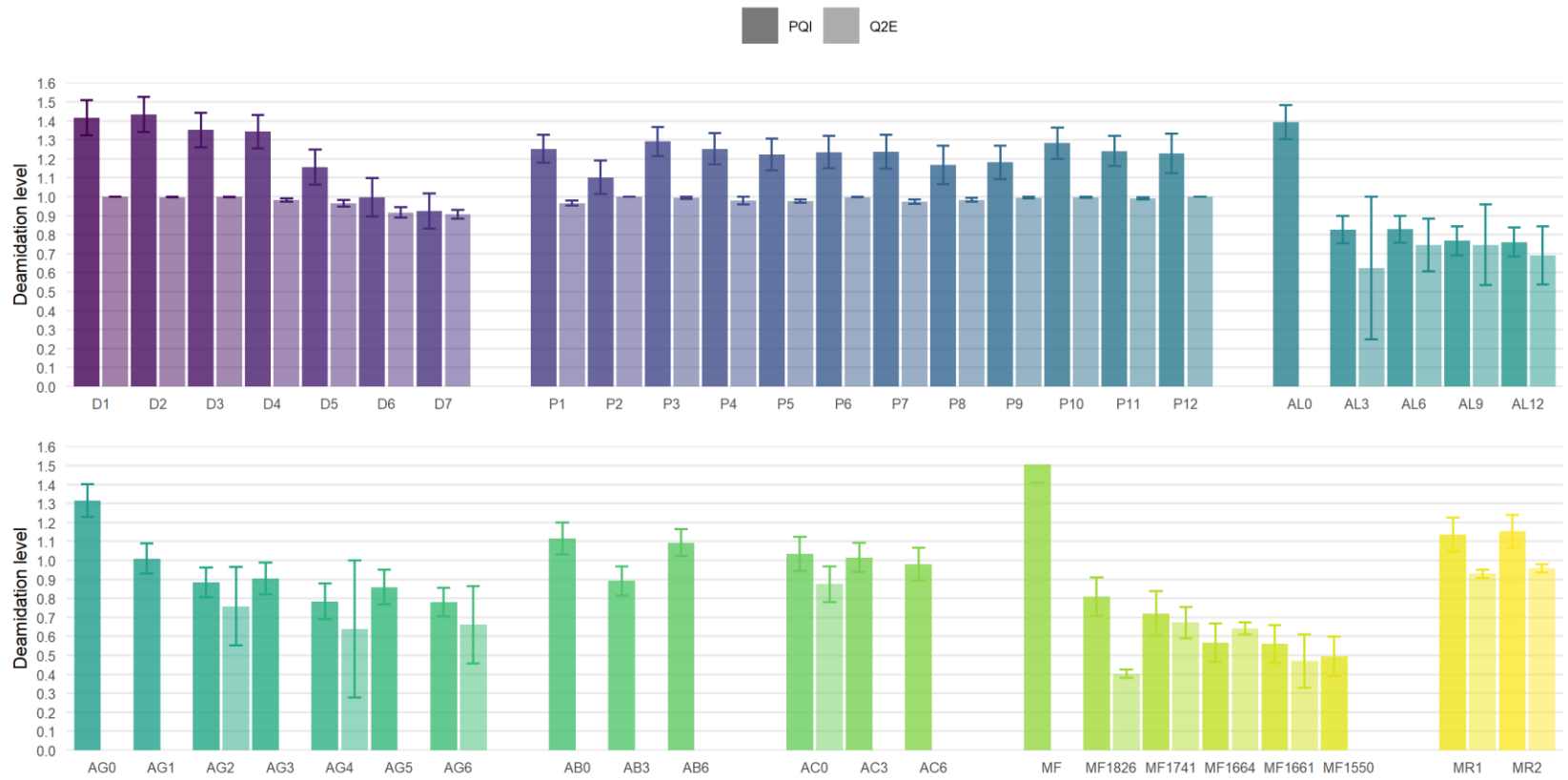


Figure 13. Q2E (light) and PQI (dark) deamidation values per sample. The error bars represent standard deviation. Q2E values have a range of 0 to 1, where 1 indicates no deamidation and 0 full deamidation. PQI calculations sometimes produce values above 1, which should be interpreted as very low deamidation but cannot be discarded. This means that for samples with very low levels of deamidation the PQI value better highlights small differences in the deamidation levels. This is particularly useful when analysing modern samples with very low levels of glutamine deamidation. Here, with the exception of sample MF1664 the PQI values are higher than the Q2E and there is a better distinction between samples. The Q2E values for three samples were capped at 1 and for twelve samples the calculation could not be computed**.** The Q2E associated error seems to increase with greater levels of deamidation.

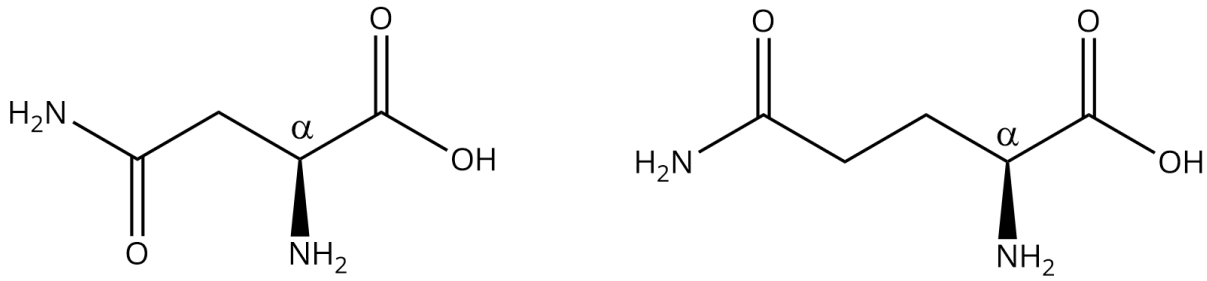
4.3.1.2 deamiDATE 1.0

Bulk deamidation

The total rates of deamidation were assessed for each sample (Figure 15). These values don't take into account the half-time of the deamidation positions, which will be discussed in the next section. The commercial collagen and parchment samples displayed relatively undamaged collagen. On average, 53.2% of asparagine and 89.9% of glutamine residues appeared undamaged for these samples. In contrast, the aged leather samples show, on average, 71% deamidated asparagine and 66.6% deamidated glutamine. These values are similar to those exhibited by leather samples from the library in Mafra, Portugal. The library samples present, on average, 78.4% deamidated asparagine and 60.9% deamidated glutamine. In contrast, the leather fragments recovered from the Mary Rose have 21.6% asparagine and 89.5% glutamine remaining. A table with the bulk deamidation values can be seen in Appendix B (Table B2).

In eight of the aged leather samples kept in acidic conditions in an ageing chamber – AG1, AG5, AC6, AB6, and AL3 to AL12 - the glutamine deamidation level is higher than that of asparagine. In acidic conditions, we assume that deamidation occurs primarily by side chain hydrolysis. In the case of asparagine, the formation of the succinimide intermediate is very slow at pH < 5 (Patel and Borchardt, 1990b, 1990a; Clarke, 2003) and deamidation is slowest at a pH between 4 and 6 (Robinson *et al.*, 2004).

The observed deamidation levels in these samples suggest that, in these conditions, the rate of deamidation of glutamine (by side chain hydrolysis) can be faster than that of asparagine. One possible explanation for this is that the side chain of glutamine is more susceptible to hydrolysis due to it being longer and therefore the functional group is at a greater distance from the α-carbon when compared to asparagine (Figure 14), leaving the side chain more exposed (Wright, 1991) . This is the case when the loss of nitrogen in free amino acids has been studied. Glutamine rapidly loses its first nitrogen, then forms a stable pyroGlu, the cyclisation preventing the loss of the second nitrogen, while in the case of Asn, both the side chain and alpha nitrogens are lost (Sohn and Ho, 1995).



Asparagine Glutamine

Figure 14. Structure of glutamine and asparagine with annotated α-carbon

The leather samples from the Mary Rose show a low glutamine deamidation level, while asparagine is much more deamidated. These samples were in a marine waterlogged environment from 1545, when the ship sank, until1982 when it was raised by the Mary Rose Trust. According to the European Environment Agency, the average pH of seawater during this period went from 8.2 to 8.1 (European Environment Agency, 2021). In alkaline conditions, the rate of deamidation of asparagine is known to be far greater than that of glutamine (Robinson and Robinson, 2001a) which is consistent with the deamidation levels of these samples.

Site-specific deamidation

When looking at site-specific deamidation of modern samples, we expect to see high levels of deamidation at sites with low half-times (e.g. Xxx-Gly), with sites at high half-times (> 5000 days) remaining mostly non-deamidated (Ramsøe *et al.*, 2020), when deamidation occurs via a cyclic intermediate. The rate data was established based upon flexible pentapeptides, and is not relevant if the amino acids are still retained in a polyproline helix, a feature of collagen, the dominant protein in our study.

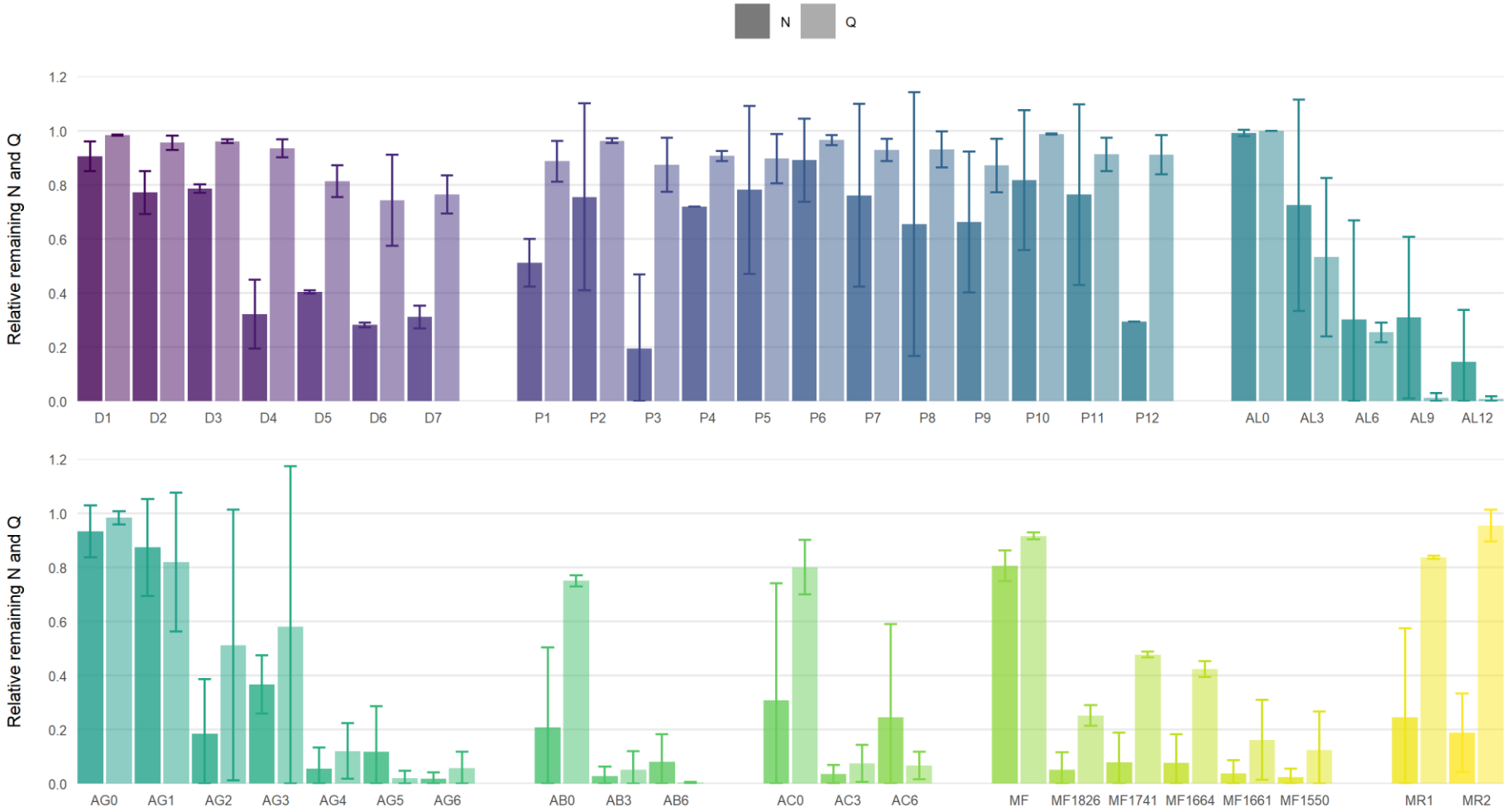


Figure 15. Relative level of non-deamidated Q (dark) and N (light) per sample for collagen type I α1 and α2. The y-axis shows the relative non-deamidated portion (1 would mean no deamidation, 0 complete deamidation). The error bars represent standard deviation.

It is worth noting that the ancient samples used as model dataset for the development of deamiDATE 1.0 range between 12K and 2.5M years old. By that standard, all our samples are modern collagen and we don't expect to see many instances of high deamidation levels at very high half-times. However, deamidation rates are affected by changes in pH and temperature, and the deamidation half-times used by deamiDATE 1.0 (Ramsøe *et al.*, 2020) were calculated at physiological conditions, i.e. 37°C and pH 7.4 (Robinson *et al.*, 2004). The influence of pH on the rates of deamidation of Asn has been widely studied as these are much more rapid than for Gln. This is, in part, because the cyclic intermediate Asu occurs much more readily than the equivalent six membered heterocycle Glu. Consequently, Gln deamidation is slower and of less biological relevance, while the pH dependence seen for Asx hydrolysis versus Asn deamidation (the former favoured at low pH and the latter at high pH) is less evident for Gln, which is largely driven by side chain hydrolysis.

Due to our samples being produced in alkaline media (parchment, commercial collagen) or exposed to acidic environments (aged leather), some deamidation at high half-times will occur. Parchment is much more resistant to acidic environments than leather, as $Ca(OH)_2$ is retained in the leather slowly converting to $CaCO_3$ by reaction with CO_2 generating a considerable buffering capacity. The site-specific deamidation patterns for each sample group are shown in Figure 16. A table with the site-specific deamidation data per sample can be seen in Appendix B (Table B3) along with the associated plots.

The commercial collagen and parchment samples exhibit very little deamidation, even at low half-times. This is consistent with their production and use history, and we can assume that any deamidation present in these samples is the result of the liming process during manufacturing.

Except for the unshaved goat aged leather samples, which exhibit a high level of deamidation but show no deamidation at high half-times, all other aged leather samples display a very high level of deamidation at low half times, and present one fully deamidated site at 10K days. The bovine leather samples also present a fully deamidated site at 5.2K and 7.2K days, and the buffalo samples display a further two sites at 6.8K and 8.9K days. None of these samples show partial deamidation at high

half-times and the control samples exhibit low deamidation levels. The deamidated sites at high half-times for these samples occur due to their exposure to a harsh acidic environment during ageing.

The deamidation pattern of the leather samples from Mafra, which present very high deamidation at low half-times, some partial deamidation at high half-times, and 3 fully deamidated sites, looks somewhat similar to that of the aged leather samples, although with higher intensities at sites with half-times above 5K days.

In contrast, the leather fragments from the Mary Rose, which show high deamidation at low half-times and low deamidation at high half-times, resemble the patterns seen in the commercial collagen and parchment samples. The low deamidation displayed by these samples is likely due to the alkaline marine environment in which they were found.

Rate of deamidation

During our analysis we found that, for the aged leather (goat) samples, the rate of deamidation of a site with low half-time was slower than expected and, on further analysis, we identified other half-times of interest. The three residue combinations associated to these half-times involve proline (P), valine (V), and alanine (A), the most common residues in collagen after glycine (G). We analysed the rate of reaction for four residue triplets (half-time): VNG (1.08 days), AQG (610 days), PQG (630 days), and VQG (640 days). The deamidation trend for the goat aged leather samples for the triplets mentioned above is illustrated in Figure 17. The plot is fitted with exponential relationships, characteristic of first order reactions, where the reaction rate is linearly dependent on the concentration of only one reactant. In Figure 17, we can see that the deamidation of VNG, which has a half-time of 1.08 days, has a slower deamidation rate than the PQG and VQG triplets, with half-times of 630 and 640 days, respectively. Unlike the aforementioned triplets, the deamidation of AQG doesn't follow a first order reaction trend but, without more data points, we cannot explain its behaviour. However, the trends observed here are further indication that the rate of deamidation of

glutamine is faster than that of asparagine when side chain hydrolysis is the preferred mechanism, as is the case for these samples, which were aged under acidic conditions.

In contrast, when we look at the deamidation rate trend for commercial collagen samples (Figure 18), prepared under alkaline conditions, we can see that the observed triplets, seemingly, follow the behaviour predicted by deamiDATE 1.0 (Robinson *et al.*, 2004; Ramsøe *et al.*, 2020), and the rate of deamidation at the VNG site is much faster than those for the glutamine sites.

While the rates of deamidation of asparagine are well studied, the opposite is true for glutamine. Robinson *et al.* (2004) reported deamidation rate constants for pentapeptides of the GlyXxxAsnYyyGly and GlyXxxGlnYyyGly forms, but go on to explain that, in proteins, where the mechanisms of deamidation are affected by the three-dimensional structure of the protein, the rates of deamidation are quantitatively different (Robinson *et al.*, 2004). Previously, (van Duin and Collins, 1998), have shown that racemization of Asx (in part a product of Asn deamidation) is predicted (and observed) to be very slow in the intact collagen triple helix, but very rapid once the protein is converted to (flexible) gelatine. These results show that, in future experiments, under controlled conditions, we could use LC-MS/MS and deamiDATE 1.0 to further investigate the kinetics of this reaction. This can then be compared and, where possible, correlated to other measurements like the melting and shrinkage temperatures of collagen to further our understanding of the damage and degradation patterns of collagen.

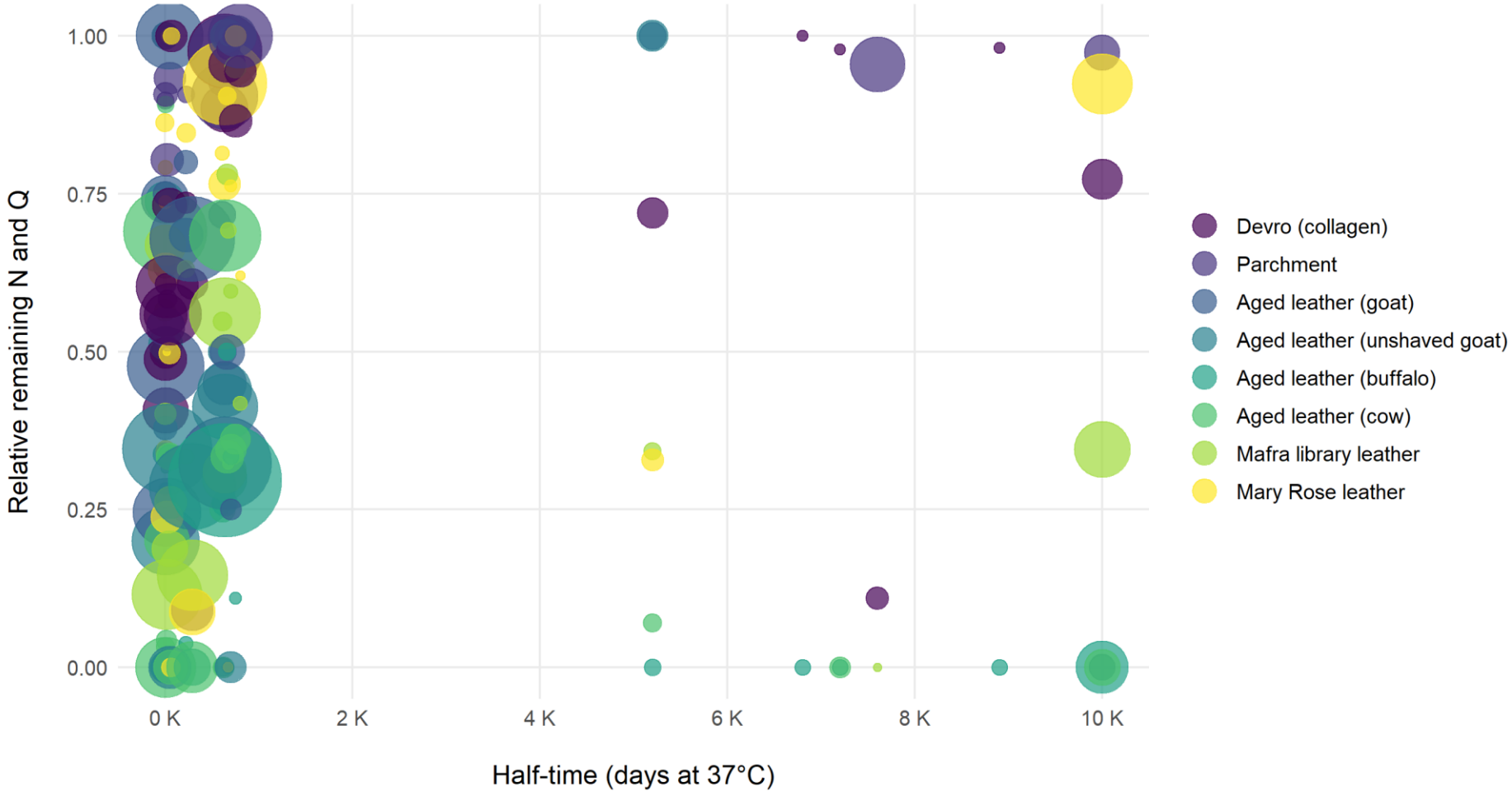


Figure 16. Site-specific deamidation of collagen by sample group. Each point represents a specific three residue combination. The size of the point represents that site's intensity, relative to the total intensity of all peptides in the same sample (Ramsøe *et al.*, 2020).

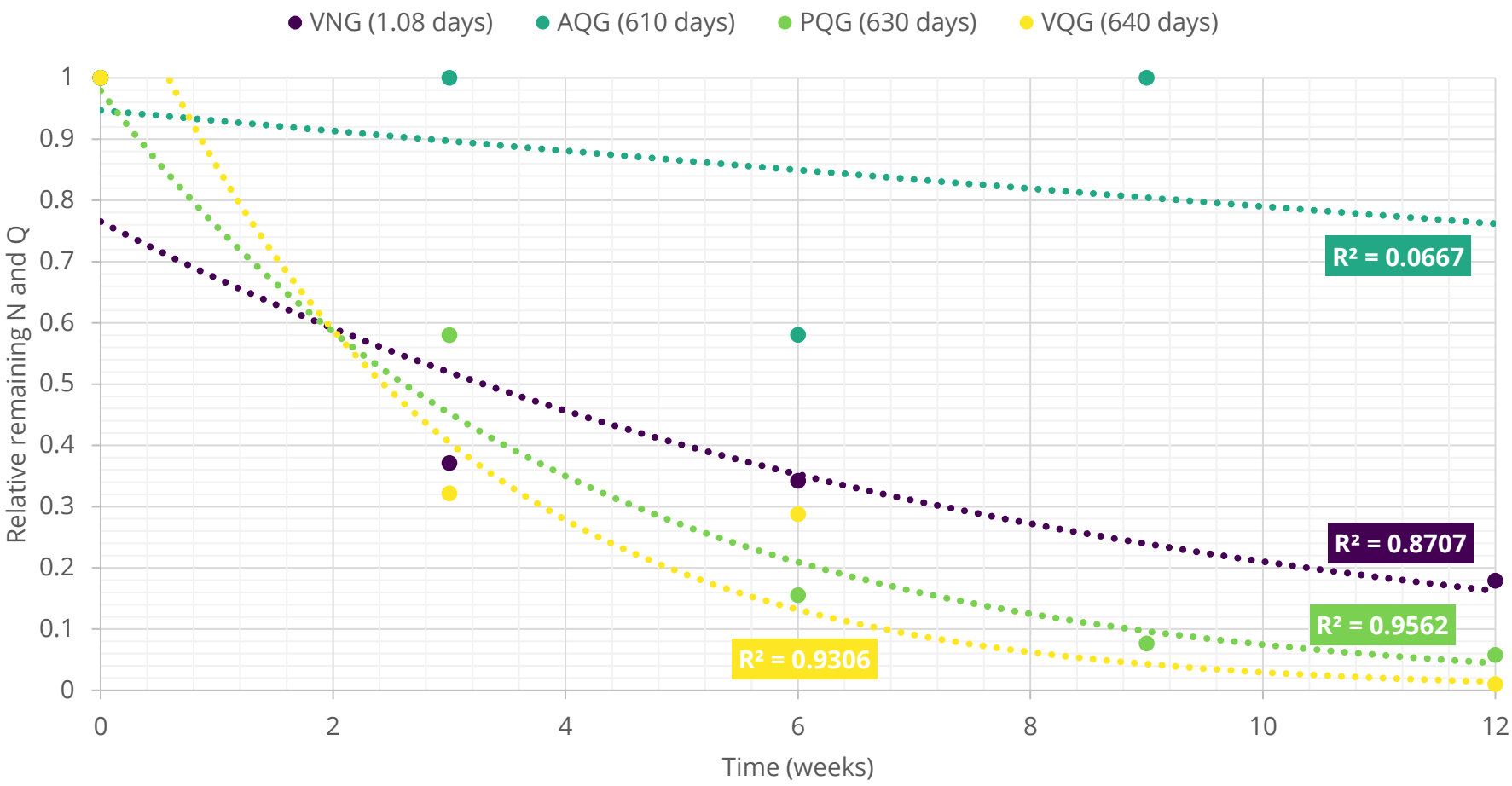


Figure 17. Deamidation rate of collagen in aged leather samples (goat) for VNG, AQG, PQG, and VQG triplets. As these are pseudo-first order reactions both Figure 17 and Figure 18 are fitted with exponential relationships characteristic of first-order reactions where the reaction rate is linearly dependent on the concentration of only one reactant. Although in the case of Figure 18, the fitted lines appear as linear given the short time span of the data relating to commercial collagen samples.

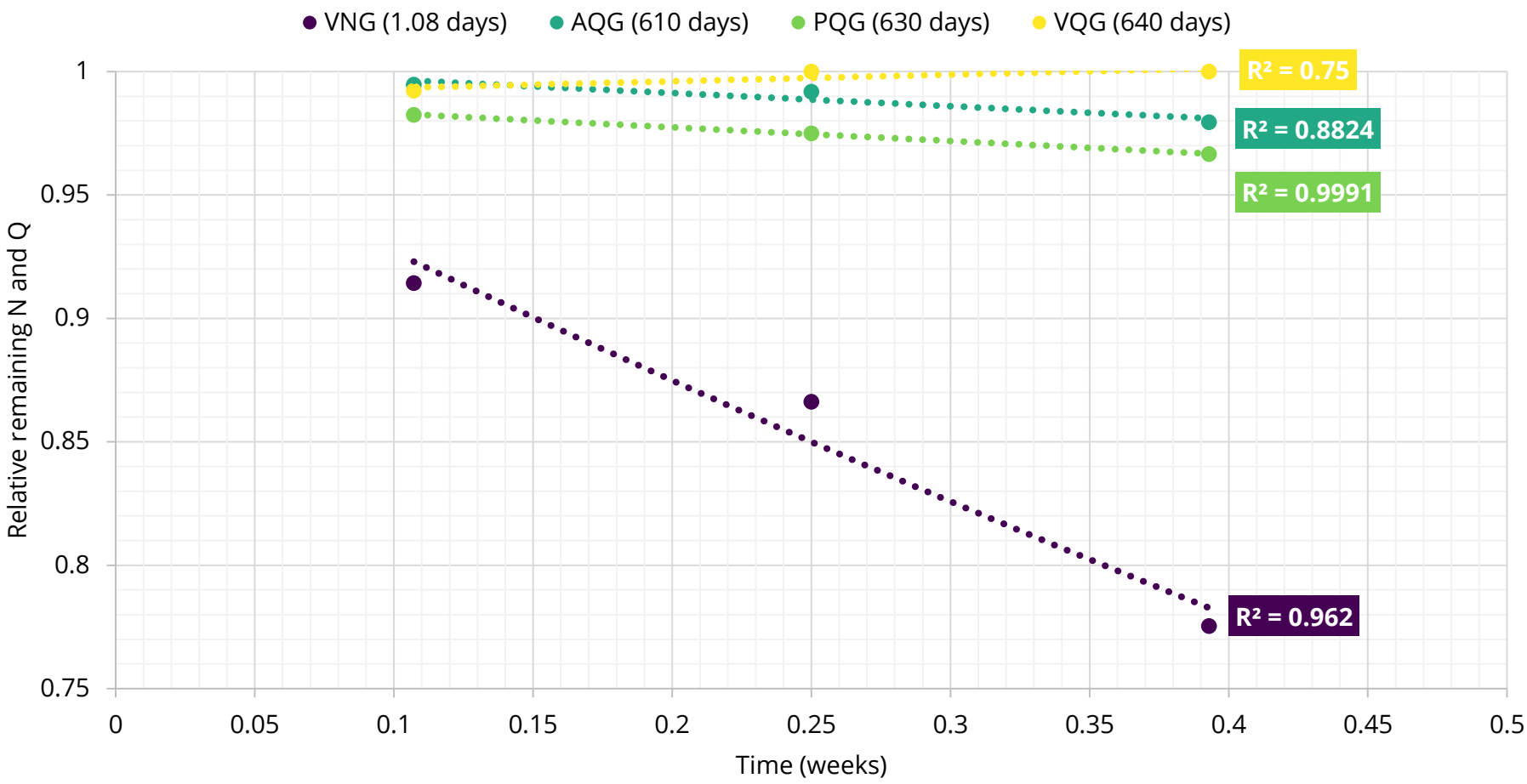


Figure 18. Deamidation rate trends in commercial collagen samples (Devro) for VNG, AQG, PQG, and VQG triplets. As these are pseudo-first order reactions both Figure 17 and are fitted with exponential relationships characteristic of first-order reactions where the reaction rate is linearly dependent on the concentration of only one reactant. Although in the case of Figure 18, the fitted lines appear as linear given the short time span of the data relating to commercial collagen samples.

4.3.1.3 Deamidation patterns

So far, bioinformatics tools have been used to determine the levels of deamidation of glutamine and asparagine in each sample. In this section a visual analysis of the LC-MS/MS data has been generated to look for patterns in deamidation that can inform our view of the manufacturing and use history of the samples. This was done for collagen type I α1 (CO1A1) and α2 (CO1A2), and collagen type III α1 (CO3A1).

In all samples, the coverage of CO1A2 is better than that of CO1A1 and CO3A1 has a low sequence coverage (Table 10). The commercial collagen sample set presents a very high sequence coverage for CO1A2 (75%) which can act as a benchmark when looking at more degraded samples. The historical leather samples from Mafra and the Mary Rose show better sequence preservation than the aged leathers. It is interesting to consider the possible role that localised deamidation would have on triple helix structure. Under acidic conditions, the rate of Asx-Xxx peptide bond cleavage is higher than under alkaline conditions, but, overall, the rates of total peptide bond cleavage in collagen are, in acid conditions, only one third of the rates observed under alkaline conditions (Collins *et al.*, 1995). Given the assumption that localised disorganisation would lead to the total melting of the triple helix the differences in overall collagen coverage are surprising. Additionally, the low sequence coverage of CO1A1 when compared to CO1A2 is strange given that CO1A1 is the most common chain, and, from experience, has the higher coverage. The tannings of leather could inhibit the digestion of the collagen or the detection of some collagen peptides, but in a marine waterlogged environment, some of the tannings may leach from the leather, which could explain the improved sequencing of the Mary Rose leather samples. The sequence coverage for each sample can be seen in Appendix B (Table B4).

Table 10. Sequence coverage of collagen type I and III per sample group.

Group	CO1A1	CO1A2	CO3A1
Devro (commercial collagen)	28.1%	75.0%	12.4%
Parchment	13.0%	40.4%	2.9%
Aged leather (goat, unshaved)	12.1%	33.0%	1.8%
Aged leather (cow)	15.5%	38.2%	6.7%
Aged leather (buffalo)	16.6%	35.7%	7.2%
Aged leather (goat)	12.7%	31.3%	3.4%
Mafra library leather	16.0%	49.7%	6.9%
Mary Rose leather	13.5%	43.9%	6.4%

The modern collagen samples from Devro show more deamidation in samples D4 – D7. This is consistent with their manufacturing history as these samples were limed for the longest times. The deamidation of glutamine has been proposed as a method of quality control for the food industry (European Union, 2020).

The parchment samples are an interesting group as they all come from the same skin, which means their liming process was identical. This suggests that any differences in the deamidated sites would be due to the treatments applied to the skin before and after drying, some of which are acidic, like yoghurt. Some differences in deamidation patterns can be seen in the region around positions 820 – 860 and sample P11, which was soaked in yoghurt (an acidic substance), has two deamidated glutamines at positions 669 and 848, and one deamidated asparagine at 654 that don't appear in the other samples (Figure 19).

Aged leather samples display more deamidated sites than the rest of the modern samples (Figure 20). Parchment and commercial collagen samples were prepared under alkaline conditions. For parchment, this translates into a reservoir of calcium carbonate ($CaCO_3$) that acts like a buffer and can prevent direct hydrolysis. In contrast, leather is more sensitive to hydrolysis, especially under acidic conditions as is the case for these samples. Interestingly, leather samples that were exposed to acidic conditions for longer times have a better sequence coverage than the control samples. This is likely

due to the amount of gelatinised collagen in each sample, since the more damaged the sample, the more gelatine there is and the more peptides are detected.

Deamidation on the leather samples from the Mafra library is consistent across samples, with some non-deamidated sites in the reference (MF) and youngest sample (MF1826, Figure 21). The leather fragment from the Mary Rose (MR1) shows similar deamidation sites to the ones found in the Mafra samples, while the shoe sole leather fragment (MR2) only displays 5 deamidation sites and has a lower sequence coverage. Plots for the rest of the samples can be found in Appendix B (Figures B7 - B24).

The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). This means that in areas in the triple helix with a low melting temperature, deamidation of asparagine via Asu is more favourable. In the region between positions 480 and 520, which shows two points where the melting temperature decreases, peptides were not observed for CO1A1, and the opposite is true for CO1A2, except for the unshaved goat aged leather. In CO1A2, we don't see any peptides in the 500 and 950 regions, except for in historical leather samples. Due to the highly alkaline or acid conditions to which most of the samples were subjected, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible.

The difference between samples in this study puts into context the challenges in the interpretation of deamidation levels of samples that were manufactured and processed in different environments, from different raw materials, and with varying degrees of quality. Results from tools such as deamiDATE 1.0 (Ramsøe *et al.*, 2020) where the underlying data is based on physiological conditions (i.e. pH 7.4, 37°C) do not take into consideration the influence of pH and temperature on the rate of deamidation, or how a sample that has been limed (i.e. damaged) for a longer period of time during its manufacturing process might have a less stable collagen chain which is more susceptible to degradation reactions than other similar materials. For this reason, it is difficult to compare the extent to which deamidation is due to age or processing in heavily degraded samples, although the comparison of samples with a shared history or source is possible through these methods and provides valuable information about the

degradation processes in a family of samples. Nevertheless, the raw material, the initial quality of the material and variables such as use history, handling and storage conditions must be taken into consideration when looking at the source of damage and the rate at which degradation processes occur in any given sample.

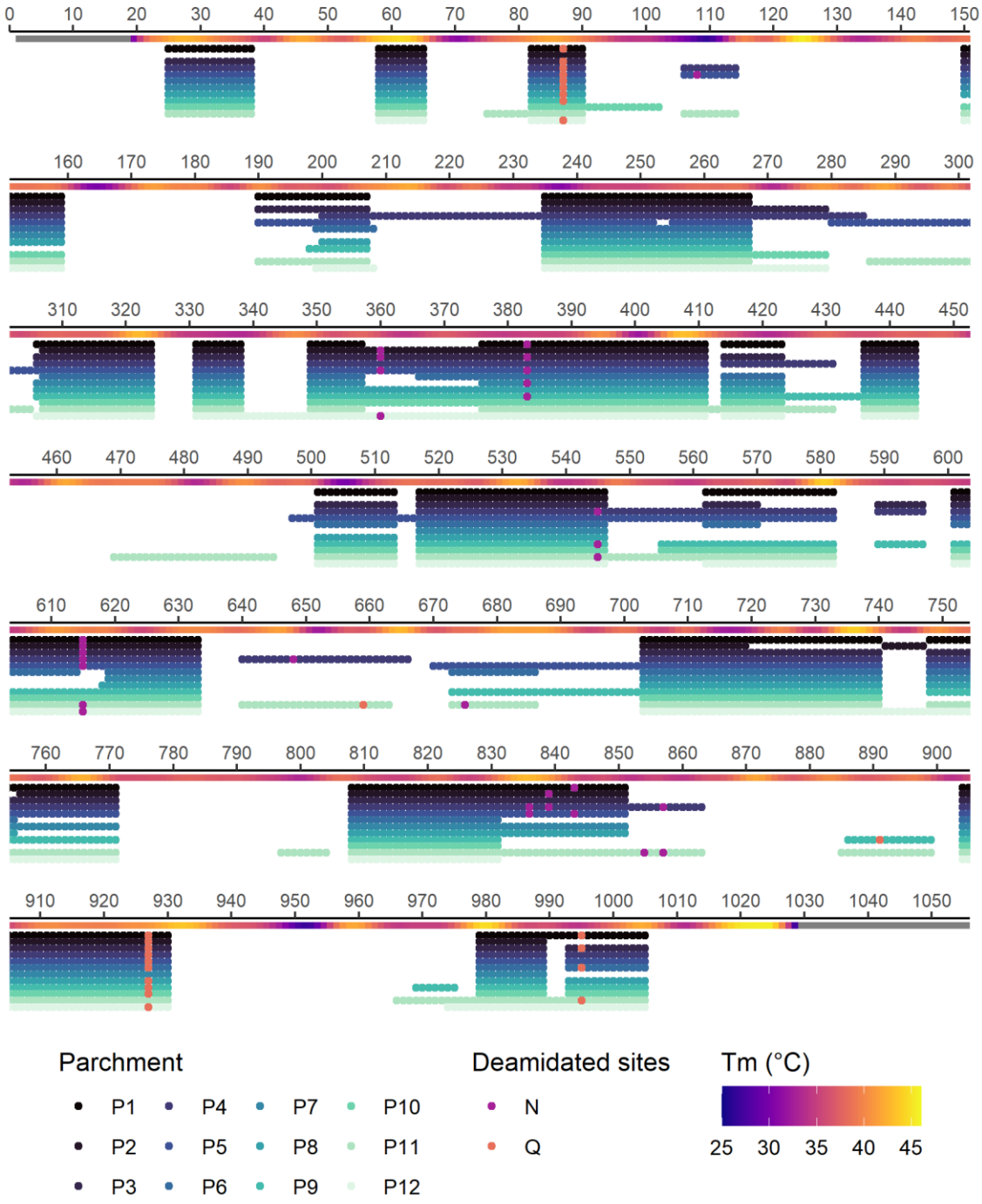


Figure 19. Collagen type I α2 from parchment samples identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

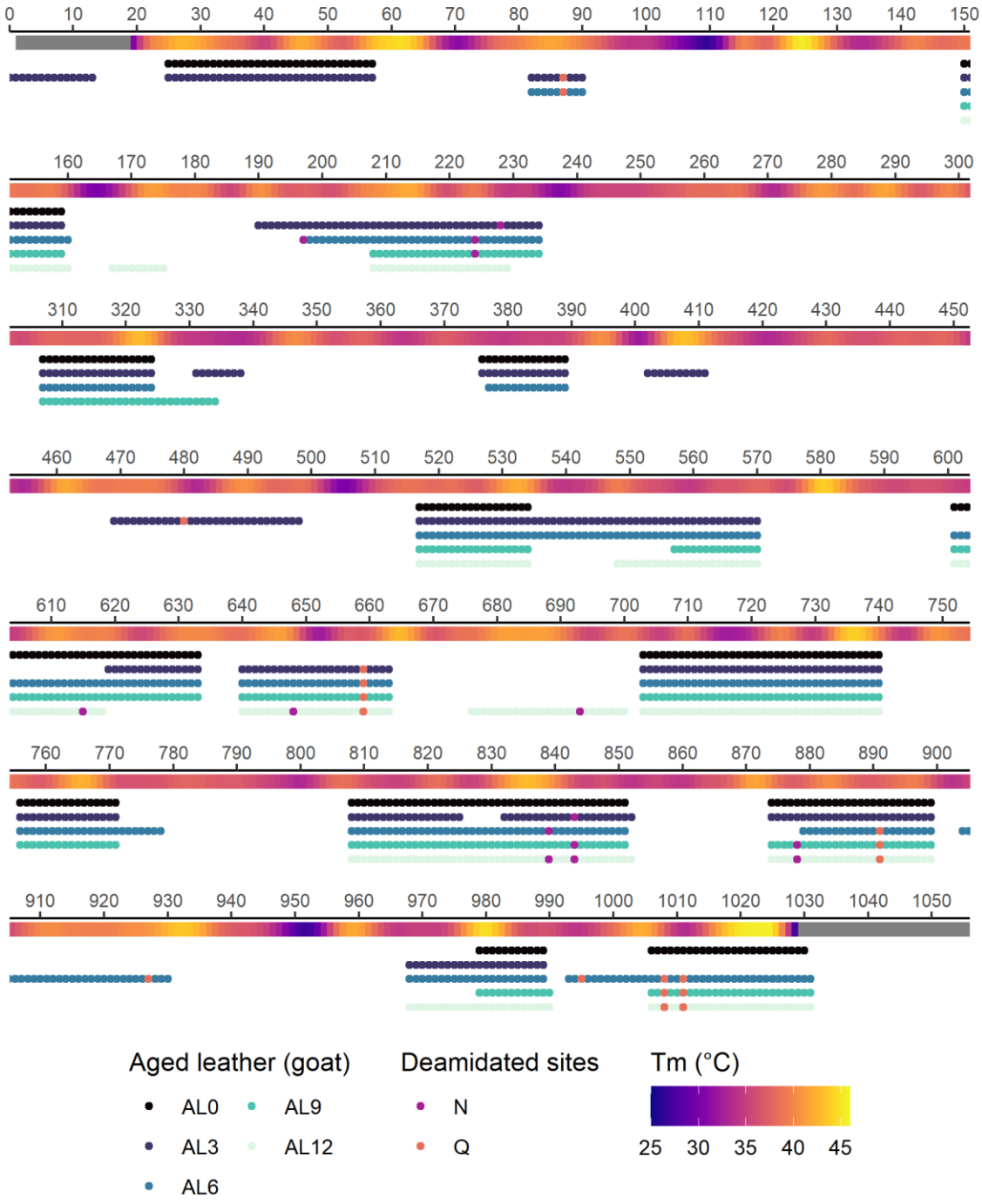


Figure 20. Collagen type I α2 from aged leather samples (goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

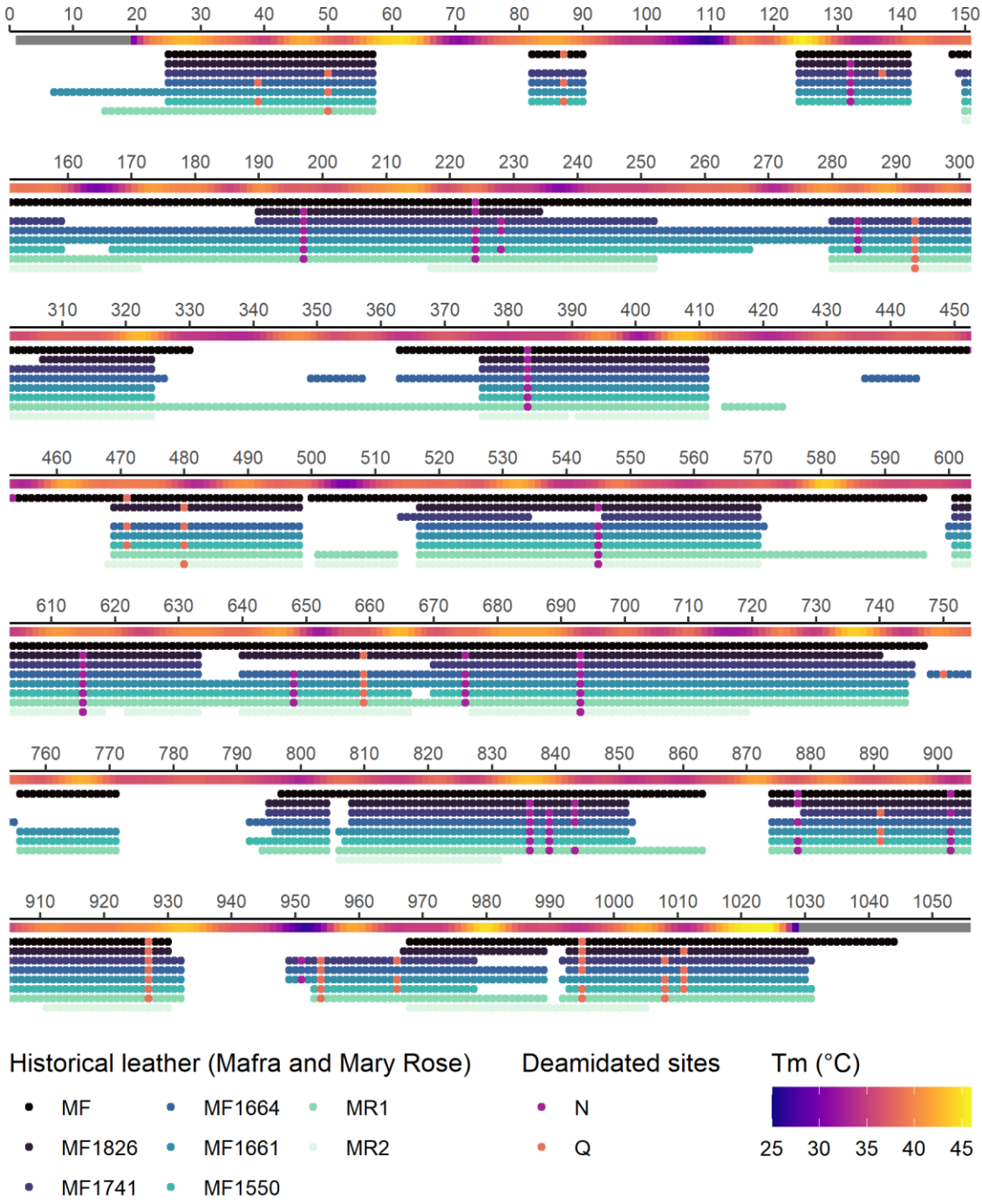


Figure 21. Collagen type I α2 from historical leather samples (Mafra and Mary Rose) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins et al., 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm)

4.3.2 Proline hydroxylation patterns

While the focus of this study is on deamidation, the patterns of proline hydroxylation in collagen deserve mention due to the abundance of Pro and Hyp in the collagen sequence. Given the role that hydroxyproline plays in the stabilisation of the collagen molecule and the way in which P4H catalyses proline hydroxylation into 4-hyroxyproline, the presence of Hyp in the Y position of the $(GXY)_n$ repeats in collagen is expected. However, in this study, we see the presence of Hyp in the X position, as well as the presence of the Hyp-Hyp-Gly motif, for example, in the 710 – 730 and 810 - 820 regions of goat aged leather samples seen in Figure 22, which suggests the presence of 3-Hyp. Weis *et al.* (2010) proposed that 3-Hyp plays a role in the ordered self-assembly of collagen supramolecular structures by forming hydrogen bonds between adjacent collagen triple helices and identified four 3-Hyp sites in human and bovine collagen types I and V. There is no way to differentiate between 4-Hyp and 3-Hyp from LC-MS/MS results, so further experiments would need to be done to confirm this. The plots for all samples can be seen in Appendix B (Figures B25 - B42).

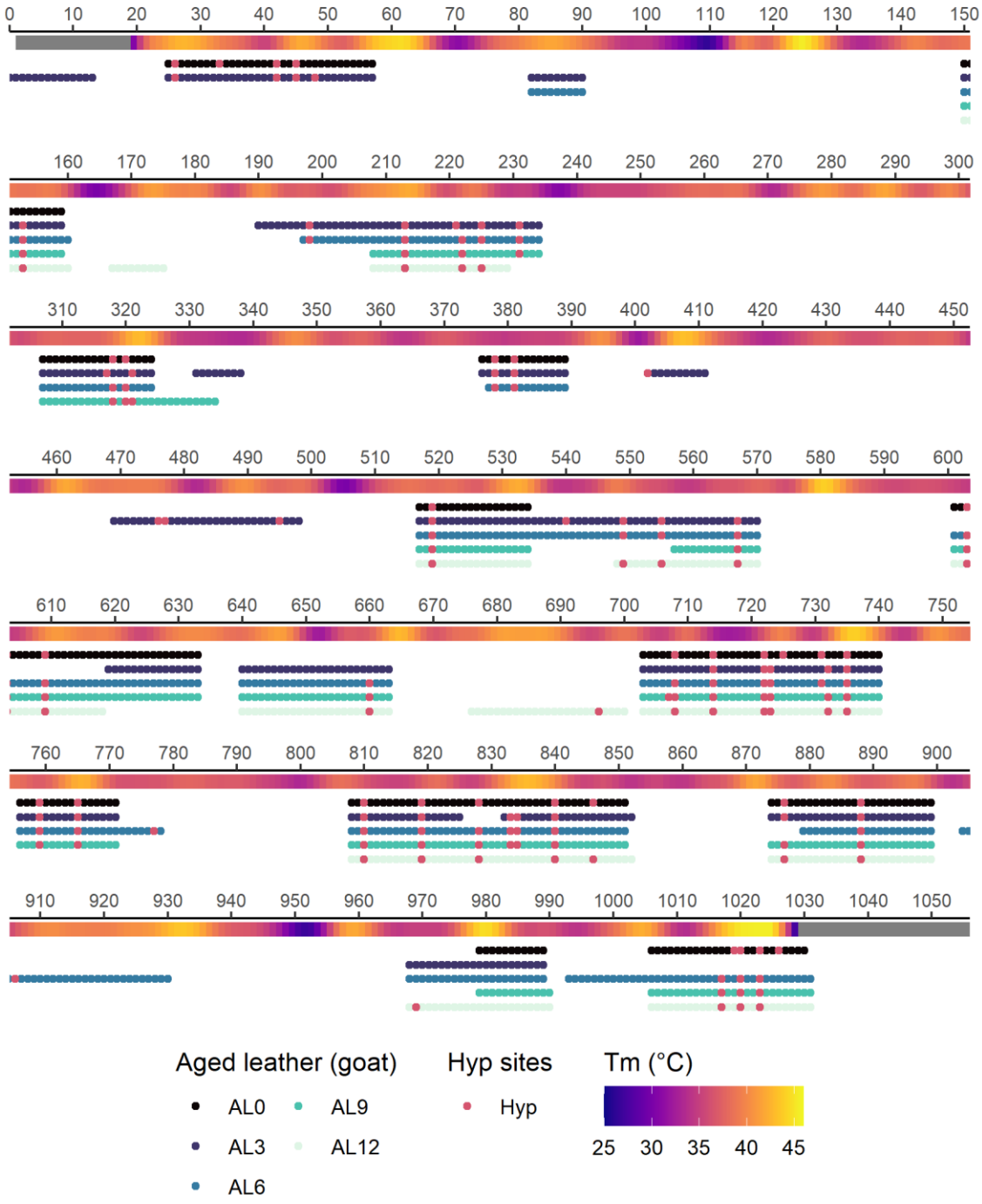


Figure 22. Collagen type I α2 from aged leather samples (goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

4.4 Conclusions

Proteins undergo physical, chemical and biological degradation processes which make their lifespan highly variable. Post-translational modifications (PTMs) of proteins can occur biologically or be introduced by diagenesis, ageing, and other factors. Analysing these chemical modifications by proteomics is relevant to increase overall peptide identifications, learn about ageing conditions, and how a sample was processed. Understanding the degradation patterns of collagen is an important step to understand the use and conservation history of archaeological and historical objects made from hide materials such as parchment and leather and can be further applied to the modern leather and food industries, both of which continue to make goods from collagen based materials. This work shows the available methods for assessing the level of deamidation of a sample and emphasises the importance of further studies of glutamine deamidation kinetics and mechanisms to better estimate damage to the collagen molecule.

Chapter 5: ZooMS as a fast and effective method to measure deamidation levels in commercial collagen samples

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Relevance: In this chapter the use of ZooMS as a quality control method suitable for the modern collagen food industry is demonstrated.

Abstract: The development and improvement of scientific and technological innovations is a critical step towards more sustainable patterns of production of goods and services. Collagen-rich by-products from the slaughter of livestock, like skin and bones, generate opportunities to minimise waste and produce high-value derivatives from slaughtered animals and are widely used in the food and beverage industries. Particular protein modifications, like deamidation, which result from external chemical, physical or biological processes acting on the proteins can be detected by mass spectrometry and used to assess the damage and overall degradation state of a protein. This study shows the use of deamidation level measurements (PQI) designed for the analysis of ancient proteins applied to the food industry as a quality control method. Using ZooMS and PQI measurements we were able to reduce the analysis time by 66% and achieved better sample separation when compared to the in-house method.

Implementing ZooMS and PQI measurements for quality control and assurance would enable the measurement of slight variations in deamidation levels which can then be correlated to the physicochemical and mechanical properties of edible collagen films and casings and inform the continuous improvement and development of new and existing products

5.1 Introduction

The development and improvement of scientific and technological innovations is a critical step towards more sustainable patterns of production of goods and services. This is reflected in several initiatives worldwide which promote the prevention of food waste. In 2015, the United Nations adopted the 2030 Agenda for Sustainable Development. Two of the Sustainable Development Goals (SDGs), which are at the heart of the agenda, are 'to end hunger, achieve food security and improved nutrition and promote sustainable agriculture' (goal 2), and 'to ensure sustainable consumption and production patterns' (goal 12, (United Nations, 2015). Similarly, the European Commission committed to reduce food losses along production and supply chains and halving the global per capita food waste at the retail and consumption levels by 2030 in the European Action Plan for the Circular Economy (European Commission, 2015). Hence, in recent years, the design and development of innovative products and methods in the food, cosmetics, and biomedical industries have gained increasing interest (Irastorza *et al.*, 2021). In this regard, collagen-rich by-products from the slaughter of livestock, like skin and bones, generate opportunities to minimise waste and produce high-value derivatives from slaughtered animals (Hashim *et al.*, 2015; Irastorza *et al.*, 2021; Tang *et al.*, 2022).

5.1.1 Collagen in the food industry

Collagen, the most abundant protein of animal origin, is widely used in the food and beverage industries as a texturising agent, food thickener, protein dietary supplement, and as edible films and coatings, among other applications.

Edible films and coatings are materials applied to foods in thin layers to cover their surface. The main applications of collagen films and coatings are as a barrier to protect against oxidation and moisture, whilst providing structural integrity and permeability and as a means to prolonging the shelf-life of foods (Greene, 2003; Bourtoom, 2008). Collagen films have the potential to substitute non-biodegradable plastic packaging materials, and the use of collagen for the production of sausage casings is a well-established technology, which will be the main focus of this study (Gennadios, Hanna and Kurth, 1997; Neklyudov, 2003; Hashim *et al.*, 2015; Ma *et al.*, 2020).

The basic processing methods of animal skins in the food industry mimic the historical methods used in the production of parchment and leather. Once the skin is removed from the animal, it is placed in a highly alkaline solution. This process, called liming, facilitates the removal of hair and epidermis by breaking the disulphide bonds in the keratinous tissue (Bienkiewicz, 1983; Covington, 2009); removes cutaneous lipids by saponification, (Koppenhoefer, 1938, 1939); and, lowers the collagen's iso-electric point by the hydrolysis of amide groups attached to asparagine and glutamine residues, which enables the removal of non-collagenous proteins from the skin (Menderes *et al.*, 1999; Covington, 2009). After liming, the skin is fleshed to remove the epidermis and fats, leaving the collagen-rich dermis layer which is then further processed into collagen casings. Although the physicochemical and mechanical properties of collagen casings can be manipulated by cross-linking, they are directly linked to the length of exposure to lime, and quality control measures have to be taken if they are to be successfully utilised without rupturing or separating from the meat stuffing during filling or cooking (Corthals *et al.*, 2012; Tang *et al.*, 2022).

In this context, particular protein modifications, like deamidation, which result from external chemical, physical or biological processes acting on the proteins can be

detected by mass spectrometry and used to assess the damage and overall degradation state of a protein. Deamidation in collagen can be directly linked to the length of exposure to an extreme pH environment like liming. High levels of deamidation indicate denaturing of collagen which translates into a weak and brittle casing. Thus, the deamidation level of the protein can be used as a quality control measure during the casings manufacturing process.

5.1.2 Deamidation

Deamidation is a protein modification occurring on asparagine (Asn) and glutamine (Gln) residues. Overall, the chemical reaction is a nucleophilic acyl substitution on the ω-carbon of the side chain of the two amino acids. The amide group is transformed into a carboxylic acid, producing aspartic (Asp) and glutamic (Glu) acids. The reaction can occur enzymatically in living organisms (Mycek and Waelsch, 1960; Imada *et al.*, 1973; Wriston and Yellin, 1973; Curthoys and Watford, 1995), but it is also known to occur spontaneously and non-enzymatically over time in all protein-based materials following, mainly, two mechanisms: the direct hydrolysis of the amide, or the formation of a cyclic amide followed by hydrolysis (Robinson *et al.*, 2004). Deamidation is often considered an indicator of protein damage, since it naturally occurs during protein ageing (Robinson and Robinson, 2001a).

At constant pH, the deamidation of Asn and Gln residues follows first-order kinetics (Geiger and Clarke, 1987; Patel and Borchardt, 1990a). Because the deamidation rates of Asn can be up to 10 times faster than Gln (Robinson, Scotchler and McKerrow, 1973; Robinson and Robinson, 2001a) it has been suggested that the investigation of the deamidation level of Gln residues is a better source of information regarding protein damage for collagen based materials in the food and leather industries, and in ancient proteins (Maffia *et al.*, 2004; Leo *et al.*, 2011; Van Doorn *et al.*, 2012; Nair *et al.*, 2022).

This study shows that measuring the glutamine deamidation levels of collagen samples analysed by peptide mass fingerprinting (or ZooMS), a method originally designed for the analysis of ancient proteins, can be applied to the food industry as a quality control

method. This is of importance to reduce waste and achieve the right physicochemical and mechanical properties needed for the intended use of the material.

5.2 Materials and Methods

5.2.1 Collagen samples

Seven bovine collagen samples, described in Table 11, were provided by Devro plc (Devro plc, 2022). The samples were limed in a lime (calcium hydroxide) and sulphide solution for 18 h, then delimed and split. Samples DV2 and DV3 were then re-limed in lime for a further 24 h and 48 h, respectively. Samples DV4 – DV7 were re-limed in lime for an unknown amount of time, possibly for weeks, without temperature control. The samples were delimed before drying and milling.

Table 11. Collagen samples provided by Devro plc.

Sample	Original sample name	Description
DV1	High Split	Bovine collagen. Limed for 18 h in lime and sulphide. The hide was split after 18 h and had a 'high' free amide level (low deamidation level).
DV2	Medium Split	Bovine collagen. Limed for 18 h in lime and sulphide. The hide was split after 18 h. After splitting the hide was re-limed without the presence of sulphide for a further 24 h. The hide had a 'medium' free amide level (medium deamidation level)
DV3	Low Split	Bovine collagen. Limed for 18 h in lime and sulphide. The hide was split after 18 h. After splitting the hide was re-limed without the presence of sulphide for a further 48 h. The hide had a 'low' free amide level (high deamidation level)
DV4	U-SCO-18-06-001-S	Bovine collagen. Limed for 18 h in lime and sulphide. The hide was split after 18 h. After

Sample	Original sample name	Description
		splitting the hide was re-limed without the presence of sulphide for an unknown period of time, different from the rest of the samples.
DV5	U-SCO-18-06-002-S	Bovine collagen. Limed for 18 h in lime and sulphide. The hide was split after 18 h. After splitting the hide was re-limed without the presence of sulphide for an unknown period of time, different from the rest of the samples.
DV6	U-SCO-18-06-004-S	Bovine collagen. Limed for 18 h in lime and sulphide. The hide was split after 18 h. After splitting the hide was re-limed without the presence of sulphide for an unknown period of time, different from the rest of the samples.
DV7	U-SCO-18-06-003-S	Bovine collagen. Limed for 18 h in lime and sulphide. The hide was split after 18 h. After splitting the hide was re-limed without the presence of sulphide for an unknown period of time, different from the rest of the samples.

5.2.2 Sampling

A small amount (< 2 mg) of dried collagen was put in individual 1.5 mL microcentrifuge tubes. Nitrile gloves were worn throughout the sampling process to avoid keratin (human skin) contamination. All samples were stored at room temperature until required.

5.2.3 ZooMS

ZooMS analysis was performed according to the protocol developed by (Fiddyment *et al.*, 2015). Samples were spun down at maximum speed on a benchtop centrifuge for 1 min. Then, 75 µL of 0.05 M ammonium bicarbonate (AmBic) buffer (pH 8) and 1 µL of trypsin (0.4 µg/µL) was added to each sample. The samples were heated at 37 °C for 4 h. After incubation with trypsin, the digests were spun down at maximum speed on a benchtop

centrifuge for 1 min and 1 µL of 5% (vol/vol) trifluoroacetic acid (TFA) was added. Samples were desalted and concentrated using C18 resin (Millipore), following the manufacturer's instructions. Peptides were eluted in a final volume of 50 µL of 50% acetonitrile (ACN)/0.1% TFA (vol/vol). One microliter of eluted peptides was mixed on a ground steel plate with 1 µL of α-cyano-4-hydroxycinnamic acid matrix solution [1% in 50% ACN/0.1% TFA (vol/vol/vol)] and air-dried. All samples were spotted in triplicate. Samples were analysed using a calibrated Ultraflex III (NLD1; Bruker Daltonics) MALDI-TOF instrument in reflector mode.

5.2.4 Parchment glutamine index

The R (R Core Team, 2021) package MALDIpqi was used to obtain the Parchment Glutamine Index (PQI), a measure of deamidation, for each sample. The MALDIpqi package pre-processes the data and utilises weighted least-squares linear regression, followed by a linear mixed effect model to predict the overall deamidation level of the sample (Nair *et al.*, 2022). Pre-processing of the spectra is performed using the R package MALDIquant (Gibb and Strimmer, 2012). A half-window size of 3 was used for smoothening with the Savitzky-Golay filter (Savitzky and Golay, 1964). The default values for the rest of the parameters were used and the peptide markers reported by (Nair *et al.*, 2022) were used in this analysis (Table 12). Each sample was submitted in triplicate.

Table 12. List of peptides used in the analysis. Adapted from: (Nair *et al.*, 2022)

Peptide	m/z	nQ	Sequence
COL1α1 508-519	1105.58	1	GVQGPPGPAGPR (1 Hyp)
COL1α1 270-291	2019.95	1	GEPGPTGIQGPPGPAGEEGKR (2 Hyp)
COL1α1 375-396	2040.97	1	TGPPGPAGQDGRPGPPGPPGAR (3 Hyp)
COL1α1 934-963	2689.25	2	GFSGLQGPPGPPGSPGEQGPSGASGPAGPR (2 Hyp)
COL1α2 756-789	3033.5	1	GPSGEPGTAGPPGTPGPQGLLGAPGFLGLPGSR (5 Hyp)
COL1α2 535-567	3093.48	1	GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR (5 Hyp)
COL1α1 9-42	3084.42	2	GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR (5 Hyp)
COL1α1 9-42	3116.4	2	GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR (7 Hyp?)

5.3 Results & Discussion

The PQI of each sample was measured and compared to the in-house 'free amide level' values obtained by Devro plc. This comparison highlights the benefits of using the described methods as a quality control measure in the food industry.

5.3.1 Parchment Glutamine Index

The PQI of each sample was obtained using the R package MALDIpqi. The half-window size was set to 3, and for every other parameter the default value was used. The power in the q estimates was 0.053 (Nair *et al.*, 2022). In theory, the PQI values should fall between 0 and 1, where 1 signifies no deamidation and 0 complete deamidation. In practice, the noise and baseline corrections applied to the spectra sometimes produce values above 1 which is interpreted as very low deamidation. Since the samples provided by Devro are modern, we expect there to be little deamidation compared to an ancient or historical sample, and PQI values greater than 1 are not surprising.

The PQI values, seen in Table 13, are consistent with the provided description of the samples. Samples DV1 and DV2 show the lowest levels of deamidation and sample DV7 the highest. The difference in deamidation levels between samples DV1 and DV2, which underwent 18 h and 42 h of liming, respectively, is minimal. Indeed, DV2 presents a lower level of deamidation than DV1. This might be attributed to differences in the reaction conditions, like pH and temperature, which affect the deamidation rate. Samples DV3 and DV4 have very similar PQIs, which indicates they underwent similar liming times. Furthermore, it can be deduced that the liming times for DV5, DV6, and DV7 were each longer than the other, respectively.

Table 13. Parchment glutamine index of commercial collagen samples.

Sample	Parchment glutamine index (PQI)	Standard deviation
DV1	1.417	0.093
DV2	1.433	0.093
DV3	1.352	0.091
DV4	1.344	0.089
DV5	1.155	0.093
DV6	0.997	0.102
DV7	0.925	0.092

As mentioned above, several factors can affect the rate of deamidation – pH, ionic strength, temperature, amino acid sequence and structure of the protein, and matrix, all have an effect on the kinetics of the reaction. But, given a constant environment, the deamidation of glutamine residues follows first-order kinetics, i.e. the rate of deamidation is proportional to the concentration of the reagents. Hence, given the liming times of DV1-DV3, the liming time for the rest of the samples can be estimated using a simple linear forecast function. Using this approach it is estimated that the damage seen in DV4, DV5, DV6, DV7 is equivalent to the skins being limed, in constant conditions, for approximately 3, 9, 14, and 16 days, respectively. While these values are consistent with the sample descriptions provided by Devro, the reaction conditions were not controlled and these estimates, likely, don't reflect the real liming time, but are still a useful guideline to inform on the degradation state of the collagen samples.

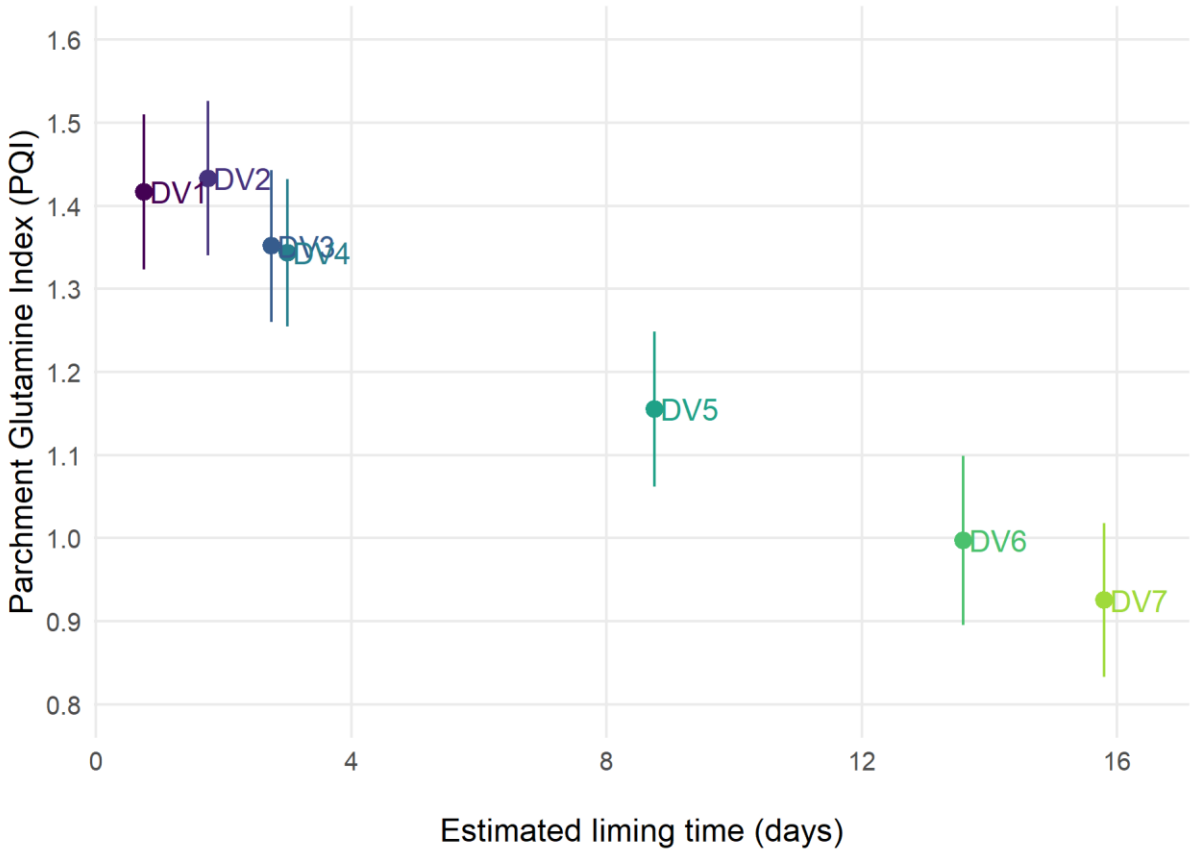

Figure 23. Parchment Glutamine Index of collagen samples vs estimated liming time in days.

5.3.2 Comparing PQI to in-house deamidation levels

Devro plc provided in-house measurements of 'free amide level' for each sample. These values, seen in Table 14, are obtained by a Devro proprietary method and are a measure of the available amide groups in the samples which can be translated into levels of deamidation. The in-house analysis takes around 24 h per batch and has a precision of around 0.02 % w/w collagen. After analysis, samples are classified as having a high, medium, or low free amide level, which is then used as a quality control measure. A high free amide level means the sample has a low deamidation level and a low free amide level means a high level of deamidation.

Table 14. Free amide level values of commercial collagen samples.

Sample	Free amide level % w/w collagen
DV1	0.65%
DV2	0.61%
DV3	0.57%
DV4	0.45%
DV5	0.37%
DV6	0.30%
DV7	0.27%

In Figure 24, the free amide levels are plotted alongside the PQI. The free amide levels show significant overlap with one another, and the difference between samples is not easy to interpret. In contrast, the difference in deamidation from the PQI values is obvious. The sample separation achieved using the PQI value indicates that this method is able to pick up on subtle changes in protein damage that could be used to enhance quality control and assurance methods in collagen based products. Additionally, this method gives a better understanding, at a glance, of the protein degradation in each sample. The small differences in deamidation between DV1 and DV2, and DV3 and DV4 are easily picked up by looking at the PQI. And, the difference between the deamidation levels in DV4 – DV7 is better highlighted by the PQI value.

Implementing the methods described here for quality control and assurance would enable the measurement of slight variations in deamidation levels, which can then be correlated to the physicochemical and mechanical properties of edible collagen films and casings. Such analyses are integral to the continuous improvement and development of new and existing products. Additionally, processing of a ZooMS sample, from sampling to analysis takes around 8 – 10 h which is a 66% time reduction versus the current in-house method.

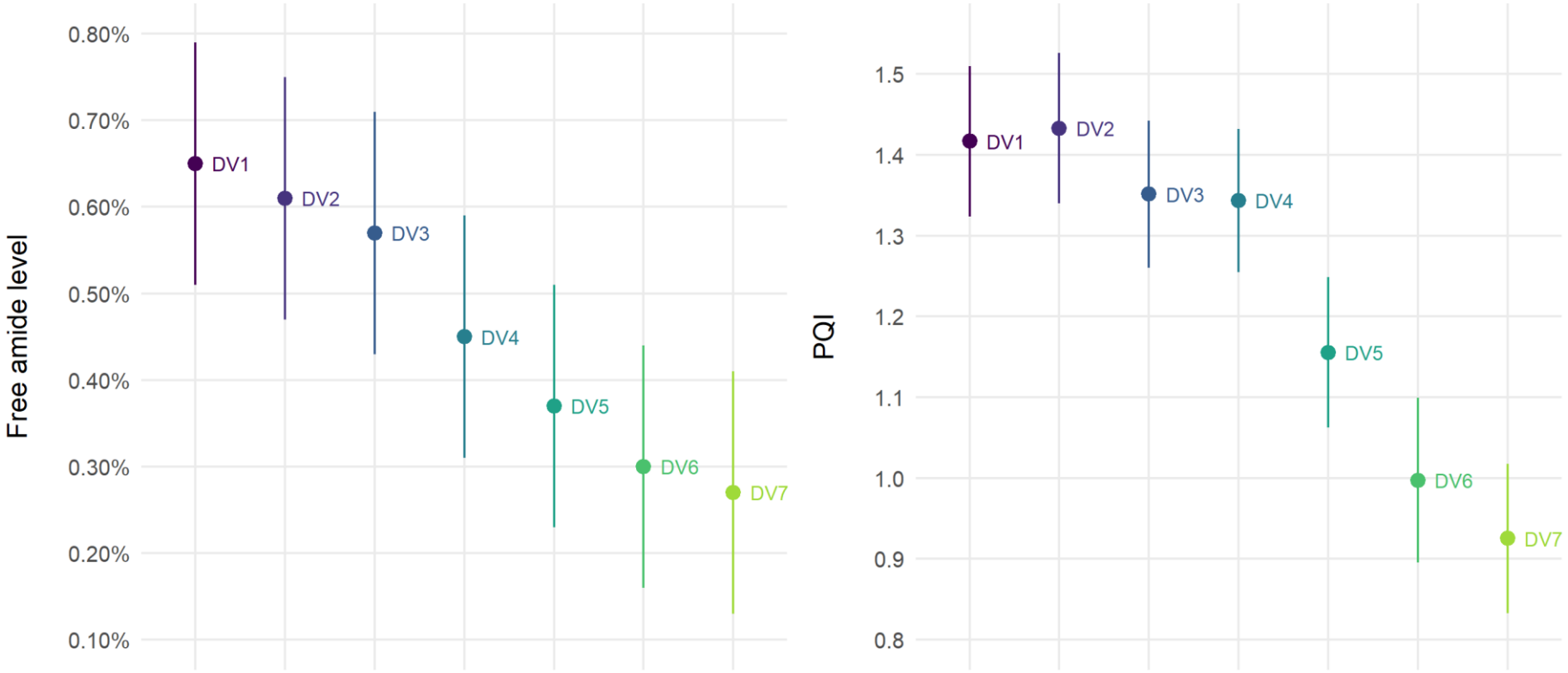

Figure 24. Comparison of PQI and Free amide levels by sample. left: Free amide levels measured by Devro plc; right: Parchment Glutamine Index (PQI) obtained with MALDIpqi. In both cases a high value indicates a low deamidation level and a low value indicates a high deamidation level. Sample separation is better achieved by PQI when compared to the in-house method. Implementing ZooMS and PQI measurement for quality control and assurance would enable the measurement of slight variations in deamidation levels which can then be correlated to the physicochemical and mechanical properties of edible collagen films and casings and inform the continuous improvement and development of new and existing product while reducing the sample processing time by 66%.

5.4 Conclusion

ZooMS and MALDIpqi were used to measure the overall deamidation levels of commercial collagen samples used in the manufacture of sausage casings. This measure was then compared to the free amide level values obtained by the in-house process used by Devro plc. Measuring the PQI via ZooMS was found to be faster and more reliable method to measure deamidation as a quality control method for collagen materials in the food industry. This work shows the application of methods developed for the study of ancient proteins to the analysis and quality control and assurance of modern collagen materials. This work was given mention by the European Commission's Innovation Radar as a tech ready innovation having a 'Noteworthy' level of Market Creation Potential and contributing to the UN sustainable development goal to 'end hunger, achieve food security and improve nutrition and promote sustainable agriculture' (European Union, 2020).

Chapter 6: A qualitative peptide biomarker approach to identify piscine gelatine to support food security

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Relevance: This chapter is the product of a secondment at Fera and discusses the application of proteomics methods for determination of piscine gelatine by identification of piscine collagen peptide markers and its importance in food safety and security.

Abstract: Pressure for commercial gelatine suppliers to provide gelatines of known species origin is driven by due diligence, requiring certification, inspection and audit. Following the Europewide adulteration of processed foods with horse meat in 2013, the 2014 Elliott Review into the Integrity and Assurance of Food Supply Networks highlighted the requirement for analytical surveillance methods to support due diligence. Additionally, for piscine gelatine, there is a food labelling requirement regarding the inclusion of fish-derived ingredients on a food label due to concerns over elicitation of an allergic response. We present a targeted peptide biomarker approach by

liquid chromatography-mass spectrometry, suitable to the type of instrumentation available to food enforcement officers, to determine the presence of piscine gelatine. The method was successfully applied to gelatine granules, capsules and composite retail food products. The obtained data indicates the method is reproducible between replicates of sub-samples with a limit of detection of 0.1% (w/w).

Keywords: gelatine, piscine, authenticity, mass spectrometry, allergen, enforcement

6.1 Introduction

Processed foods and other consumer products require accurate labelling according to the meat species they contain. Further to declaring the authenticity of the product, health and safety regulations must be met, which requires inclusion of allergen information. Where a product contains any of the regulated allergens as an ingredient or processing aid, it must be included on the label ('Regulation (EU) No 1169/2011', 2011). This is the case for foods incorporating ingredients derived from fish.

The pressure for commercial gelatine suppliers to provide gelatines of known species provenance is driven by due diligence, requiring certification, inspection and audit with regards to the animal origin of the gelatine. In response to the Europewide adulteration of processed foods with horsemeat in 2013, the 2014 Elliott Review into the Integrity and Assurance of Food Supply Networks (Elliott, 2014) highlighted the requirement for analytical surveillance methods to support such due diligence and, critically, to promote food safety. The current work supports the development of such laboratory services in food security to determine piscine gelatine. The aim of this research was to develop a method using liquid chromatography triple quadrupole tandem mass spectrometry (LC-TQMS/MS), a high-throughput technology known to have high sensitivity and specificity (Peng *et al.*, 2014). LC-TQMS/MS is a low-cost technology when compared to other mass spectrometers, such as Matrix Assisted Laser Desorption/Ionisation-Time-of-Flight tandem mass spectrometry (MALDI-TOF MS/MS), previously used to determine collagen species provenance in discovery methods in research and development. Additionally,

LC-TQMS/MS is already available and widely used in Official Control Laboratories (MacDonald and Bradley, 2019) to support regulatory enforcement in determining pesticide and veterinary drugs. This technology can be easily adapted to determine peptide biomarkers to address issues in food labelling verification and authenticity with minimal additional cost. The question of cost is critical since enforcement laboratories often have limited funds to invest in new instrumentation.

Gelatine, a cleavage product of collagen protein, is widely used in the food industry to impact on texture and act as a binding agent. Highly processed gelatine, or hydrolysed collagen, has also been used as a water retention agent in meat products, and undeclared bovine gelatine, or hydrolysed bovine collagen, was reported in meat injection powders (Food Standards Agency, 2009). A unique feature associated with the structure of collagen is that every third amino acid is usually glycine (G, Gly) which gives a repeat of the (G-X-Y)n. motif. Proline constitutes around 18% of the amino acid composition of collagen and is often subject to hydroxylation during collagen synthesis. Additionally, asparaginyl (N, Asn) and glutaminyl (Q, Gln) residues within collagen undergo deamidation during gelatine manufacture (Shoulders and Raines, 2009).

Gelatine is manufactured as a by-product of the meat and fish industry. Sources of collagen include porcine skin, cattle hide and bone, and skin and bones from a range of fish species. The highly denaturing process required to produce gelatine can destroy or denature much of the DNA in a sample (Menderes *et al.*, 1999; Cai *et al.*, 2012), often compromising the opportunity for application of genomic methods including real-time PCR (Grundy *et al.*, 2016; Jannat *et al.*, 2018). The collagen protein is also denatured during gelatine manufacture, and protein detection methods, including enzyme linked-immunosorbent assay (ELISA), are also compromised, with authors reporting false positive and false negative results (Doi *et al.*, 2009; Grundy *et al.*, 2016). Collagen peptides, however, are more robust, in terms of integrity, following gelatine manufacture (Sha *et al.*, 2014, 2018; Grundy *et al.*, 2016; Guo *et al.*, 2018; Kleinnijenhuis, van Holthoon and Herregods, 2018).

Piscine gelatine can be prepared from the skin of a wide range of fish species. Food grade piscine gelatine is prepared on a commercial scale from over 100 species of

farmed, warm water fish in only three gelatine manufacturing plants worldwide (personal correspondence), often from farmed tilapia genus. This gelatine has a higher melting temperature than bovine and porcine gelatines.

Methods have been reported to determine the species provenance of bovine and porcine gelatine by collagen peptide marker identification by liquid chromatography coupled to mass spectrometry (LC-MS/MS) (Sha *et al.*, 2014, 2018; Grundy *et al.*, 2016; Guo *et al.*, 2018; Kleinnijenhuis, van Holthoon and Herregods, 2018). Regarding the determination of piscine collagen, data is more limited. Authors have reported success in differentiating bovine, porcine and fish gelatine using chemometric analysis of an liquid chromatography mass spectrometry dataset (Jannat *et al.*, 2018). Much of the work on piscine collagen focuses on archaeological studies rather than studies of food gelatine: collagen peptide sequences have been reported in archaeological cold water fish remains (Harvey, Daugnora and Buckley, 2018) and collagen sequences have been reported for eight cold water fish species (Richter *et al.*, 2011a; Korzow Richter *et al.*, 2020). Four piscine collagen peptide sequences derived from cold water fish (sturgeon) have been reported as markers of archaeological glue (Dallongeville *et al.*, 2011; Kumazawa *et al.*, 2018). Finally, authors reported the application of the protein sequence of a characteristic parasitic bacteria to predict the presence of piscine gelatine among bovine and porcine gelatines (Ward, Powles and Page, 2018).

Taking into account the labelling requirements of foods containing fish-derived ingredients, and the requirement to support due diligence with scientific testing methods for food safety and authenticity, we report a method to determine piscine gelatine using identification of piscine collagen marker peptides found in gelatines used in the food industry. To support the role of Official Control Laboratories in food security, we report a targeted LC-TQMS/MS method for the determination of fish-derived gelatine in gelatine granules, capsules, and composite food products.

6.2 Materials and methods

6.2.1 Test materials

Given that piscine gelatine is prepared in a limited number of manufacturing plants globally and from a wide variety of warm water fish species, it was important to source piscine gelatines over a number of years, to yield a set of representative samples.

Eleven dry gelatines of piscine origin, sourced from suppliers across Europe over a period of approximately sixteen years and stored according to the manufacturer's instructions were included, as detailed in Table 15. Authentic reference gelatines were also kindly provided by Gelatine Manufacturers of Europe, the European trade body which represents gelatine manufacturers (Ref. QC1, QC2 and TSO in Table 15).

Table 15. Table detailing the samples used during the study.

Sample ref.	Sample type	Sample Description	No. of replicates
CAN	Fish gelatine capsule	Supplied by Euro Caps Limited UK, reference 401448, Lot 1605052, Year 2016	2
CAP	Fish gelatine capsule	Supplied by Euro Caps Limited UK, reference 401548, Lot 1605107, Year 2008	2
CAT	Fish gelatine capsule	Supplied by Euro Caps Limited UK, reference 402625, Lot 1604104, Year 2016	2
FTS	Granular gelatine	Supplied by Weishardt International, France, Ref. 32G 1002616AR, Year 2007	7
TNO	Granular gelatine	Supplied by Lapi Gelatine S.p.A, Ref. 3858, Year 2007	7
TOO	Granular gelatine	Supplied by Healan Ingredients Limited, UK, Ref. G2141, Year 2007	7
FGS	Granular gelatine	Supplied by Croda Europe Limited, UK, Ref. ex LAPI, Year 2007	7
FSO	Granular gelatine	Supplied by Sigma-Aldrich Limited, UK, Ref. G7041, Lot. SLBW3543, Year 2017	7
FGO	Granular gelatine	Supplied by Healan Ingredients Limited, UK, Ref. 50000186, Year 2017	7

Sample ref.	Sample type	Sample Description	No. of replicates
SGO	Granular gelatine	Supplied by Sigma-Aldrich Limited, UK , Ref. G7041 023K0976, Year 2003	7
TSO	Reference material	Supplied by Gelatine Manufacturers of Europe, Piscine skin gelatine, Ref. DQ/14/1025-006, Year 2014	7
ROM	Granular gelatine	Supplied by Romer Labs UK Limited, Ref. COKAL0206A 2019	7
BLO	Granular gelatine	Sigma fish gelatine, Ref. G7041 Lot 023K0976, 2003	7
MOU	Composite ready meal	Fish mousse 'ready meal', purchased from UK supermarket, 2019.	2
TER	Composite ready meal	Fish terrine 'ready meal', purchased from UK supermarket, 2019.	2
QC1	Reference material	Supplied by Gelatine Manufacturers of Europe, Bovine hide gelatine lime process, Ref. DQ/14/1025-004, Year 2014, used for Quality Control	2
QC2	Reference material	Supplied by Gelatine Manufacturers of Europe, Porcine skin gelatine acid process, Ref. DQ/14/1025-001, Year 2014, used for Quality Control.	2

6.2.2 Methods

6.2.2.1 Gelatine preparation from test materials

For each granular gelatine or gelatine capsule sample, 5mg/mL preparations of gelatine, dissolved in 50 mM ammonium bicarbonate, were prepared. 20 µL (100 µg) was digested with 2 µg of Trypsin Gold (Promega Corp.) for 16 hours at 37°C. Tryptic collagen peptides were cleaned up using C18 Solid Phase Extraction (Discovery® DSC-18 SPE tube, 100 mg bed weight, volume 1 mL, Sigma-Aldrich). Contaminants were removed with equilibration in 0.1% (v/v) formic acid and peptides were eluted in 50% (v/v) acetonitrile, 0.1% formic acid, prior to drying by vacuum centrifugation and analysis by mass spectrometry.

6.2.2.2 Gelatine isolation and preparation from composite food products

Ready meal food products, purchased from UK retailers, were analysed in duplicate (Ref. MOU and TER). A third replicate was also prepared as a matrix-match positive control by spiking the food, prior to extraction, with a bovine and a porcine reference gelatine (Ref. QC1 and QC2) at the 0.1% (w/w) level. Gelatine was extracted from the samples and analysed according to the method reported by (Grundy *et al.*, 2016). In brief, proteins were precipitated for 10 minutes by incubation at 80°C in 50 mM acetic acid. Following centrifugation to remove and discard insoluble proteins, proteins of a molecular mass below 30 kilodaltons (kDa) were discarded by molecular weight sieving (Pierce™ Protein Concentrator PES, 30 kDa, Thermo Fisher 88531 30 kDa). The gelatine yield was determined according to the methods of the Association of Official Analytical Chemists (Kolar, 1990) and 100 µg of gelatine was digested with 2 µg of Trypsin Gold (Promega Corp.) at 37°C for 16 hours. Tryptic peptides were then isolated from the sample by solid phase extraction and dried as above prior to analysis.

6.2.2.3 Peptide biomarker discovery by High-Resolution Accurate-Mass Mass Spectrometry

Samples were initially analysed by full scan electrospray ionisation-liquid chromatography High-Resolution Accurate-Mass Mass Spectrometry (HRAM LC-MS/MS) to identify suitable candidate peptides for use as species markers. Following determination of suitable target peptide markers, the samples were analysed by a targeted LC-TQMS/MS method, described below.

The HRAM LC-MS/MS method used nano-flow liquid chromatography (Dionex Ultimate 3000, Thermo Scientific, UK) with C18 5 µm trap (300 µm x 5 mm). 1 µg of extract was injected onto an EASY-Spray PepMap RSLC C18 100Å 2 µm column (75 µm x 500 mm, Thermo Scientific, UK) using gradient elution with 0 - 50% acetonitrile, 0.1% formic acid, at 300 nL/min, 40ºC during a 35 minute period prior to column washing and re-equilibration. The nanoLC system was interfaced with a LTQ Velos Pro Orbitrap Mass

Spectrometer (Thermo Scientific, UK) with an EASY-Spray source (Thermo Scientific, UK), operated in a collision-induced dissociation mode under the synchronization of Xcalibur 2.1.0 software as well as LTQ Tune Plus software (Thermo-Fisher Scientific), full scan, resolution 60,000 FWHM (mass range, m/z 350–2000), normalized CE of 35% and activation time of 10 milliseconds for mass spectral acquisition.

A database was prepared in collaboration with Kristine Korzow Richter (Department of Archaeology, Harvard University). All available piscine-specific collagen type I sequences were mined from NCBI (NCBI Resource Coordinators, 2016) and the PhyloFish transcriptome database (Pasquier *et al.*, 2016), genetic sequences were aligned to the annotated collagen genes or transcripts from *Danio rerio* (zebrafish) and then translated. Protein sequences were then assigned to the α1, α2, or α3 chain and then aligned. Sequences which were less than 50% complete or had a lower than 75% identity to the zebrafish collagen protein sequences (Accession no. AAH63249.1, AAH66384.1, AH71278.1) were removed. The resulting dataset contained protein sequences from 79 species for α1 chain, 94 species for the α2 chain, and 61 species for the α3 chain. Sequences for all three chains were included for several warm water species (optimal temperatures in the range of 24 - 32°C) including *Oreochromis niloticus* (Nile tilapia), *Cyprinus carpio* (common carp), *Ictalurus punctatus* (channel catfish), and α1 and α2 chains from *Ctenopharyngodn idella* (grass carp). The data was interrogated against this database using the Mascot search engine (Perkins *et al.*, 1999) with a fixed modification of carbamidomethylation of cysteine, and variable modifications set as hydroxylation of proline and lysine, deamidation of asparagine and glutamine, glucosylgalactosylation of lysine, oxidation of methionine, and acetylation of the protein N-terminus. A peptide mass tolerance of ±10 ppm, fragment mass tolerance of ±0.07 Da, and maximum of one missed cleavage were set, and the data was also interrogated against a decoy database.

6.2.2.4 LC-TQMS/MS Method Development

Thirty piscine collagen marker peptides (F1-F30) identified in the samples were considered for suitability for a subsequent targeted method. Using the BLAST alignment search tool (Altschul *et al.*, 1990), these peptides were compared to sequences of mammalian and avian species to verify that there was no sequence overlap to establish the suitability of these peptides as markers of piscine collagen. The list of peptides along with a targeted method was created for the detection of the thirty peptides using the Skyline MacCoss Lab software, University of Washington (MacLean *et al.*, 2010) for detection with a Liquid Chromatography-Triple Quadrupole Mass Spectrometry (LC-TQMS/MS) instrument and the final method was optimised for the best-resolved sixteen peptides (Table 16).

Ten micrograms (µg) of sample were analysed by LC-TQMS/MS. Positive quality controls (QCs) were included in the form of solvent standards comprised of bovine and porcine collagen peptides, synthesised by Eurogentec Limited, and also by over-spiking sample matrices with gelatines QC1 and QC2. Chromatography was optimised for an Agilent 6490 TQMS/MS with an Agilent 1200 HPLC and InfinityLab Poroshell120 EC C18, 2.1x100 mm, 2.7 µM reverse phase column in a gradient of acetonitrile, 0.1% formic acid (v/v). Regarding the mass spectrometer source parameters, the gas temperature was 290ºC with a gas flow of 11 L/min. with nebulizer pressure of 30 psi, sheath gas temperature of 300ºC with a sheath gas flow of 11 L/min. While all peptide transitions were determined in positive mode, both positive and negative modes were applied to mitigate any charging affects in the mass spectrometer at a capillary voltage of 3500 V. The nozzle voltage was 500 V for positive and 0 V for negative mode. Regarding the ion funnel parameters, the high-pressure RF was 110 V for both positive and negative modes. The low-pressure radio frequency voltage was 60 V for both positive and negative modes.

Species identification was accepted when a minimum of two species marker peptides were detected. A peptide was designated as 'detected' when each of the four following criteria were met:

i. detected peaks were resolved at the same retention time as the peptide in the matrix spike or solvent standard (± 0.1 minutes);
ii. peaks were detected in all transitions for the peptide, with minimum signal-to-noise ratio of three;
iii. peak area showed a clear increase in comparison to preceding solvent blank (negative QC) injection to discount carry-over from the previous injection;
iv. peak was resolved into a symmetrical shape.

Table 16. Dynamic multiple reaction monitoring parameters of the targeted LC-MS/MS method for each piscine peptide (annotated with F in the Peptide Identifier), porcine peptides (Po) and bovine peptides (Bo).

Peptide identifier	Precursor Ion Mass (m/z)	Product Ion Mass (m/z)	Ret. Time (min)	Delta Ret. Time	Collision Energy (eV)	Cell Accelerator Voltage (V)	Polarity
F1	771.9	932.5	9	2	24.9	4	Positive
F1	771.9	861.4	9	2	24.9	4	Positive
F1	514.9	733.4	9	2	13.7	4	Positive
F1	514.9	611.3	9	2	13.7	4	Positive
F5	784.9	1128.6	9.3	2	25.3	4	Positive
F5	784.9	958.5	9.3	2	25.3	4	Positive
F5	784.9	887.4	9.3	2	25.3	4	Positive
F5	523.6	759.4	9.3	2	14	4	Positive
F6	735.4	1090.5	7.8	2	23.8	4	Positive
F6	490.6	926.4	7.8	2	12.9	4	Positive
F6	490.6	779.4	7.8	2	12.9	4	Positive
F6	490.6	544.3	7.8	2	12.9	4	Positive
F9	771.9	932.5	9	2	24.9	4	Positive
F9	771.9	861.4	9	2	24.9	4	Positive
F9	771.9	810.4	9	2	24.9	4	Positive
F9	514.9	733.4	9	2	13.7	4	Positive
F10	586.8	885.5	8.4	2	19.2	4	Positive
F10	586.8	828.5	8.4	2	19.2	4	Positive

Peptide identifier	Precursor Ion Mass (m/z)	Product Ion Mass (m/z)	Ret. Time (min)	Delta Ret. Time	Collision Energy (eV)	Cell Accelerator Voltage (V)	Polarity
F10	586.8	757.4	8.4	2	19.2	4	Positive
F10	391.5	516.3	8.4	2	9.3	4	Positive
F16	760.9	949.5	7.3	2	24.6	4	Positive
F16	760.9	781.4	7.3	2	24.6	4	Positive
F16	507.6	797.3	7.3	2	13.5	4	Positive
F16	507.6	556.3	7.3	2	13.5	4	Positive
F17	774.4	1019.5	9.8	2	25	4	Positive
F17	774.4	849.4	9.8	2	25	4	Positive
F17	516.6	857.4	9.8	2	13.8	4	Positive
F17	516.6	544.3	9.8	2	13.8	4	Positive
F18	715.3	1090.5	7.5	2	23.2	4	Positive
F18	715.3	849.4	7.5	2	23.2	4	Positive
F18	715.3	748.4	7.5	2	23.2	4	Positive
F18	477.2	544.3	7.5	2	12.4	4	Positive
F2	738.9	978.5	6.6	2	23.9	4	Positive
F2	738.9	921.5	6.6	2	23.9	4	Positive
F2	492.9	554.3	6.6	2	12.9	4	Positive
F2	492.9	497.3	6.6	2	12.9	4	Positive
F20	735.4	1187.6	7.9	2	23.8	4	Positive
F20	735.4	1090.5	7.9	2	23.8	4	Positive

Peptide identifier	Precursor Ion Mass (m/z)	Product Ion Mass (m/z)	Ret. Time (min)	Delta Ret. Time	Collision Energy (eV)	Cell Accelerator Voltage (V)	Polarity
F20	490.6	779.4	7.9	2	12.9	4	Positive
F20	490.6	544.3	7.9	2	12.9	4	Positive
F21	689.3	960.5	7.9	2	22.4	4	Positive
F21	689.3	813.4	7.9	2	22.4	4	Positive
F21	689.3	756.4	7.9	2	22.4	4	Positive
F21	459.9	515.3	7.9	2	11.8	4	Positive
F26	625.8	1025.5	5.6	2	20.4	4	Positive
F26	625.8	897.5	5.6	2	20.4	4	Positive
F26	417.6	542.3	5.6	2	10.2	4	Positive
F27	642.3	856.5	7	2	20.9	4	Positive
F27	642.3	785.4	7	2	20.9	4	Positive
F27	428.5	884.4	7	2	10.6	4	Positive
F27	428.5	771.3	7	2	10.6	4	Positive
F28	598.8	943.5	7.2	2	19.6	4	Positive
F28	598.8	758.4	7.2	2	19.6	4	Positive
F28	399.5	531.3	7.2	2	9.6	4	Positive
F29	586.3	888.4	7.4	2	19.2	4	Positive
F29	586.3	645.3	7.4	2	19.2	4	Positive
F29	391.2	532.2	7.4	2	9.3	4	Positive
F29	391.2	527.3	7.4	2	9.3	4	Positive

Peptide identifier	Precursor Ion Mass (m/z)	Product Ion Mass (m/z)	Ret. Time (min)	Delta Ret. Time	Collision Energy (eV)	Cell Accelerator Voltage (V)	Polarity
F30	578.3	888.4	5.5	2	18.9	4	Positive
F30	578.3	773.4	5.5	2	18.9	4	Positive
F30	578.3	645.3	5.5	2	18.9	4	Positive
F30	385.9	511.3	5.5	2	9.1	4	Positive
Bo 1	769.9	928.4	6.5	2	25	4	Positive
Bo 1	769.9	1056.4	6.5	2	30	4	Positive
Bo 1	769.9	999.4	6.5	2	25	4	Positive
Bo 1	769.9	706	6.5	2	20	4	Positive
Bo 2	516.8	878.5	5.3	2	20	4	Positive
Bo 2	516.8	765.4	5.3	2	20	4	Positive
Bo 2	516.8	637.3	5.3	2	17	4	Positive
Bo 2	516.8	636.9	5.3	2	20	4	Positive
Bo 2	516.8	523.3	5.3	2	17	4	Positive
Po 1	596.8	908.4	6.4	2	20	4	Positive
Po 1	596.8	851.5	6.4	2	19.4	4	Positive
Po 1	596.8	584.3	6.4	2	19.4	4	Positive
Po 1	596.8	539.4	6.4	2	20	4	Positive
Po 2	727.4	1283.6	10.9	2	23.5	4	Positive
Po 2	727.4	984.5	10.9	2	30	4	Positive
Po 2	727.4	837.3	10.9	2	30	4	Positive

Peptide identifier	Precursor Ion Mass (m/z)	Product Ion Mass (m/z)	Ret. Time (min)	Delta Ret. Time	Collision Energy (eV)	Cell Accelerator Voltage (V)	Polarity
Po 2	727.4	667.3	10.9	2	30	4	Positive
negative transition	596.9	894.5	9.1	14	20	4	Negative

6.2.3 Results

The sequence data of the peptides determined as biomarkers of piscine gelatine, from analysis of piscine gelatine samples, are detailed in

Table 17, along with the associated amino acid modifications and retention time.

The results of the analyses to verify the suitability of the method developed are summarised in Table 18 which shows the number of piscine marker peptides detected in each sample and the total number of these markers detected in each of the two replicates of capsule and composite food samples or three replicates of the dry gelatine samples.

As shown in Table 18, between four and eleven piscine peptides were detected in each sample and the number of peptides detected for each replicate of a sample was highly reproducible, demonstrating the suitability of the method to determine piscine gelatine.

Indeed, the same peptides are detected for each replicate for twelve out of the fifteen samples. This provides positive evidence for the repeatability of the method although repeatability must be formally determined in the future in a full validation study.

As expected, no bovine or porcine marker peptides were detected in any of the piscine gelatine samples. Bovine and porcine gelatine was detected as appropriate for the matrix-matched QC samples at the 0.1% (w/w) level.

While a full method validation was outside of the scope of this funded work, the method was challenged by analysing two additional gelatine granule samples in triplicate (references BLO, sourced in 2003, and ROM sourced in 2019). As shown in Table 18, seven piscine collagen marker peptides were detected in each of the replicates of BLO and eight in each of the ROM replicates, all with perfect reproducibility with respect to the particular marker peptides detected in the three sub-samples, again indicating strong prospects with respect to the reproducibility of this method. Concerning the composite ready meal products, seven piscine marker peptides were detected in each replicate of the mousse (MOU) and terrine (TER) sub-samples (Table 18).

Table 17. Piscine collagen peptides selected for the targeted method (F#), the bovine QC peptides (Bo 1 and Bo 2), and the porcine QC peptides (Po 1 and Po 2). Modifications positions are indicated with an asterisk (*) next to the modified amino acid.

Peptide ID	Peptide sequence	Modifications	RT (min)
F1	GAP*GAAGIAGAP*GFP*GAR	3 Pro->Hyp (P)	9
F2	GESGPAGPAGAAGPAGPR		8.4
F5	GAP*GAAGIAGAP*GFPGP*R	3 Pro->Hyp (P)	7.3
F6	GPAGPP*GATGFPGSAGR	Pro->Hyp (P)	9.8
F9	GSPGAAGIAGAP*GFPGSR	Pro->Hyp (P)	7.5
F10	GVMGAIGAP*GAAGK	Pro->Hyp (P)	6.6
F16	GESGPSGPAGPAGPAGVR		7.9
F17	GETGP*AGLTGFP*GAAGR	2 Pro->Hyp (P)	7.9
F18	GGAGPP*GATGFP*GAAGR	2 Pro->Hyp (P)	7
F20	GPAGPP*GATGFP*GAAGR	2 Pro->Hyp (P)	7.2
F21	GESGSFGPSGPSGVR		7.4
F26	GPAGAQGGLGAP*GPK	Pro->Hyp (P)	5.5
F27	GPSGEAGASGLAGPR		9.3
F28	GVPGGAGGLGEP*GR	Pro->Hyp (P)	9.3
F29	LGLN*GAP*GQDGR	Deamidated (NQ); Pro->Hyp (P)	7.8
F30	LGPN*GAP*GQDGR	Deamidated (NQ); Pro->Hyp (P)	9
Bo 1	GAP*GAIGAP*GPAGADGDR	2 Pro->Hyp (P)	6.5
Bo 2	GPP*GAGGPPGPR	1 Pro->Hyp (P)	5.3
Po 1	GGP*GGPGLP*GPP*GK	3 Pro->Hyp (P)	6.4
Po 2	GIP*GEFGLP*GPAGPR	2 Pro->Hyp (P)	10.9

Table 18. Peptides detected for each sample using the optimised protocol. The number of peptides determined in each replicate is annotated. Where all replicates have the same number of identified peptides the number only appears once.

Sample ref.	Piscine Peptide Identifier																Number of piscine peptides determined in each of the replicate samples
	F1	F2	F5	F6	F9	F10	F16	F17	F18	F20	F21	F26	F27	F28	F29	F30	
FSO				x						x	x	x	x	x	x	x	8
SGO				x						x	x	x	x	x	x	x	8
FGO		x	x	x		x		x	x	x							7
FGS	x			x	x					x							4,7,4
TSO											x		x	x		x	4
FTS	x	x	x	x	x	x	x	x	x	x		x					11
TNO		x	x	x		x		x	x	x						x	8,7,7
TOO	x	x	x	x	x	x	x		x	x		x					10,6,6
CAN	x	x				x	x	x	x	x		x					8
CAP	x	x	x	x	x	x	x	x	x	x		x					11
CAT	x	x				x	x	x	x	x		x					8
BLO		x	x	x		x		x	x	x							7
ROM				x						x	x	x	x	x	x	x	8
MOU		x	x	x		x		x	x	x							7
TER		x	x	x		x		x	x	x							7

6.2.4 Discussion and Conclusions

Differently from research aimed to determine piscine species marker peptides in cold water fish for archaeological purposes (Dallongeville *et al.*, 2011; Richter *et al.*, 2011a; Harvey, Daugnora and Buckley, 2018; Kumazawa *et al.*, 2018; Korzow Richter *et al.*, 2020), this work focused on determining warm water species marker peptides to determine piscine food gelatine with the aim to support the work of control and regulatory bodies in the food industry. Furthermore, in contrast to data reported elsewhere (Ward, Powles and Page, 2018), this method identifies piscine collagen sequence markers rather than a marker sequence of a parasitic bacterium common to fish, providing confidence of the presence of piscine gelatine rather than bacterial contamination.

In order to support enforcement in the food supply chain, it is vital that a method exists which is accessible to Official Control Laboratories where funding is often limited. It is critical that methods can be implemented using the instrumentation available to these enforcement officers and that the analysis has high-throughput capability. Therefore, methods developed on high cost discovery instrumentation such as MALDI-TOF MS (Buckley *et al.*, 2009; Harvey, Daugnora and Buckley, 2018) are not suitable for use in food enforcement laboratories. This method is based on LC-TQMS/MS instrumentation which is already available to enforcement officers due to its use in long-established testing areas such as pesticide and veterinary drug monitoring, and which can easily be applied to peptide identification.

The method was successfully applied to piscine gelatine granules, food supplement capsules and retail composite food products. The data indicates that the method is reproducible between replicates of sub-samples throughout this study. While validation was outside of the scope of the available funding, initial analysis suggests the limit of detection (LOD) is 0.1% (w/w), based on samples in this study which have been over-spiked with bovine and porcine gelatine. In support of this data, outside of this study on piscine gelatine, a comprehensive validation study has been completed using these methods to determine bovine and porcine gelatine in composite food products ('Defra Project FA0177'). The validation included accuracy, repeatability, specificity, robustness,

stability, and limit of detection studies. Composite food samples included chocolate mousse, marshmallows, jelly confectionery, terrine, food supplement capsules, and pork pie gelatine. Using the same extraction methods, and determination of bovine and porcine peptides on the same instrumentation, the limit of detection was determined to be 0.1% (w/w) ('Defra Project FA0177'). This technology has the potential for future application by Official Control Laboratories to verify food labelling claims, and to support due diligence and the paper trail which underpins the species authenticity of gelatine, in line with the requirements of the 2014 Elliott Review into the Integrity and Assurance of Food Supply Networks (Elliott, 2014).

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Chapter 7: Summary and Discussion

This chapter will outline how the aims of the thesis, proposed in Chapter 1, were met (7.1). Next, it will discuss the challenges faced during this research (7.2), future work (7.3), and the thesis will be concluded (7.4).

7.1 Achievement of aims

This thesis has explored the available tools in the field of palaeoproteomics to **assess changes in proteins present in hide materials caused by manufacturing processes and use history** by demonstrating a novel use for the ZooMS methodology which will further our understanding of the history of a sample, and help with sample screening for sequencing and further studies (Chapter 3), by using sequence and post-translational modification information to assess the damage and degradation of collagen in different environments, and by highlighting the importance of further studies on the kinetics of deamidation reactions, particularly for glutamine (Chapter 4). Furthermore, this thesis has applied **palaeoproteomics methods to the modern-day processing of collagen in the food industry** by demonstrating the use of ZooMS as a suitable quality control method for collagen processed in the food industry (Chapter 5), and by supporting food safety by developing and optimising a method for the determination of piscine gelatine in food and food supplements (Chapter 6).

7.2 Challenges

7.2.1 Deamidation: age vs environment

One of the biggest challenges this research faced is the interpretation of deamidation levels of samples that were manufactured and processed in different environments, from different raw materials, and with varying degrees of quality. Results from tools such as deamiDATE 1.0 (Ramsøe *et al.*, 2020) where the underlying data is based on

physiological conditions (i.e. pH 7.4, 37°C) don't take into consideration the influence of pH and temperature on the rate of deamidation, or how a sample that has been limed (i.e. damaged) for a longer period of time during its manufacturing process might have a less stable collagen chain which is more susceptible to degradation reactions than other similar materials. For this reason, it is difficult to compare the extent to which deamidation is due to age or processing in heavily degraded samples, although the comparison of samples with a shared history or source is possible through these methods and provides valuable information about the degradation processes in a family of samples. Nevertheless, studies on the kinetics of glutamine deamidation and other degradation reactions are needed to gain an understanding of the variation in degradation rates and patterns in collagen materials with different qualities and manufacturing processes. The raw material, the initial quality of the material and variables such as use history, handling and storage conditions must be taken into consideration when looking at the source of damage and the rate at which degradation processes occur in any given sample.

7.2.2 COVID-19 pandemic

The main blocker and biggest challenge for this PhD was the COVID-19 pandemic. Data processing and, consequently, analysis, was delayed due to the restrictions imposed between 2020 and 2022. A batch of commercial collagen samples, provided by Devro, could not be analysed due to the travel restrictions and university and laboratories closures associated with the pandemic. The analysis of these samples was intended as a further study of the application of ZooMS as a quality control measure in the food industry (Chapter 5). Unfortunately, this analysis was not possible and is not included in this thesis.

Similarly, a big collaborative research effort, involving hundreds of samples, on the degradation patterns of collagen from hide materials, with colleagues at the University of Copenhagen and the University of Cambridge, is underway, but due to the pandemic restrictions, this work was severely delayed and its completion was not compatible with

the submission deadline of this thesis. Consequently, a smaller study on collagen degradation with a focus on deamidation is presented in this thesis (Chapter 4).

7.3 Future work

Based on the results presented in this thesis, several areas of opportunity have been identified to further this research:

The identification of peptide markers from milk, egg, and wheat proteins from ZooMS spectra, as reported in Chapter 3 is the first step into obtaining information about the processing and use history of parchment samples from a single analysis. One of the advantages of this approach is that, with some automation, it can be retroactively applied to all the parchment samples which have been analysed by ZooMS. At the moment around 7000 samples are available which can be used to advance this research. These approach can be further used for the screening of samples made from leather and can potentially be used as an aid in quality control and assurance in the modern leather and food industries.

Chapter 4 explored the available tools and methods to assess collagen damage and degradation patterns and highlights the importance of studies on the kinetics of glutamine deamidation. To further this work, a collaborative effort is underway to consolidate data from a large number of samples and make a comparative study of the degradation patterns in collagen that expands on the work presented in this thesis. This includes the comparison of results from different database search software, and further analysis of the rates of deamidation for samples from a variety of pH environments. The development of this knowledge will have a great impact in the understanding of the mechanisms of degradation of collagen and its correlation to the quality and longevity of cultural heritage materials.

A full validation of ZooMS as a quality control method in the food industry is required for the effective use of this technology in an industrial setting on the basis of the results presented in Chapter 5. In the food safety field, the consolidation of the targeted

method for determination of piscine gelatine developed and tested in Chapter 6, with existing methods for the identification of bovine and porcine gelatine, would enhance the support to officers and its use for the analysis of collagen mixtures like the ones found in glue used in conservation practices could be tested. This thesis highlights the importance of continued collaboration with industrial partners to keep driving innovation and development both in the study of ancient proteins and in the food industry which contribute to sustainable development and food security.

Lastly, the comparison and, where possible, correlation of the bulk of the results presented in this thesis with physicochemical measurements commonly used in the food and leather industries and by conservation experts, like the melting and shrinkage temperatures of collagen, and analysis by differential scanning calorimetry (DSC) and infrared spectroscopy (IR), is a task that will further our understanding of the degradation processes of this protein and enhance the methods used in the conservation field to preserve our cultural heritage.

7.4 Conclusion

This thesis aimed to explore the available tools in the field of palaeoproteomics to (i) assess changes in proteins present in hide materials caused by manufacturing processes and use history and (ii) assess the relevance and application of palaeoproteomics methods to the modern-day processing of collagen in the food industry.

First, we propose two novel uses of the ZooMS methodology 1) as a fast and low cost tool for the preliminary identification of proteins that aid in sample screening where there is limited time and/or resources. Usually, ZooMS is used as a species identification tool based on the collagen fingerprint and is not used for the analysis of very complex samples. In this work, twenty two peptide markers are proposed for proteins of milk, egg, and wheat origin from ZooMS spectra, showing that it is possible to make a preliminary identification of these proteins alongside species identification based on the collagen fingerprint. The presence of these proteins can provide information about the

manufacturing processes, use history, and/or conservation treatments in a sample, and act as a screening method for the selection of samples for further analysis. And 2) as a suitable method of quality control in the processing of collagen in the food industry. Here, the deamidation level (PQI) of processed collagen samples used in the manufacture of sausage casings from Devro was calculated using a method developed for the deamidation of parchment samples, and then compared to in-house measures of free amide level, a measure used as a quality control method in the industry. The adapted method resulted in a faster analysis with better sample separation and was able to pick up smaller differences between samples than the in-house method, making it a suitable substitute for the in-house quality control method currently in use. Additionally, this shows the possibilities of PQI for the analysis of subtle differences in seemingly undamaged skins.

Furthermore, a targeted method for the determination of piscine gelatine in food products and its importance in food safety and security is presented. The creation of a piscine collagen database was made possible by gathering sequences from studies of archaeological fish remains and applied to the development and optimisation of the method, which proposes sixteen peptide markers for piscine gelatine. The method has been successfully applied to gelatine granules, capsules and composite retail food products.

Last, the work presented on this thesis on the analysis of the degradation patterns based on the deamidation of a variety of samples processed in both alkaline and acidic environments, and the difference in those patterns according to their processing conditions, highlights the need for studies on the kinetics of glutamine deamidation under varied pH conditions to further our understanding of the forces behind protein degradation and damage. Understanding these patterns is an important step to understand the use and conservation history of archaeological and historical objects and can be further applied to the modern leather and food industries. This study explored the available methods for assessing the level of deamidation of a sample and emphasised the importance of further studies of glutamine deamidation kinetics and mechanisms to better estimate damage to the collagen molecule. This is highlighted by

the difference in the deamidation patterns, rates of reaction and reaction pathways of samples that have been subjected to acidic conditions (leather) when compared to those processed in an alkaline environment (parchment), where glutamine deamidation is faster than that of asparagine in samples aged under acidic conditions.

Together, the results of this thesis are evidence of the importance of interdisciplinary research to drive innovation and its significance in the advancement of palaeoproteomics and the preservation of cultural heritage.

List of Abbreviations

ACN	acetonitrile
AGC	automatic gain control
AmBic	ammonium bicarbonate
BCE	before the Common Era
CE	collision energy
CH	Cultural Heritage
CID	collision-induced dissociation
CL	chemiluminescence
CO1A1	collagen type I a1
CO1A2	collagen type I a2
CO3A1	collagen type III a1
CoEMS	Centre of Excellence for Mass Spectrometry
CPH	University of Copenhagen
cRAP	common Repository of Adventitious Proteins
DESI	desorption electrospray ionisation
DNA	deoxyribonucleic acid
DSC	differential scanning calorimetry
EI	electron impact
ELISA	enzyme-linked immunosorbent assay
EPRSC	Engineering and Physical Sciences Research Council
ESI	electrospray ionisation
ETN	European Training Network
EVA	ethyl-vinyl acetate
FA	formic acid
FDR	false discovery rate
FT-ICR	Fourier Transform Ion Cyclotron Resonance
FWHM	full width at half maximum
GPM	Global Proteome Machine
HCD	higher-energy C-trap dissociation
HILIC	hydrophilic interaction liquid chromatography
HRAM	high-resolution accurate-mass
IC	internal calibration

ICLT	Institute for Creative Leather Technologies
IMF	immunofluorescence
IR	infrared spectroscopy
ITN	innovative training network
iTRAQ	isobaric tag for relative and absolute quantitation
LC	liquid chromatography
LOD	limit of detection
m/z	mass to charge ratio
MALDI	matrix-assisted laser desorption/ionisation
mgf	Mascot generic format
MRM	multiple reaction monitoring
MS	mass spectrometry
MS/MS	tandem mass spectrometry
MS1	first mass spectrometer
MS2	second mass spectrometer
NCBI	National Center for Biotechnology Information
NCE	normalised collision energy
OVAL	ovalbumin
OVALY	ovalbumin-related protein Y
P4H	Prolyl 4-Hydroxylase
PCA	principal component analysis
PCR	polymerase chain reaction
PMF	Peptide Mass Fingerprinting
PNGaseF	Peptide-N-Glycosidase F
PQI	parchment glutamine index
pRIA	protein radioimmunoassay
PRIDE	proteomics identification database
PSM	peptide-spectrum matches
PTM	post-translational modification
PVC	polyvinyl chloride
Q2E	glutamine to glutamic acid
QC	quality control
RF	radio frequency
SDG	Sustainable Development Goals

SERS	surface-enhanced Raman scattering
SIMCA	soft independent modelling of class analogy
SIMS	secondary ion mass spectrometry
SPE	solid-phase extraction
TEMPERA	Teaching Emerging Methods in Palaeoproteomics for the European Research Area
TFA	trifluoroacetic acid
TMT	tandem mass tag
TOF	time-of-flight
TQMS	triple quadrupole mass spectrometry
TRFE	ovotransferrin
UN	United Nations
UPLC	ultra performance liquid chromatography
ZooMS	zooarchaeology by mass spectrometry

Appendix A

Table A1. Protein identifications per sample. Showing the protein, species, accession number, sequence coverage, number of peptide matches, and number of unique peptide matches. The ID corresponds to the sample number.

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
1	COL1A3	Amazon molly (Poecilia formosa)	XP.007571557.1	6.2	33	3
1	COL1A3	Arrowtail (Melanonus zugmayeri)	Melanonus_zugmayeri__Bfish16_col1a3_translation	6.5	74	2
1	COL1A2	Asian arowana (Scleropages formosus)	XP.018587334.1	5.6	65	3
1	COL1A1	Asian arowana (Scleropages formosus)	XP.018620194.1	10.2	112	10
1	COL1A2	Black ghost knifefish (Apteronotus albifrons)	Apteronotus_albifrons__A2AAid:41621_col1a2	5.1	33	3
1	COL1A1	Bovine (Bos taurus)	P02453	48.7	1318	3
1	COL1A2	Bovine (Bos taurus)	P02465	47.3	733	41
1	COL3A1	Bovine (Bos taurus)	P04258	38.1	458	61
1	COL1A2	Bowfin (Amia calva)	Amia_calva__AACid:31457_col1a2	3.7	37	4
1	COL1A2	Burbot (Lota lota)	Lota_lota__Bfish11_col1a2_translation	6.2	32	1
1	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	4.4	106	4
1	Collagen I	Chub (Squalius cephalus)	EANTOCCSq_Chub	6.3	169	46

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
1	COL1A3	Eurasian carp (Cyprinus carpio)	XP.018968199.1	2.6	43	1
1	COL1A1	Forkbeard (Phycis phycis)	Phycis_phycis__Bfish09_col1a1	4.3	95	26
1	Collagen I	Gar (Lepisosteidae)	EANSL_Col1_Lepisosteidae	20	329	117
1	COL1A1	Goat (Capra hircus)	A0A452FHU9	50.3	1429	114
1	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	5.2	168	55
1	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	5.5	168	55
1	COL1A2	Japanese sturgeon (Acipenser schrenckii)	A0A0S3P5T6	2.3	26	2
1	COL1A1	Marbled moray cod (Muraenolepis marmoratus)	Muraenolepis_marmoratus__Bfish20_col1a1	4.1	99	4
1	Collagen I	Nile tilapia (Oreochromis niloticus)	EANTENAAPPLC_Col1_Oreochromis_Tilapia	7.8	225	54
1	Collagen I	Pacific salmon and trout (Oncorhynchus)	EANTEPSSS_Col1_Oncorhynchus	4.1	146	21
1	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	4.6	151	26
1	COL1A1	Red piranha (Pygocentrus nattereri)	XP.017540674.1	7.5	97	2
1	COL1A3	Red piranha (Pygocentrus nattereri)	XP.017580869.1	3.4	63	16
1	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	7.7	344	173

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
1	COL1A3	Sailfin molly (Poecilia latipinna)	XP.014886816.1	6.2	33	3
1	COL2A1b	Sea lamprey	Q2I8X9	3.1	47	47
1	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	4.6	70	2
1	COL1A2	Sheep (Ovis aries)	W5NTT7	56.3	981	262
1	COL3A1	Sheep (Ovis aries)	W5Q4S0	34.9	570	173
1	COL1A3	Shortfin molly (Poecilia mexicana)	XP.014866612.1	6.2	29	4
1	COL1A1	Small-spotted catshark (Scyliorhinus canicula)	D0PQF7	4.4	68	44
1	COL1A3	Southern platyfish (Xiphophorus maculatus)	XP.005794759.1	4.4	31	1
1	COL1A1	Spotted gar (Lepisosteus oculatus)	XP.006638297.1	15.4	329	117
1	Collagen I	Stickleback (Gasterosteus)	EANTENAAPGGG__Col1_Gasterosteus_stickleback	4.4	130	5
1	Collagen I	Tench (Tinca tinca)	EANTOCC_Tench	6.1	305	105
1	COL1A2	Tongue sole (Cynoglossus semilaevis)	A0A3P8VXI7	4.5	37	4
1	Collagen I	Zebra mbuna (Maylandia zebra)	EANTENAAPPLC_Col1__Maylandia_zebra	2.9	60	4
1	COL1A3	Zebrafish (Danio rerio)	Q6NZ15	4.1	6	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
1	COL1A3	Zebrafish (Danio rerio)	DANIO-annotatedgenome-col1a3-protein	4.1	6	1
1	Collagen I	Zebrafish (Danio rerio)	EANTOCC_Col1__Danio_rerio	5.8	165	9
2	COL1A1	Amazon molly (Poecilia formosa)	XP.007565541.1	9.3	61	22
2	COL1A1	Asian arowana (Scleropages formosus)	XP.018620194.1	8.5	43	6
2	COL1A1	Atlantic herring (Clupea harengus)	XP.012697307.1	4	26	2
2	COL1A2	Barramundi (Lates calcarifer)	XP.018522130.1	5.7	30	24
2	COL1A1	Beira killifish (Nothobranchius kuhntae)	A0A1A8K041	6.6	34	1
2	COL1A2	Black ghost knifefish (Apteronotus albifrons)	Apteronotus_albifrons__A2AAid:41621_col1a2	4.4	26	2
2	COL2A1	Bovine (Bos taurus)	P02459	3.6	45	1
2	COL1A2	Bovine (Bos taurus)	P02465	30	190	7
2	COL3A1	Bovine (Bos taurus)	P04258	21.5	71	5
2	Collagen I	Bream (Abramis)	EANTOCC_Col1_Abramis_Bream	5.1	152	46
2	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	2.6	64	2
2	Ovalbumin	Chicken (Gallus gallus)	P01012	3.4	2	2
2	Ovalbumin	Chicken (Gallus gallus)	P01012	3.4	2	2
2	Ovalbumin-related protein Y	Chicken (Gallus gallus)	P01014	2.3	1	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
2	Ovotransferrin	Chicken (Gallus gallus)	P02789	1.4	1	1
2	Collagen I	Chub (Squalius cephalus)	EANTOCCSq_Chub	4.6	75	6
2	Collagen I	Flounder (Paralichthys)	EANTENAAPPPPP_Col1_Paralichthys_Flounder	2	50	3
2	Collagen I	Gar (Lepisosteidae)	EANSL_Col1_Lepisosteidae	17.5	116	35
2	COL1A1	Goat (Capra hircus)	A0A452FHU9	46.5	404	326
2	COL1A1	Golden-line barbel (Sinocyclocheilus grahami)	XP.016113605.1	1.5	19	6
2	COL1A1	Guppy (Poecilia reticulata)	A0A3P9NHJ7	9.3	61	22
2	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	4.2	60	15
2	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	4.2	60	15
2	Collagen I	Pacific salmon and trout (Oncorhynchus)	EANTEPSSS_Col1_Oncorhynchus	3.8	61	5
2	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	3.1	67	7
2	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	6.9	135	60
2	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	3.1	28	4
2	COL1A2	Sheep (Ovis aries)	W5NTT9	34.3	243	62
2	COL3A1	Sheep (Ovis aries)	W5Q4S1	19	98	32

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
2	COL1A1	Shortfin molly (Poecilia mexicana)	XP.014880315.1	9.3	61	22
2	COL1A3	Sinocyclocheilus anshuiensis	XP.016343587.1	1.5	19	6
2	COL1A3	Sinocyclocheilus rhinocerous	XP.016383096.1	1.5	19	6
2	COL1A3	Southern platyfish (Xiphophorus maculatus)	XP.005794759.1	3	15	1
2	COL1A1	Spotted gar (Lepisosteus oculatus)	XP.006638297.1	13.5	116	35
2	Collagen I	Zebra mbuna (Maylandia zebra)	EANTENAAPPLC_Col1__Maylandia_zebra	1.7	18	4
4	COL1A2	African butterflyfish (Pantodon buchholzi)	Pantodon_buchlozi__C2PBid:18493_col1a2	1.5	25	17
4	COL1A1	Amazon molly (Poecilia formosa)	XP.007565541.1	9	156	28
4	COL1A3	Amazon molly (Poecilia formosa)	XP.007571557.1	5.3	36	2
4	COL1A2	Asian swamp eel (Monopterus albus)	XM_020614246.1	5.3	27	2
4	COL1A2	Atlantic herring (Clupea harengus)	A0A6P3W0U2	3.7	18	1
4	COL1A1	Atlantic herring (Clupea harengus)	XP.012697307.1	3.9	73	1
4	Histone H3.3	Barley (Hordeum vulgare)	P06353	8.8	1	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
4	COL1A3	Bicolour Damselfish (Stegastes partitus)	A0A3B5AFM4	5.1	79	1
4	COL1A2	Black ghost knifefish (Apteronotus albifrons)	Apteronotus_albifrons__A2AAid:41621_col1a2	3.8	25	1
4	COL1A1	Black rockcod (Notothenia coriiceps)	A0A6I9MX97	3.2	188	119
4	COL1A1	Bovine (Bos taurus)	P02453	54.6	1666	10
4	COL2A1	Bovine (Bos taurus)	P02459	6.4	103	7
4	COL1A2	Bovine (Bos taurus)	P02465	48.7	850	52
4	COL3A1	Bovine (Bos taurus)	P04258	45.9	669	43
4	COL1A2	Bowfin (Amia calva)	Amia_calva__AACid:31457_col1a2	3.3	29	11
4	Collagen I	Bream (Abramis)	EANTOCC_Col1_Abramis_Bream	9.3	386	71
4	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	3.2	99	9
4	Lysozyme C	Chicken (Gallus gallus)	P00698	25.2	32	32
4	Protein TENP	Chicken (Gallus gallus)	O42273	14.3	20	20
4	Ovalbumin	Chicken (Gallus gallus)	P01012	45.9	228	228
4	Lysozyme C	Chicken (Gallus gallus)	P00698	25.2	32	32
4	Ovomucoid	Chicken (Gallus gallus)	P01005	4.8	7	7
4	Ovalbumin	Chicken (Gallus gallus)	P01012	45.9	228	228
4	Ovalbumin-related protein X	Chicken (Gallus gallus)	P01013	15.1	20	20
4	Ovalbumin-related protein Y	Chicken (Gallus gallus)	P01014	18.8	51	51

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
4	Ovotransferrin	Chicken (Gallus gallus)	P02789	27.9	163	163
4	Histone H2B	Chicken (Gallus gallus)	P0C1H3	7.1	1	1
4	Ovoinhibitor	Chicken (Gallus gallus)	P10184	4.4	3	3
4	Ovostatin	Chicken (Gallus gallus)	P20740	7.5	17	17
4	Extracellular fatty acid-binding protein	Chicken (Gallus gallus)	P21760	6.2	1	1
4	Mucin-5B	Chicken (Gallus gallus)	Q98UI9	6.7	20	20
4	Collagen I	Chub (Squalius cephalus)	EANTOCCSq_Chub	8.7	165	34
4	Collagen I	Cod (Gadus)	EANTENAPGGG_Col1_Cod-genome	2.7	70	1
4	Collagen I	Cod (Gadus)	EANTENAPGGG_Col1_Gadoid	2.4	70	1
4	COL1A3	Coho salmon (Oncorhynchus kisutch)	XP.020316038.1	2.2	30	1
4	Collagen I	Flounder (Paralichthys)	EANTENAAPPPPP_Col1_Paralichthys_Flounder	3.9	105	6
4	COL1A1	Forkbeard (Phycis phycis)	Phycis_phycis__Bfish09_col1a1	3.7	87	26
4	COL1A1	Goat (Capra hircus)	A0A452FHU9	56	1786	32
4	COL1A2	Goat (Capra hircus)	A0A452G3V6	43.4	641	1
4	COL1A2	Great Blue-spotted Mudskipper (Boleophthalmus pectinirostris)	XM_020940167.1	6	47	2
4	COL1A1	Guinean codling (Laemonema laureysi)	Laemonema_laureysi__Bfish23_col1a1	4.4	49	5

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
4	COL1A1	Guppy (Poecilia reticulata)	A0A3P9NHJ7	9	156	28
4	COL1A1	Japanese eel (Anguilla japonica)	A0A090B2K5	9	158	43
4	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	4.8	217	85
4	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	5.1	217	85
4	COL1A2	Japanese sturgeon (Acipenser schrenckii)	A0A0S3P5T6	1.5	9	1
4	COL1A1	Killifish (Austrofundulus limnaeus)	XP.013888853.1	6.9	110	1
4	Collagen I	Nile tilapia (Oreochromis niloticus)	EANTENAAPPLC_Col1_Oreochromis_Tilapia	6.3	256	74
4	Collagen I	Pacific salmon and trout (Oncorhynchus)	EANTEPSSS_Col1_Oncorhynchus	4.2	138	19
4	COL1A2	Pollock (Pollachius virens)	Pollachius_virens__Bfish04_col1a2_translation	2.3	11	11
4	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	5.4	149	16
4	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	9.5	432	201
4	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	4.9	80	4
4	COL1A2	Sheep (Ovis aries)	W5NTT16	58.4	1101	141
4	COL1A1	Sheep (Ovis aries)	W5P481	53.1	1738	32

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
4	COL3A1	Sheep (Ovis aries)	W5Q4S11	39.2	822	196
4	COL1A3	Sheepshead Minnow (Cyprinodon variegatus)	XP.015257153.1	1.8	3	1
4	COL1A1	Shortfin molly (Poecilia mexicana)	XP.014880315.1	9	156	28
4	COL1A3	Shortfin molly (Poecilia mexicana)	XP.014866612.1	4.4	32	2
4	COL1A1	Small-spotted catshark (Scyliorhinus canicula)	D0PQF7	5.8	74	42
4	COL1A1	Southern platyfish (Xiphophorus maculatus)	XP.005817058.1	7.1	90	3
4	Collagen I	Stickleback (Gasterosteus)	EANTENAAPGGG__Col1_Gasterosteus_stickleback	5.1	124	5
4	Histone H3.2	Wheat (Triticum aestivum)	P68428	5.1	1	1
4	Collagen I	Zebra mbuna (Maylandia zebra)	EANTENAAPPLC_Col1__Maylandia_zebra	1.9	78	15
5	COL1A3	Amazon molly (Poecilia formosa)	XP.007571557.1	5.9	55	3
5	COL1A3	Arrowtail (Melanonus zugmayeri)	Melanonus_zugmayeri__Bfish16_col1a3_translation	6.5	88	1
5	COL1A1	Asian arowana (Scleropages formosus)	XP.018620194.1	9.6	127	5
5	COL1A2	Atlantic herring (Clupea harengus)	A0A6P3W0U2	3.7	25	12

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
5	COL1A1	Atlantic herring (Clupea harengus)	XP.012697307.1	3.9	82	1
5	Histone H3.3	Barley (Hordeum vulgare)	P06353	16.2	4	4
5	Elongation factor 1-alpha	Barley (Hordeum vulgare)	P34824	2.5	1	1
5	Elongation factor 1-alpha	Barley (Hordeum vulgare)	Q40034	2.5	1	1
5	COL1A1	Barramundi (Lates calcarifer)	XP.018553992.1	11	121	1
5	COL1A1	Beira killifish (Nothobranchius kuhntae)	A0A1A8K041	9	110	1
5	COL1A3	Bicolour Damselfish (Stegastes partitus)	A0A3B5AFM4	6.2	88	1
5	COL1A2	Black ghost knifefish (Apteronotus albifrons)	Apteronotus_albifrons__A2AAid:41621_col1a2	5.8	40	4
5	COL1A3	Black rockcod (Notothenia coriiceps)	A0A6I9N4J7	4.9	113	25
5	COL1A1	Bovine (Bos taurus)	P02453	53.6	1520	14
5	COL2A1	Bovine (Bos taurus)	P02459	7.2	96	7
5	COL3A1	Bovine (Bos taurus)	P04258	42.2	590	73
5	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	3.6	130	11
5	Ovalbumin	Chicken (Gallus gallus)	P01012	4.4	1	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
5	Ovalbumin	Chicken (Gallus gallus)	P01012	4.4	1	1
5	Collagen I	Chub (Squalius cephalus)	EANTOCCSq_Chub	7.5	195	40
5	Collagen I	Cod (Gadus)	EANTENAPGGG_Col1_Cod-genome	3	71	3
5	COL1A1	Forkbeard (Phycis phycis)	Phycis_phycis__Bfish09_col1a1	6.3	102	27
5	Collagen I	Gar (Lepisosteidae)	EANSL_Col1_Lepisosteidae	16.7	335	118
5	COL1A1	Goat (Capra hircus)	A0A452FHU9	55.6	1664	26
5	COL1A2	Goat (Capra hircus)	A0A452G3V6	40	670	4
5	COL1A3	Japanese eel (Anguilla japonica)	A0A090AZH6	7.1	63	10
5	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	5.4	213	66
5	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	5.7	213	66
5	COL1A2	Korthausae Killifish (Notobranchius korthausae)	A0A1A8FIG3	4.1	30	1
5	COL1A3	Mexican tetra (Astyanax mexicanus)	XP.007233638.1	1.3	2	1
5	COL1A1	Mummichog (Fundulus heteroclitus)	XP.012716616.1	5.3	77	1
5	Collagen I	Nile tilapia (Oreochromis niloticus)	EANTENAAPPLC_Col1_Oreochromis_Tilapia	8	270	72
5	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	5.7	196	26

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
5	COL1A2	Red piranha (Pygocentrus nattereri)	XP.017550401.1	3.8	38	3
5	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	11.5	426	203
5	COL1A3	Sailfin molly (Poecilia latipinna)	XP.014886816.1	5.9	55	3
5	COL2A1b	Sea lamprey (Petromyzon marinus)	Q2I8X9	3.1	43	43
5	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	7.3	88	2
5	COL1A2	Sheep (Ovis aries)	W5NTT15	56.2	1098	387
5	COL1A1	Sheep (Ovis aries)	W5P481	52.6	1624	30
5	COL3A1	Sheep (Ovis aries)	W5Q4S9	38.7	751	234
5	COL1A1	Small-spotted catshark (Scyliorhinus canicula)	D0PQF7	7.2	77	42
5	COL1A3	Southern platyfish (Xiphophorus maculatus)	XP.005794759.1	4.1	55	3
5	COL1A1	Spotted gar (Lepisosteus oculatus)	XP.006638297.1	12.9	335	118
5	Collagen I	Tench (Tinca tinca)	EANTOCC_Tench	8.5	379	154
5	COL1A2	Tiger tail seahorse (Hippocampus comes)	XM_019889715.1	6.2	37	7
5	COL1A2	Tongue sole (Cynoglossus semilaevis)	A0A3P8VXI7	3.9	51	3

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
5	COL1A1	Western softhead grenadier (Malacocephalus occidentalis)	Malacocephalus_occidentalis__Bfish18_col1a1	5	54	1
5	Histone H2A.1	Wheat (Triticum aestivum)	P02275	6.2	2	2
5	Histone H2A.2.1	Wheat (Triticum aestivum)	P02276	6	2	2
5	Histone H2A.2.2	Wheat (Triticum aestivum)	P02277	6	2	2
5	Cold shock protein CS66	Wheat (Triticum aestivum)	P46526	1.9	1	1
5	Histone H4 variant TH011	Wheat (Triticum aestivum)	P62785	11.7	1	1
5	Histone H4 variant TH091	Wheat (Triticum aestivum)	P62786	11.7	1	1
5	Histone H3.2	Wheat (Triticum aestivum)	P68428	9.6	4	4
5	Elongation factor 1-alpha	Wheat (Triticum aestivum)	Q03033	2.5	1	1
5	Serpin-Z1A	Wheat (Triticum aestivum)	Q41593	7.8	5	5
5	Histone H2A.4	Wheat (Triticum aestivum)	Q43208	6.7	2	2
5	Protein H2A.5	Wheat (Triticum aestivum)	Q43213	6.2	2	2

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
5	Protein H2A.6	Wheat (Triticum aestivum)	Q43214	6.1	2	2
5	Protein H2A.7	Wheat (Triticum aestivum)	Q43312	6.7	2	2
5	Collagen I	Zebra mbuna (Maylandia zebra)	EANTENAAPPLC_Col1__Maylandia_zebra	2.6	72	8
5	COL1A3	Zebrafish (Danio rerio)	Q6NZ15	2.6	8	1
5	COL1A3	Zebrafish (Danio rerio)	DANIO-annotatedgenome-col1a3-protein	2.6	8	1
5	Collagen I	Zebrafish (Danio rerio)	EANTOCC_Col1__Danio_rerio	4.2	180	30
6	COL1A1	Amazon molly (Poecilia formosa)	XP.007565541.1	11.2	105	23
6	COL1A2	Asian arowana (Scleropages formosus)	XP.018587334.1	3.9	69	2
6	COL1A1	Asian arowana (Scleropages formosus)	XP.018620194.1	7.1	97	20
6	COL1A2	Ballan wrasse (Labrus bergylta)	XM_020631662.1	4.1	23	4
6	Histone H3.3	Barley (Hordeum vulgare)	P06353	16.2	2	2
6	COL1A2	Barramundi (Lates calcarifer)	XP.018522130.1	3.5	33	14
6	COL1A2	Bicolour Damselfish (Stegastes partitus)	A0A3B4ZDV7	2.8	30	4
6	COL1A3	Black rockcod (Notothenia coriiceps)	A0A6I9N4J7	4.9	70	14
6	COL1A1	Bovine (Bos taurus)	P02453	42	939	30

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
6	COL1A2	Bovine (Bos taurus)	P02465	36.1	539	28
6	COL3A1	Bovine (Bos taurus)	P04258	31.8	365	30
6	COL1A2	Bowfin (Amia calva)	Amia_calva__AACid:31457_col1a2	2.6	29	1
6	Collagen I	Bream (Abramis)	EANTOCC_Col1_Abramis_Bream	7.7	249	7
6	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	3.5	107	2
6	Collagen I	Chub (Squalius cephalus)	EANTOCCSq_Chub	5.8	149	24
6	Collagen I	Flounder (Paralichthys)	EANTENAAPPPPP_Col1_Paralichthys_Flounder	3.5	88	2
6	COL1A1	Forkbeard (Phycis phycis)	Phycis_phycis__Bfish09_col1a1	4.4	63	15
6	COL1A1	Goat (Capra hircus)	A0A452FHU9	44	1039	130
6	COL1A1	Guppy (Poecilia reticulata)	A0A3P9NHJ7	11.2	105	23
6	COL1A3	Haplochromis burtoni	XP.005913627.1	4.9	85	1
6	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	5.6	166	65
6	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	5.8	166	65
6	COL1A2	Mangrove killifish (Kryptolebias marmoratus)	XP.017279795.1	1.5	4	1
6	Collagen I	Pacific salmon and trout (Oncorhynchus)	EANTEPSSS_Col1_Oncorhynchus	3.7	118	17
6	COL1A3	Pundamilia nyererei	XP.005725945.1	4.9	85	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
6	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	7.7	293	133
6	COL1A1	Sailfin molly (Poecilia latipinna)	XP.014880315.1	10.9	83	1
6	COL2A1a	Sea lamprey (Petromyzon marinus)	Q2I8Y0	3	9	9
6	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	5.4	65	1
6	COL1A2	Sheep (Ovis aries)	W5NTT13	40.8	612	125
6	COL3A1	Sheep (Ovis aries)	W5Q4S8	29	429	94
6	COL1A1	Sheepshead Minnow (Cyprinodon variegatus)	A0A3Q2CSU4	6.2	59	2
6	COL1A1	Shortfin molly (Poecilia mexicana)	XP.014880315.1	11.2	105	23
6	COL1A3	Southern platyfish (Xiphophorus maculatus)	XP.005794759.1	5.7	28	5
6	Collagen I	Tench (Tinca tinca)	EANTOCC_Tench	5.6	274	45
6	Histone H3.2	Wheat (Triticum aestivum)	P68428	9.6	2	2
6	Serpin-Z1B	Wheat (Triticum aestivum)	P93693	2.5	1	1
6	Serpin-Z1A	Wheat (Triticum aestivum)	Q41593	2.5	1	1
6	Serpin-Z1C	Wheat (Triticum aestivum)	Q9ST58	2.5	1	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
6	COL1A1	Zebra mbuna (Maylandia zebra)	A0A3P9BM02	4.9	85	1
6	Collagen I	Zebrafish (Danio rerio)	EANTOCC_Col1__Danio_rerio	5.8	150	16
7	COL1A3	Amazon molly (Poecilia formosa)	XP.007571557.1	3.3	27	1
7	COL1A2	Asian arowana (Scleropages formosus)	XP.018587334.1	5.6	53	12
7	COL1A1	Barramundi (Lates calcarifer)	XP.018553992.1	8.2	75	8
7	COL1A3	Bicolour Damselfish (Stegastes partitus)	A0A3B5AFM4	5.7	62	1
7	COL1A2	Black ghost knifefish (Apteronotus albifrons)	Apteronotus_albifrons__A2AAid:41621_col1a2	5.1	41	5
7	COL1A1	Bovine (Bos taurus)	P02453	47.7	1031	10
7	COL2A1	Bovine (Bos taurus)	P02459	4.2	76	3
7	COL1A2	Bovine (Bos taurus)	P02465	41.6	587	30
7	COL1A1	Brown trout (Salmo trutta)	A0A674DI56	4.7	76	1
7	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	3.4	108	7
7	Ovalbumin-related protein Y	Chicken (Gallus gallus)	P01014	2.3	1	1
7	Proteinase inhibitor	Flax (Linum usitatissimum)	P82381	15.9	1	1
7	COL1A1	Forkbeard (Phycis phycis)	Phycis_phycis__Bfish09_col1a1	3.1	85	21

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
7	Collagen I	Gar (Lepisosteidae)	EANSL_Col1_Lepisosteidae	17.7	288	107
7	COL1A1	Goat (Capra hircus)	A0A452FHU9	48.3	1105	84
7	COL1A1b	Guppy (Poecilia reticulata)	A0A3P9NZJ7	3.3	27	1
7	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	4.6	124	30
7	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	4.9	124	30
7	COL1A2	Mangrove killifish (Kryptolebias marmoratus)	XP.017279795.1	2	7	2
7	COL1A1	Mummichog (Fundulus heteroclitus)	XP.012716616.1	5.6	54	2
7	Collagen I	Nile tilapia (Oreochromis niloticus)	EANTENAAPPLC_Col1_Oreochromis_Tilapia	6.7	182	45
7	Collagen I	Pacific salmon and trout (Oncorhynchus)	EANTEPSSS_Col1_Oncorhynchus	3.6	126	16
7	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	4.9	142	52
7	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	7.7	280	137
7	COL1A3	Sailfin molly (Poecilia latipinna)	XP.014886816.1	3.3	27	1
7	COL1A1	Sailfin molly (Poecilia latipinna)	XP.014880315.1	9.5	89	3
7	COL2A1b	Sea lamprey (Petromyzon marinus)	Q2I8X9	3.1	41	41

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
7	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	6.7	59	5
7	COL1A2	Sheep (Ovis aries)	W5NTT11	51.3	764	202
7	COL3A1	Sheep (Ovis aries)	W5Q4S5	32.2	406	370
7	COL1A1	Sheepshead Minnow (Cyprinodon variegatus)	A0A3Q2CSU4	7.4	57	2
7	COL1A3	Shortfin molly (Poecilia mexicana)	XP.014866612.1	2.6	26	1
7	COL1A3	Southern platyfish (Xiphophorus maculatus)	XP.005794759.1	3.5	28	2
7	COL1A1	Spotted gar (Lepisosteus oculatus)	XP.006638297.1	13.6	288	107
7	COL1A2	Spotted gar (Lepisosteus oculatus)	XP.015213472.1	3.1	49	3
7	Collagen I	Tench (Tinca tinca)	EANTOCC_Tench	6.5	261	115
7	COL1A2	Tiger tail seahorse (Hippocampus comes)	XM_019889715.1	5.6	41	6
7	COL1A2	West Indian Ocean coelacanth (Latimeria chalumnae)	XM_006011624.2	0.6	1	1
7	Collagen I	Zebra mbuna (Maylandia zebra)	EANTENAAPPLC_Col1__Maylandia_zebra	2.3	41	3
8	COL1A2	African butterflyfish (Pantodon buchholzi)	Pantodon_buchlozi__C2PBid:18493_col1a2	1.5	27	12

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
8	COL1A3	Amazon molly (Poecilia formosa)	XP.007571557.1	5.5	41	3
8	COL1A2	Asian arowana (Scleropages formosus)	XP.018587334.1	3.9	64	8
8	Histone H3.3	Barley (Hordeum vulgare)	P06353	8.8	1	1
8	Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic	Barley (Hordeum vulgare)	P08477	7.5	2	2
8	Elongation factor 1-alpha	Barley (Hordeum vulgare)	P34824	4.7	3	3
8	Elongation factor 1-alpha	Barley (Hordeum vulgare)	Q40034	4.7	3	3
8	COL1A2	Barramundi (Lates calcarifer)	XP.018522130.1	5.6	43	33
8	COL1A1	Barramundi (Lates calcarifer)	XP.018553992.1	7	92	3
8	COL1A3	Bicolour Damselfish (Stegastes partitus)	A0A3B5AFM4	4.3	70	1
8	COL1A2	Black ghost knifefish (Apteronotus albifrons)	Apteronotus_albifrons__A2AAid:41621_col1a2	3.8	26	1
8	Albumin	Bovine (Bos taurus)	P02769	2.5	1	1
8	COL2A1	Bovine (Bos taurus)	P02459	4.2	78	2
8	COL1A2	Bovine (Bos taurus)	P02465	34.5	602	35
8	Collagen I	Bream (Abramis)	EANTOCC_Col1_Abramis_Bream	7.3	240	21

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
8	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	3.8	104	17
8	COL1A3	Channel catfish (Ictalurus punctatus)	A0A2D0SA79	3.2	11	1
8	Mucin-6	Chicken (Gallus gallus)	F1NBL0	0.7	1	1
8	Lysozyme C	Chicken (Gallus gallus)	P00698	25.2	18	18
8	Protein TENP	Chicken (Gallus gallus)	O42273	5.5	14	14
8	Ovalbumin	Chicken (Gallus gallus)	P01012	19.7	17	17
8	Lysozyme C	Chicken (Gallus gallus)	P00698	25.2	18	18
8	Ovomucoid	Chicken (Gallus gallus)	P01005	4.8	2	2
8	Ovalbumin	Chicken (Gallus gallus)	P01012	19.7	17	17
8	Ovalbumin-related protein X	Chicken (Gallus gallus)	P01013	2.6	4	4
8	Ovalbumin-related protein Y	Chicken (Gallus gallus)	P01014	10.8	8	8
8	Avidin	Chicken (Gallus gallus)	P02701	13.8	3	3
8	Ovotransferrin	Chicken (Gallus gallus)	P02789	21.4	45	45
8	Histone H2B	Chicken (Gallus gallus)	P0C1H3	7.1	1	1
8	Ovostatin	Chicken (Gallus gallus)	P20740	1.2	2	2
8	Extracellular fatty acid-binding protein	Chicken (Gallus gallus)	P21760	6.2	1	1
8	Mucin-5B	Chicken (Gallus gallus)	Q98UI9	4	22	22
8	Collagen I	Gar (Lepisosteidae)	EANSL_Col1_Lepisosteidae	16	284	79

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
8	COL1A1	Goat (Capra hircus)	A0A452FHU9	42.8	1065	821
8	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	4.1	178	64
8	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	4.4	178	64
8	Collagen I	Nile tilapia (Oreochromis niloticus)	EANTENAAPPLC_Col1_Oreochromis_Tilapia	6.9	201	55
8	COL1A3	Northern pike (Esox lucius)	XP.010886968.2	1.5	4	4
8	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	4.3	124	22
8	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	9.7	284	158
8	COL1A3	Sailfin molly (Poecilia latipinna)	XP.014886816.1	5.5	41	3
8	COL1A1	Sailfin molly (Poecilia latipinna)	XP.014880315.1	8.6	98	4
8	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	2.9	67	1
8	COL1A2	Sheep (Ovis aries)	W5NTT12	42.8	734	161
8	COL3A1	Sheep (Ovis aries)	W5Q4S6	27.5	624	596
8	COL1A3	Shortfin molly (Poecilia mexicana)	XP.014866612.1	4.6	32	3
8	COL1A1	Sinocyclocheilus anshuiensis	XP.016307878.1	6.6	115	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
8	COL1A1	Small-spotted catshark (Scyliorhinus canicula)	D0PQF7	4.9	60	30
8	COL1A1	Spotted gar (Lepisosteus oculatus)	XP.006638297.1	12.3	284	79
8	Collagen I	Tench (Tinca tinca)	EANTOCC_Tench	6.4	233	59
8	COL1A1	Tongue sole (Cynoglossus semilaevis)	A0A3P8W8U6	5.4	74	1
8	Histone H2B.2	Wheat (Triticum aestivum)	P05621	6	1	1
8	Histone H2B.1	Wheat (Triticum aestivum)	P27807	5.9	1	1
8	Eukaryotic initiation factor 4A	Wheat (Triticum aestivum)	P41378	2.4	1	1
8	Histone H4 variant TH011	Wheat (Triticum aestivum)	P62785	11.7	1	1
8	Histone H4 variant TH091	Wheat (Triticum aestivum)	P62786	11.7	1	1
8	Histone H3.2	Wheat (Triticum aestivum)	P68428	5.1	1	1
8	Serpin-Z1B	Wheat (Triticum aestivum)	P93693	4.8	6	6
8	Elongation factor 1-alpha	Wheat (Triticum aestivum)	Q03033	4.7	3	3
8	Serpin-Z1A	Wheat (Triticum aestivum)	Q41593	4.8	6	6

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
8	Histone H2B.4	Wheat (Triticum aestivum)	Q43215	6.7	1	1
8	Histone H2B.5	Wheat (Triticum aestivum)	Q43216	6.6	1	1
8	Histone H2B.3	Wheat (Triticum aestivum)	Q43217	6.5	1	1
8	Serpin-Z1C	Wheat (Triticum aestivum)	Q9ST58	4.8	6	6
8	Collagen I	Zebrafish (Danio rerio)	EANTOCC_Col1__Danio_rerio	6.8	171	13
9	COL1A2	African butterflyfish (Pantodon buchholzi)	Pantodon_buchlozi__C2PBid:18493_col1a2	3.1	34	5
9	COL1A1	Amazon molly (Poecilia formosa)	XP.007565541.1	9.1	126	39
9	COL1A2	Atlantic herring (Clupea harengus)	A0A6P3W0U2	3.7	10	1
9	COL1A2	Black ghost knifefish (Apteronotus albifrons)	Apteronotus_albifrons__A2AAid:41621_col1a2	5.2	38	3
9	Alpha-S1-casein	Bovine (Bos taurus)	P02662	10.3	2	2
9	Alpha-S2-casein	Bovine (Bos taurus)	P02663	17.1	12	12
9	Alpha-S2-casein	Bovine (Bos taurus)	P02663	5.8	3	3
9	COL1A2	Bovine (Bos taurus)	P02465	39.5	640	28
9	Alpha-S1-casein	Bovine (Bos taurus)	P02662	10.3	2	2
9	Alpha-S1-casein	Bovine (Bos taurus)	P02662	17.1	12	12
9	Beta-casein	Bovine (Bos taurus)	P02666	5.8	3	3

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
9	Beta-lactoglobulin	Bovine (Bos taurus)	P02754	5.1	8	8
9	COL1A3	Brown trout (Salmo trutta)	Salmo_trutta_v2_NSTid:31221X73256_col1a3	1.7	22	1
9	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	3.5	106	1
9	Ovalbumin	Chicken (Gallus gallus)	P01012	5.7	3	3
9	Ovalbumin	Chicken (Gallus gallus)	P01012	5.7	3	3
9	Ovotransferrin	Chicken (Gallus gallus)	P02789	2.4	2	2
9	Collagen I	Chub (Squalius cephalus)	EANTOCCSq_Chub	5.5	148	24
9	Collagen I	Fathead minnow (Pimephales promelas)	EANTOCCP_Col1_Fathead_Minnow	5.4	158	6
9	COL1A1	Forkbeard (Phycis phycis)	Phycis_phycis__Bfish09_col1a1	4.6	72	12
9	Collagen I	Gar (Lepisosteidae)	EANSL_Col1_Lepisosteidae	15.8	305	126
9	COL1A1	Goat (Capra hircus)	A0A452FHU9	51.7	1147	903
9	COL1A1	Golden-line barbel (Sinocyclocheilus grahami)	XP.016113605.1	2.7	63	26
9	COL1A1	Guppy (Poecilia reticulata)	A0A3P9NHJ7	9.1	126	39
9	Collagen I	Nile tilapia (Oreochromis niloticus)	EANTENAAPPLC_Col1_Oreochromis_Tilapia	7	180	32
9	COL1A2	Pacific bluefin tuna (Thunnus orientalis)	A0A060N2D3	5.5	67	5

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
9	Collagen I	Pacific salmon and trout (Oncorhynchus)	EANTEPSSS_Col1_Oncorhynchus	3.5	128	15
9	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	5	148	29
9	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	8.5	295	137
9	COL2A1b	Sea lamprey (Petromyzon marinus)	Q2I8X9	3.1	48	48
9	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	5.4	63	3
9	COL1A2	Sheep (Ovis aries)	W5NTT14	47.9	810	194
9	COL3A1	Sheep (Ovis aries)	W5Q4S7	34.6	533	498
9	COL1A1	Shortfin molly (Poecilia mexicana)	XP.014880315.1	9.1	126	39
9	COL1A3	Sinocyclocheilus anshuiensis	XP.016343587.1	2.7	63	26
9	COL1A3	Sinocyclocheilus rhinocerous	XP.016383096.1	2.7	63	26
9	COL1A3	Southern platyfish (Xiphophorus maculatus)	XP.005794759.1	4.8	29	5
9	COL1A1	Spotted gar (Lepisosteus oculatus)	XP.006638297.1	12.2	305	126
9	COL1A2	Spotted gar (Lepisosteus oculatus)	XP.015213472.1	4.2	51	2
9	Collagen I	Stickleback (Gasterosteus)	EANTENAAPGGG__Col1_Gasterosteus_stickleback	5	125	10

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
9	Collagen I	Tench (Tinca tinca)	EANTOCC_Tench	5.7	286	70
9	COL1A2	Tongue sole (Cynoglossus semilaevis)	A0A3P8VXI7	2.9	36	1
9	COL1A1	Vaillant's grenadier (Bathygadus melanobranchus)	Bathygadus_melanobranchus__Bfish19_col1a1	4.4	98	1
9	COL1A2	West Indian Ocean coelacanth (Latimeria chalumnae)	XM_006011624.2	0.9	1	1
9	Collagen I	Zebrafish (Danio rerio)	EANTOCC_Col1__Danio_rerio	4.9	148	25
10	COL1A1	Amazon molly (Poecilia formosa)	XP.007565541.1	10.6	111	34
10	COL1A3	Arrowtail (Melanonus zugmayeri)	Melanonus_zugmayeri__Bfish16_col1a3_translation	4.9	49	1
10	COL1A2	Asian arowana (Scleropages formosus)	XP.018587334.1	3.9	31	2
10	COL1A2	Ballan wrasse (Labrus bergylta)	XM_020631662.1	3.4	22	17
10	COL1A1	Beira killifish (Nothobranchius kuhntae)	A0A1A8K041	8.7	82	2
10	COL1A1	Black rockcod (Notothenia coriiceps)	A0A6I9MX97	3.2	51	5
10	COL1A2	Bovine (Bos taurus)	P02465	34.1	372	27
10	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	3.5	96	3

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
10	Ovalbumin	Chicken (Gallus gallus)	P01012	7.8	13	13
10	Ovalbumin	Chicken (Gallus gallus)	P01012	7.8	13	13
10	COL1A1	Cusk (Brosme brosme)	Brosme_brosme__Bfish12_col1a1	4.4	73	2
10	Collagen I	Flounder (Paralichthys)	EANTENAAPPPPP_Col1_Paralichthys_Flounder	2.6	70	1
10	COL1A1	Goat (Capra hircus)	A0A452FHU9	45.5	746	5
10	COL1A1	Guppy (Poecilia reticulata)	A0A3P9NHJ7	9.3	110	34
10	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	5.2	107	30
10	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	5.2	107	30
10	COL1A1	Mangrove killifish (Kryptolebias marmoratus)	XP.017267796.1	2.4	47	1
10	Collagen I	Nile tilapia (Oreochromis niloticus)	EANTENAAPPLC_Col1_Oreochromis_Tilapia	6.1	164	38
10	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	3.3	102	34
10	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	6.6	219	131
10	COL1A3	Sailfin molly (Poecilia latipinna)	XP.014886816.1	4.2	33	2
10	COL1A1	Sailfin molly (Poecilia latipinna)	XP.014880315.1	10.3	78	1
10	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	4.9	57	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
10	COL1A2	Sheep (Ovis aries)	W5NTT7	39.1	445	102
10	COL1A1	Sheep (Ovis aries)	W5P481	42.3	743	2
10	COL3A1	Sheep (Ovis aries)	W5Q4S3	23.9	216	180
10	COL1A1	Shortfin molly (Poecilia mexicana)	XP.014880315.1	10.6	111	34
10	COL1A1	Small-spotted catshark (Scyliorhinus canicula)	D0PQF7	5.5	58	28
10	COL1A3	Southern platyfish (Xiphophorus maculatus)	XP.005794759.1	3	36	5
10	COL1A2	Spotted gar (Lepisosteus oculatus)	XP.015213472.1	3.8	29	2
10	Collagen I	Tench (Tinca tinca)	EANTOCC_Tench	6	220	93
10	COL1A1	Turquoise killifish (Nothobranchius furzeri)	Nothobranchius_furzeri_v1_BS48189.1_col1a1	8.7	82	2
10	COL1A1	Turquoise killifish (Nothobranchius furzeri)	XP.015824467.1	8.7	82	2
10	Collagen I	Zebra mbuna (Maylandia zebra)	EANTENAAPPLC_Col1__Maylandia_zebra	1.7	40	18
10	Collagen I	Zebrafish (Danio rerio)	EANTOCC_Col1__Danio_rerio	4.7	120	19
11	COL1A2	African butterflyfish (Pantodon buchholzi)	Pantodon_buchlozi__C2PBid:18493_col1a2	1.5	37	18
11	COL1A3	Asian arowana (Scleropages formosus)	XP.018597555.1	8.2	108	4

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
11	COL1A1	Asian arowana (Scleropages formosus)	XP.018620194.1	11.7	122	12
11	COL1A2	Atlantic herring (Clupea harengus)	A0A6P3W0U2	3.7	11	3
11	COL1A2	Barramundi (Lates calcarifer)	XP.018522130.1	4.5	33	27
11	COL1A2	Bicolour Damselfish (Stegastes partitus)	A0A3B4ZDV7	3	26	1
11	Albumin	Bovine (Bos taurus)	P02769	1.5	1	1
11	Alpha-S1-casein	Bovine (Bos taurus)	P02662	13.6	3	3
11	Alpha-S2-casein	Bovine (Bos taurus)	P02663	19.8	7	7
11	Alpha-S2-casein	Bovine (Bos taurus)	P02663	5.8	10	10
11	COL1A2	Bovine (Bos taurus)	P02465	46.9	789	34
11	Alpha-S1-casein	Bovine (Bos taurus)	P02662	13.6	3	3
11	Alpha-S1-casein	Bovine (Bos taurus)	P02662	19.8	7	7
11	Beta-casein	Bovine (Bos taurus)	P02666	5.8	10	10
11	COL3A1	Bovine (Bos taurus)	P04258	43.4	676	61
11	Glycosylation-dependent cell adhesion molecule 1	Bovine (Bos taurus)	P80195	4.6	1	1
11	COL1A2	Bowfin (Amia calva)	Amia_calva__AACid:31457_col1a2	3.2	34	7
11	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	4.9	99	11
11	Growth/differentiation factor 8	Chicken (Gallus gallus)	O42220	1.9	1	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
11	Heat shock cognate 71 kDa protein	Chicken (Gallus gallus)	O73885	1.1	1	1
11	Ovalbumin	Chicken (Gallus gallus)	P01012	28.2	32	32
11	Ovomucoid	Chicken (Gallus gallus)	P01005	4.3	1	1
11	Ovalbumin	Chicken (Gallus gallus)	P01012	28.2	32	32
11	Ovotransferrin	Chicken (Gallus gallus)	P02789	6.5	4	4
11	Histone H2B	Chicken (Gallus gallus)	P0C1H3	7.1	1	1
11	COL1A3	European eel (Anguilla anguilla)	Anguilla_anguilla_DAAid:26647_col1a3_cut	6.5	69	10
11	COL1A1	Forkbeard (Phycis phycis)	Phycis_phycis__Bfish09_col1a1	5.2	72	19
11	Collagen I	Gar (Lepisosteidae)	EANSL_Col1_Lepisosteidae	17.7	334	109
11	COL1A1	Goat (Capra hircus)	A0A452FHU9	55.4	1489	1183
11	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	4.7	212	87
11	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	5	212	87
11	COL1A2	Mangrove killifish (Kryptolebias marmoratus)	XP.017279795.1	1.2	6	1
11	COL1A3	Mexican tetra (Astyanax mexicanus)	XP.007233638.1	2.8	4	1
11	Collagen I	Nile tilapia (Oreochromis niloticus)	EANTENAAPPLC_Col1_Oreochromis_Tilapia	6.6	204	45

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
11	Collagen I	Pacific salmon and trout (Oncorhynchus)	EANTEPSSS_Col1_Oncorhynchus	4.7	148	18
11	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	5.5	143	37
11	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	10.4	375	186
11	COL2A1b	Sea lamprey (Petromyzon marinus)	Q2I8X9	3.1	53	53
11	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	6.1	90	4
11	COL1A2	Sheep (Ovis aries)	W5NTT17	55.6	998	198
11	COL3A1	Sheep (Ovis aries)	W5Q4S10	37.2	845	230
11	COL1A1	Small-spotted catshark (Scyliorhinus canicula)	D0PQF7	5.6	54	28
11	COL1A1	Spotted gar (Lepisosteus oculatus)	XP.006638297.1	13.6	334	109
11	Collagen I	Stickleback (Gasterosteus)	EANTENAAPGGG__Col1_Gasterosteus_stickleback	5	149	14
11	Collagen I	Tench (Tinca tinca)	EANTOCC_Tench	7.1	333	127
11	Histone H2A.1	Wheat (Triticum aestivum)	P02275	6.2	1	1
11	Histone H2A.2.1	Wheat (Triticum aestivum)	P02276	6	1	1
11	Histone H2A.2.2	Wheat (Triticum aestivum)	P02277	6	1	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
11	Histone H2A.4	Wheat (Triticum aestivum)	Q43208	6.7	1	1
11	Protein H2A.5	Wheat (Triticum aestivum)	Q43213	6.2	1	1
11	Protein H2A.6	Wheat (Triticum aestivum)	Q43214	6.1	1	1
11	Protein H2A.7	Wheat (Triticum aestivum)	Q43312	6.7	1	1
11	COL1A3	Yellow croaker (Larimichthys crocea)	XP.010747796.1	4.5	92	1
11	Collagen I	Zebra mbuna (Maylandia zebra)	EANTENAAPPLC_Col1__Maylandia_zebra	1.9	81	13
11	Collagen I	Zebrafish (Danio rerio)	EANTOCC_Col1__Danio_rerio	6.1	169	19
12	COL1A1	Amazon molly (Poecilia formosa)	XP.007565541.1	7.7	86	21
12	COL1A3	Amazon molly (Poecilia formosa)	XP.007571557.1	3.5	31	1
12	COL1A2	Asian arowana (Scleropages formosus)	XP.018587334.1	5.8	44	19
12	COL1A2	Atlantic herring (Clupea harengus)	A0A6P3W0U2	3.7	16	1
12	COL1A3	Atlantic salmon (Salmo salar)	A0A1S3Q7E3	1.7	25	1
12	COL1A3	Atlantic salmon (Salmo salar)	A0A1S3Q7E3	3	26	2

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
12	COL1A2	Barramundi (Lates calcarifer)	XP.018522130.1	4.5	34	24
12	COL1A2	Black ghost knifefish (Apteronotus albifrons)	Apteronotus_albifrons__A2AAid:41621_col1a2	4.4	29	2
12	Alpha-S1-casein	Bovine (Bos taurus)	P02662	23.4	7	7
12	Alpha-S2-casein	Bovine (Bos taurus)	P02663	8.6	12	12
12	Alpha-S2-casein	Bovine (Bos taurus)	P02663	12.5	9	9
12	COL1A1	Bovine (Bos taurus)	P02453	39.4	679	1
12	COL2A1	Bovine (Bos taurus)	P02459	3.5	57	1
12	COL1A2	Bovine (Bos taurus)	P02465	32.4	466	22
12	Alpha-S1-casein	Bovine (Bos taurus)	P02662	23.4	7	7
12	Alpha-S1-casein	Bovine (Bos taurus)	P02662	8.6	12	12
12	Beta-casein	Bovine (Bos taurus)	P02666	12.5	9	9
12	Glycosylation-dependent cell adhesion molecule 1	Bovine (Bos taurus)	P80195	4.6	1	1
12	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	3.4	88	6
12	Ovocleidin-116	Chicken (Gallus gallus)	F1NSM7	1.2	1	1
12	Lysozyme C	Chicken (Gallus gallus)	P00698	29.9	30	30
12	Protein TENP	Chicken (Gallus gallus)	O42273	19.1	14	14
12	Ovalbumin	Chicken (Gallus gallus)	P01012	50.8	403	403
12	Lysozyme C	Chicken (Gallus gallus)	P00698	29.9	30	30
12	Ovomucoid	Chicken (Gallus gallus)	P01005	4.8	8	8

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
12	Ovalbumin	Chicken (Gallus gallus)	P01012	50.8	403	403
12	Ovalbumin-related protein X	Chicken (Gallus gallus)	P01013	28	38	38
12	Ovalbumin-related protein Y	Chicken (Gallus gallus)	P01014	31.4	95	95
12	Cystatin	Chicken (Gallus gallus)	P01038	7.9	1	1
12	Avidin	Chicken (Gallus gallus)	P02701	5.3	3	3
12	Ovotransferrin	Chicken (Gallus gallus)	P02789	36.6	241	241
12	Ovostatin	Chicken (Gallus gallus)	P20740	7	31	31
12	Mucin-5B	Chicken (Gallus gallus)	Q98UI9	3.6	12	12
12	Collagen I	Chub (Squalius cephalus)	EANTOCCSq_Chub	4.8	116	29
12	Collagen I	Cod (Gadus)	EANTENAPGGG_Col1_Cod-genome	1.2	28	1
12	Collagen I	Cod (Gadus)	EANTENAPGGG_Col1_Gadoid	1.2	28	1
12	COL1A1	Coryphaenoides yaquinae	BAV03979.1	4.1	49	1
12	COL1A1	Cusk (Brosme brosme)	Brosme_brosme__Bfish12_col1a1	4.8	87	1
12	COL1A1	European bass (Dicentrarchus labrax)	E6ZHW3	6.6	52	2
12	Collagen I	European bass (Dicentrarchus labrax)	EANTENAAPPPM_Col1_Dicentrarchus_Sea_bass	2.9	52	2
12	Collagen I	Fathead minnow (Pimephales promelas)	EANTOCCP_Col1_Fathead_Minnow	4.8	132	41
12	Collagen I	Gar (Lepisosteidae)	EANSL_Col1_Lepisosteidae	17.2	203	76

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
12	COL1A1	Goat (Capra hircus)	A0A452FHU9	42.8	750	72
12	COL1A3	Golden-line barbel (Sinocyclocheilus grahami)	XP.016102039.1	3.5	25	4
12	COL1A1	Guppy (Poecilia reticulata)	A0A3P9NHJ7	7.7	86	21
12	COL1A1b	Guppy (Poecilia reticulata)	A0A3P9NZJ7	3.5	31	1
12	COL1A2	Haplochromis burtoni	A0A3Q2W722	2.8	5	1
12	COL1A2	Mangrove killifish (Kryptolebias marmoratus)	XP.017279795.1	2.7	7	4
12	Collagen I	Nile tilapia (Oreochromis niloticus)	EANTENAAPPLC_Col1_Oreochromis_Tilapia	4.7	124	26
12	COL1A3	Northern pike (Esox lucius)	XP.010886968.2	2.2	4	3
12	Collagen I	Pacific salmon and trout (Oncorhynchus)	EANTEPSSS_Col1_Oncorhynchus	3.2	100	14
12	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	4.1	103	19
12	Collagen I	Pufferfish (Tetraodon)	EANTENAAPTTTT_Col1_Tetraodon_Pufferfish	3.6	98	6
12	COL1A2	Pundamilia nyererei	A0A3B4GSB9	2.8	5	1
12	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	6.1	194	95
12	COL1A3	Sailfin molly (Poecilia latipinna)	XP.014886816.1	3.5	31	1

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
12	COL1A1	Sailfin molly (Poecilia latipinna)	XP.014880315.1	7.3	66	1
12	COL2A1b	Sea lamprey (Petromyzon marinus)	Q2I8X9	3.1	28	28
12	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	3	47	1
12	COL1A2	Sheep (Ovis aries)	W5NTT8	42	600	157
12	COL3A1	Sheep (Ovis aries)	W5Q4S4	27.7	326	302
12	COL1A1	Shortfin molly (Poecilia mexicana)	XP.014880315.1	7.7	86	21
12	COL1A3	Shortfin molly (Poecilia mexicana)	XP.014866612.1	3.5	29	4
12	COL1A1	Spotted gar (Lepisosteus oculatus)	XP.006638297.1	13.3	203	76
12	Collagen I	Stickleback (Gasterosteus)	EANTENAAPGGG__Col1_Gasterosteus_stickleback	3.4	86	3
12	COL1A1	Yellow croaker (Larimichthys crocea)	XP.010745684.1	2.8	46	1
13		Wheat (Triticum aestivum)	tr|Q2I8X9|Q2I8X9_PETMA	7.6	12	12
12	COL1A2	Zebra mbuna (Maylandia zebra)	A0A3P9BM02	3.7	10	1
13	COL1A1	Amazon molly (Poecilia formosa)	XP.007565541.1	11.4	63	2

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
13	COL1A2	Amazon molly (Poecilia formosa)	XP.007573076.1	2.5	33	1
13	COL1A2	Asian arowana (Scleropages formosus)	XP.018587334.1	5	40	1
13	COL1A3	Asian arowana (Scleropages formosus)	XP.018597555.1	6.6	42	1
13	COL1A1	Asian arowana (Scleropages formosus)	XP.018620194.1	7.5	54	3
13	COL1A1	Bowfin (Amia calva)	Amia_calva__AACid:1433_col1a1	9.8	94	2
13	COL1A2	Bowfin (Amia calva)	Amia_calva__AACid:31457_col1a2	3.1	30	3
13	Collagen I	Bream (Abramis)	EANTOCC_Col1_Abramis_Bream	4.8	156	8
13	Collagen I	Channel catfish (Ictalurus punctatus)	EANTOSI_Col1_Ictalurus_punctatus_	3.2	55	3
13	Heat shock cognate 71 kDa protein	Chicken (Gallus gallus)	O73885	1.1	1	1
13	Ovalbumin	Chicken (Gallus gallus)	P01012	7.5	2	2
13	Ovalbumin	Chicken (Gallus gallus)	P01012	7.5	2	2
13	Collagen I	Cod (Gadus)	EANTENAPGGG_Col1_Cod-genome	1.5	25	1
13	Collagen I	Cod (Gadus)	EANTENAPGGG_Col1_Gadoid	1.5	25	1
13	COL1A3	Eurasian carp (Cyprinus carpio)	XP.018968199.1	3.4	27	2
13	COL1A1	European grayling (Thymallus thymallus)	Thymallus_thymallus__ITTid:56712_col1a1	4	34	4
13	COL1A1	Forkbeard (Phycis phycis)	Phycis_phycis__Bfish09_col1a1	4.7	37	20

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
13	COL1A1	Goat (Capra hircus)	A0A452FHU9	46.3	664	536
13	COL1A2	Goat (Capra hircus)	A0A452G3V6	31.2	341	9
13	COL1A1	Golden-line barbel (Sinocyclocheilus grahami)	XP.016113605.1	1.5	27	7
13	COL1A1	Guppy (Poecilia reticulata)	A0A3P9NHJ7	11.4	63	2
13	COL1A1	Haplochromis burtoni	A0A3Q3CY74	7.9	46	8
13	COL1A23	Japanese rice fish (Oryzias latipes)	EANTENAAPABAOO_Col1A23_Oryzias_latipes_concat	3.9	62	14
13	Collagen I	Japanese rice fish (Oryzias latipes)	rEANTENAAPABAOO_Col1_Oryzias_latipes	3.9	62	14
13	COL1A1	Japanese sturgeon (Acipenser schrenckii)	A0A0F7R0Z6	7.6	81	5
13	COL1A1	Japanese sturgeon (Acipenser schrenckii)	A0A0F7R0Z6	7.6	81	5
13	COL1A1	Mummichog (Fundulus heteroclitus)	XP.012716616.1	7.4	45	2
13	COL1A2	Northern pike (Esox lucius)	A0A3P8YWE6	2.8	31	1
13	Collagen I	Pufferfish (Takifugu)	EANTENAAPTTT_Col1_Takifugu_Pufferfish	3.4	80	6
13	Collagen I	Pufferfish (Tetraodon)	EANTENAAPTTTT_Col1_Tetraodon_Pufferfish	3.5	80	6
13	Collagen I	Roach (Rutilus)	EANTOCC_Rutilus_Roach	7.1	178	69

ID	Protein	Species	Uniprot or NCBI accession number	Sequence coverage	Peptide matches	Unique peptide matches
13	COL1A3	Shallow-water Cape hake (Merluccius capensis)	Merluccius_capensis__Bfish14_col1a3_translation	4	34	5
13	COL1A2	Sheep (Ovis aries)	W5NTT7	40.4	501	160
13	COL3A1	Sheep (Ovis aries)	W5Q4S0	30.4	160	151
13	COL1A1	Shortfin molly (Poecilia mexicana)	XP.014880315.1	11.4	63	2
13	COL1A2	Shortfin molly (Poecilia mexicana)	XP.014852900.1	3.4	35	1
13	COL1A1	Silver carp (Hypophthalmichthys molitrix)	A0A077B3P8	7.8	94	33
13	COL1A3	Sinocyclocheilus anshuiensis	XP.016348621.1	1.7	22	2
13	COL1A3	Sinocyclocheilus anshuiensis	XP.016343587.1	1.5	27	7
13	COL1A1	Sinocyclocheilus rhinocerous	XP.016379370.1	3.4	30	1
13	COL1A3	Sinocyclocheilus rhinocerous	XP.016383096.1	1.5	27	7
13	COL1A1	Southern platyfish (Xiphophorus maculatus)	XP.005817058.1	8.8	41	1
13	Collagen I	Tench (Tinca tinca)	EANTOCC_Tench	5.4	147	27
13	Collagen I	Zebrafish (Danio rerio)	EANTOCC_Col1__Danio_rerio	5.4	103	10

Table A2. Peptide matches per protein. Showing protein, accession number (Acc.), slice, miscleavages (Mis.), mass-to-charge ratio (m/z), charge (z), sequence, and mass error.

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[237-243]	1	800.4009	1	k.PGRPGER.g [2xOxidation]	0.0197
COL1A2	A0A452G3V6	[599-606]	0	802.369	1	r.GDQGPVGR.t [1xDeamidation; 1xOxidation]	-0.0166
COL1A2	A0A452G3V6	[1082-1087]	1	806.4043	1	k.KTNEWK.k [1xDeamidation]	-0.0118
COL1A2	A0A452G3V6	[1083-1088]	1	806.4043	1	k.TNEWKK.t [1xDeamidation]	-0.0118
COL1A1	A0A452FHU9	[1310-1315]	0	811.3985	1	k.NWYISK.n [1xDeamidation]	-0.0076
COL1A2	A0A452G3V6	[924-929]	1	820.4094	1	r.TCRDLR.l [1xCarbamidomethyl]	0.0029
COL1A1	A0A452FHU9	[244-252]	0	836.4373	1	r.GPPGPQGAR.g	-0.0104
COL1A1	A0A452FHU9	[1084-1092]	0	836.4373	1	r.GPAGPQGPR.g	-0.0104
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0032
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	-0.0081
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	-0.0081
COL1A1	A0A452FHU9	[1217-1224]	0	859.4268	1	r.ADDANVVR.d	0.0126
COL1A2	A0A452G3V6	[111-120]	0	868.4635	1	r.VGAPGPAGAR.g [1xOxidation]	-0.0158
COL1A2	A0A452G3V6	[759-767]	0	868.4635	1	r.GPSGPQGIR.g	-0.0158
COL1A1	A0A452FHU9	[361-369]	0	886.4377	1	r.GSEGPQGVR.g	0.0049
COL1A2	A0A452G3V6	[335-344]	0	892.4999	1	r.PGPIGPAGAR.g	-0.0151
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.007

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[361-369]	0	902.4326	1	r.GSEGPQGVR.g [1xOxidation]	0.0198
COL1A2	A0A452G3V6	[335-344]	0	908.4948	1	r.PGPIGPAGAR.g [1xOxidation]	-0.0074
COL1A2	A0A452G3V6	[816-826]	0	909.4789	1	r.GPAGPTGPAGK.d	-0.0171
COL1A1	A0A452FHU9	[564-573]	0	918.4792	1	r.PGPPGPPGAR.g [1xOxidation]	-0.009
COL1A2	A0A452G3V6	[335-344]	0	924.4898	1	r.PGPIGPAGAR.g [2xOxidation]	0.005
COL1A1	A0A452FHU9	[1141-1151]	0	925.4738	1	r.GPPGSAGTPGK.d	-0.0002
COL1A1	A0A452FHU9	[564-573]	0	934.4741	1	r.PGPPGPPGAR.g [2xOxidation]	0.0073
COL1A1	A0A452FHU9	[564-573]	0	950.469	1	r.PGPPGPPGAR.g [3xOxidation]	0.0154
COL1A2	A0A452G3V6	[968-976]	0	997.5201	1	r.AQPEDIPVK.n [1xDeamidation]	0.0075
COL1A2	A0A452G3V6	[1-8]	0	1010.4975	1	.MLSFVDTR.t [1xAcetyl]	0.0171
COL1A2	A0A452G3V6	[299-308]	0	1010.5088	1	r.PGEPGLMGPR.g	0.0058
COL1A2	A0A452G3V6	[968-976]	0	1012.531	1	r.AQPEDIPVK.n [1xOxidation]	-0.0126
COL1A2	A0A452G3V6	[968-976]	0	1029.5099	1	r.AQPEDIPVK.n [1xDeamidation; 2xOxidation]	0.017
COL1A2	A0A452G3V6	[1120-1128]	0	1048.5496	1	r.LNIGPVCFK. [1xCarbamidomethyl; 1xDeamidation]	-0.0129
COL1A1	A0A452FHU9	[310-321]	1	1063.5756	1	r.GRPGAPGPAGAR.g	-0.0043
COL1A2	A0A452G3V6	[1120-1128]	0	1064.5445	1	r.LNIGPVCFK. [1xCarbamidomethyl; 1xDeamidation; 1xOxidation]	0.0032
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	0.008
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	0.0095
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.0049
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0171

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[1089-1097]	1	1110.6041	1	k.TIIEYKTNK.p [1xDeamidation]	-0.0057
COL1A1	A0A452FHU9	[685-696]	0	1122.5538	1	r.GVQGPPGPAGPR.g [1xDeamidation; 2xOxidation]	-0.0031
COL1A1	A0A452FHU9	[685-696]	0	1137.5647	1	r.GVQGPPGPAGPR.g [3xOxidation]	0.0194
COL1A1	A0A452FHU9	[1084-1095]	1	1137.5647	1	r.GPAGPQGPRGDK.g [1xDeamidation]	0.0194
COL1A2	A0A452G3V6	[323-334]	0	1138.5851	1	k.EGPAGLPGIDGR.p	-0.0111
COL1A1	A0A452FHU9	[1310-1318]	1	1150.5891	1	k.NWYISKNPK.d [1xDeamidation]	0.0198
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.0107
COL1A2	A0A452G3V6	[759-770]	1	1168.6069	1	r.GPSGPQGIRGDK.g	-0.0135
COL1A2	A0A452G3V6	[345-356]	0	1185.5899	1	r.GEPGNIGFPGPK.g [1xOxidation]	0.0175
COL1A1	A0A452FHU9	[1236-1245]	0	1188.6219	1	k.SLSQQIENIR.s [1xDeamidation]	0.005
COL1A1	A0A452FHU9	[598-611]	0	1192.6321	1	r.GVPGPPGAVGPAGK.d [2xOxidation]	-0.004
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.019
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	0.01
COL1A2	A0A452G3V6	[881-891]	1	1229.6233	1	r.ADQPRSPASLR.p [2xOxidation]	0
COL1A2	A0A452G3V6	[214-228]	0	1251.6804	1	r.GIPGPVGAAGATGAR.g	-0.0034
COL1A2	A0A452G3V6	[214-228]	0	1267.6753	1	r.GIPGPVGAAGATGAR.g [1xOxidation]	0.0169
COL1A1	A0A452FHU9	[970-983]	0	1296.6583	1	r.GFPGLPGPSGEPGK.q	0.0102
COL1A1	A0A452FHU9	[415-429]	0	1332.6543	1	r.GPSGPQGPSGPPGPK.g [1xOxidation]	0.0101
COL1A2	A0A452G3V6	[26-37]	1	1334.7097	1	k.CLQLVSGSLGKR.l [1xCarbamidomethyl; 1xDeamidation; 1xOxidation]	-0.001
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0191

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.02
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0145
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	0.0033
COL1A2	A0A452G3V6	[827-842]	1	1508.7928	1	k.DGRTGQPGAVGPAGIR.g	-0.0199
COL1A1	A0A452FHU9	[253-267]	1	1512.7587	1	r.GLPGTAGLPGMKGHR.g [4xOxidation]	0.0109
COL1A1	A0A452FHU9	[1152-1167]	0	1529.8071	1	k.DGLNGLPGPIGPPGPR.g [1xOxidation]	-0.0039
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	-0.0037
COL1A1	A0A452FHU9	[397-414]	0	1569.7768	1	k.GANGAPGIAGAPGFPGAR.g [2xOxidation]	0.0079
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0169
COL1A1	A0A452FHU9	[487-504]	1	1599.7874	1	r.GGPGSRGFPGSDGVAGPK.g	0.0197
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0.0067
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	0.0027
COL1A1	A0A452FHU9	[612-630]	0	1706.7729	1	k.DGEAGAQGPPGPAGPAGER.g [1xOxidation]	0.0138
COL1A2	A0A452G3V6	[345-361]	1	1759.861	1	r.GEPGNIGFPGPKGPTVR.i [5xOxidation]	0.0083
COL1A1	A0A452FHU9	[882-902]	0	1765.8868	1	r.VGPPGPSGNAGPPGPPGPAGK.e [1xDeamidation]	0.0071
COL1A2	A0A452G3V6	[903-918]	0	1774.8705	1	k.SLNNQIETLLTPEGSR.k [3xDeamidation]	0.0121
COL1A1	A0A452FHU9	[657-675]	0	1783.8093	1	k.PGEQGVPGDLGAPGPSGAR.g [1xDeamidation; 4xOxidation]	0.0154
COL1A1	A0A452FHU9	[352-369]	1	1783.8318	1	k.GEAGPQGPRGSEGPQGVR.g [3xOxidation]	-0.007
COL1A2	A0A452G3V6	[903-918]	0	1788.8974	1	k.SLNNQIETLLTPEGSR.k [1xDeamidation; 1xOxidation]	-0.0168
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	-0.003

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	0.0118
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	0.0023
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0042
COL1A1	A0A452FHU9	[448-467]	0	1848.861	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 1xOxidation]	0.0188
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0049
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0121
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.0159
COL1A1	A0A452FHU9	[934-957]	0	2073.9948	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 1xOxidation]	-0.0041
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	-0.0056
COL1A1	A0A452FHU9	[934-957]	0	2089.9897	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 2xOxidation]	0.0062
COL1A1	A0A452FHU9	[528-551]	1	2104.0669	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t	0.0054
COL1A2	A0A452G3V6	[434-457]	0	2151.0313	1	k.GEPGVVGAPGTAGPSGPSGLPGER.g [3xOxidation]	-0.0055
COL1A1	A0A452FHU9	[1036-1061]	0	2153.0622	1	r.GETGPAGPPGAPGAPGAPGPVGPAGK.s [2xOxidation]	-0.0105
COL1A1	A0A452FHU9	[685-708]	1	2179.9963	1	r.GVQGPPGPAGPRGANGAPGNDGAK.g [1xDeamidation; 5xOxidation]	0.0197
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	-0.0018
COL1A1	A0A452FHU9	[709-732]	0	2199.9571	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [1xDeamidation; 4xOxidation]	0.0135
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.0071
COL1A1	A0A452FHU9	[882-906]	1	2263.0473	1	r.VGPPGPSGNAGPPGPPGPAGKEGSK.g [1xDeamidation; 6xOxidation]	0.0185
COL1A2	A0A452G3V6	[599-622]	1	2285.0793	1	r.GDQGPVGRTGEPGAAGPPGFVGEK.g [3xOxidation]	0.0102
COL1A1	A0A452FHU9	[442-467]	1	2394.1056	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 2xOxidation]	-0.0004

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[442-467]	1	2409.1165	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [3xOxidation]	0.0021
COL1A1	A0A452FHU9	[442-467]	1	2410.1005	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 3xOxidation]	0.0155
COL1A2	A0A452G3V6	[565-591]	0	2484.1678	1	r.GDGGPPVSTYPGFGISGPPGPPGPAGK.e [4xOxidation]	0.0189
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	-0.0045
COL1A1	A0A452FHU9	[1288-1309]	0	2578.1258	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 2xOxidation]	0.0074
COL1A1	A0A452FHU9	[322-351]	0	2581.1801	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 5xOxidation]	-0.0191
COL1A1	A0A452FHU9	[322-351]	0	2613.1699	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 7xOxidation]	0.0094
COL1A2	A0A452G3V6	[535-564]	0	2677.2085	1	k.GENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [7xOxidation]	0.015
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0124
COL1A1	A0A452FHU9	[1111-1140]	0	2753.2398	1	r.GFSGLQGPPGPPGSPGEQGPSGASGPAGPR.g [6xOxidation]	0.0128
COL1A2	A0A452G3V6	[711-740]	1	2766.2714	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [2xDeamidation; 6xOxidation]	0.0172
COL1A2	A0A452G3V6	[532-564]	1	2879.4031	1	k.GPKGENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.0151
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.002
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0131
COL1A1	A0A452FHU9	[709-741]	1	2883.4166	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g	-0.0165
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.0074
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.0071
COL1A2	A0A452G3V6	[422-457]	1	3212.5091	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [1xDeamidation; 3xOxidation]	0.0055
COL1A2	A0A452G3V6	[422-457]	1	3227.52	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [4xOxidation]	0.0108
COL1A2	A0A452G3V6	[780-815]	1	3365.721	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [3xOxidation]	-0.0026

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[780-815]	1	3366.705	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 3xOxidation]	-0.0152
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	-0.0072
COL1A2	A0A452G3V6	[843-880]	0	3652.5524	1	r.GSQGSQGPAGPPGPPGPPGPPGPSGGGYDFGFDGDFYR.a [1xDeamidation; 4xOxidation]	-0.015
COL1A2	A0A452G3V6	[599-606]	0	802.369	1	r.GDQGPVGR.t [1xDeamidation; 1xOxidation]	-0.0015
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0115
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	-0.0116
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	-0.0116
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.0147
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.0147
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.0147
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0163
COL1A2	A0A452G3V6	[759-767]	0	901.4374	1	r.GPSGPQGIR.g [1xDeamidation; 2xOxidation]	0.0087
COL1A1	A0A3P9NHJ7	[484-493]	0	952.4847	1	r.PGPPGPVGAR.g [3xOxidation]	-0.0094
COL1A2	A0A452G3V6	[968-976]	0	997.5201	1	r.AQPEDIPVK.n [1xDeamidation]	0.0128
COL1A2	A0A452G3V6	[968-976]	0	1029.5099	1	r.AQPEDIPVK.n [1xDeamidation; 2xOxidation]	-0.0193
COL1A2	A0A452G3V6	[1120-1128]	0	1048.5496	1	r.LNIGPVCFK. [1xCarbamidomethyl; 1xDeamidation]	-0.0113
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	0.0029
COL1A1	A0A6I9MX97	[762-772]	1	1087.5603	1	k.GNRGETGIAGR.a	-0.0073
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	0.0009

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.011
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.0142
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0083
COL1A1	A0A452FHU9	[733-744]	1	1111.5854	1	r.GAAGLPGPKGDR.g [1xOxidation]	0.0186
COL1A1	A0A452FHU9	[685-696]	0	1138.5487	1	r.GVQGPPGPAGPR.g [1xDeamidation; 3xOxidation]	0.0105
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.0062
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0148
COL1A1	A0A3P9NHJ7	[1206-1214]	1	1183.5928	1	k.NWYMSKNIK.e	0.0146
COL1A2	A0A452G3V6	[759-770]	1	1185.5858	1	r.GPSGPQGIRGDK.g [1xDeamidation; 1xOxidation]	0.0057
COL1A2	A0A452G3V6	[345-356]	0	1185.5899	1	r.GEPGNIGFPGPK.g [1xOxidation]	0.0017
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	0.0136
COL1A2	A0A452G3V6	[881-891]	1	1229.6233	1	r.ADQPRSPASLR.p [2xOxidation]	-0.0132
COL1A1	A0A6I9MX97	[1079-1089]	1	1260.643	1	r.DRDLEVDGTLK.s	0.0175
COL1A2	A0A452G3V6	[26-37]	1	1333.7256	1	k.CLQLVSGSLGKR.l [1xCarbamidomethyl; 1xOxidation]	-0.0075
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0116
COL1A1	A0A3P9NHJ7	[1267-1280]	0	1455.6784	1	k.NSIAYMDAAAGNLK.k [1xDeamidation; 1xOxidation]	0.0195
COL1A1	A0A452FHU9	[1386-1398]	0	1457.7846	1	k.ALLLQGSNEIEIR.a [2xDeamidation]	-0.0129
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.0119
COL1A1	A0A3P9NHJ7	[877-891]	0	1473.6856	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation; 4xOxidation]	0.0102
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0164

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	0.0051
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	0.0058
COL1A1	A0A452FHU9	[1152-1167]	0	1546.786	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	0.0198
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	0.0145
COL1A2	A0A452G3V6	[196-213]	0	1562.8285	1	k.GAAGLPGVAGAPGLPGPR.g [3xOxidation]	0.0014
COL1A1	A0A1A8K041	[503-519]	1	1570.782	1	r.GAPGLVGPKGASGEPGR.t [4xOxidation]	0.0169
COL1A1	A0A3P9NHJ7	[514-531]	1	1583.7959	1	k.PGERGVMGPTGAAGAAGK.d	0.0158
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0124
COL1A1	A0A452FHU9	[397-414]	0	1586.7558	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 3xOxidation]	0.0168
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0.0017
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	-0.0023
COL1A1	A0A1A8K041	[959-975]	1	1658.8133	1	r.GERGFPGLPGPAGETGK.v [2xOxidation]	0.0088
COL1A1	A0A452FHU9	[612-630]	0	1690.778	1	k.DGEAGAQGPPGPAGPAGER.g	0.0112
COL1A1	A0A452FHU9	[612-630]	0	1706.7729	1	k.DGEAGAQGPPGPAGPAGER.g [1xOxidation]	0.0137
COL1A1	A0A1A8K041	[1006-1024]	1	1740.8147	1	r.EGTPGTEGAAGRDGAPGPK.g [1xOxidation]	-0.0189
COL1A1	A0A1A8K041	[1006-1024]	1	1756.8096	1	r.EGTPGTEGAAGRDGAPGPK.g [2xOxidation]	-0.0112
COL1A1	A0A452FHU9	[1152-1169]	1	1759.9086	1	k.DGLNGLPGPIGPPGPRGR.t [1xDeamidation; 2xOxidation]	0.0199
COL1A1	A0A452FHU9	[352-369]	1	1783.8318	1	k.GEAGPQGPRGSEGPQGVR.g [3xOxidation]	-0.001
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	-0.0033

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1236-1251]	1	1802.8879	1	k.SLSQQIENIRSPEGSR.k [2xDeamidation]	-0.0165
COL1A1	A0A1A8K041	[773-793]	1	1804.9049	1	k.GEPGAAGPVGAAGARGAPGER.g	0.0052
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	0.0088
COL1A1	A0A1A8K041	[773-793]	1	1820.8998	1	k.GEPGAAGPVGAAGARGAPGER.g [1xOxidation]	-0.0192
COL1A1	A0A452FHU9	[882-902]	0	1828.8824	1	r.VGPPGPSGNAGPPGPPGPAGK.e [4xOxidation]	-0.0115
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	0.0028
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0037
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0018
COL1A1	A0A1A8K041	[1054-1075]	1	2011.9064	1	k.SGDRGETGPAGPAGPAGPAGPR.g [5xOxidation]	-0.0145
COL1A1	A0A452FHU9	[448-468]	1	2019.973	1	k.GEPGPTGIQGPPGPAGEEGKR.g [2xOxidation]	0.0029
COL1A2	A0A452G3V6	[323-344]	1	2028.0621	1	k.EGPAGLPGIDGRPGPIGPAGAR.g [1xOxidation]	-0.0179
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0132
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.01
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	0.0012
COL1A1	A0A452FHU9	[528-551]	1	2104.0669	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t	-0.0031
COL1A1	A0A6I9MX97	[1240-1258]	1	2105.0292	1	k.AMLLQGSNEIEIRAEGNSR.f [1xDeamidation; 1xOxidation]	-0.0067
COL1A1	A0A1A8K041	[1028-1053]	0	2145.0207	1	r.GESGPAGAPGAPGPSGAPGPVGPAGK.s [3xOxidation]	0.0187
COL1A1	A0A452FHU9	[528-551]	1	2152.0517	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t [3xOxidation]	-0.0078
COL1A1	A0A1A8K041	[902-925]	1	2180.0214	1	r.GETGPAGRPGEVGAAGPPGPSGEK.g [3xOxidation]	-0.0037

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	-0.0012
COL1A1	A0A452FHU9	[709-732]	0	2199.9571	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [1xDeamidation; 4xOxidation]	0.0197
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.0064
COL1A2	A0A452G3V6	[711-736]	0	2263.1102	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGK.h [2xOxidation]	-0.0142
COL1A2	A0A452G3V6	[599-622]	1	2285.0793	1	r.GDQGPVGRTGEPGAAGPPGFVGEK.g [3xOxidation]	0.0149
COL1A1	A0A6I9MX97	[486-511]	0	2316.0851	1	r.GEQGAGGAGGFQGLPGPQGAIGESGK.p [2xOxidation]	0.0149
COL1A2	A0A452G3V6	[169-195]	0	2368.2143	1	r.GEVGLPGLSGPVGPPGNPGANGLPGAK.g [2xDeamidation]	0.0002
COL1A1	A0A452FHU9	[442-467]	1	2394.1056	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 2xOxidation]	0.0171
COL1A1	A0A452FHU9	[442-467]	1	2409.1165	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [3xOxidation]	0.0147
COL1A1	A0A452FHU9	[442-467]	1	2410.1005	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 3xOxidation]	0.0192
COL1A1	A0A1A8K041	[1133-1159]	1	2469.1827	1	r.GPPGPVGPAGKDGSNGMPGPIGPPGPR.g [1xDeamidation; 3xOxidation]	-0.0013
COL1A1	A0A1A8K041	[1133-1159]	1	2485.1776	1	r.GPPGPVGPAGKDGSNGMPGPIGPPGPR.g [1xDeamidation; 4xOxidation]	0.0114
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	0.0085
COL1A1	A0A3P9NHJ7	[1184-1205]	1	2574.1521	1	k.VYCNMDTGETCITPTQPEVAKK.n [2xCarbamidomethyl; 2xOxidation]	-0.0048
COL1A1	A0A452FHU9	[1288-1309]	0	2578.1258	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 2xOxidation]	0.0161
COL1A1	A0A452FHU9	[322-351]	0	2581.1801	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 5xOxidation]	-0.0158
COL1A1	A0A452FHU9	[322-351]	0	2596.191	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [6xOxidation]	-0.0012
COL1A1	A0A1A8K041	[1103-1132]	0	2678.2077	1	r.GFTGAQGPPGPPGPSGDQGATGPAGPAGQR.g [2xDeamidation; 2xOxidation]	0.017
COL1A1	A0A6I9MX97	[966-995]	0	2686.2162	1	r.GFTGMQGPIGPSGSNGEAGPAGTSGPAGPR.g [1xDeamidation; 1xOxidation]	-0.0142

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[404-433]	1	2705.2398	1	r.GPPGESGAAGPTGPIGSRGPSGPPGPDGNK.g [5xOxidation]	-0.0173
COL1A1	A0A3P9NHJ7	[333-361]	1	2717.2325	1	r.GPPGPQGAAGAPGPKGNTFQGDVGAPGFK.g [3xDeamidation; 5xOxidation]	0.0167
COL1A1	A0A452FHU9	[1111-1140]	0	2737.2448	1	r.GFSGLQGPPGPPGSPGEQGPSGASGPAGPR.g [5xOxidation]	0.0102
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0084
COL1A1	A0A452FHU9	[1111-1140]	0	2753.2398	1	r.GFSGLQGPPGPPGSPGEQGPSGASGPAGPR.g [6xOxidation]	0.0047
COL1A2	A0A452G3V6	[711-740]	1	2766.2714	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [2xDeamidation; 6xOxidation]	0.0091
COL1A1	A0A452FHU9	[994-1025]	1	2866.3537	1	r.GPPGPMGPPGLAGPPGESGREGAPGAEGSPGR.d [1xOxidation]	0.0047
COL1A2	A0A452G3V6	[532-564]	1	2879.4031	1	k.GPKGENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.0133
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.0099
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0176
COL1A1	A0A452FHU9	[397-429]	1	2932.382	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [1xDeamidation; 6xOxidation]	0.0136
COL1A1	A0A452FHU9	[709-741]	1	2932.3854	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g [1xDeamidation; 3xOxidation]	0.0102
COL1A1	A0A3P9NHJ7	[902-933]	1	3001.3341	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 5xOxidation]	0.0013
COL1A1	A0A3P9NHJ7	[902-933]	1	3002.3181	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 5xOxidation]	-0.004
COL1A1	A0A3P9NHJ7	[902-933]	1	3017.329	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 6xOxidation]	0.0058
COL1A1	A0A3P9NHJ7	[902-933]	1	3018.313	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 6xOxidation]	0.013
COL1A1	A0A3P9NHJ7	[551-582]	1	3018.342	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [1xDeamidation; 5xOxidation]	-0.016
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.0076
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.01
COL1A1	A0A1A8K041	[353-388]	1	3116.39	1	r.GPEGPAGARGEPGNAGPAGPAGPSGNPGADGAAGPK.g [6xOxidation]	-0.0107

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[422-457]	1	3211.525	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [3xOxidation]	-0.0047
COL1A1	A0A1A8K041	[314-352]	1	3315.5261	1	r.GNDGAAGAAGPPGPTGPAGPPGFPGGPGSKGDVGAQGAR.g [2xDeamidation; 2xOxidation]	-0.015
COL1A2	A0A452G3V6	[780-815]	1	3366.705	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 3xOxidation]	0.0105
COL1A1	A0A452FHU9	[1433-1463]	1	3381.6559	1	k.TSRLPIIDVAPLDVGAPDQEFGFDIGSVCFL. [1xCarbamidomethyl; 1xDeamidation; 2xOxidation]	0.0029
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	0.0028
COL1A2	A0A452G3V6	[843-880]	0	3652.5524	1	r.GSQGSQGPAGPPGPPGPPGPPGPSGGGYDFGFDGDFYR.a [1xDeamidation; 4xOxidation]	-0.0018
Ovalbumin	P01012	[201-207]	0	821.3887	1	r.VTEQESK.p [1xDeamidation]	-0.0054
Ovalbumin	P01012	[220-227]	0	822.4026	1	r.VASMASEK.m	0.0175
Ovalbumin	P01012	[208-219]	0	1514.7494	1	k.PVQMMYQIGLFR.v [2xOxidation]	0.0175
COL1A2	A0A452G3V6	[599-606]	0	801.385	1	r.GDQGPVGR.t [1xOxidation]	0.0173
COL1A2	A0A452G3V6	[282-290]	0	801.4213	1	r.GATGPAGVR.g [1xOxidation]	-0.0191
COL1A2	A0A3B4ZDV7	[152-160]	0	814.4054	1	k.GEPGAAGQK.g	-0.0183
COL1A2	A0A3B4ZDV7	[1066-1072]	0	821.3458	1	r.ADQPAMR.a [1xDeamidation; 2xOxidation]	0.0173
Ovotransferrin	P02789	[38-43]	1	822.3774	1	k.KCNNLR.d [1xCarbamidomethyl; 2xDeamidation; 1xOxidation]	-0.0033
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.001
COL1A2	A0A6P3W0U2	[176-185]	1	845.4476	1	r.KGEGGAAGAK.g	0.0036
COL1A2	A0A6P3W0U2	[168-175]	0	851.4006	1	r.GYNGIDGR.k	-0.0023
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.0101
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.0101

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.0101
COL1A1	A0A452FHU9	[361-369]	0	886.4377	1	r.GSEGPQGVR.g	-0.0187
COL1A2	A0A6P3W0U2	[884-893]	0	898.4741	1	r.LGPAGASGPR.g [1xOxidation]	0.0138
COL1A1	A0A452FHU9	[1026-1035]	1	943.4592	1	r.DGAPGAKGDR.g	-0.002
Ovalbumin	P01012	[86-93]	0	945.5251	1	r.DILNQITK.p [1xDeamidation]	-0.0048
COL1A1	A0A452FHU9	[564-573]	0	950.469	1	r.PGPPGPPGAR.g [3xOxidation]	0.0051
COL1A1	A0A452FHU9	[1026-1035]	1	959.4541	1	r.DGAPGAKGDR.g [1xOxidation]	-0.0118
COL1A2	A0A3B4ZDV7	[151-160]	1	975.4742	1	r.KGEPGAAGQK.g [1xDeamidation; 2xOxidation]	0.0034
COL1A2	A0A3B4ZDV7	[361-370]	0	988.488	1	r.TGPIGMPGAR.g [2xOxidation]	0.0096
COL1A2	A0A3B4ZDV7	[1066-1074]	1	988.488	1	r.ADQPAMRAK.d [1xDeamidation]	0.0096
COL1A2	A0A452G3V6	[1-8]	0	1010.4975	1	.MLSFVDTR.t [1xAcetyl]	0.0044
COL1A2	A0A452G3V6	[299-308]	0	1010.5088	1	r.PGEPGLMGPR.g	-0.0068
COL1A1	A0A452FHU9	[1-8]	0	1030.5026	1	.MFSFVDLR.l [1xOxidation]	0.0197
COL1A2	A0A6P3W0U2	[210-221]	1	1069.5497	1	r.GRAGPSGPAGAR.g [1xOxidation]	-0.0058
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	-0.0009
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	0.006
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.0044
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0047
COL1A1	A0A452FHU9	[733-744]	1	1111.5854	1	r.GAAGLPGPKGDR.g [1xOxidation]	0.0178
COL1A1	A0A452FHU9	[733-744]	1	1127.5804	1	r.GAAGLPGPKGDR.g [2xOxidation]	-0.0016

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[253-264]	0	1130.5874	1	r.GLPGTAGLPGMK.g [2xOxidation]	-0.0031
COL1A1	A0A452FHU9	[1310-1318]	1	1150.5891	1	k.NWYISKNPK.d [1xDeamidation]	0.0069
COL1A2	A0A452G3V6	[323-334]	0	1154.58	1	k.EGPAGLPGIDGR.p [1xOxidation]	0.0018
COL1A1	A0A452FHU9	[574-585]	0	1161.5721	1	r.GQAGVMGFPGPK.g [1xOxidation]	0.0186
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0048
COL1A2	A0A452G3V6	[759-770]	1	1185.5858	1	r.GPSGPQGIRGDK.g [1xDeamidation; 1xOxidation]	-0.0066
COL1A2	A0A452G3V6	[345-356]	0	1185.5899	1	r.GEPGNIGFPGPK.g [1xOxidation]	-0.0106
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.0068
COL1A2	A0A452G3V6	[759-770]	1	1200.5967	1	r.GPSGPQGIRGDK.g [2xOxidation]	0.0134
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	0.0029
COL1A2	A0A6P3W0U2	[474-485]	0	1203.6004	1	r.GQPGTIGFPGPK.g [3xOxidation]	0.0186
COL1A2	A0A452G3V6	[881-891]	1	1230.6073	1	r.ADQPRSPASLR.p [1xDeamidation; 2xOxidation]	0.0197
COL1A2	A0A452G3V6	[214-228]	0	1251.6804	1	r.GIPGPVGAAGATGAR.g	0.0192
COL1A2	A0A3B4ZDV7	[1002-1015]	1	1273.6396	1	r.GPAGPHGPAGKDGR.a	-0.0018
COL1A2	A0A6P3W0U2	[870-883]	0	1288.6314	1	r.GLPGMAGGVGEVGR.l [2xOxidation]	0.0176
COL1A2	A0A6P3W0U2	[494-506]	1	1288.6492	1	k.AGEKGPTGPTGLR.g [3xOxidation]	-0.0001
COL1A2	A0A3B4ZDV7	[1002-1015]	1	1289.6345	1	r.GPAGPHGPAGKDGR.a [1xOxidation]	-0.0142
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0124
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.011
COL1A1	A0A452FHU9	[253-267]	1	1480.7689	1	r.GLPGTAGLPGMKGHR.g [2xOxidation]	0.0017
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0102

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	-0.001
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	-0.0162
COL1A1	A0A452FHU9	[1152-1167]	0	1546.786	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	0.0047
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	0.0118
COL1A2	A0A452G3V6	[196-213]	0	1562.8285	1	k.GAAGLPGVAGAPGLPGPR.g [3xOxidation]	-0.0051
COL1A2	A0A452G3V6	[59-72]	1	1568.7672	1	r.NSCLTHPKGLMGPR.g [1xCarbamidomethyl; 1xDeamidation]	0.0084
COL1A1	A0A452FHU9	[397-414]	0	1570.7608	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 2xOxidation]	0.0133
COL1A2	A0A452G3V6	[404-421]	0	1580.7663	1	r.GPPGESGAAGPTGPIGSR.g [1xOxidation]	0.0167
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0122
COL1A1	A0A452FHU9	[397-414]	0	1586.7558	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 3xOxidation]	0.0116
COL1A2	A0A3B4ZDV7	[290-307]	1	1596.7976	1	r.GLAGDPGAQGVKGDGGPK.g [1xOxidation]	0.0022
COL1A2	A0A3B4ZDV7	[521-538]	1	1596.8089	1	r.GIPGDQGVAGAAGGKGER.g	-0.0091
COL1A1	A0A452FHU9	[487-504]	1	1599.7874	1	r.GGPGSRGFPGSDGVAGPK.g	0.0038
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0.0055
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	0.0014
COL1A2	A0A3B4ZDV7	[1143-1156]	1	1632.8163	1	r.ETCIYAHPASIARK.n [1xCarbamidomethyl; 1xOxidation]	0.0152
COL1A1	A0A452FHU9	[612-630]	0	1690.778	1	k.DGEAGAQGPPGPAGPAGER.g	0.0056
COL1A1	A0A452FHU9	[612-630]	0	1706.7729	1	k.DGEAGAQGPPGPAGPAGER.g [1xOxidation]	0.007
COL1A1	A0A452FHU9	[1152-1169]	1	1759.9086	1	k.DGLNGLPGPIGPPGPRGR.t [1xDeamidation; 2xOxidation]	0.0128
COL1A1	A0A452FHU9	[657-675]	0	1783.8093	1	k.PGEQGVPGDLGAPGPSGAR.g [1xDeamidation; 4xOxidation]	0.0157

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[352-369]	1	1783.8318	1	k.GEAGPQGPRGSEGPQGVR.g [3xOxidation]	-0.0068
COL1A2	A0A452G3V6	[903-918]	0	1788.8974	1	k.SLNNQIETLLTPEGSR.k [1xDeamidation; 1xOxidation]	-0.014
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	-0.007
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	0.0042
COL1A1	A0A452FHU9	[574-593]	1	1828.901	1	r.GQAGVMGFPGPKGAAGEPGK.a [1xOxidation]	0.0039
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	-0.0016
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0081
COL1A1	A0A452FHU9	[994-1013]	0	1848.8545	1	r.GPPGPMGPPGLAGPPGESGR.e [4xOxidation]	-0.0006
COL1A1	A0A452FHU9	[448-467]	0	1848.861	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 1xOxidation]	-0.0072
COL1A2	A0A6P3W0U2	[474-493]	1	1872.9086	1	r.GQPGTIGFPGPKGPGGEAGK.a [4xOxidation]	0.008
COL1A2	A0A6P3W0U2	[474-493]	1	1888.9035	1	r.GQPGTIGFPGPKGPGGEAGK.a [5xOxidation]	0.0161
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0038
COL1A2	A0A3B4ZDV7	[308-328]	1	2011.9064	1	k.GEPGNAGPQGAPGSQGEEGKR.g [2xOxidation]	-0.0122
COL1A2	A0A3B4ZDV7	[412-433]	1	2015.953	1	k.EGPAGPAGQDGRSGPPGPTGPR.g [1xDeamidation]	0.0038
COL1A1	A0A452FHU9	[448-468]	1	2019.973	1	k.GEPGPTGIQGPPGPAGEEGKR.g [2xOxidation]	0.0005
COL1A2	A0A6P3W0U2	[1272-1290]	1	2028.0469	1	k.AVLLQGSNDVELRAEGNSR.f	-0.0054
COL1A2	A0A3B4ZDV7	[830-853]	1	2056.0683	1	r.GTPGGAGALGEPGRVGPAGPPGAR.g	-0.0002
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0047
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.0101

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[934-957]	0	2073.9948	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 1xOxidation]	0.0065
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	-0.0081
COL1A1	A0A452FHU9	[934-957]	0	2089.9897	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 2xOxidation]	0.0116
COL1A1	A0A452FHU9	[528-551]	1	2104.0669	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t	-0.0128
COL1A2	A0A3B4ZDV7	[424-445]	1	2105.041	1	r.SGPPGPTGPRGQPGNIGFPGPK.g [1xDeamidation; 2xOxidation]	-0.0007
COL1A2	A0A6P3W0U2	[369-392]	1	2142.0534	1	r.GSTGEQGASGPAGLLGPRGASGTR.g [1xDeamidation]	0.0118
COL1A2	A0A452G3V6	[434-457]	0	2151.0313	1	k.GEPGVVGAPGTAGPSGPSGLPGER.g [3xOxidation]	-0.0063
COL1A1	A0A452FHU9	[1036-1061]	0	2153.0622	1	r.GETGPAGPPGAPGAPGAPGPVGPAGK.s [2xOxidation]	-0.0087
COL1A1	A0A452FHU9	[685-708]	1	2179.9963	1	r.GVQGPPGPAGPRGANGAPGNDGAK.g [1xDeamidation; 5xOxidation]	0.0131
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	0.0074
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.0149
COL1A2	A0A452G3V6	[599-622]	1	2301.0742	1	r.GDQGPVGRTGEPGAAGPPGFVGEK.g [4xOxidation]	-0.0065
COL1A2	A0A3B4ZDV7	[230-256]	0	2368.164	1	r.GEPGPNGAVGPVGPPGNPGANGLNGAK.g [1xOxidation]	0.0133
COL1A2	A0A452G3V6	[502-528]	1	2409.1542	1	r.GEVGPAGPNGFAGPAGAAGQPGAKGER.g [2xOxidation]	-0.002
COL1A1	A0A452FHU9	[442-467]	1	2410.1005	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 3xOxidation]	0.0121
COL1A2	A0A6P3W0U2	[45-71]	0	2465.1732	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation]	0.0125
COL1A2	A0A6P3W0U2	[45-71]	0	2481.1681	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 1xOxidation]	0.0073
COL1A2	A0A3B4ZDV7	[695-724]	0	2485.1702	1	k.GEVGPSGPAGPAGQSGPAGPSGPSGPAGAR.g [1xDeamidation]	0.0127
COL1A2	A0A6P3W0U2	[45-71]	0	2497.163	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 2xOxidation]	-0.0008
COL1A2	A0A6P3W0U2	[45-71]	0	2513.1579	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 3xOxidation]	-0.0114
COL1A2	A0A3B4ZDV7	[695-724]	0	2580.1557	1	k.GEVGPSGPAGPAGQSGPAGPSGPSGPAGAR.g [6xOxidation]	-0.0011

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A6P3W0U2	[933-961]	1	2582.1826	1	k.GDRGEPGSNGPSGLSGAPGPAGPAGAVGR.p [5xOxidation]	-0.0104
COL1A1	A0A452FHU9	[322-351]	0	2613.1699	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 7xOxidation]	0.0115
COL1A2	A0A3B4ZDV7	[972-1001]	0	2653.206	1	r.GHPGLQGMPGPSGPSGDTGAAGPNGPAGPR.g [2xDeamidation]	0.0107
COL1A2	A0A6P3W0U2	[222-251]	0	2654.1965	1	r.GADGNTGPSGPAGPLGAAGPPGFPGAPGPK.g [8xOxidation]	-0.0054
COL1A2	A0A3B4ZDV7	[972-1001]	0	2669.2009	1	r.GHPGLQGMPGPSGPSGDTGAAGPNGPAGPR.g [2xDeamidation; 1xOxidation]	0.0054
COL1A1	A0A452FHU9	[796-825]	1	2703.2394	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [4xOxidation]	-0.0168
COL1A2	A0A452G3V6	[404-433]	1	2705.2398	1	r.GPPGESGAAGPTGPIGSRGPSGPPGPDGNK.g [5xOxidation]	-0.0128
COL1A1	A0A452FHU9	[984-1013]	1	2727.2904	1	k.QGPSGASGERGPPGPMGPPGLAGPPGESGR.e [1xOxidation]	0.0031
COL1A1	A0A452FHU9	[796-825]	1	2736.2132	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [1xDeamidation; 6xOxidation]	0.0017
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	0.0124
COL1A2	A0A3B4ZDV7	[656-685]	1	2767.2666	1	r.GTPGERGEVGPAGAPGFAGPPGADGQPGAR.g [5xOxidation]	0.0119
COL1A2	A0A6P3W0U2	[1115-1139]	1	2769.32	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [3xDeamidation; 1xOxidation]	0.0036
COL1A2	A0A6P3W0U2	[1115-1139]	1	2784.3309	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [2xDeamidation; 2xOxidation]	0.0026
COL1A2	A0A6P3W0U2	[1115-1139]	1	2785.3149	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [3xDeamidation; 2xOxidation]	0.0092
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.0028
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0083
COL1A1	A0A452FHU9	[709-741]	1	2883.4166	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g	-0.0117
COL1A1	A0A452FHU9	[763-795]	1	2883.4231	1	r.GLTGPIGPPGPAGAPGDKGETGPSGPAGPTGAR.g [2xOxidation]	-0.0182
COL1A2	A0A6P3W0U2	[834-866]	0	2921.3773	1	k.GSPGESGPAGAPGTAGPQGQLGSQGFNGLPGGR.g [1xDeamidation]	-0.0014

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[397-429]	1	2932.382	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [1xDeamidation; 6xOxidation]	-0.0157
COL1A1	A0A452FHU9	[709-741]	1	2932.3854	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g [1xDeamidation; 3xOxidation]	-0.019
COL1A2	A0A6P3W0U2	[834-866]	0	3001.3518	1	k.GSPGESGPAGAPGTAGPQGQLGSQGFNGLPGGR.g [1xDeamidation; 5xOxidation]	-0.007
COL1A2	A0A6P3W0U2	[834-866]	0	3002.3358	1	k.GSPGESGPAGAPGTAGPQGQLGSQGFNGLPGGR.g [2xDeamidation; 5xOxidation]	-0.0037
COL1A2	A0A6P3W0U2	[1008-1040]	1	3060.4453	1	k.GLRGHPGLQGMPGPNGPPGDSGPAGSTGHSGPR.g [1xDeamidation]	0.0043
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.0134
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.0006
COL1A2	A0A452G3V6	[422-457]	1	3227.52	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [4xOxidation]	0.0039
COL1A2	A0A3B4ZDV7	[1278-1308]	1	3366.7402	1	k.PNRLPLLDIAPLDIGGADQEFGLDIGPVCFK. [1xCarbamidomethyl; 1xOxidation]	-0.0082
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	0.0047
COL1A1	A0A452FHU9	[322-360]	1	3414.5945	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPR.g [1xDeamidation; 4xOxidation]	0.0027
COL1A2	A0A452G3V6	[843-880]	0	3651.5684	1	r.GSQGSQGPAGPPGPPGPPGPPGPSGGGYDFGFDGDFYR.a [4xOxidation]	-0.0051
COL1A2	A0A452G3V6	[843-880]	0	3652.5524	1	r.GSQGSQGPAGPPGPPGPPGPPGPSGGGYDFGFDGDFYR.a [1xDeamidation; 4xOxidation]	0.0041
Ovotransferrin	P02789	[680-688]	0	1057.5928	1	k.FYTVISSLK.t	0.0196
Alpha-S2-casein	P02663	[204-212]	1	1162.5925	1	k.AMKPWIQPK.t [4xOxidation]	-0.0038
Alpha-S2-casein	P02663	[130-140]	0	1229.6372	1	r.NAVPITPTLNR.e [2xDeamidation; 2xOxidation]	0.0069
Alpha-S2-casein	P02663	[129-140]	1	1383.7703	1	k.RNAVPITPTLNR.e [2xOxidation]	-0.0005
Alpha-S2-casein	P02663	[129-140]	1	1385.7383	1	k.RNAVPITPTLNR.e [2xDeamidation; 2xOxidation]	0.0116

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
Alpha-S1-casein	P02662	[135-147]	1	1508.7526	1	r.LHSMKEGIHAQQK.e [2xDeamidation]	0.0006
Ovalbumin	P01012	[86-105]	1	2316.1242	1	r.DILNQITKPNDVYSFSLASR.l [3xDeamidation; 2xOxidation]	-0.0171
Ovotransferrin	P02789	[517-539]	1	2574.1745	1	r.LCQLCQGSGGIPPEKCVASSHEK.y [3xCarbamidomethyl; 2xOxidation]	-0.0183
Protein TENP	O42273	[306-312]	0	801.4465	1	r.VVLEEGR.a	0.0178
Ovotransferrin	P02789	[38-43]	1	806.3825	1	k.KCNNLR.d [1xCarbamidomethyl; 2xDeamidation]	-0.0098
Ovalbumin	P01012	[86-93]	0	944.5411	1	r.DILNQITK.p	-0.0105
Ovalbumin-related protein Y	P01014	[259-266]	1	1006.568	1	k.TINFDKLR.e	-0.0104
COL1A2	A0A6P3W0U2	[144-152]	0	805.3799	1	r.GTAGSQGAR.g [1xDeamidation]	-0.0161
COL1A1	A0A452FHU9	[1310-1315]	0	811.3985	1	k.NWYISK.n [1xDeamidation]	-0.0072
COL1A1	A0A1S3Q7E3	[102-110]	0	813.3737	1	k.GPQGGDGPK.g [1xDeamidation]	0.0157
COL1A2	A0A6P3W0U2	[34-41]	1	815.4006	1	r.GPKGPDGR.p [2xOxidation]	0.0171
COL1A2	A0A6P3W0U2	[37-44]	1	815.4006	1	k.GPDGRPGK.p [2xOxidation]	0.0171
COL1A2	A0A452G3V6	[924-929]	1	820.4094	1	r.TCRDLR.l [1xCarbamidomethyl]	-0.0194
COL1A2	A0A452G3V6	[1082-1087]	1	821.4152	1	k.KTNEWK.k [1xOxidation]	0.0082
COL1A2	A0A452G3V6	[1083-1088]	1	821.4152	1	k.TNEWKK.t [1xOxidation]	0.0082
COL1A2	A0A452G3V6	[1082-1087]	1	822.3992	1	k.KTNEWK.k [1xDeamidation; 1xOxidation]	-0.0169
COL1A2	A0A452G3V6	[1083-1088]	1	822.3992	1	k.TNEWKK.t [1xDeamidation; 1xOxidation]	-0.0169
COL1A1	A0A452FHU9	[244-252]	0	836.4373	1	r.GPPGPQGAR.g	-0.0114
COL1A1	A0A452FHU9	[1084-1092]	0	836.4373	1	r.GPAGPQGPR.g	-0.0114

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0051
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	-0.0126
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	-0.0126
COL1A1	A0A452FHU9	[1217-1224]	0	859.4268	1	r.ADDANVVR.d	0.0024
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.02
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.02
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.02
COL1A1	A0A452FHU9	[361-369]	0	887.4217	1	r.GSEGPQGVR.g [1xDeamidation]	-0.0034
COL1A3	E6ZHW3	[299-308]	0	892.4635	1	r.PGPPGPSGAR.g	0.0054
COL1A3	E6ZHW3	[551-560]	0	892.4635	1	r.PGPPGPAGSR.g	0.0054
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0117
COL1A1	A0A452FHU9	[361-369]	0	902.4326	1	r.GSEGPQGVR.g [1xOxidation]	0.0098
COL1A1	A0A452FHU9	[564-573]	0	950.469	1	r.PGPPGPPGAR.g [3xOxidation]	0.0137
COL1A1	A0A3P9NHJ7	[484-493]	0	952.4847	1	r.PGPPGPVGAR.g [3xOxidation]	-0.0072
Ovalbumin-related protein Y	P01014	[259-266]	1	1007.552	1	k.TINFDKLR.e [1xDeamidation]	-0.0041
Ovalbumin-related protein Y	P01014	[48-56]	1	1022.4935	1	r.GNTESQMKK.v	0.0147
COL1A2	A0A452G3V6	[968-976]	0	1012.531	1	r.AQPEDIPVK.n [1xOxidation]	0.0038
Ovalbumin-related protein Y	P01014	[48-56]	1	1023.4775	1	r.GNTESQMKK.v [1xDeamidation]	0.0017
Alpha-S2-casein	P02663	[207-214]	1	1029.5728	1	k.PWIQPKTK.v [2xOxidation]	-0.0099

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A3Q2W722	[176-186]	1	1024.5534	1	k.GEPGGAGPKVR.r	-0.0195
Ovotransferrin	P02789	[540-548]	0	1047.5258	1	k.YFGYTGALR.c	0.0148
COL1A1	A0A1S3Q7E3	[896-906]	1	1031.4977	1	r.GGRGETGNAGR.p	0.0009
Ovostatin	P20740	[1278-1286]	1	1098.5313	1	k.INSKNTFEK.v [2xDeamidation; 1xOxidation]	-0.0042
Mucin-5B	Q98UI9	[1722-1731]	0	1144.6572	1	r.EVIVDTLLSR.n	-0.0125
COL1A2	A0A452G3V6	[1120-1128]	0	1048.5496	1	r.LNIGPVCFK. [1xCarbamidomethyl; 1xDeamidation]	-0.0162
COL1A1	A0A452FHU9	[121-131]	1	1050.5439	1	r.GPRGPAGPPGR.d [2xOxidation]	0.0104
Ovalbumin-related protein X	P01013	[207-216]	0	1216.6725	1	r.ADHPFLFLIK.h [1xOxidation]	0.0136
COL1A2	A0A6P3W0U2	[210-221]	1	1069.5497	1	r.GRAGPSGPAGAR.g [1xOxidation]	-0.0141
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	0.0091
Alpha-S2-casein	P02663	[130-140]	0	1228.6532	1	r.NAVPITPTLNR.e [1xDeamidation; 2xOxidation]	-0.0072
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	-0.0049
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.0048
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0061
COL1A1	A0A452FHU9	[733-744]	1	1111.5854	1	r.GAAGLPGPKGDR.g [1xOxidation]	0.0134
COL1A2	A0A6P3W0U2	[1310-1318]	1	1124.5946	1	k.TVIEYRTNK.p [1xDeamidation]	-0.0057
COL1A2	A0A3P9BM02	[931-942]	1	1125.5647	1	r.GAPGPAGPRGEK.g [2xOxidation]	-0.006
COL1A1	A0A452FHU9	[733-744]	1	1127.5804	1	r.GAAGLPGPKGDR.g [2xOxidation]	-0.0131
COL1A1	A0A452FHU9	[253-264]	0	1130.5874	1	r.GLPGTAGLPGMK.g [2xOxidation]	0.0039
COL1A2	A0A452G3V6	[323-334]	0	1138.5851	1	k.EGPAGLPGIDGR.p	-0.008

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A3P9BM02	[436-447]	0	1143.6157	1	r.GLSGNIGFPGPK.g	0.0059
COL1A1	A0A452FHU9	[1310-1318]	1	1149.6051	1	k.NWYISKNPK.d	0.003
COL1A1	A0A452FHU9	[574-585]	0	1161.5721	1	r.GQAGVMGFPGPK.g [1xOxidation]	0.0129
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.0091
Mucin-5B	Q98UI9	[1611-1621]	0	1295.5936	1	r.YCNPGISEPVK.i [1xCarbamidomethyl; 2xOxidation]	0.0184
COL1A1	A0A452FHU9	[1310-1318]	1	1165.6	1	k.NWYISKNPK.d [1xOxidation]	-0.0043
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0014
COL1A1	A0A3P9NHJ7	[1206-1214]	1	1183.5928	1	k.NWYMSKNIK.e	-0.0098
COL1A2	A0A452G3V6	[759-770]	1	1185.5858	1	r.GPSGPQGIRGDK.g [1xDeamidation; 1xOxidation]	-0.0035
COL1A2	A0A452G3V6	[345-356]	0	1185.5899	1	r.GEPGNIGFPGPK.g [1xOxidation]	-0.0075
COL1A2	A0A6P3W0U2	[474-485]	0	1187.6055	1	r.GQPGTIGFPGPK.g [2xOxidation]	0.0119
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.0096
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	-0.0046
COL1A1	A0A3P9NHJ7	[1133-1142]	0	1203.6216	1	k.SLSQQIEQIR.s [2xDeamidation]	-0.0056
Mucin-5B	Q98UI9	[1704-1714]	1	1295.5936	1	r.DQVYKPCGEAK.r [1xCarbamidomethyl; 1xDeamidation]	0.0184
Mucin-5B	Q98UI9	[2020-2029]	1	1295.63	1	r.SMKEQYIVHK.h [1xDeamidation; 2xOxidation]	-0.0179
COL1A2	A0A452G3V6	[881-891]	1	1229.6233	1	r.ADQPRSPASLR.p [2xOxidation]	0.0121
COL1A1	A0A452FHU9	[958-969]	1	1240.6757	1	r.GVVGLPGQRGER.g [1xOxidation]	-0.0009
COL1A1	A0A452FHU9	[958-969]	1	1241.6597	1	r.GVVGLPGQRGER.g [1xDeamidation; 1xOxidation]	-0.0146

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[214-228]	0	1251.6804	1	r.GIPGPVGAAGATGAR.g	0.0046
COL1A2	A0A3P9BM02	[117-129]	1	1263.6553	1	k.PGDRGVPGPQGAR.g	0.0118
Ovalbumin	P01012	[371-382]	0	1345.7375	1	k.HIATNAVLFFGR.c	0.006
Ovostatin	P20740	[1370-1381]	1	1349.7093	1	k.RSSSNMVIIDVK.m [1xDeamidation]	-0.0034
Alpha-S2-casein	P02663	[141-152]	1	1379.6649	1	r.EQLSTSEENSKK.t	0.0199
COL1A1	A0A3P9NHJ7	[1111-1121]	1	1307.6525	1	r.MFRADDANVLR.d	0.0167
COL1A2	A0A452G3V6	[892-902]	1	1310.6474	1	r.PKDYEVDATLK.s [2xOxidation]	0.0081
COL1A1	A0A452FHU9	[415-429]	0	1332.6543	1	r.GPSGPQGPSGPPGPK.g [1xOxidation]	0.0178
COL1A2	A0A3P9BM02	[332-346]	0	1343.6914	1	r.GPTGELGATGLAGAR.g [1xOxidation]	0.009
COL1A1	A0A1S3Q7E3	[1233-1244]	1	1344.6754	1	k.VENIRSPEGSQK.n [1xDeamidation]	0.0016
Mucin-5B	Q98UI9	[1393-1404]	0	1387.725	1	k.LSSITCPPQQLK.l [1xCarbamidomethyl; 1xOxidation]	0.0065
COL1A2	A0A3P9BM02	[278-292]	0	1351.6349	1	r.GGPGPQGPQGAAGPR.g [3xOxidation]	0.018
Mucin-5B	Q98UI9	[1393-1404]	0	1389.693	1	k.LSSITCPPQQLK.l [1xCarbamidomethyl; 2xDeamidation; 1xOxidation]	0.0045
Ovalbumin-related protein Y	P01014	[373-384]	0	1412.7321	1	r.YNPTNAILFFGR.y	0.0032
Ovalbumin-related protein X	P01013	[217-228]	0	1418.7175	1	k.HNPTNTIVYFGR.y	0.0085
COL1A1	A0A3P9NHJ7	[877-891]	0	1409.706	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation]	-0.0001
COL1A1	A0A3P9NHJ7	[772-788]	0	1411.7077	1	r.GAAGPPGATGFPGAAGR.v	-0.0116
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0017
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	-0.0014

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[253-267]	1	1464.774	1	r.GLPGTAGLPGMKGHR.g [1xOxidation]	0.0172
COL1A1	A0A3P9NHJ7	[877-891]	0	1473.6856	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation; 4xOxidation]	-0.0123
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	-0.0018
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	-0.0131
COL1A2	A0A6P3W0U2	[153-167]	1	1508.7791	1	r.GFPGTPGLPGMKGHR.g	-0.0093
COL1A2	A0A3P9BM02	[712-728]	0	1530.7295	1	r.GDNGPSGLTGFPGAAGR.v	0.0114
COL1A1	A0A452FHU9	[1152-1167]	0	1546.786	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	0.011
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	-0.0081
COL1A2	A0A452G3V6	[196-213]	0	1562.8285	1	k.GAAGLPGVAGAPGLPGPR.g [3xOxidation]	-0.0112
COL1A1	A0A3P9NHJ7	[431-447]	1	1568.8027	1	r.GAPGLVGPKGSTGEPGR.t [2xOxidation]	0.0037
COL1A1	A0A452FHU9	[397-414]	0	1570.7608	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 2xOxidation]	0.0031
COL1A2	A0A452G3V6	[404-421]	0	1580.7663	1	r.GPPGESGAAGPTGPIGSR.g [1xOxidation]	0.0079
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	-0.002
COL1A1	A0A452FHU9	[430-447]	1	1586.7405	1	k.GNSGEPGAPGSKGDTGAK.g	0.0109
COL1A1	A0A452FHU9	[397-414]	0	1586.7558	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 3xOxidation]	-0.0043
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	-0.0067
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	-0.0107
COL1A2	A0A452G3V6	[151-168]	0	1632.7976	1	k.GELGPVGNPGPAGPAGPR.g [1xDeamidation; 2xOxidation]	0.0199
COL1A2	A0A452G3V6	[968-980]	1	1632.8016	1	r.AQPEDIPVKNWYR.n [1xDeamidation; 1xOxidation]	0.0158
COL1A3	E6ZHW3	[1214-1227]	1	1636.8276	1	r.DQEVDTTLKTLTQK.v [1xDeamidation; 1xOxidation]	0.0061
COL1A1	A0A452FHU9	[520-537]	1	1655.7984	1	k.GSPGEAGRPGEAGLPGAK.g [3xOxidation]	0.0197

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[493-510]	1	1655.8136	1	r.GFPGSDGVAGPKGPAGER.g	0.0045
COL1A1	A0A1S3Q7E3	[871-891]	0	1687.8398	1	r.VGPPGGSGAPGSAGPPGPAGK.e [1xOxidation]	-0.0111
COL1A3	E6ZHW3	[750-767]	0	1693.8504	1	r.GITGSIGVPGPHGAQGEK.g [2xOxidation]	-0.0095
COL1A1	A0A1S3Q7E3	[752-769]	0	1740.7857	1	r.GMTGPIGPPGPTGAHGEK.g [5xOxidation]	-0.0015
COL1A1	A0A1S3Q7E3	[646-664]	0	1742.794	1	k.AGEQGVPGEVGGPGPSGSR.g [3xOxidation]	0.0029
COL1A2	A0A452G3V6	[1036-1050]	1	1744.8058	1	k.NSIAYMDEETGNLKK.a [2xOxidation]	0.0148
COL1A1	A0A452FHU9	[1152-1169]	1	1759.9086	1	k.DGLNGLPGPIGPPGPRGR.t [1xDeamidation; 2xOxidation]	-0.008
COL1A2	A0A452G3V6	[903-918]	0	1773.8865	1	k.SLNNQIETLLTPEGSR.k [2xDeamidation]	-0.0136
COL1A1	A0A3P9NHJ7	[941-961]	0	1775.8559	1	k.AGAPGAPGPPGAPGPVGPAGK.t [6xOxidation]	0.0086
COL1A1	A0A3P9NHJ7	[874-891]	1	1782.8769	1	r.GERGFPGPPGPAQGEIGK.p [2xOxidation]	0.0139
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	-0.0165
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	-0.0175
COL1A2	A0A3P9BM02	[841-860]	0	1836.9021	1	r.GAPGNIGLPGMTGPQGEAGR.e	-0.0064
COL1A2	A0A6P3W0U2	[474-493]	1	1872.9086	1	r.GQPGTIGFPGPKGPGGEAGK.a [4xOxidation]	-0.009
COL1A2	A0A6P3W0U2	[474-493]	1	1888.9035	1	r.GQPGTIGFPGPKGPGGEAGK.a [5xOxidation]	-0.0043
COL1A2	A0A6P3W0U2	[144-164]	1	1975.9654	1	r.GTAGSQGARGFPGTPGLPGMK.g [2xOxidation]	0.0066
COL1A2	A0A3P9BM02	[121-141]	1	2010.0226	1	r.GVPGPQGARGFPGTPGLPGMK.g [2xOxidation]	0.0092
COL1A2	A0A6P3W0U2	[452-473]	1	2016.9482	1	k.DGPAGPAGQDGRSGPPGPTGPR.g [1xOxidation]	-0.0041
COL1A2	A0A452G3V6	[323-344]	1	2028.0621	1	k.EGPAGLPGIDGRPGPIGPAGAR.g [1xOxidation]	-0.0159
COL1A1	A0A1S3Q7E3	[1378-1396]	1	2056.0669	1	k.ALLLQGANEIEIRAEGNSR.f [2xDeamidation]	-0.0004

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	-0.0002
COL1A1	A0A452FHU9	[552-573]	1	2072.9744	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [5xOxidation]	0.0124
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	-0.0004
COL1A1	A0A452FHU9	[564-585]	1	2094.0073	1	r.PGPPGPPGARGQAGVMGFPGPK.g [1xDeamidation; 4xOxidation]	-0.0024
COL1A1	A0A3P9NHJ7	[484-505]	1	2105.0597	1	r.PGPPGPVGARGQPGVMGFPGPK.g [3xOxidation]	-0.0111
COL1A1	A0A3P9NHJ7	[617-640]	0	2144.0189	1	k.GEPGAPGAPGAAGPPGLQGMPGER.g [1xOxidation]	0.0181
COL1A1	A0A452FHU9	[685-708]	1	2179.9963	1	r.GVQGPPGPAGPRGANGAPGNDGAK.g [1xDeamidation; 5xOxidation]	0.0188
COL1A2	A0A3P9BM02	[883-908]	0	2199.0095	1	r.GEPGSAGAMGLAGAPGPAGPTGAAGR.p [4xOxidation]	-0.0129
COL1A1	A0A1S3Q7E3	[748-769]	1	2199.9757	1	k.DGMRGMTGPIGPPGPTGAHGEK.g [5xOxidation]	0.0101
COL1A1	A0A452FHU9	[970-993]	1	2255.0687	1	r.GFPGLPGPSGEPGKQGPSGASGER.g [2xOxidation]	-0.0123
COL1A1	A0A452FHU9	[970-993]	1	2271.0636	1	r.GFPGLPGPSGEPGKQGPSGASGER.g [3xOxidation]	-0.0032
COL1A1	A0A452FHU9	[442-467]	1	2409.1165	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [3xOxidation]	0.0091
COL1A1	A0A452FHU9	[442-467]	1	2410.1005	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 3xOxidation]	0.0075
COL1A2	A0A6P3W0U2	[315-341]	1	2421.1389	1	r.GGNGPQGPSGPSGQRGLSGDPGPSGVK.g [1xDeamidation; 1xOxidation]	0.0081
COL1A2	A0A452G3V6	[565-591]	0	2468.1728	1	r.GDGGPPVSTYPGFGISGPPGPPGPAGK.e [3xOxidation]	0.0194
COL1A2	A0A6P3W0U2	[45-71]	0	2481.1681	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 1xOxidation]	0.019
COL1A3	E6ZHW3	[1020-1048]	1	2485.1888	1	k.GDRGESGMAGPPGPPGAPGAPGAVGPSGK.s	0.0097
COL1A1	A0A452FHU9	[277-303]	1	2494.0899	1	k.GDAGPAGPKGEPGSPGENGAPGQMGPR.g [1xDeamidation; 3xOxidation]	0.0182
COL1A2	A0A6P3W0U2	[45-71]	0	2497.163	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 2xOxidation]	0.0055
COL1A1	A0A452FHU9	[322-351]	0	2501.2055	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation]	-0.0171
COL1A2	A0A6P3W0U2	[45-71]	0	2513.1579	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 3xOxidation]	0.0146

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[322-351]	0	2549.1903	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 3xOxidation]	-0.0044
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	0.0121
COL1A2	A0A3P9BM02	[37-61]	1	2563.1592	1	r.NFAAQYDGVKGPDPGPGPMGLMGPR.g [2xDeamidation; 2xOxidation]	-0.0026
COL1A2	A0A3P9BM02	[37-61]	1	2578.1701	1	r.NFAAQYDGVKGPDPGPGPMGLMGPR.g [1xDeamidation; 3xOxidation]	-0.0129
COL1A2	A0A3P9BM02	[37-61]	1	2579.1541	1	r.NFAAQYDGVKGPDPGPGPMGLMGPR.g [2xDeamidation; 3xOxidation]	0.0145
COL1A1	A0A452FHU9	[322-351]	0	2581.1801	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 5xOxidation]	-0.0054
COL1A2	A0A6P3W0U2	[222-251]	0	2591.2009	1	r.GADGNTGPSGPAGPLGAAGPPGFPGAPGPK.g [1xDeamidation; 4xOxidation]	-0.0071
COL1A2	A0A3Q2W722	[509-538]	1	2594.219	1	r.GNPGAAGSTGPQGPIGARGPAGTPGADGGK.g [4xOxidation]	0.0019
COL1A2	A0A452G3V6	[535-564]	0	2597.2339	1	k.GENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.0066
COL1A2	A0A452G3V6	[708-736]	1	2607.2434	1	k.GERGYPGNAGPVGAAGAPGPQGPVGPTGK.h [2xDeamidation; 2xOxidation]	0.0131
COL1A2	A0A3P9BM02	[185-214]	0	2653.2012	1	r.GADGNVGPTGPAGPLGAAGPPGFPGGPGPK.g [1xDeamidation; 8xOxidation]	0.0123
COL1A2	A0A452G3V6	[496-525]	1	2698.2452	1	r.GSPGERGEVGPAGPNGFAGPAGAAGQPGAK.g [5xOxidation]	-0.0001
COL1A2	A0A452G3V6	[711-740]	1	2701.3077	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [1xDeamidation; 2xOxidation]	-0.0181
COL1A1	A0A452FHU9	[796-825]	1	2703.2394	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [4xOxidation]	-0.0092
COL1A2	A0A452G3V6	[404-433]	1	2705.2398	1	r.GPPGESGAAGPTGPIGSRGPSGPPGPDGNK.g [5xOxidation]	-0.0179
COL1A2	A0A452G3V6	[711-740]	1	2717.3026	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [1xDeamidation; 3xOxidation]	0.0069
COL1A3	E6ZHW3	[1098-1127]	1	2725.2747	1	r.GFSGMQGLPGPAGPSGERGPAGASGPAGPR.g [3xOxidation]	0.0072
COL1A3	E6ZHW3	[783-812]	1	2727.2241	1	r.GAPGERGETGPAGPAGFAGPPGADGQPGAK.g [6xOxidation]	0.0002
COL1A1	A0A1S3Q7E3	[785-814]	1	2743.2455	1	r.GSPGERGEHGAPGPAGFAGPPGADGQPGNK.g [1xDeamidation; 1xOxidation]	0.0071
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0011
COL1A1	A0A452FHU9	[984-1013]	1	2759.2802	1	k.QGPSGASGERGPPGPMGPPGLAGPPGESGR.e [3xOxidation]	-0.0053

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[711-740]	1	2766.2714	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [2xDeamidation; 6xOxidation]	0.017
COL1A1	A0A1S3Q7E3	[587-619]	1	2792.3082	1	r.GEAGAVGGLGAPGKDGDSGAPGAQGPAGAQGEK.g [1xDeamidation]	-0.0099
COL1A1	A0A1S3Q7E3	[587-619]	1	2793.2922	1	r.GEAGAVGGLGAPGKDGDSGAPGAQGPAGAQGEK.g [2xDeamidation]	-0.0029
COL1A1	A0A452FHU9	[598-630]	1	2865.3762	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [1xDeamidation; 2xOxidation]	0.0101
COL1A1	A0A452FHU9	[397-429]	1	2867.4183	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [2xOxidation]	0.0016
COL1A1	A0A452FHU9	[763-795]	1	2867.4282	1	r.GLTGPIGPPGPAGAPGDKGETGPSGPAGPTGAR.g [1xOxidation]	-0.0083
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0094
COL1A1	A0A452FHU9	[709-741]	1	2883.4166	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g	-0.0128
COL1A1	A0A452FHU9	[763-795]	1	2883.4231	1	r.GLTGPIGPPGPAGAPGDKGETGPSGPAGPTGAR.g [2xOxidation]	-0.0193
COL1A2	A0A6P3W0U2	[609-641]	1	2915.3337	1	k.GEPGAVGPAGAPGHQGPAGMPGERGAGGTPGAK.g [1xDeamidation; 4xOxidation]	-0.0049
COL1A1	A0A3P9NHJ7	[551-582]	1	3001.3631	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [4xOxidation]	-0.0025
COL1A1	A0A3P9NHJ7	[551-582]	1	3002.3471	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [1xDeamidation; 4xOxidation]	-0.0056
COL1A1	A0A3P9NHJ7	[902-933]	1	3017.329	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 6xOxidation]	0.0146
COL1A1	A0A3P9NHJ7	[551-582]	1	3017.358	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [5xOxidation]	-0.0144
COL1A1	A0A3P9NHJ7	[902-933]	1	3018.313	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 6xOxidation]	0.0199
COL1A1	A0A3P9NHJ7	[551-582]	1	3018.342	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [1xDeamidation; 5xOxidation]	-0.0091
COL1A2	A0A3P9BM02	[781-813]	0	3069.4396	1	k.GPSGESGPPGPPGAPGTSGPLGLQGFVGLPGSR.g [8xOxidation]	-0.0155
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.0095
COL1A2	A0A3Q2W722	[755-787]	0	3084.4392	1	k.GPSGESGPPGPPGTPGTSGPLGLQGFVGLPGSR.g [1xDeamidation; 7xOxidation]	-0.0048
COL1A2	A0A452G3V6	[623-655]	0	3093.4912	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [5xOxidation]	0.0112
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.0089

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A1S3Q7E3	[815-850]	1	3116.4264	1	k.GEAGNNGPKGEAGAPGPGGPVGAPGPQGPAGNSGAK.g [5xOxidation]	0.003
COL1A2	A0A452G3V6	[623-655]	0	3157.4709	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [9xOxidation]	0.0015
COL1A3	E6ZHW3	[852-889]	1	3166.5664	1	r.GGAGTPGATGFPGPAGRVGPPGPSGAGGPPGPAGPVGK.d [3xOxidation]	-0.0117
COL1A2	A0A452G3V6	[422-457]	1	3227.52	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [4xOxidation]	-0.017
COL1A2	A0A452G3V6	[780-815]	1	3350.7101	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 2xOxidation]	0.0107
COL1A1	A0A452FHU9	[1433-1463]	1	3380.6719	1	k.TSRLPIIDVAPLDVGAPDQEFGFDIGSVCFL. [1xCarbamidomethyl; 2xOxidation]	0.0186
COL1A1	A0A452FHU9	[1433-1463]	1	3396.6668	1	k.TSRLPIIDVAPLDVGAPDQEFGFDIGSVCFL. [1xCarbamidomethyl; 3xOxidation]	0.0007
COL1A1	A0A452FHU9	[1433-1463]	1	3397.6508	1	k.TSRLPIIDVAPLDVGAPDQEFGFDIGSVCFL. [1xCarbamidomethyl; 1xDeamidation; 3xOxidation]	0.0127
COL1A2	A0A6P3W0U2	[1011-1051]	1	3722.6484	1	r.GHPGLQGMPGPNGPPGDSGPAGSTGHSGPRGPAGPSGPSGK.d [1xDeamidation; 6xOxidation]	-0.0188
COL1A1	A0A452FHU9	[1111-1151]	1	3723.6753	1	r.GFSGLQGPPGPPGSPGEQGPSGASGPAGPRGPPGSAGTPGK.d [10xOxidation]	-0.0012
Ovostatin	P20740	[147-158]	1	1439.7351	1	k.PIYKPGQSVMFR.v [1xDeamidation; 1xOxidation]	0.0154
Ovalbumin	P01012	[208-219]	0	1515.7334	1	k.PVQMMYQIGLFR.v [1xDeamidation; 2xOxidation]	0.0129
Ovotransferrin	P02789	[141-154]	0	1534.8489	1	r.SAGWNIPIGTLLHR.g	-0.0086
Ovalbumin	P01012	[188-200]	1	1555.721	1	k.AFKDEDTQAMPFR.v	0.0192
Mucin-5B	Q98UI9	[941-955]	1	1677.833	1	r.IQEIATDPGAEKNYK.v [1xDeamidation]	-0.0182
Ovalbumin-related protein Y	P01014	[111-124]	1	1686.852	1	k.TFSVLPEYLSCARK.f [1xCarbamidomethyl; 1xOxidation]	-0.009
Ovotransferrin	P02789	[602-616]	0	1709.8639	1	r.ECNLAEVPTHAVVVR.p [1xCarbamidomethyl; 1xOxidation]	-0.0127
Ovotransferrin	P02789	[602-616]	0	1710.8479	1	r.ECNLAEVPTHAVVVR.p [1xCarbamidomethyl; 1xDeamidation; 1xOxidation]	0.0061
Alpha-S1-casein	P02662	[23-37]	0	1761.913	1	k.HQGLPQEVLNENLLR.f [2xDeamidation]	0.0038

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
Ovalbumin	P01012	[371-386]	1	1804.9163	1	k.HIATNAVLFFGRCVSP. [1xCarbamidomethyl; 1xOxidation]	-0.0142
Avidin	P02701	[34-50]	0	1837.8385	1	k.WTNDLGSNMTIGAVNSR.g [2xDeamidation]	-0.014
Ovalbumin	P01012	[144-159]	0	1859.9498	1	r.ELINSWVESQTNGIIR.n [1xDeamidation]	-0.0106
Protein TENP	O42273	[51-71]	0	2239.1063	1	k.EPQTCSLAPWSPAGTELPAVK.v [1xCarbamidomethyl]	0.0012
Ovostatin	P20740	[666-685]	1	2241.1042	1	r.PLTSGLGPDVYQFLRDMGMK.f [1xOxidation]	-0.0027
Ovalbumin	P01012	[124-143]	1	2266.1099	1	k.ELYRGGLEPINFQTAADQAR.e [1xDeamidation; 1xOxidation]	-0.0161
Alpha-S2-casein	P02663	[130-151]	1	2445.2104	1	r.NAVPITPTLNREQLSTSEENSK.k [1xDeamidation; 1xOxidation]	-0.0158
Alpha-S2-casein	P02663	[130-151]	1	2461.2053	1	r.NAVPITPTLNREQLSTSEENSK.k [1xDeamidation; 2xOxidation]	-0.017
Ovotransferrin	P02789	[95-119]	1	2713.3719	1	k.PIAAEVYEHTEGSTTSYYAVAVVKK.g	-0.0005
Ovotransferrin	P02789	[67-94]	1	2879.4421	1	k.AIANNEADAISLDGGQAFEAGLAPYKLK.p [2xOxidation]	-0.0164
Ovotransferrin	P02789	[67-94]	1	2880.4262	1	k.AIANNEADAISLDGGQAFEAGLAPYKLK.p [1xDeamidation; 2xOxidation]	-0.0071
Ovalbumin	P01012	[21-47]	0	3067.4726	1	k.VHHANENIFYCPIAIMSALAMVYLGAK.d [1xCarbamidomethyl; 2xDeamidation; 2xOxidation]	0.0149
Ovostatin	P20740	[159-185]	1	3167.5129	1	r.VVALDFNFKPVQEMYPLIAVQDPQNNR.i [6xDeamidation; 1xOxidation]	0.0052
Ovostatin	P20740	[159-185]	1	3211.5616	1	r.VVALDFNFKPVQEMYPLIAVQDPQNNR.i [2xDeamidation; 4xOxidation]	0.003
Ovalbumin-related protein Y	P01014	[153-182]	1	3381.7287	1	k.ETNGQIKDLLVSSSIDFGTTMVFINTIYFK.g	0.0177
Ovalbumin	P01012	[86-93]	0	944.5411	1	r.DILNQITK.p	-0.019
Ovalbumin	P01012	[48-56]	1	1062.5538	1	k.DSTRTQINK.v	0.0029
COL1A2	A0A6P3W0U2	[144-152]	0	805.3799	1	r.GTAGSQGAR.g [1xDeamidation]	0.005
COL1A2	A0A452G3V6	[1082-1087]	1	806.4043	1	k.KTNEWK.k [1xDeamidation]	-0.0063
COL1A2	A0A452G3V6	[1083-1088]	1	806.4043	1	k.TNEWKK.t [1xDeamidation]	-0.0063

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1310-1315]	0	811.3985	1	k.NWYISK.n [1xDeamidation]	-0.0014
COL1A1	A0A3Q3CY74	[346-354]	0	813.385	1	r.GPEGPGGAR.g [1xOxidation]	-0.0104
COL1A2	A0A6P3W0U2	[34-41]	1	815.4006	1	r.GPKGPDGR.p [2xOxidation]	0.0115
COL1A2	A0A6P3W0U2	[37-44]	1	815.4006	1	k.GPDGRPGK.p [2xOxidation]	0.0115
COL1A2	A0A452G3V6	[924-929]	1	820.4094	1	r.TCRDLR.l [1xCarbamidomethyl]	0.0034
COL1A1	A0A452FHU9	[244-252]	0	836.4373	1	r.GPPGPQGAR.g	-0.0054
COL1A1	A0A452FHU9	[1084-1092]	0	836.4373	1	r.GPAGPQGPR.g	-0.0054
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	0.0078
COL1A2	A0A6P3W0U2	[1303-1309]	0	844.3948	1	r.HTGQWSK.t [1xDeamidation]	0.0112
COL1A2	A0A6P3W0U2	[651-658]	0	849.4213	1	r.GLEGNFGR.d	0.0002
COL1A1	A0A452FHU9	[312-321]	0	850.453	1	r.PGAPGPAGAR.g	-0.0056
COL1A1	A0A452FHU9	[268-276]	0	851.4258	1	r.GFSGLDGAK.g	0.0195
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	0.0057
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	0.0057
COL1A2	A0A6P3W0U2	[212-221]	0	856.4272	1	r.AGPSGPAGAR.g [1xOxidation]	0.0125
COL1A2	A0A452G3V6	[111-120]	0	868.4635	1	r.VGAPGPAGAR.g [1xOxidation]	-0.0089
COL1A2	A0A452G3V6	[759-767]	0	868.4635	1	r.GPSGPQGIR.g	-0.0089
COL1A1	A0A452FHU9	[361-369]	0	886.4377	1	r.GSEGPQGVR.g	0.0043
COL1A2	A0A452G3V6	[335-344]	0	892.4999	1	r.PGPIGPAGAR.g	-0.0109
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0009

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[272-281]	0	902.4513	1	r.AGVMGPAGSR.g	0.0088
COL1A2	A0A3P8YWE6	[914-922]	1	904.4483	1	k.GVAGEKGDR.g [1xOxidation]	0.0121
COL1A1	A0A3Q3CY74	[549-558]	0	905.4588	1	r.PGPPGPGGNR.g	0.0004
COL1A2	A0A452G3V6	[335-344]	0	908.4948	1	r.PGPIGPAGAR.g [1xOxidation]	0.0016
COL1A2	A0A452G3V6	[816-826]	0	909.4789	1	r.GPAGPTGPAGK.d	-0.0152
COL1A1	A0A452FHU9	[564-573]	0	918.4792	1	r.PGPPGPPGAR.g [1xOxidation]	-0.0079
COL1A1	A0A452FHU9	[564-573]	0	934.4741	1	r.PGPPGPPGAR.g [2xOxidation]	0
COL1A2	A0A6P3W0U2	[642-650]	1	936.4534	1	k.GEKGEGGFR.g	0.0025
COL1A1	A0A3P9NHJ7	[484-493]	0	952.4847	1	r.PGPPGPVGAR.g [3xOxidation]	-0.0002
COL1A3	A0A2D0SA79	[1015-1024]	1	969.4748	1	r.DGAPGPKGDR.g	0.0166
COL1A1	A0A077B3P8	[514-523]	0	974.4248	1	r.NGEPGMPGSK.g [1xDeamidation]	0.0175
COL1A2	A0A6P3W0U2	[926-935]	1	975.5007	1	r.PGAAGFKGDR.g	-0.0126
COL1A2	A0A6P3W0U2	[633-644]	1	1029.5323	1	r.GAGGTPGAKGEK.g	0.0132
COL1A1	A0A452FHU9	[1-8]	0	1030.5026	1	.MFSFVDLR.l [1xOxidation]	0.0055
COL1A2	A0A3P8YWE6	[128-139]	1	1037.5599	1	r.GRAGPAGPAGAR.g	-0.0137
COL1A2	A0A452G3V6	[1120-1128]	0	1048.5496	1	r.LNIGPVCFK. [1xCarbamidomethyl; 1xDeamidation]	-0.0114
COL1A1	A0A452FHU9	[121-131]	1	1050.5439	1	r.GPRGPAGPPGR.d [2xOxidation]	-0.0166
COL1A2	A0A6P3W0U2	[210-221]	1	1053.5548	1	r.GRAGPSGPAGAR.g	0.0101
COL1A2	A0A6P3W0U2	[633-644]	1	1061.5222	1	r.GAGGTPGAKGEK.g [2xOxidation]	-0.0001
COL1A1	A0A452FHU9	[310-321]	1	1063.5756	1	r.GRPGAPGPAGAR.g	-0.017
COL1A2	A0A6P3W0U2	[210-221]	1	1069.5497	1	r.GRAGPSGPAGAR.g [1xOxidation]	-0.0071

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A3	A0A2D0SA79	[1073-1084]	1	1071.5541	1	r.GAVGPAGARGDK.g [1xOxidation]	-0.0031
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	0.0084
COL1A1	A0A3P9NHJ7	[472-483]	0	1085.5334	1	k.IGASGAPGQDGR.p	0.0108
COL1A1	A0A3P9NHJ7	[389-400]	1	1085.5446	1	r.GSRGEPGAAGAR.g	-0.0004
COL1A1	A0A452FHU9	[493-504]	0	1088.5371	1	r.GFPGSDGVAGPK.g	0.0167
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	0.0098
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.0004
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0144
COL1A2	A0A3P8YWE6	[902-913]	1	1109.5698	1	r.GAPGPAGPRGEK.g [1xOxidation]	-0.0096
COL1A1	A0A0F7R0Z6	[727-738]	1	1111.6218	1	r.GAAGLPGIKGDR.g	-0.006
COL1A2	A0A6P3W0U2	[1310-1318]	1	1123.6106	1	k.TVIEYRTNK.p	0.0061
COL1A2	A0A452G3V6	[1089-1097]	1	1125.615	1	k.TIIEYKTNK.p [1xOxidation]	0.0172
COL1A1	A0A452FHU9	[253-264]	0	1130.5874	1	r.GLPGTAGLPGMK.g [2xOxidation]	0.0179
COL1A2	A0A452G3V6	[323-334]	0	1138.5851	1	k.EGPAGLPGIDGR.p	0.0047
COL1A1	A0A0F7R0Z6	[727-738]	1	1143.6117	1	r.GAAGLPGIKGDR.g [2xOxidation]	0.02
COL1A1	A0A452FHU9	[1310-1318]	1	1149.6051	1	k.NWYISKNPK.d	-0.0025
COL1A1	A0A077B3P8	[1295-1303]	1	1154.5841	1	k.NWYTSKNIK.e [1xDeamidation]	0.0187
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.01
COL1A1	A0A452FHU9	[1310-1318]	1	1165.6	1	k.NWYISKNPK.d [1xOxidation]	0.009

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0159
COL1A1	A0A3P9NHJ7	[1206-1214]	1	1183.5928	1	k.NWYMSKNIK.e	0.0049
COL1A2	A0A452G3V6	[759-770]	1	1185.5858	1	r.GPSGPQGIRGDK.g [1xDeamidation; 1xOxidation]	0.0129
COL1A2	A0A452G3V6	[345-356]	0	1185.5899	1	r.GEPGNIGFPGPK.g [1xOxidation]	0.0089
COL1A3	A0A2D0SA79	[1222-1231]	1	1188.6583	1	k.SISQKIENIR.s [1xDeamidation]	0.0019
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.0055
COL1A2	A0A452G3V6	[759-770]	1	1200.5967	1	r.GPSGPQGIRGDK.g [2xOxidation]	0.0099
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	0.0161
COL1A1	A0A3P9NHJ7	[1133-1142]	0	1203.6216	1	k.SLSQQIEQIR.s [2xDeamidation]	0.0174
COL1A1	A0A3P9NHJ7	[1133-1142]	0	1204.6056	1	k.SLSQQIEQIR.s [3xDeamidation]	0.011
COL1A2	A0A3P8YWE6	[973-985]	0	1215.6341	1	r.AGSHGAIGPVGHR.g	0.0184
COL1A2	A0A452G3V6	[881-891]	1	1229.6233	1	r.ADQPRSPASLR.p [2xOxidation]	0.0067
COL1A1	A0A3P9NHJ7	[865-876]	1	1239.6804	1	r.GIVGLPGQRGER.g [1xDeamidation]	0.0121
COL1A2	A0A6P3W0U2	[494-506]	1	1240.6644	1	k.AGEKGPTGPTGLR.g	-0.0167
COL1A2	A0A3P8YWE6	[58-70]	1	1241.5981	1	k.PGDRGGPGTQGAR.g [1xOxidation]	0.0159
COL1A3	A0A2D0SA79	[1227-1237]	1	1243.6641	1	k.IENIRSPEGTK.t	0.0146
COL1A2	A0A452G3V6	[214-228]	0	1251.6804	1	r.GIPGPVGAAGATGAR.g	-0.0057
COL1A2	A0A452G3V6	[309-322]	0	1255.643	1	r.GFPGSPGNIGPAGK.e	-0.0027
COL1A2	A0A3P8YWE6	[788-801]	0	1260.6695	1	k.GLPGAPGPVGEPGR.l	0
COL1A2	A0A452G3V6	[214-228]	0	1267.6753	1	r.GIPGPVGAAGATGAR.g [1xOxidation]	0.0122

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A3P8YWE6	[788-801]	0	1292.6593	1	k.GLPGAPGPVGEPGR.l [2xOxidation]	-0.0004
COL1A2	A0A6P3W0U2	[387-400]	1	1295.7179	1	r.GASGTRGLPGLPGR.a	-0.0107
COL1A3	A0A2D0SA79	[461-475]	0	1305.6546	1	r.GEPGGTGPVGPPGAR.g	0.0042
COL1A2	A0A6P3W0U2	[387-400]	1	1311.7128	1	r.GASGTRGLPGLPGR.a [1xOxidation]	-0.0193
COL1A2	A0A3P8YWE6	[305-318]	1	1324.708	1	r.GGVGNRGVPGLEGR.a	-0.0085
COL1A3	A0A2D0SA79	[1372-1384]	0	1401.722	1	k.ALLLQGSNDAEIR.a [2xDeamidation]	0.0195
COL1A1	A0A3P9NHJ7	[877-891]	0	1409.706	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation]	0.02
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0097
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.0077
COL1A1	A0A077B3P8	[904-919]	0	1464.7329	1	r.TGEIGTPGPPGAPGEK.g	-0.0009
COL1A1	A0A3P9NHJ7	[877-891]	0	1473.6856	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation; 4xOxidation]	0.0067
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0052
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	-0.006
COL1A2	A0A452G3V6	[827-842]	1	1508.7928	1	k.DGRTGQPGAVGPAGIR.g	-0.0093
COL1A2	A0A3P8YWE6	[286-301]	1	1515.751	1	k.RGSTGEPGATGPAGLR.g [2xOxidation]	0.0069
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	0.0008
COL1A1	A0A452FHU9	[1152-1167]	0	1546.786	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	0.0097
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	0.003
COL1A1	A0A452FHU9	[1152-1167]	0	1561.7969	1	k.DGLNGLPGPIGPPGPR.g [3xOxidation]	0.0169
COL1A2	A0A452G3V6	[196-213]	0	1562.8285	1	k.GAAGLPGVAGAPGLPGPR.g [3xOxidation]	-0.0034

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[397-414]	0	1569.7768	1	k.GANGAPGIAGAPGFPGAR.g [2xOxidation]	-0.0022
COL1A3	A0A2D0SA79	[386-403]	0	1570.7972	1	k.GSPGAAGITGAPGFPGTR.g	-0.0161
COL1A2	A0A452G3V6	[404-421]	0	1580.7663	1	r.GPPGESGAAGPTGPIGSR.g [1xOxidation]	0.0156
COL1A2	A0A452G3V6	[59-72]	1	1583.7781	1	r.NSCLTHPKGLMGPR.g [1xCarbamidomethyl; 1xOxidation]	0.0151
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0036
COL1A1	A0A452FHU9	[397-414]	0	1586.7558	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 3xOxidation]	0.0137
COL1A2	A0A6P3W0U2	[1303-1315]	1	1604.818	1	r.HTGQWSKTVIEYR.t	-0.0175
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	-0.004
COL1A1	A0A452FHU9	[268-285]	1	1617.7867	1	r.GFSGLDGAKGDAGPAGPK.g [1xOxidation]	0.0052
COL1A2	A0A452G3V6	[968-980]	1	1632.8016	1	r.AQPEDIPVKNWYR.n [1xDeamidation; 1xOxidation]	0.0191
COL1A2	A0A6P3W0U2	[369-386]	0	1643.7984	1	r.GSTGEQGASGPAGLLGPR.g [2xOxidation]	-0.0006
COL1A1	A0A0F7R0Z6	[961-977]	1	1658.8133	1	r.GERGFSGLPGPTGEPGK.q [1xOxidation]	0.0007
COL1A1	A0A0F7R0Z6	[961-977]	1	1690.8031	1	r.GERGFSGLPGPTGEPGK.q [3xOxidation]	-0.0046
COL1A1	A0A452FHU9	[612-630]	0	1706.7729	1	k.DGEAGAQGPPGPAGPAGER.g [1xOxidation]	0.0063
COL1A1	A0A3P9NHJ7	[587-604]	1	1709.8718	1	r.GFPGERGAPGPIGPAGTR.g [1xOxidation]	-0.0046
COL1A1	A0A3Q3CY74	[867-887]	0	1722.8922	1	r.VGPPGPAGNAGPPGAPGPAGK.e	-0.0155
COL1A1	A0A3Q3CY74	[579-596]	1	1745.8123	1	k.PGERGTMGPTGPVGAPGK.d [5xOxidation]	0.0125
COL1A1	A0A452FHU9	[352-369]	1	1783.8318	1	k.GEAGPQGPRGSEGPQGVR.g [3xOxidation]	0.0003
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	-0.0083
COL1A1	A0A3Q3CY74	[867-887]	0	1802.8668	1	r.VGPPGPAGNAGPPGAPGPAGK.e [5xOxidation]	-0.0181

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1236-1251]	1	1803.8719	1	k.SLSQQIENIRSPEGSR.k [3xDeamidation]	0.0192
COL1A1	A0A0F7R0Z6	[1230-1245]	1	1804.8923	1	k.SLSQQIENIRSPEGTK.k [2xDeamidation; 1xOxidation]	0.0157
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	-0.0086
COL1A1	A0A452FHU9	[882-902]	0	1828.8824	1	r.VGPPGPSGNAGPPGPPGPAGK.e [4xOxidation]	-0.0091
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	-0.0075
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.014
COL1A1	A0A3Q3CY74	[433-452]	0	1837.8563	1	k.GEAGVSGVQGPPGPPGEEGK.r [2xOxidation]	0.0129
COL1A1	A0A452FHU9	[994-1013]	0	1848.8545	1	r.GPPGPMGPPGLAGPPGESGR.e [4xOxidation]	0.0052
COL1A1	A0A452FHU9	[448-467]	0	1848.861	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 1xOxidation]	-0.0013
COL1A3	A0A2D0SA79	[437-456]	0	1868.8145	1	k.GEPGPAGPQGLAGPPGDEGK.r [1xDeamidation; 5xOxidation]	0.0096
COL1A2	A0A6P3W0U2	[474-493]	1	1872.9086	1	r.GQPGTIGFPGPKGPGGEAGK.a [4xOxidation]	0.0114
COL1A2	A0A6P3W0U2	[474-493]	1	1888.9035	1	r.GQPGTIGFPGPKGPGGEAGK.a [5xOxidation]	0.0161
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0126
COL1A1	A0A0F7R0Z6	[546-567]	1	2011.9064	1	k.TGPAGPAGQDGRAGPPGPSGAR.g [1xDeamidation; 5xOxidation]	-0.0137
COL1A1	A0A3Q3CY74	[537-558]	1	2015.9464	1	k.MGPSGAPGQDGRPGPPGPGGNR.g	-0.0117
COL1A1	A0A452FHU9	[448-468]	1	2019.973	1	k.GEPGPTGIQGPPGPAGEEGKR.g [2xOxidation]	0.0054
COL1A2	A0A452G3V6	[323-344]	1	2028.0621	1	k.EGPAGLPGIDGRPGPIGPAGAR.g [1xOxidation]	-0.0198
COL1A1	A0A452FHU9	[552-573]	1	2040.9846	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [3xOxidation]	-0.0092
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0062

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.0046
COL1A1	A0A452FHU9	[934-957]	0	2073.9948	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 1xOxidation]	0.0037
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	0.0081
COL1A1	A0A452FHU9	[528-551]	1	2104.0669	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t	-0.0001
COL1A1	A0A3P9NHJ7	[484-505]	1	2106.0437	1	r.PGPPGPVGARGQPGVMGFPGPK.g [1xDeamidation; 3xOxidation]	-0.0016
COL1A1	A0A452FHU9	[528-551]	1	2120.0618	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t [1xOxidation]	0.0136
COL1A1	A0A452FHU9	[1036-1061]	0	2153.0622	1	r.GETGPAGPPGAPGAPGAPGPVGPAGK.s [2xOxidation]	-0.0032
COL1A1	A0A3Q3CY74	[513-536]	1	2180.0288	1	r.TGEPGLPGAKGMTGSPGNPGPDGK.m [1xDeamidation]	-0.0123
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	0.0173
COL1A1	A0A077B3P8	[514-537]	1	2199.9645	1	r.NGEPGMPGSKGMTGSPGSPGPDGK.t [1xDeamidation]	0.0154
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.0096
COL1A1	A0A452FHU9	[442-467]	1	2377.1266	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xOxidation]	0.0158
COL1A2	A0A452G3V6	[502-528]	1	2409.1542	1	r.GEVGPAGPNGFAGPAGAAGQPGAKGER.g [2xOxidation]	0.006
COL1A1	A0A452FHU9	[442-467]	1	2410.1005	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 3xOxidation]	0.0155
COL1A2	A0A6P3W0U2	[45-71]	0	2465.1732	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation]	0.0132
COL1A2	A0A6P3W0U2	[45-71]	0	2481.1681	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 1xOxidation]	0.0059
COL1A2	A0A6P3W0U2	[45-71]	0	2497.163	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 2xOxidation]	-0.0012
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	0.0063
COL1A2	A0A3P8YWE6	[620-646]	1	2563.1444	1	r.GEVGPAGPPGFAGPHGADGQPGPRGDK.g [1xDeamidation; 5xOxidation]	0.0009
COL1A1	A0A3P9NHJ7	[1184-1205]	1	2574.1521	1	k.VYCNMDTGETCITPTQPEVAKK.n [2xCarbamidomethyl; 2xOxidation]	0.0028
COL1A2	A0A3P8YWE6	[620-646]	1	2578.1553	1	r.GEVGPAGPPGFAGPHGADGQPGPRGDK.g [6xOxidation]	0.0026

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A0F7R0Z6	[829-858]	1	2580.1921	1	k.GDAGSPGPAGPTGAPGPAGNVGATGPKGSR.g [1xDeamidation; 4xOxidation]	-0.019
COL1A2	A0A6P3W0U2	[933-961]	1	2582.1826	1	k.GDRGEPGSNGPSGLSGAPGPAGPAGAVGR.p [5xOxidation]	-0.0184
COL1A2	A0A6P3W0U2	[222-251]	0	2591.2009	1	r.GADGNTGPSGPAGPLGAAGPPGFPGAPGPK.g [1xDeamidation; 4xOxidation]	-0.0022
COL1A3	A0A2D0SA79	[1022-1050]	1	2613.1924	1	k.GDRGESGHAGAPGAPGPPGPPGPVGPSGK.h [6xOxidation]	0.0123
COL1A1	A0A3Q3CY74	[1096-1125]	0	2670.1849	1	r.GFTGMQGPPGPAGPSGESGPAGAAGPAGPR.g [5xOxidation]	0.0122
COL1A2	A0A3P8YWE6	[929-958]	0	2689.2206	1	r.GHGGLQGMPGPNGPAGETGASGMTGPAGPR.g [1xOxidation]	-0.0089
COL1A1	A0A3Q3CY74	[781-810]	1	2701.2601	1	r.GPPGERGEAGPPGPAGFAGPPGADGQPGAK.g [3xOxidation]	0.011
COL1A2	A0A3P8YWE6	[929-958]	0	2705.2155	1	r.GHGGLQGMPGPNGPAGETGASGMTGPAGPR.g [2xOxidation]	0.0013
COL1A3	A0A2D0SA79	[1025-1054]	1	2718.2615	1	r.GESGHAGAPGAPGPPGPPGPVGPSGKHGDR.g [4xOxidation]	-0.0118
COL1A2	A0A3P8YWE6	[802-831]	1	2735.2988	1	r.LGPAGASGPRGPVGNIGMPGMNGAQGEAGR.e [2xDeamidation]	-0.0103
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0042
COL1A2	A0A452G3V6	[711-740]	1	2766.2714	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [2xDeamidation; 6xOxidation]	0.0108
COL1A1	A0A0F7R0Z6	[1105-1134]	0	2767.2554	1	r.GFTGLQGLPGPAGHSGEQGPAGASGPAGPR.g [2xDeamidation; 5xOxidation]	0.0051
COL1A2	A0A6P3W0U2	[1115-1139]	1	2769.32	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [3xDeamidation; 1xOxidation]	-0.0065
COL1A2	A0A6P3W0U2	[1115-1139]	1	2784.3309	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [2xDeamidation; 2xOxidation]	-0.0139
COL1A2	A0A6P3W0U2	[1115-1139]	1	2785.3149	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [3xDeamidation; 2xOxidation]	-0.0039
COL1A1	A0A077B3P8	[788-820]	1	2864.3446	1	r.GETGAPGPAGFAGPPGADGLPGAKGEAGDNGAK.g [1xOxidation]	0.0117
COL1A2	A0A6P3W0U2	[609-641]	1	2867.3489	1	k.GEPGAVGPAGAPGHQGPAGMPGERGAGGTPGAK.g [1xDeamidation; 1xOxidation]	0.0054

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.0148
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0177
COL1A1	A0A452FHU9	[397-429]	1	2899.4082	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [4xOxidation]	-0.0117
COL1A1	A0A452FHU9	[709-741]	1	2899.4115	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g [1xOxidation]	-0.0151
COL1A1	A0A3P9NHJ7	[902-933]	1	3001.3341	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 5xOxidation]	0.0145
COL1A1	A0A3P9NHJ7	[551-582]	1	3001.3631	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [4xOxidation]	-0.0145
COL1A1	A0A3P9NHJ7	[902-933]	1	3002.3181	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 5xOxidation]	0.0099
COL1A1	A0A3P9NHJ7	[551-582]	1	3002.3471	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [1xDeamidation; 4xOxidation]	-0.0191
COL1A1	A0A3P9NHJ7	[902-933]	1	3017.329	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 6xOxidation]	-0.0046
COL1A1	A0A3P9NHJ7	[902-933]	1	3018.313	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 6xOxidation]	0.006
COL1A3	A0A2D0SA79	[923-958]	1	3084.4729	1	r.GSPGSDGPAGPAGAPGPQGIGGGVGIAGSPGQRGER.g [2xDeamidation]	-0.0137
COL1A3	A0A2D0SA79	[815-850]	1	3100.3839	1	k.GEHGDTGPKGDAGPPGPSGPGGASGPQGPAGATGAK.g [1xDeamidation; 3xOxidation]	-0.0005
COL1A3	A0A2D0SA79	[350-385]	1	3100.3951	1	r.GSEGPQGARGEPGNSGPAGAAGPSGPPGNDGSPGAK.g [1xDeamidation]	-0.0118
COL1A2	A0A452G3V6	[422-457]	1	3227.52	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [4xOxidation]	0.0119
COL1A2	A0A452G3V6	[780-815]	1	3365.721	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [3xOxidation]	0.0116
Ovalbumin	P01012	[208-219]	0	1514.7494	1	k.PVQMMYQIGLFR.v [2xOxidation]	0.0015
COL1A1	A0A452FHU9	[237-243]	1	800.4009	1	k.PGRPGER.g [2xOxidation]	0.0171
COL1A2	A0A452G3V6	[1082-1087]	1	806.4043	1	k.KTNEWK.k [1xDeamidation]	-0.0133
COL1A2	A0A452G3V6	[1083-1088]	1	806.4043	1	k.TNEWKK.t [1xDeamidation]	-0.0133
COL1A1	A0A452FHU9	[1310-1315]	0	811.3985	1	k.NWYISK.n [1xDeamidation]	-0.0107

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A3P9NHJ7	[210-218]	0	815.3894	1	k.GDTGPAGPK.g [1xOxidation]	0.0109
COL1A2	A0A452G3V6	[1082-1087]	1	822.3992	1	k.KTNEWK.k [1xDeamidation; 1xOxidation]	-0.0031
COL1A2	A0A452G3V6	[1083-1088]	1	822.3992	1	k.TNEWKK.t [1xDeamidation; 1xOxidation]	-0.0031
COL1A1	A0A452FHU9	[244-252]	0	836.4373	1	r.GPPGPQGAR.g	-0.0131
COL1A1	A0A452FHU9	[1084-1092]	0	836.4373	1	r.GPAGPQGPR.g	-0.0131
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0115
COL1A1	A0A3P9NHJ7	[177-185]	0	842.4115	1	r.GPSGPQGAR.g [1xOxidation]	0.0173
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	0.002
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	0.002
COL1A1	A0A452FHU9	[244-252]	0	853.4163	1	r.GPPGPQGAR.g [1xDeamidation; 1xOxidation]	0.0037
COL1A1	A0A452FHU9	[1084-1092]	0	853.4163	1	r.GPAGPQGPR.g [1xDeamidation; 1xOxidation]	0.0037
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.0176
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.0176
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.0176
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.013
COL1A1	A0A452FHU9	[361-369]	0	902.4326	1	r.GSEGPQGVR.g [1xOxidation]	0.0125
COL1A1	A0A3P9NHJ7	[892-901]	0	942.4275	1	k.PGPAGPGGER.g [3xOxidation]	0.0138
COL1A1	A0A452FHU9	[564-573]	0	950.469	1	r.PGPPGPPGAR.g [3xOxidation]	0.0049
COL1A1	A0A3P9NHJ7	[484-493]	0	952.4847	1	r.PGPPGPVGAR.g [3xOxidation]	-0.0187

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[51-58]	0	953.4509	1	k.TSLSGMWR.n [1xOxidation]	0.0087
COL1A2	A0A452G3V6	[1-8]	0	1010.4975	1	.MLSFVDTR.t [1xAcetyl]	0.0018
COL1A2	A0A452G3V6	[299-308]	0	1010.5088	1	r.PGEPGLMGPR.g	-0.0095
COL1A1	A0A452FHU9	[1-8]	0	1030.5026	1	.MFSFVDLR.l [1xOxidation]	0.0013
COL1A2	A0A452G3V6	[1120-1128]	0	1048.5496	1	r.LNIGPVCFK. [1xCarbamidomethyl; 1xDeamidation]	-0.0056
COL1A1	A0A452FHU9	[310-321]	1	1063.5756	1	r.GRPGAPGPAGAR.g	-0.0124
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	0.0066
COL1A1	A0A3P9NHJ7	[472-483]	0	1085.5334	1	k.IGASGAPGQDGR.p	0.0042
COL1A1	A0A3P9NHJ7	[389-400]	1	1085.5446	1	r.GSRGEPGAAGAR.g	-0.0071
COL1A1	A0A452FHU9	[907-917]	1	1086.5287	1	k.GPRGETGPAGR.p [2xOxidation]	-0.0094
COL1A1	A0A452FHU9	[493-504]	0	1088.5371	1	r.GFPGSDGVAGPK.g	-0.0027
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	0.0046
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.0032
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0133
COL1A1	A0A452FHU9	[733-744]	1	1127.5804	1	r.GAAGLPGPKGDR.g [2xOxidation]	-0.0188
COL1A2	A0A452G3V6	[323-334]	0	1138.5851	1	k.EGPAGLPGIDGR.p	-0.0142
COL1A1	A0A452FHU9	[574-585]	0	1145.5772	1	r.GQAGVMGFPGPK.g	0.0193
COL1A1	A0A452FHU9	[253-264]	0	1146.5823	1	r.GLPGTAGLPGMK.g [3xOxidation]	0.0122
COL1A2	A0A452G3V6	[323-334]	0	1154.58	1	k.EGPAGLPGIDGR.p [1xOxidation]	0.0149
COL1A1	A0A3P9NHJ7	[518-531]	0	1160.5728	1	r.GVMGPTGAAGAAGK.d [1xOxidation]	0.0092
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.011

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0172
COL1A1	A0A3P9NHJ7	[1206-1214]	1	1183.5928	1	k.NWYMSKNIK.e	0.0089
COL1A2	A0A452G3V6	[759-770]	1	1185.5858	1	r.GPSGPQGIRGDK.g [1xDeamidation; 1xOxidation]	0.0077
COL1A2	A0A452G3V6	[345-356]	0	1185.5899	1	r.GEPGNIGFPGPK.g [1xOxidation]	0.0037
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.0156
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	0.0152
COL1A1	A0A3P9NHJ7	[1133-1142]	0	1203.6216	1	k.SLSQQIEQIR.s [2xDeamidation]	0.0071
COL1A1	A0A3P9NHJ7	[653-666]	1	1228.5917	1	r.GDQGAKGADGAPGK.d	-0.0138
COL1A2	A0A452G3V6	[49-58]	1	1251.6303	1	k.WKTSLSGMWR.n	0.0113
COL1A1	A0A3P9NHJ7	[865-876]	1	1254.6913	1	r.GIVGLPGQRGER.g [1xOxidation]	-0.0191
COL1A1	A0A3P9NHJ7	[333-347]	0	1259.6379	1	r.GPPGPQGAAGAPGPK.g [1xDeamidation]	-0.0088
COL1A2	A0A452G3V6	[214-228]	0	1267.6753	1	r.GIPGPVGAAGATGAR.g [1xOxidation]	0.0178
COL1A2	A0A452G3V6	[309-322]	0	1288.6168	1	r.GFPGSPGNIGPAGK.e [1xDeamidation; 2xOxidation]	0.0091
COL1A1	A0A452FHU9	[970-983]	0	1296.6583	1	r.GFPGLPGPSGEPGK.q	0.009
COL1A1	A0A452FHU9	[472-486]	0	1387.6965	1	r.GEPGPAGLPGPPGER.g	-0.0053
COL1A1	A0A3P9NHJ7	[877-891]	0	1408.7219	1	r.GFPGPPGPAQGEIGK.p	-0.0181
COL1A1	A0A3P9NHJ7	[877-891]	0	1409.706	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation]	0.0199
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.0184
COL1A1	A0A3P9NHJ7	[877-891]	0	1473.6856	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation; 4xOxidation]	0.0089
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0134
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	0.0022

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[827-842]	1	1508.7928	1	k.DGRTGQPGAVGPAGIR.g	-0.0198
COL1A1	A0A452FHU9	[1152-1167]	0	1529.8071	1	k.DGLNGLPGPIGPPGPR.g [1xOxidation]	0.0074
COL1A1	A0A452FHU9	[1152-1167]	0	1530.7911	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 1xOxidation]	-0.0118
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	0.004
COL1A2	A0A452G3V6	[59-72]	1	1568.7672	1	r.NSCLTHPKGLMGPR.g [1xCarbamidomethyl; 1xDeamidation]	0.0109
COL1A1	A0A452FHU9	[397-414]	0	1569.7768	1	k.GANGAPGIAGAPGFPGAR.g [2xOxidation]	0.0151
COL1A1	A0A1A8K041	[503-519]	1	1570.782	1	r.GAPGLVGPKGASGEPGR.t [4xOxidation]	0.0027
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0172
COL1A1	A0A3P9NHJ7	[1267-1281]	1	1598.7843	1	k.NSIAYMDAAAGNLKK.s [2xOxidation]	0.0012
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0.0107
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	0.0066
COL1A1	A0A1A8K041	[959-975]	1	1658.8133	1	r.GERGFPGLPGPAGETGK.v [2xOxidation]	0.0181
COL1A1	A0A3P9NHJ7	[587-604]	1	1709.8718	1	r.GFPGERGAPGPIGPAGTR.g [1xOxidation]	-0.0192
COL1A1	A0A1A8K041	[1006-1024]	1	1740.8147	1	r.EGTPGTEGAAGRDGAPGPK.g [1xOxidation]	-0.0188
COL1A1	A0A1A8K041	[1006-1024]	1	1756.8096	1	r.EGTPGTEGAAGRDGAPGPK.g [2xOxidation]	-0.0186
COL1A1	A0A3P9NHJ7	[874-891]	1	1782.8769	1	r.GERGFPGPPGPAQGEIGK.p [2xOxidation]	-0.0109
COL1A1	A0A452FHU9	[657-675]	0	1783.8093	1	k.PGEQGVPGDLGAPGPSGAR.g [1xDeamidation; 4xOxidation]	0.016
COL1A1	A0A452FHU9	[352-369]	1	1783.8318	1	k.GEAGPQGPRGSEGPQGVR.g [3xOxidation]	-0.0065
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	0.0049

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A1A8K041	[773-793]	1	1804.9049	1	k.GEPGAAGPVGAAGARGAPGER.g	0.0141
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	0.0115
COL1A1	A0A1A8K041	[773-793]	1	1820.8998	1	k.GEPGAAGPVGAAGARGAPGER.g [1xOxidation]	-0.0108
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	0.0062
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0004
COL1A1	A0A452FHU9	[448-467]	0	1848.861	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 1xOxidation]	0.0192
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0005
COL1A1	A0A1A8K041	[544-565]	1	2015.9716	1	k.MGPAGSPGQDGRPGPPGPVGAR.g [1xDeamidation]	-0.0166
COL1A1	A0A3P9NHJ7	[472-493]	1	2019.9843	1	k.IGASGAPGQDGRPGPPGPVGAR.g [1xDeamidation; 3xOxidation]	0.0141
COL1A2	A0A452G3V6	[323-344]	1	2028.0621	1	k.EGPAGLPGIDGRPGPIGPAGAR.g [1xOxidation]	-0.0143
COL1A1	A0A452FHU9	[552-573]	1	2040.9846	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [3xOxidation]	-0.0185
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0111
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.0072
COL1A1	A0A452FHU9	[934-957]	0	2073.9948	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 1xOxidation]	0.007
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	0.0093
COL1A1	A0A452FHU9	[528-551]	1	2104.0669	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t	-0.0093
COL1A1	A0A3P9NHJ7	[484-505]	1	2106.0437	1	r.PGPPGPVGARGQPGVMGFPGPK.g [1xDeamidation; 3xOxidation]	0.0004
COL1A1	A0A3P9NHJ7	[617-640]	0	2144.0189	1	k.GEPGAPGAPGAAGPPGLQGMPGER.g [1xOxidation]	-0.0166
COL1A1	A0A452FHU9	[528-551]	1	2152.0517	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t [3xOxidation]	-0.0001
COL1A1	A0A1A8K041	[902-925]	1	2180.0214	1	r.GETGPAGRPGEVGAAGPPGPSGEK.g [3xOxidation]	0.0031
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	0.0074

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	0.0016
COL1A1	A0A1A8K041	[1162-1187]	0	2263.0626	1	r.SGETGPSGPPGNPGPPGPPGPPGPGI. [2xOxidation]	0.0115
COL1A2	A0A452G3V6	[711-736]	0	2264.0942	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGK.h [1xDeamidation; 2xOxidation]	-0.001
COL1A2	A0A452G3V6	[299-322]	1	2264.1128	1	r.PGEPGLMGPRGFPGSPGNIGPAGK.e [1xDeamidation; 1xOxidation]	-0.0197
COL1A1	A0A3P9NHJ7	[877-901]	1	2285.1309	1	r.GFPGPPGPAQGEIGKPGPAGPGGER.g [1xDeamidation]	-0.0116
COL1A1	A0A452FHU9	[442-467]	1	2394.1056	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 2xOxidation]	0.008
COL1A2	A0A452G3V6	[502-528]	1	2409.1542	1	r.GEVGPAGPNGFAGPAGAAGQPGAKGER.g [2xOxidation]	-0.0159
COL1A1	A0A452FHU9	[442-467]	1	2410.1005	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 3xOxidation]	0.0186
COL1A1	A0A1A8K041	[1133-1159]	1	2468.1987	1	r.GPPGPVGPAGKDGSNGMPGPIGPPGPR.g [3xOxidation]	-0.0001
COL1A1	A0A1A8K041	[1133-1159]	1	2484.1936	1	r.GPPGPVGPAGKDGSNGMPGPIGPPGPR.g [4xOxidation]	0.0145
COL1A1	A0A452FHU9	[322-351]	0	2501.2055	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation]	-0.0046
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	-0.0003
COL1A1	A0A3P9NHJ7	[1184-1205]	1	2574.1521	1	k.VYCNMDTGETCITPTQPEVAKK.n [2xCarbamidomethyl; 2xOxidation]	-0.0013
COL1A1	A0A452FHU9	[1288-1309]	0	2578.1258	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 2xOxidation]	0.0127
COL1A1	A0A1A8K041	[1133-1159]	1	2580.1631	1	r.GPPGPVGPAGKDGSNGMPGPIGPPGPR.g [10xOxidation]	-0.0056
COL1A1	A0A1A8K041	[827-856]	1	2582.1713	1	k.GDAGAPGPAGATGGAGPQGPVGNTGPKGAR.g [2xDeamidation; 5xOxidation]	-0.004
COL1A2	A0A452G3V6	[535-564]	0	2597.2339	1	k.GENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.0036
COL1A2	A0A452G3V6	[535-564]	0	2677.2085	1	k.GENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [7xOxidation]	0.0023
COL1A2	A0A452G3V6	[73-102]	0	2728.271	1	r.GPPGASGAPGPQGFQGPPGEPGEPGQTGAR.g [1xOxidation]	-0.0173

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0099
COL1A1	A0A452FHU9	[1111-1140]	0	2753.2398	1	r.GFSGLQGPPGPPGSPGEQGPSGASGPAGPR.g [6xOxidation]	0.0072
COL1A2	A0A452G3V6	[532-564]	1	2879.4031	1	k.GPKGENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.0081
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.0017
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0086
COL1A1	A0A452FHU9	[709-741]	1	2883.4166	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g	-0.0119
COL1A1	A0A452FHU9	[763-795]	1	2883.4231	1	r.GLTGPIGPPGPAGAPGDKGETGPSGPAGPTGAR.g [2xOxidation]	-0.0185
COL1A1	A0A452FHU9	[397-429]	1	2899.4082	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [4xOxidation]	-0.0166
COL1A1	A0A452FHU9	[709-741]	1	2899.4115	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g [1xOxidation]	-0.0199
COL1A1	A0A3P9NHJ7	[902-933]	1	2921.3595	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation]	-0.0097
COL1A1	A0A3P9NHJ7	[551-582]	1	3001.3631	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [4xOxidation]	-0.0076
COL1A1	A0A3P9NHJ7	[902-933]	1	3002.3181	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 5xOxidation]	0.0058
COL1A1	A0A3P9NHJ7	[902-933]	1	3017.329	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 6xOxidation]	0.0142
COL1A1	A0A3P9NHJ7	[551-582]	1	3017.358	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [5xOxidation]	-0.0148
COL1A1	A0A3P9NHJ7	[902-933]	1	3018.313	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 6xOxidation]	0.0076
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.004
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.0094
COL1A1	A0A3P9NHJ7	[1070-1104]	0	3227.5466	1	r.SGEMGPAGPPGPPGPPGPPGAPGGGFDIGFITQEK.a	0.0026
COL1A2	A0A452G3V6	[422-457]	1	3228.504	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [1xDeamidation; 4xOxidation]	0.0161
COL1A2	A0A452G3V6	[780-815]	1	3365.721	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [3xOxidation]	0.0181

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[780-815]	1	3366.705	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 3xOxidation]	-0.004
COL1A1	A0A452FHU9	[1433-1463]	1	3380.6719	1	k.TSRLPIIDVAPLDVGAPDQEFGFDIGSVCFL. [1xCarbamidomethyl; 2xOxidation]	0.0029
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	-0.0052
COL1A1	A0A452FHU9	[322-360]	1	3397.6156	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPR.g [3xOxidation]	0.0186
COL1A1	A0A452FHU9	[1433-1463]	1	3397.6508	1	k.TSRLPIIDVAPLDVGAPDQEFGFDIGSVCFL. [1xCarbamidomethyl; 1xDeamidation; 3xOxidation]	-0.0167
COL1A1	A0A452FHU9	[312-351]	1	3412.6153	1	r.PGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 5xOxidation]	0.0196
COL1A1	A0A452FHU9	[322-360]	1	3414.5945	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPR.g [1xDeamidation; 4xOxidation]	0.0115
Ovalbumin	P01012	[86-93]	0	945.5251	1	r.DILNQITK.p [1xDeamidation]	-0.0095
Ovalbumin-related protein Y	P01014	[259-266]	1	1007.552	1	k.TINFDKLR.e [1xDeamidation]	-0.0187
Ovalbumin-related protein Y	P01014	[259-266]	1	1022.5629	1	k.TINFDKLR.e [1xOxidation]	0.0093
Ovotransferrin	P02789	[594-601]	1	1024.4993	1	r.RANVMDYR.e	0.0186
Ovotransferrin	P02789	[625-632]	1	1030.5527	1	r.DLLERQEK.r	0.0013
Ovotransferrin	P02789	[219-228]	1	1035.5469	1	k.DGKGDVAFVK.h	0.0107
Ovotransferrin	P02789	[447-458]	1	1295.7106	1	r.PASYFAVAVARK.d [1xOxidation]	-0.0044
COL1A1	A0A452FHU9	[1310-1315]	0	811.3985	1	k.NWYISK.n [1xDeamidation]	-0.0174
COL1A1	A0A3P9NHJ7	[210-218]	0	815.3894	1	k.GDTGPAGPK.g [1xOxidation]	0.0187
COL1A2	A0A452G3V6	[1082-1087]	1	822.3992	1	k.KTNEWK.k [1xDeamidation; 1xOxidation]	0.0188

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[1083-1088]	1	822.3992	1	k.TNEWKK.t [1xDeamidation; 1xOxidation]	0.0188
COL1A1	A0A452FHU9	[244-252]	0	836.4373	1	r.GPPGPQGAR.g	-0.0181
COL1A1	A0A452FHU9	[1084-1092]	0	836.4373	1	r.GPAGPQGPR.g	-0.0181
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0027
COL1A1	A0A3P9NHJ7	[177-185]	0	842.4115	1	r.GPSGPQGAR.g [1xOxidation]	0.0097
COL1A1	A0A3P9NHJ7	[177-185]	0	843.3955	1	r.GPSGPQGAR.g [1xDeamidation; 1xOxidation]	0.0183
COL1A1	A0A3P9NHJ7	[279-287]	0	843.3955	1	r.GPEGPAGAR.g [2xOxidation]	0.0183
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	-0.0077
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	-0.0077
COL1A1	A0A3P9NHJ7	[177-185]	0	858.4064	1	r.GPSGPQGAR.g [2xOxidation]	0.0191
COL1A1	A0A3P9NHJ7	[733-741]	0	860.3745	1	k.GEPGDNGAK.g [1xOxidation]	0.0077
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.016
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.016
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.016
COL1A1	A0A452FHU9	[361-369]	0	886.4377	1	r.GSEGPQGVR.g	0.0091
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0117
COL1A2	A0A452G3V6	[272-281]	0	902.4513	1	r.AGVMGPAGSR.g	0.002
COL1A2	A0A452G3V6	[272-281]	0	918.4462	1	r.AGVMGPAGSR.g [1xOxidation]	0.005
COL1A1	A0A3P9NHJ7	[892-901]	0	942.4275	1	k.PGPAGPGGER.g [3xOxidation]	0.0194
COL1A1	A0A452FHU9	[1026-1035]	1	943.4592	1	r.DGAPGAKGDR.g	0.0046

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[564-573]	0	950.469	1	r.PGPPGPPGAR.g [3xOxidation]	0.0021
COL1A1	A0A3P9NHJ7	[484-493]	0	952.4847	1	r.PGPPGPVGAR.g [3xOxidation]	-0.0147
COL1A2	A0A452G3V6	[968-976]	0	1013.515	1	r.AQPEDIPVK.n [1xDeamidation; 1xOxidation]	-0.0087
COL1A1	A0A3P9NHJ7	[1124-1132]	0	1019.5255	1	r.DLEVDSTLK.s	-0.0012
COL1A1	A0A452FHU9	[676-684]	1	1020.4857	1	r.GERGFPGER.g [1xOxidation]	0.0085
COL1A2	A0A060N2D3	[674-685]	0	1036.5534	1	r.GAPGIGGPTGPR.g	0.0135
COL1A2	A0A452G3V6	[1120-1128]	0	1048.5496	1	r.LNIGPVCFK. [1xCarbamidomethyl; 1xDeamidation]	-0.0111
COL1A1	A0A452FHU9	[121-131]	1	1050.5439	1	r.GPRGPAGPPGR.d [2xOxidation]	0.0081
COL1A1	A0A452FHU9	[310-321]	1	1063.5756	1	r.GRPGAPGPAGAR.g	-0.0026
COL1A2	A0A060N2D3	[1073-1084]	1	1069.5385	1	r.GPAGPAGAKGDR.g [1xOxidation]	0.0035
COL1A2	A0A452G3V6	[458-469]	1	1073.5586	1	r.GAAGIPGGKGEK.v [2xOxidation]	0.0196
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	0.008
COL1A2	A0A060N2D3	[722-733]	1	1085.5698	1	r.GAGGLPGAKGER.g [1xOxidation]	0.0092
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	-0.0018
COL1A1	A0A674DI56	[247-258]	0	1094.6204	1	r.GTPGTPGLPGIK.g	-0.0114
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.0142
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.0109
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0106
COL1A2	A0A452G3V6	[1089-1097]	1	1110.6041	1	k.TIIEYKTNK.p [1xDeamidation]	-0.0066
COL1A2	A0A060N2D3	[587-600]	0	1126.5851	1	r.GPAGATGSVGAPGK.d	-0.0186

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[733-744]	1	1127.5804	1	r.GAAGLPGPKGDR.g [2xOxidation]	0.0009
COL1A2	A0A452G3V6	[323-334]	0	1138.5851	1	k.EGPAGLPGIDGR.p	0.0053
COL1A2	A0A060N2D3	[458-469]	1	1139.5552	1	r.GPRGEPGGSGPR.g [1xOxidation]	0.0169
COL1A2	A0A060N2D3	[587-600]	0	1142.58	1	r.GPAGATGSVGAPGK.d [1xOxidation]	-0.0196
COL1A1	A0A452FHU9	[1310-1318]	1	1149.6051	1	k.NWYISKNPK.d	0.015
COL1A1	A0A452FHU9	[1310-1318]	1	1150.5891	1	k.NWYISKNPK.d [1xDeamidation]	0.019
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.014
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0106
COL1A1	A0A3P9NHJ7	[1206-1214]	1	1183.5928	1	k.NWYMSKNIK.e	0.008
COL1A1	A0A452FHU9	[1236-1245]	0	1188.6219	1	k.SLSQQIENIR.s [1xDeamidation]	0.0158
COL1A1	A0A674DI56	[1233-1242]	1	1190.6375	1	k.SLSQKVENIR.s [1xDeamidation; 1xOxidation]	0.0076
COL1A1	A0A674DI56	[1233-1242]	1	1191.6216	1	k.SLSQKVENIR.s [2xDeamidation; 1xOxidation]	0.002
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.0162
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	0.0091
COL1A1	A0A3P9NHJ7	[1133-1142]	0	1203.6216	1	k.SLSQQIEQIR.s [2xDeamidation]	0.0042
COL1A2	A0A452G3V6	[881-891]	1	1229.6233	1	r.ADQPRSPASLR.p [2xOxidation]	0.0023
COL1A1	A0A452FHU9	[958-969]	1	1240.6757	1	r.GVVGLPGQRGER.g [1xOxidation]	-0.018
COL1A2	A0A452G3V6	[49-58]	1	1251.6303	1	k.WKTSLSGMWR.n	0.0094
COL1A1	A0A3P9NHJ7	[865-876]	1	1254.6913	1	r.GIVGLPGQRGER.g [1xOxidation]	0.0156

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A060N2D3	[404-418]	0	1261.6535	1	r.GPAGAQGPVGAPGPK.g [1xDeamidation]	0.0063
COL1A2	A0A452G3V6	[214-228]	0	1267.6753	1	r.GIPGPVGAAGATGAR.g [1xOxidation]	0.0139
COL1A2	A0A452G3V6	[309-322]	0	1287.6328	1	r.GFPGSPGNIGPAGK.e [2xOxidation]	-0.0095
COL1A2	A0A452G3V6	[309-322]	0	1288.6168	1	r.GFPGSPGNIGPAGK.e [1xDeamidation; 2xOxidation]	-0.0072
COL1A1	A0A452FHU9	[240-252]	1	1292.6342	1	r.PGERGPPGPQGAR.g [1xDeamidation; 1xOxidation]	0.0104
COL1A1	A0A3P9NHJ7	[425-439]	1	1378.7437	1	k.GAPGERGAPGLVGPK.g [1xOxidation]	-0.0045
Ovalbumin	P01012	[208-219]	0	1514.7494	1	k.PVQMMYQIGLFR.v [2xOxidation]	0.0153
COL1A1	A0A452FHU9	[1386-1398]	0	1457.7846	1	k.ALLLQGSNEIEIR.a [2xDeamidation]	0.0009
COL1A1	A0A3P9NHJ7	[1282-1294]	0	1458.7798	1	k.SLLLQGSNEIEVR.a [1xDeamidation]	-0.0057
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.0162
COL1A1	A0A452FHU9	[253-267]	1	1464.774	1	r.GLPGTAGLPGMKGHR.g [1xOxidation]	-0.0029
COL1A1	A0A3P9NHJ7	[877-891]	0	1473.6856	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation; 4xOxidation]	0.0085
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0156
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	0.0043
COL1A1	A0A674DI56	[247-261]	1	1508.7816	1	r.GTPGTPGLPGIKGHR.g [4xOxidation]	-0.0106
COL1A1	A0A452FHU9	[1152-1167]	0	1513.8122	1	k.DGLNGLPGPIGPPGPR.g	-0.0108
COL1A1	A0A452FHU9	[1152-1167]	0	1529.8071	1	k.DGLNGLPGPIGPPGPR.g [1xOxidation]	0.012
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	-0.0052
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	0.016

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[397-414]	0	1569.7768	1	k.GANGAPGIAGAPGFPGAR.g [2xOxidation]	0.0131
COL1A1	A0A452FHU9	[397-414]	0	1570.7608	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 2xOxidation]	0.0189
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0133
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0.0183
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	0.0143
COL1A1	A0A452FHU9	[612-630]	0	1706.7729	1	k.DGEAGAQGPPGPAGPAGER.g [1xOxidation]	0.013
COL1A1	A0A3P9NHJ7	[587-604]	1	1709.8718	1	r.GFPGERGAPGPIGPAGTR.g [1xOxidation]	-0.0051
COL1A1	A0A674DI56	[757-774]	0	1740.7857	1	r.GMTGPIGPPGPTGAHGEK.g [5xOxidation]	0.0117
COL1A2	A0A060N2D3	[668-685]	1	1743.8409	1	r.GFPGERGAPGIGGPTGPR.g [4xOxidation]	-0.0179
COL1A1	A0A452FHU9	[862-881]	1	1759.847	1	k.GARGSAGPPGATGFPGAAGR.v [3xOxidation]	0.0185
COL1A1	A0A452FHU9	[882-902]	0	1765.8868	1	r.VGPPGPSGNAGPPGPPGPAGK.e [1xDeamidation]	0.0169
COL1A1	A0A3P9NHJ7	[902-921]	0	1768.8799	1	r.GPPGPMGPPGLAGAPGEPGR.e	-0.0134
COL1A1	A0A452FHU9	[352-369]	1	1783.8318	1	k.GEAGPQGPRGSEGPQGVR.g [3xOxidation]	0.0168
COL1A2	A0A452G3V6	[903-918]	0	1788.8974	1	k.SLNNQIETLLTPEGSR.k [1xDeamidation; 1xOxidation]	0.0069
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	-0.0023
COL1A1	A0A3P9NHJ7	[1133-1148]	1	1815.9195	1	k.SLSQQIEQIRSPDGTR.k [1xDeamidation]	0.0054
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	0.0086
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	0.0008
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0057
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0042

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A3P9NHJ7	[472-493]	1	2019.9843	1	k.IGASGAPGQDGRPGPPGPVGAR.g [1xDeamidation; 3xOxidation]	0.0141
COL1A1	A0A452FHU9	[552-573]	1	2040.9846	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [3xOxidation]	-0.0155
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0179
COL1A1	A0A452FHU9	[934-957]	0	2057.0159	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g	-0.0184
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.013
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	0.0026
COL1A1	A0A452FHU9	[528-551]	1	2104.0669	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t	-0.006
COL1A1	A0A3P9NHJ7	[484-505]	1	2106.0437	1	r.PGPPGPVGARGQPGVMGFPGPK.g [1xDeamidation; 3xOxidation]	0.001
COL1A1	A0A452FHU9	[564-585]	1	2109.0182	1	r.PGPPGPPGARGQAGVMGFPGPK.g [5xOxidation]	-0.0006
COL1A1	A0A452FHU9	[528-551]	1	2152.0517	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t [3xOxidation]	-0.0024
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	0.0059
COL1A1	A0A674DI56	[753-774]	1	2199.9757	1	k.DGMRGMTGPIGPPGPTGAHGEK.g [5xOxidation]	0.0033
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.002
COL1A1	A0A452FHU9	[442-467]	1	2394.1056	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 2xOxidation]	0.0078
COL1A1	A0A452FHU9	[442-467]	1	2409.1165	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [3xOxidation]	0.0145
COL1A2	A0A452G3V6	[502-528]	1	2410.1382	1	r.GEVGPAGPNGFAGPAGAAGQPGAKGER.g [1xDeamidation; 2xOxidation]	-0.0143
COL1A1	A0A674DI56	[961-987]	1	2461.1702	1	r.GPSGSPGVPGQAGEPGKQGPGGPVGER.g [3xOxidation]	-0.0001
COL1A2	A0A452G3V6	[565-591]	0	2468.1728	1	r.GDGGPPVSTYPGFGISGPPGPPGPAGK.e [3xOxidation]	0.0161
COL1A1	A0A674DI56	[1135-1161]	1	2484.2048	1	r.GPHGSSGSTGKDGMNGLPGPIGPPGPR.g	-0.0129
COL1A1	A0A674DI56	[1135-1161]	1	2485.1888	1	r.GPHGSSGSTGKDGMNGLPGPIGPPGPR.g [1xDeamidation]	0.0025
COL1A2	A0A452G3V6	[683-707]	1	2501.1916	1	r.WATVSLSGNPGNDGPPGRDGQPGHK.g	-0.0188

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	0.0014
COL1A1	A0A3P9NHJ7	[1184-1205]	1	2574.1521	1	k.VYCNMDTGETCITPTQPEVAKK.n [2xCarbamidomethyl; 2xOxidation]	-0.0173
COL1A1	A0A452FHU9	[1288-1309]	0	2578.1258	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 2xOxidation]	0.0166
COL1A1	A0A452FHU9	[322-351]	0	2581.1801	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 5xOxidation]	-0.0037
COL1A1	A0A674DI56	[829-858]	1	2591.2081	1	k.GDAGAPGPGGPVGAPGPQGPAGNAGTKGTR.g [1xDeamidation; 4xOxidation]	-0.0194
COL1A1	A0A452FHU9	[322-351]	0	2597.175	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 6xOxidation]	0.0077
COL1A1	A0A3P9NHJ7	[333-361]	1	2714.2805	1	r.GPPGPQGAAGAPGPKGNTFQGDVGAPGFK.g [5xOxidation]	0.0116
COL1A1	A0A452FHU9	[1111-1140]	0	2737.2448	1	r.GFSGLQGPPGPPGSPGEQGPSGASGPAGPR.g [5xOxidation]	0.0055
COL1A2	A0A452G3V6	[711-740]	1	2750.2765	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [2xDeamidation; 5xOxidation]	0.0062
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0154
COL1A2	A0A452G3V6	[711-740]	1	2766.2714	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [2xDeamidation; 6xOxidation]	0.0187
COL1A2	A0A452G3V6	[532-564]	1	2879.4031	1	k.GPKGENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.0142
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.0112
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0175
COL1A1	A0A3P9NHJ7	[902-933]	1	2921.3595	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation]	0.0069
COL1A1	A0A3P9NHJ7	[902-933]	1	3001.3341	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 5xOxidation]	0.0011
COL1A1	A0A3P9NHJ7	[902-933]	1	3002.3181	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 5xOxidation]	0.0058
COL1A1	A0A3P9NHJ7	[902-933]	1	3017.329	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 6xOxidation]	0.0002
COL1A1	A0A3P9NHJ7	[902-933]	1	3018.313	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 6xOxidation]	0.0084
COL1A1	A0A674DI56	[1433-1460]	0	3049.4421	1	r.LPIIDIAPMDVGAPDQEFGVEVGPVCFV. [1xCarbamidomethyl; 1xDeamidation; 4xOxidation]	0.0173

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1263-1287]	1	3069.2699	1	k.MCHPDWKSGEYWIDPNQGCNLDAIK.v [2xCarbamidomethyl; 3xDeamidation; 2xOxidation]	0.0169
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.0139
COL1A1	A0A674DI56	[820-855]	1	3084.4366	1	k.GEAGNNGPKGDAGAPGPGGPVGAPGPQGPAGNAGTK.g [3xOxidation]	0.0152
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.0106
COL1A2	A0A452G3V6	[1101-1128]	1	3111.6395	1	r.LPILDIAPLDIGGADQEIRLNIGPVCFK. [1xCarbamidomethyl; 4xOxidation]	-0.0019
COL1A2	A0A452G3V6	[422-457]	1	3212.5091	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [1xDeamidation; 3xOxidation]	0.015
COL1A1	A0A3P9NHJ7	[1070-1104]	0	3227.5466	1	r.SGEMGPAGPPGPPGPPGPPGAPGGGFDIGFITQEK.a	0.0048
COL1A2	A0A452G3V6	[422-457]	1	3228.504	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [1xDeamidation; 4xOxidation]	0.012
COL1A2	A0A452G3V6	[780-815]	1	3350.7101	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 2xOxidation]	-0.0018
COL1A2	A0A452G3V6	[780-815]	1	3365.721	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [3xOxidation]	-0.0031
COL1A2	A0A452G3V6	[780-815]	1	3366.705	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 3xOxidation]	0.0042
COL1A2	A0A452G3V6	[780-815]	1	3381.7159	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [4xOxidation]	-0.012
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	-0.0008
COL1A2	A0A452G3V6	[843-880]	0	3651.5684	1	r.GSQGSQGPAGPPGPPGPPGPPGPSGGGYDFGFDGDFYR.a [4xOxidation]	-0.0155
COL1A2	A0A452G3V6	[843-880]	0	3652.5524	1	r.GSQGSQGPAGPPGPPGPPGPPGPSGGGYDFGFDGDFYR.a [1xDeamidation; 4xOxidation]	-0.0008
Ovalbumin	P01012	[371-386]	1	1804.9163	1	k.HIATNAVLFFGRCVSP. [1xCarbamidomethyl; 1xOxidation]	-0.0031
Ovalbumin-related protein Y	P01014	[292-309]	0	2047.0239	1	k.YNLTSILMALGMTDLFSR.s [1xDeamidation]	-0.0141
Ovotransferrin	P02789	[662-667]	1	822.4655	1	k.CLFKVR.e [1xCarbamidomethyl]	0.0041

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
Mucin-5B	Q98UI9	[1519-1526]	1	901.5353	1	k.KVVPDISK.n [1xOxidation]	0.0087
Ovalbumin	P01012	[86-93]	0	944.5411	1	r.DILNQITK.p	-0.0133
Ovostatin	P20740	[370-378]	0	1038.5619	1	r.GIPYFGQIK.l [1xOxidation]	-0.0145
Mucin-5B	Q98UI9	[743-751]	1	1163.6024	1	k.LLCKCIQGR.l [2xCarbamidomethyl; 1xOxidation]	0.0088
Protein TENP	O42273	[425-434]	1	1266.6762	1	k.DYVLVPCKLK.l [1xCarbamidomethyl; 2xOxidation]	0.01
Ovalbumin	P01012	[371-382]	0	1345.7375	1	k.HIATNAVLFFGR.c	0.009
Ovostatin	P20740	[8-18]	0	1384.7293	1	r.EILSFFCLTVR.k [1xCarbamidomethyl]	0.0124
Ovotransferrin	P02789	[459-470]	1	1388.6917	1	k.DSNVNWNNLKGK.k	-0.0084
Ovalbumin-related protein Y	P01014	[373-384]	0	1412.7321	1	r.YNPTNAILFFGR.y	0.0079
Ovotransferrin	P02789	[141-154]	0	1534.8489	1	r.SAGWNIPIGTLLHR.g	0.0025
COL1A1	A0A452FHU9	[237-243]	1	800.4009	1	k.PGRPGER.g [2xOxidation]	-0.0168
COL1A1	A0A452FHU9	[277-285]	0	801.3737	1	k.GDAGPAGPK.g [2xOxidation]	0.0171
COL1A1	A0A452FHU9	[826-834]	0	801.3737	1	k.GEPGDAGAK.g	0.0171
COL1A1	A0A452FHU9	[1310-1315]	0	811.3985	1	k.NWYISK.n [1xDeamidation]	0
COL1A1	A0A3B5AFM4	[418-426]	0	813.385	1	r.GEPGGAGPR.g [1xOxidation]	0.0107
COL1A1	A0A090B2K5	[300-309]	0	814.4166	1	r.AGPAGAAGAR.g [1xOxidation]	-0.0087
COL1A1	A0A452FHU9	[244-252]	0	836.4373	1	r.GPPGPQGAR.g	-0.011
COL1A1	A0A452FHU9	[1084-1092]	0	836.4373	1	r.GPAGPQGPR.g	-0.011
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	0.0072
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	-0.0152

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	-0.0152
COL1A1	A0A452FHU9	[244-252]	0	853.4163	1	r.GPPGPQGAR.g [1xDeamidation; 1xOxidation]	0.0106
COL1A1	A0A452FHU9	[1084-1092]	0	853.4163	1	r.GPAGPQGPR.g [1xDeamidation; 1xOxidation]	0.0106
COL1A2	A0A452G3V6	[111-120]	0	868.4635	1	r.VGAPGPAGAR.g [1xOxidation]	-0.0116
COL1A2	A0A452G3V6	[759-767]	0	868.4635	1	r.GPSGPQGIR.g	-0.0116
COL1A1	A0A3B5AFM4	[506-515]	0	892.4635	1	r.PGPPGPSGAR.g	0.0004
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0072
COL1A2	A0A452G3V6	[272-281]	0	902.4513	1	r.AGVMGPAGSR.g	0.0049
COL1A1	A0A3P9NHJ7	[484-493]	0	952.4847	1	r.PGPPGPVGAR.g [3xOxidation]	-0.0143
COL1A1	A0A090B2K5	[298-309]	1	1027.5392	1	r.GRAGPAGAAGAR.g [1xOxidation]	0.0064
COL1A2	A0A452G3V6	[968-976]	0	1028.5259	1	r.AQPEDIPVK.n [2xOxidation]	0.017
COL1A2	A0A6P3W0U2	[633-644]	1	1029.5323	1	r.GAGGTPGAKGEK.g	0.0181
COL1A2	A0A452G3V6	[1120-1128]	0	1047.5656	1	r.LNIGPVCFK. [1xCarbamidomethyl]	-0.01
COL1A2	A0A452G3V6	[1120-1128]	0	1048.5496	1	r.LNIGPVCFK. [1xCarbamidomethyl; 1xDeamidation]	0.0035
COL1A1	A0A3B5AFM4	[612-623]	0	1068.5069	1	r.GGPGPVGPGGPR.g [4xOxidation]	-0.0037
COL1A2	A0A6P3W0U2	[210-221]	1	1069.5497	1	r.GRAGPSGPAGAR.g [1xOxidation]	-0.0048
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	0.0082
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	-0.0029
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.0189
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.0062

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0081
COL1A2	A0A452G3V6	[1089-1097]	1	1110.6041	1	k.TIIEYKTNK.p [1xDeamidation]	0.0157
COL1A1	A0A090B2K5	[721-732]	1	1111.6218	1	r.GAAGLPGLKGDR.g	-0.0104
COL1A1	A0A3B5AFM4	[540-553]	0	1112.5695	1	r.GPAGAAGAVGAPGK.d [2xOxidation]	0.0144
COL1A2	A0A452G3V6	[323-334]	0	1138.5851	1	k.EGPAGLPGIDGR.p	0.0046
COL1A2	A0A452G3V6	[26-36]	0	1161.6296	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl]	-0.0127
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.0093
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0107
COL1A1	A0A3P9NHJ7	[1206-1214]	1	1183.5928	1	k.NWYMSKNIK.e	0.0146
COL1A1	A0A452FHU9	[958-969]	1	1224.6807	1	r.GVVGLPGQRGER.g	0.0015
COL1A1	A0A452FHU9	[958-969]	1	1225.6648	1	r.GVVGLPGQRGER.g [1xDeamidation]	-0.0148
COL1A2	A0A452G3V6	[816-829]	1	1237.6284	1	r.GPAGPTGPAGKDGR.t	-0.0162
COL1A1	A0A452FHU9	[958-969]	1	1240.6757	1	r.GVVGLPGQRGER.g [1xOxidation]	0.0134
COL1A2	A0A452G3V6	[214-228]	0	1251.6804	1	r.GIPGPVGAAGATGAR.g	-0.0093
COL1A2	A0A452G3V6	[214-228]	0	1267.6753	1	r.GIPGPVGAAGATGAR.g [1xOxidation]	0.013
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0134
COL1A1	A0A6I9MX97	[720-736]	0	1457.7132	1	r.GTAGPPGATGFPGAAGR.v [1xOxidation]	0.0183
COL1A1	A0A452FHU9	[918-933]	0	1458.7223	1	r.PGEVGPPGPPGPAGEK.g [1xOxidation]	0.0182
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.01
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0126
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	0.0014

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A6P3W0U2	[153-167]	1	1508.7791	1	r.GFPGTPGLPGMKGHR.g	-0.0103
Mucin-5B	Q98UI9	[941-955]	1	1677.833	1	r.IQEIATDPGAEKNYK.v [1xDeamidation]	0.0086
Ovalbumin-related protein Y	P01014	[111-124]	1	1686.852	1	k.TFSVLPEYLSCARK.f [1xCarbamidomethyl; 1xOxidation]	-0.0102
Ovalbumin	P01012	[128-143]	0	1687.8398	1	r.GGLEPINFQTAADQAR.e	-0.0119
Ovalbumin	P01012	[144-159]	0	1858.9658	1	r.ELINSWVESQTNGIIR.n	-0.0067
COL1A1	A0A452FHU9	[1152-1167]	0	1546.786	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	0.0077
Ovostatin	P20740	[1082-1098]	0	1871.8626	1	k.TDGCFQSTGILVNNAMK.g [1xCarbamidomethyl; 1xOxidation]	0.0116
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	0.0035
COL1A2	A0A452G3V6	[196-213]	0	1562.8285	1	k.GAAGLPGVAGAPGLPGPR.g [3xOxidation]	0.0023
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0029
COL1A1	A0A452FHU9	[397-414]	0	1586.7558	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 3xOxidation]	0.0161
COL1A2	A0A452G3V6	[151-168]	0	1631.8136	1	k.GELGPVGNPGPAGPAGPR.g [2xOxidation]	-0.0005
COL1A2	A0A452G3V6	[968-980]	1	1631.8176	1	r.AQPEDIPVKNWYR.n [1xOxidation]	-0.0045
COL1A2	A0A6P3W0U2	[420-437]	1	1643.7368	1	r.GGPGDSGRAGEPGQTGAR.g [1xDeamidation; 1xOxidation]	0.02
COL1A2	A0A6P3W0U2	[561-578]	1	1643.762	1	r.GSPGDQGASGPAGVKGER.g [1xDeamidation; 1xOxidation]	-0.0052
Ovostatin	P20740	[222-239]	1	2094.0502	1	k.SGERTSHSFLVEEYVLPK.f [1xOxidation]	-0.0158
Ovostatin	P20740	[520-539]	0	2234.0897	1	k.VNIQADQNGTFMIPLVVNEK.m [4xDeamidation]	-0.0071
COL1A1	A0A452FHU9	[520-537]	1	1655.7984	1	k.GSPGEAGRPGEAGLPGAK.g [3xOxidation]	-0.0072
COL1A1	A0A452FHU9	[493-510]	1	1671.8085	1	r.GFPGSDGVAGPKGPAGER.g [1xOxidation]	-0.0014
COL1A1	A0A3P9NHJ7	[587-604]	1	1693.8769	1	r.GFPGERGAPGPIGPAGTR.g	-0.0127

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A3P9NHJ7	[587-604]	1	1709.8718	1	r.GFPGERGAPGPIGPAGTR.g [1xOxidation]	-0.0108
COL1A1	A0A452FHU9	[469-486]	1	1719.8409	1	r.GARGEPGPAGLPGPPGER.g [3xOxidation]	0.0178
COL1A1	A0A6I9MX97	[512-530]	0	1741.7987	1	k.PGEQGLSGEAGVSGPAGNR.g [2xDeamidation]	0.0029
COL1A1	A0A452FHU9	[862-881]	1	1743.8521	1	k.GARGSAGPPGATGFPGAAGR.v [2xOxidation]	-0.0092
COL1A1	A0A6I9MX97	[869-887]	1	1756.7733	1	r.EGSPGNEGSSGRDGPAGPK.g [1xDeamidation]	0.0009
COL1A2	A0A452G3V6	[1021-1035]	0	1769.8752	1	r.LLANHASQNITYHCK.n [1xCarbamidomethyl]	0.012
COL1A2	A0A452G3V6	[683-700]	0	1782.8406	1	r.WATVSLSGNPGNDGPPGR.d [1xDeamidation]	0.0056
COL1A1	A0A090B2K5	[1223-1238]	1	1804.8923	1	k.SLSQQIENIRSPEGTK.k [2xDeamidation; 1xOxidation]	0.0193
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	-0.0101
COL1A2	A0A6P3W0U2	[962-983]	1	1819.9158	1	r.PGSRGEAGPVGAGGPAGAAGAR.g	-0.0043
COL1A1	A0A3B5AFM4	[394-413]	0	1820.8661	1	k.GEPGPAGVQGLPGPSGEEGK.r [1xDeamidation]	-0.0028
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	-0.0044
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0109
COL1A1	A0A3B5AFM4	[394-413]	0	1836.861	1	k.GEPGPAGVQGLPGPSGEEGK.r [1xDeamidation; 1xOxidation]	0.0119
COL1A2	A0A6P3W0U2	[1124-1140]	1	1859.9709	1	k.SLNTQIDNLLSPEGSKK.n [1xOxidation]	-0.0131
COL1A1	A0A090B2K5	[436-455]	0	1868.8145	1	k.GEPGPSGVQGPPGPAGEEGK.r [1xDeamidation; 4xOxidation]	0.0098
COL1A2	A0A6P3W0U2	[474-493]	1	1872.9086	1	r.GQPGTIGFPGPKGPGGEAGK.a [4xOxidation]	0.0065
COL1A2	A0A6P3W0U2	[474-493]	1	1888.9035	1	r.GQPGTIGFPGPKGPGGEAGK.a [5xOxidation]	0.0071
COL1A2	A0A6P3W0U2	[576-596]	1	1922.9315	1	k.GERGNPGPAGSVGSQGPIGAR.g [2xDeamidation]	0.009

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.002
COL1A2	A0A452G3V6	[737-758]	1	1998.0264	1	k.HGSRGEPGPVGAVGPAGAVGPR.g [1xOxidation]	-0.0099
COL1A1	A0A090B2K5	[436-456]	1	2024.9156	1	k.GEPGPSGVQGPPGPAGEEGKR.g [1xDeamidation; 4xOxidation]	-0.0022
COL1A2	A0A452G3V6	[323-344]	1	2028.0621	1	k.EGPAGLPGIDGRPGPIGPAGAR.g [1xOxidation]	-0.0022
COL1A1	A0A3B5AFM4	[394-414]	1	2040.9469	1	k.GEPGPAGVQGLPGPSGEEGKR.g [1xDeamidation; 4xOxidation]	0.0111
COL1A1	A0A3B5AFM4	[1259-1277]	1	2044.0305	1	k.ALLLQGSNDVEIRAEGNSR.f [2xDeamidation]	-0.0119
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0015
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.0091
COL1A1	A0A452FHU9	[934-957]	0	2073.9948	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 1xOxidation]	0.0126
COL1A1	A0A3B5AFM4	[187-208]	1	2082.0727	1	r.GAAGPQQGARGFPGTPGLPGIK.g [3xOxidation]	0.0168
COL1A1	A0A3P9NHJ7	[484-505]	1	2089.0648	1	r.PGPPGPVGARGQPGVMGFPGPK.g [2xOxidation]	-0.0104
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	0.0058
COL1A2	A0A452G3V6	[711-736]	0	2233.0884	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGK.h [2xDeamidation]	-0.0043
COL1A1	A0A452FHU9	[970-993]	1	2239.0738	1	r.GFPGLPGPSGEPGKQGPSGASGER.g [1xOxidation]	-0.0053
COL1A1	A0A452FHU9	[970-993]	1	2255.0687	1	r.GFPGLPGPSGEPGKQGPSGASGER.g [2xOxidation]	-0.0125
COL1A2	A0A452G3V6	[711-736]	0	2265.0782	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGK.h [2xDeamidation; 2xOxidation]	0.001
COL1A1	A0A3P9NHJ7	[243-269]	1	2269.1472	1	r.GRAGPSGAAGPTGPAGPPGFPGGPGPK.g	-0.0113
COL1A1	A0A452FHU9	[970-993]	1	2271.0636	1	r.GFPGLPGPSGEPGKQGPSGASGER.g [3xOxidation]	0.0071
COL1A1	A0A3P9NHJ7	[877-901]	1	2284.1469	1	r.GFPGPPGPAQGEIGKPGPAGPGGER.g	-0.0191
COL1A1	A0A452FHU9	[835-861]	0	2323.1313	1	k.GDAGPPGPAGPAGPPGPIGNVGAPGPK.g [4xOxidation]	-0.008
COL1A1	A0A452FHU9	[442-467]	1	2394.1056	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 2xOxidation]	0.0022

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A6P3W0U2	[315-341]	1	2404.16	1	r.GGNGPQGPSGPSGQRGLSGDPGPSGVK.g	0.0045
COL1A2	A0A452G3V6	[502-528]	1	2409.1542	1	r.GEVGPAGPNGFAGPAGAAGQPGAKGER.g [2xOxidation]	-0.0158
COL1A2	A0A452G3V6	[502-528]	1	2411.1222	1	r.GEVGPAGPNGFAGPAGAAGQPGAKGER.g [2xDeamidation; 2xOxidation]	0.0179
COL1A2	A0A452G3V6	[565-591]	0	2420.1881	1	r.GDGGPPVSTYPGFGISGPPGPPGPAGK.e	0.0153
COL1A2	A0A452G3V6	[502-528]	1	2427.1171	1	r.GEVGPAGPNGFAGPAGAAGQPGAKGER.g [2xDeamidation; 3xOxidation]	0.0022
COL1A1	A0A452FHU9	[1033-1061]	1	2465.2168	1	k.GDRGETGPAGPPGAPGAPGAPGPVGPAGK.s [1xOxidation]	0.0002
COL1A1	A0A452FHU9	[1033-1061]	1	2481.2117	1	k.GDRGETGPAGPPGAPGAPGAPGPVGPAGK.s [2xOxidation]	-0.002
COL1A1	A0A452FHU9	[1141-1167]	1	2485.2318	1	r.GPPGSAGTPGKDGLNGLPGPIGPPGPR.g [1xDeamidation; 4xOxidation]	-0.0081
COL1A1	A0A3B5AFM4	[1161-1182]	1	2494.1081	1	r.VHCNMETGETCIAPSKSSIPMK.n [2xCarbamidomethyl; 1xDeamidation; 1xOxidation]	0.0028
COL1A2	A0A6P3W0U2	[45-71]	0	2497.163	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 2xOxidation]	0.0182
COL1A1	A0A452FHU9	[322-351]	0	2500.2215	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g	-0.0069
COL1A1	A0A452FHU9	[1141-1167]	1	2549.2114	1	r.GPPGSAGTPGKDGLNGLPGPIGPPGPR.g [1xDeamidation; 8xOxidation]	0.0116
COL1A2	A0A6P3W0U2	[933-961]	1	2550.1927	1	k.GDRGEPGSNGPSGLSGAPGPAGPAGAVGR.p [3xOxidation]	0.0047
COL1A1	A0A3B5AFM4	[762-791]	1	2562.1815	1	k.GDAGAPGPGGPVGAAGPQGPAGPPGAKGAR.g [1xDeamidation; 7xOxidation]	-0.0148
COL1A1	A0A3B5AFM4	[1278-1300]	1	2563.1769	1	r.FTYSVSEDGCTSHTGSWGKTVIK.y [1xCarbamidomethyl; 1xOxidation]	-0.0023
COL1A1	A0A3B5AFM4	[962-990]	1	2563.1842	1	k.GDRGESGMSGPPGPPGTPGAPGAVGPSGK.t [2xOxidation]	-0.0095
COL1A1	A0A3B5AFM4	[762-791]	1	2578.1764	1	k.GDAGAPGPGGPVGAAGPQGPAGPPGAKGAR.g [1xDeamidation; 8xOxidation]	-0.0142
COL1A1	A0A3B5AFM4	[962-990]	1	2579.1791	1	k.GDRGESGMSGPPGPPGTPGAPGAVGPSGK.t [3xOxidation]	-0.0024
COL1A2	A0A452G3V6	[470-495]	1	2595.2811	1	k.VRSPHWALTHTGEAGPAGPAGPAGPR.g [3xOxidation]	-0.0169

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[708-736]	1	2653.2601	1	k.GERGYPGNAGPVGAAGAPGPQGPVGPTGK.h [5xOxidation]	0.0041
COL1A2	A0A452G3V6	[121-150]	0	2669.2325	1	r.GSDGSVGPVGPAGPIGSAGPPGFPGAPGPK.g [8xOxidation]	-0.0048
COL1A2	A0A452G3V6	[708-736]	1	2670.239	1	k.GERGYPGNAGPVGAAGAPGPQGPVGPTGK.h [1xDeamidation; 6xOxidation]	-0.0071
COL1A1	A0A3P9NHJ7	[333-361]	1	2685.2427	1	r.GPPGPQGAAGAPGPKGNTFQGDVGAPGFK.g [3xDeamidation; 3xOxidation]	-0.0126
COL1A1	A0A6I9MX97	[966-995]	0	2686.2162	1	r.GFTGMQGPIGPSGSNGEAGPAGTSGPAGPR.g [1xDeamidation; 1xOxidation]	0.0007
COL1A2	A0A452G3V6	[404-433]	1	2689.2448	1	r.GPPGESGAAGPTGPIGSRGPSGPPGPDGNK.g [4xOxidation]	-0.0136
COL1A1	A0A452FHU9	[796-825]	1	2703.2394	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [4xOxidation]	-0.0168
COL1A2	A0A452G3V6	[404-433]	1	2705.2398	1	r.GPPGESGAAGPTGPIGSRGPSGPPGPDGNK.g [5xOxidation]	-0.0114
COL1A2	A0A452G3V6	[73-102]	0	2713.2601	1	r.GPPGASGAPGPQGFQGPPGEPGEPGQTGAR.g [1xDeamidation]	0.0151
COL1A1	A0A090B2K5	[1099-1128]	0	2715.3121	1	r.GFTGLQGLPGPAGHTGETGPAGPAGPAGPR.g [1xDeamidation; 2xOxidation]	0.0169
COL1A1	A0A452FHU9	[796-825]	1	2735.2292	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [6xOxidation]	0.0019
COL1A2	A0A6P3W0U2	[1011-1040]	0	2750.2336	1	r.GHPGLQGMPGPNGPPGDSGPAGSTGHSGPR.g [1xDeamidation; 1xOxidation]	0.003
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0037
COL1A1	A0A3B5AFM4	[540-572]	1	2767.2765	1	r.GPAGAAGAVGAPGKDGDVGAPGSSGPAGPAGEK.g [5xOxidation]	0.0134
COL1A1	A0A452FHU9	[994-1025]	1	2866.3537	1	r.GPPGPMGPPGLAGPPGESGREGAPGAEGSPGR.d [1xOxidation]	-0.0148
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.005
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0091
COL1A1	A0A452FHU9	[709-741]	1	2883.4166	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g	-0.0125
COL1A1	A0A452FHU9	[763-795]	1	2883.4231	1	r.GLTGPIGPPGPAGAPGDKGETGPSGPAGPTGAR.g [2xOxidation]	-0.019
COL1A1	A0A3P9NHJ7	[551-582]	1	3002.3471	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [1xDeamidation; 4xOxidation]	-0.006

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A6P3W0U2	[297-329]	1	3009.3933	1	k.GAAGLPGIAGTPGFPGPRGGNGPQGPSGPSGQR.g [3xDeamidation; 5xOxidation]	0.0013
COL1A1	A0A3P9NHJ7	[551-582]	1	3018.342	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [1xDeamidation; 5xOxidation]	0.0041
COL1A1	A0A6I9MX97	[963-995]	1	3068.3875	1	k.GHRGFTGMQGPIGPSGSNGEAGPAGTSGPAGPR.g [1xDeamidation; 3xOxidation]	-0.0136
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	-0.0071
COL1A1	A0A452FHU9	[187-219]	0	3084.4116	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [5xOxidation]	0.0084
COL1A1	A0A452FHU9	[187-219]	0	3085.3956	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [1xDeamidation; 5xOxidation]	0.0112
COL1A2	A0A452G3V6	[623-655]	0	3093.4912	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [5xOxidation]	-0.0126
COL1A1	A0A3B5AFM4	[921-954]	1	3100.3951	1	r.GAPGPAGPPGLSGAPGEAGREPQGSTGHDGAPGR.d [1xDeamidation; 5xOxidation]	-0.0125
COL1A2	A0A452G3V6	[623-655]	0	3157.4709	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [9xOxidation]	-0.0126
COL1A1	A0A3P9NHJ7	[605-640]	1	3184.4712	1	r.GSPGSPGNDGAKGEPGAPGAPGAAGPPGLQGMPGER.g [2xOxidation]	0.0191
COL1A1	A0A452FHU9	[697-732]	1	3195.388	1	r.GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGER.g [3xDeamidation; 3xOxidation]	-0.0134
COL1A2	A0A452G3V6	[422-457]	1	3227.52	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [4xOxidation]	0.0057
COL1A1	A0A452FHU9	[312-351]	1	3331.6567	1	r.PGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g	-0.0109
COL1A2	A0A452G3V6	[780-815]	1	3349.7261	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [2xOxidation]	-0.0062
COL1A1	A0A3B5AFM4	[1306-1336]	1	3390.6926	1	k.TSRLPIIDFAPLDVGAPDQEFGVEVGPVCFL. [1xCarbamidomethyl; 2xOxidation]	-0.0145
COL1A2	A0A452G3V6	[623-658]	1	3435.6564	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSRGER.g [5xOxidation]	-0.0114
COL1A1	A0A452FHU9	[1111-1151]	1	3723.6753	1	r.GFSGLQGPPGPPGSPGEQGPSGASGPAGPRGPPGSAGTPGK.d [10xOxidation]	0.0094
Ovostatin	P20740	[666-685]	1	2274.0781	1	r.PLTSGLGPDVYQFLRDMGMK.f [1xDeamidation; 3xOxidation]	0.0105
Ovostatin	P20740	[261-281]	1	2428.1999	1	k.ICAVYTYGQPVEGKVQLSVCR.d [2xCarbamidomethyl; 1xDeamidation]	-0.0158

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
Ovostatin	P20740	[261-281]	1	2445.1789	1	k.ICAVYTYGQPVEGKVQLSVCR.d [2xCarbamidomethyl; 2xDeamidation; 1xOxidation]	0.0151
Ovostatin	P20740	[261-281]	1	2460.1898	1	k.ICAVYTYGQPVEGKVQLSVCR.d [2xCarbamidomethyl; 1xDeamidation; 2xOxidation]	0.0138
Ovotransferrin	P02789	[517-539]	1	2591.1534	1	r.LCQLCQGSGGIPPEKCVASSHEK.y [3xCarbamidomethyl; 1xDeamidation; 3xOxidation]	0.0192
Ovostatin	P20740	[159-185]	1	3167.5129	1	r.VVALDFNFKPVQEMYPLIAVQDPQNNR.i [6xDeamidation; 1xOxidation]	0.0109
Ovostatin	P20740	[159-185]	1	3183.5078	1	r.VVALDFNFKPVQEMYPLIAVQDPQNNR.i [6xDeamidation; 2xOxidation]	-0.0063
Ovalbumin-related protein X	P01013	[72-99]	1	3210.616	1	k.MKILELPFASGDLSMLVLLPDEVSDLER.i [5xOxidation]	0.0147
Ovostatin	P20740	[430-457]	1	3226.4633	1	k.ALYKTSDQCHSEGWIEPSYPDASLSVQR.l [1xCarbamidomethyl; 2xDeamidation]	-0.0047
Ovalbumin-related protein X	P01013	[136-167]	0	3373.727	1	k.YNLTSVLMALGMTDLFIPSANLTGISSAESLK.i [1xOxidation]	-0.0039
Serpin-Z1A	Q41593	[157-171]	1	1643.885	1	r.IKDILPPGSIDNTTK.l [2xOxidation]	0.0064
COL1A2	A0A452G3V6	[282-290]	0	801.4213	1	r.GATGPAGVR.g [1xOxidation]	-0.0034
COL1A2	A0A452G3V6	[599-606]	0	802.369	1	r.GDQGPVGR.t [1xDeamidation; 1xOxidation]	-0.0006
COL1A2	A0A6P3W0U2	[144-152]	0	805.3799	1	r.GTAGSQGAR.g [1xDeamidation]	0.0129
COL1A2	A0A452G3V6	[1082-1087]	1	806.4043	1	k.KTNEWK.k [1xDeamidation]	-0.0153
COL1A2	A0A452G3V6	[1083-1088]	1	806.4043	1	k.TNEWKK.t [1xDeamidation]	-0.0153
COL1A1	A0A452FHU9	[1310-1315]	0	811.3985	1	k.NWYISK.n [1xDeamidation]	-0.0119
COL1A1	A0A1A8K041	[304-313]	0	814.4166	1	r.AGPSGAAGAR.g	-0.0119
COL1A2	A0A452G3V6	[924-929]	1	820.4094	1	r.TCRDLR.l [1xCarbamidomethyl]	-0.0044
COL1A2	A0A452G3V6	[1082-1087]	1	822.3992	1	k.KTNEWK.k [1xDeamidation; 1xOxidation]	0.0096

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[1083-1088]	1	822.3992	1	k.TNEWKK.t [1xDeamidation; 1xOxidation]	0.0096
COL1A1	A0A1A8K041	[353-361]	0	827.4006	1	r.GPEGPAGAR.g [1xOxidation]	0.0127
COL1A1	A0A452FHU9	[244-252]	0	836.4373	1	r.GPPGPQGAR.g	-0.0175
COL1A1	A0A452FHU9	[1084-1092]	0	836.4373	1	r.GPAGPQGPR.g	-0.0175
COL1A3	A0A090AZH6	[95-103]	0	839.3894	1	k.GPPGDDGPK.g	0.0197
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0095
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	-0.0067
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	-0.0067
COL1A1	A0A3B5AFM4	[307-315]	0	858.4064	1	r.GSEGPQGAR.g	0.0161
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.0141
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.0141
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.0141
COL1A2	A0A6P3W0U2	[996-1004]	1	890.4326	1	k.GTAGEKGDR.g	0.0189
COL1A1	A0A3B5AFM4	[506-515]	0	892.4635	1	r.PGPPGPSGAR.g	0.0094
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0139
COL1A1	A0A452FHU9	[361-369]	0	902.4326	1	r.GSEGPQGVR.g [1xOxidation]	0.0172
COL1A1	A0A452FHU9	[564-573]	0	950.469	1	r.PGPPGPPGAR.g [3xOxidation]	0.0004
COL1A1	A0A1A8K041	[556-565]	0	952.4847	1	r.PGPPGPVGAR.g [3xOxidation]	-0.0164
COL1A2	A0A452G3V6	[51-58]	0	953.4509	1	k.TSLSGMWR.n [1xOxidation]	0.0061

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A6I9N4J7	[1229-1237]	0	975.4629	1	k.IQSPDGTQK.s [2xDeamidation]	0.0101
COL1A2	A0A452G3V6	[1-8]	0	1010.4975	1	.MLSFVDTR.t [1xAcetyl]	-0.014
COL1A2	A0A452G3V6	[968-976]	0	1012.531	1	r.AQPEDIPVK.n [1xOxidation]	0.0028
COL1A1	A0A6I9N4J7	[669-680]	0	1024.5534	1	r.GVPGGAGPIGSR.g	-0.0191
COL1A2	A0A452G3V6	[968-976]	0	1029.5099	1	r.AQPEDIPVK.n [1xDeamidation; 2xOxidation]	0.0084
COL1A3	A0A090AZH6	[667-678]	0	1032.5334	1	r.GAPGGVGPAGHR.g	0.0177
COL1A1	A0A6I9N4J7	[968-977]	0	1048.5058	1	k.QGPAGLFGER.g [1xDeamidation; 1xOxidation]	0.0194
COL1A1	A0A452FHU9	[121-131]	1	1050.5439	1	r.GPRGPAGPPGR.d [2xOxidation]	0.0164
COL1A1	A0A452FHU9	[310-321]	1	1063.5756	1	r.GRPGAPGPAGAR.g	0.0087
COL1A1	A0A3B5AFM4	[612-623]	0	1068.5069	1	r.GGPGPVGPGGPR.g [4xOxidation]	0.0158
COL1A2	A0A6P3W0U2	[210-221]	1	1069.5497	1	r.GRAGPSGPAGAR.g [1xOxidation]	-0.0152
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	0.0018
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	0.0063
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.0117
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.0134
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0093
COL1A2	A0A452G3V6	[1089-1097]	1	1110.6041	1	k.TIIEYKTNK.p [1xDeamidation]	0.0141
COL1A1	A0A3B5AFM4	[540-553]	0	1112.5695	1	r.GPAGAAGAVGAPGK.d [2xOxidation]	0.0124
COL1A2	A0A6P3W0U2	[1310-1318]	1	1123.6106	1	k.TVIEYRTNK.p	-0.0035
COL1A2	A0A6P3W0U2	[1310-1318]	1	1124.5946	1	k.TVIEYRTNK.p [1xDeamidation]	0.0139

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A6I9N4J7	[465-476]	1	1125.5396	1	r.GPNGERGGPGAR.g [1xDeamidation]	0.0197
COL1A1	A0A452FHU9	[733-744]	1	1127.5804	1	r.GAAGLPGPKGDR.g [2xOxidation]	-0.0076
COL1A1	A0A3B5AFM4	[660-671]	1	1129.596	1	r.GAGGLPGVKGER.g [2xOxidation]	-0.0028
COL1A1	A0A3B5AFM4	[256-267]	0	1134.5902	1	r.PGPPGPSLQGAR.g [1xDeamidation]	0.0196
COL1A3	A0A090AZH6	[1293-1301]	1	1137.5687	1	k.NWYTSKNPK.e	0.0195
COL1A3	A0A090AZH6	[292-303]	1	1137.5759	1	r.GRPGPPGPAGAR.g [3xOxidation]	0.0123
COL1A2	A0A452G3V6	[323-334]	0	1138.5851	1	k.EGPAGLPGIDGR.p	0.0093
COL1A1	A0A452FHU9	[253-264]	0	1146.5823	1	r.GLPGTAGLPGMK.g [3xOxidation]	0.0179
COL1A1	A0A452FHU9	[1310-1318]	1	1150.5891	1	k.NWYISKNPK.d [1xDeamidation]	0.0026
COL1A2	A0A452G3V6	[323-334]	0	1154.58	1	k.EGPAGLPGIDGR.p [1xOxidation]	0.0131
COL1A1	A0A452FHU9	[574-585]	0	1161.5721	1	r.GQAGVMGFPGPK.g [1xOxidation]	0.0039
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0167
COL1A1	A0A6I9N4J7	[1295-1303]	1	1183.5994	1	k.NWYLSKNIK.e [2xDeamidation; 1xOxidation]	0.0067
COL1A2	A0A452G3V6	[759-770]	1	1185.5858	1	r.GPSGPQGIRGDK.g [1xDeamidation; 1xOxidation]	-0.013
COL1A2	A0A452G3V6	[345-356]	0	1185.5899	1	r.GEPGNIGFPGPK.g [1xOxidation]	-0.017
COL1A1	A0A452FHU9	[1236-1245]	0	1187.6379	1	k.SLSQQIENIR.s	-0.0148
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.0062
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	0.0098
COL1A2	A0A6P3W0U2	[474-485]	0	1203.6004	1	r.GQPGTIGFPGPK.g [3xOxidation]	0.0129
COL1A1	A0A1A8K041	[232-244]	1	1240.6029	1	r.PGERGAAGPQGAR.g [1xDeamidation; 1xOxidation]	0.0029

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[214-228]	0	1251.6804	1	r.GIPGPVGAAGATGAR.g	0.0039
COL1A1	A0A1A8K041	[407-421]	0	1259.6379	1	r.GPPGPQGAAGAPGPK.g [1xDeamidation]	-0.0041
COL1A2	A0A452G3V6	[214-228]	0	1267.6753	1	r.GIPGPVGAAGATGAR.g [1xOxidation]	0.0126
COL1A2	A0A6P3W0U2	[561-575]	0	1316.6077	1	r.GSPGDQGASGPAGVK.g [2xOxidation]	0.0048
COL1A1	A0A452FHU9	[781-795]	0	1343.6186	1	k.GETGPSGPAGPTGAR.g [2xOxidation]	0.0198
COL1A1	A0A3B5AFM4	[183-196]	1	1383.6724	1	r.PGERGAAGPQQGAR.g [2xOxidation]	0.0141
COL1A1	A0A3B5AFM4	[708-722]	0	1383.6863	1	k.GEPGALGVAGPTGPR.g [3xOxidation]	0.0002
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0149
COL1A1	A0A452FHU9	[918-933]	0	1458.7223	1	r.PGEVGPPGPPGPAGEK.g [1xOxidation]	0.0035
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.0127
COL1A3	A0A090AZH6	[847-863]	0	1473.7081	1	r.GGAGPPGATGFPGAVGR.v [3xOxidation]	-0.0122
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0082
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	-0.003
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	-0.003
COL1A1	A0A452FHU9	[1152-1167]	0	1546.786	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	0.0105
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	0.0106
COL1A2	A0A452G3V6	[196-213]	0	1562.8285	1	k.GAAGLPGVAGAPGLPGPR.g [3xOxidation]	-0.0004
COL1A1	A0A452FHU9	[1371-1384]	0	1568.7373	1	k.NSVAYMDQQTGNLK.k	-0.0004
COL1A1	A0A452FHU9	[397-414]	0	1569.7768	1	k.GANGAPGIAGAPGFPGAR.g [2xOxidation]	0.0116
COL1A1	A0A452FHU9	[397-414]	0	1570.7608	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 2xOxidation]	0.0144

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[59-72]	1	1583.7781	1	r.NSCLTHPKGLMGPR.g [1xCarbamidomethyl; 1xOxidation]	0.0159
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0104
COL1A1	A0A452FHU9	[397-414]	0	1586.7558	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 3xOxidation]	0.0181
COL1A2	A0A6P3W0U2	[1303-1315]	1	1604.818	1	r.HTGQWSKTVIEYR.t	0.0158
COL1A2	A0A6P3W0U2	[579-596]	0	1611.7721	1	r.GNPGPAGSVGSQGPIGAR.g [1xDeamidation; 2xOxidation]	0.0104
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0.0065
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	0.0025
COL1A2	A0A6P3W0U2	[1303-1315]	1	1620.8129	1	r.HTGQWSKTVIEYR.t [1xOxidation]	0.0129
COL1A1	A0A1A8K041	[959-975]	1	1658.8133	1	r.GERGFPGLPGPAGETGK.v [2xOxidation]	0.0091
COL1A1	A0A452FHU9	[612-630]	0	1706.7729	1	k.DGEAGAQGPPGPAGPAGER.g [1xOxidation]	0.0049
COL1A1	A0A1A8K041	[1006-1024]	1	1740.8147	1	r.EGTPGTEGAAGRDGAPGPK.g [1xOxidation]	-0.0181
COL1A3	A0A090AZH6	[1354-1368]	1	1743.8218	1	k.NSIAYMDQQTGNLKK.a [1xDeamidation; 2xOxidation]	-0.0074
COL1A2	A0A452G3V6	[345-361]	1	1759.861	1	r.GEPGNIGFPGPKGPTVR.i [5xOxidation]	0.0066
COL1A1	A0A6I9N4J7	[866-886]	0	1779.9752	1	r.VGPPGPSGVGGPPGPLGPVGK.e	-0.0106
COL1A1	A0A452FHU9	[352-369]	1	1784.8158	1	k.GEAGPQGPRGSEGPQGVR.g [1xDeamidation; 3xOxidation]	0.0195
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	-0.0135
COL1A1	A0A1A8K041	[773-793]	1	1804.9049	1	k.GEPGAAGPVGAAGARGAPGER.g	0.0125
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	0.0021
COL1A1	A0A3B5AFM4	[394-413]	0	1820.8661	1	k.GEPGPAGVQGLPGPSGEEGK.r [1xDeamidation]	0.0139

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	-0.0027
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0092
COL1A2	A0A6P3W0U2	[474-493]	1	1872.9086	1	r.GQPGTIGFPGPKGPGGEAGK.a [4xOxidation]	0.0114
COL1A2	A0A6P3W0U2	[474-493]	1	1888.9035	1	r.GQPGTIGFPGPKGPGGEAGK.a [5xOxidation]	0.0113
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0061
COL1A2	A0A452G3V6	[323-344]	1	2028.0621	1	k.EGPAGLPGIDGRPGPIGPAGAR.g [1xOxidation]	-0.0128
COL1A1	A0A3B5AFM4	[394-414]	1	2040.9469	1	k.GEPGPAGVQGLPGPSGEEGKR.g [1xDeamidation; 4xOxidation]	0.0002
COL1A1	A0A6I9N4J7	[1371-1389]	1	2056.0782	1	k.ALLLQGTNDVEIRAEGNSR.f	-0.0077
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0138
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.0077
COL1A1	A0A452FHU9	[934-957]	0	2073.9948	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 1xOxidation]	0.0069
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	0.0048
COL1A1	A0A1A8K041	[556-577]	1	2106.0437	1	r.PGPPGPVGARGQPGVMGFPGPK.g [1xDeamidation; 3xOxidation]	-0.0145
COL1A1	A0A1A8K041	[902-925]	1	2180.0214	1	r.GETGPAGRPGEVGAAGPPGPSGEK.g [3xOxidation]	-0.0024
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	0.0156
COL1A3	A0A090AZH6	[691-714]	0	2199.9757	1	k.GEPGAAGAPGALGAPGMQGMPGER.g [4xOxidation]	0.0124
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.0101
COL1A1	A0A3B5AFM4	[809-833]	1	2263.0949	1	r.VGPPGPAGASGPPGPVGPVGKDGAR.g [7xOxidation]	-0.0175
COL1A1	A0A1A8K041	[1058-1084]	1	2285.1017	1	r.GETGPAGPAGPAGPAGPRGPGGPAGAR.g [3xOxidation]	0.0026
COL1A1	A0A452FHU9	[442-467]	1	2394.1056	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 2xOxidation]	0.0072

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[442-467]	1	2409.1165	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [3xOxidation]	0.0034
COL1A1	A0A452FHU9	[442-467]	1	2410.1005	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 3xOxidation]	0.0112
COL1A1	A0A1A8K041	[1160-1187]	1	2445.1793	1	r.GRSGETGPSGPPGNPGPPGPPGPPGPGI. [1xDeamidation]	0.018
COL1A1	A0A1A8K041	[1133-1159]	1	2453.1878	1	r.GPPGPVGPAGKDGSNGMPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	-0.001
COL1A1	A0A1A8K041	[1160-1187]	1	2461.1742	1	r.GRSGETGPSGPPGNPGPPGPPGPPGPGI. [1xDeamidation; 1xOxidation]	0.007
COL1A2	A0A6P3W0U2	[45-71]	0	2465.1732	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation]	0.0128
COL1A2	A0A452G3V6	[565-591]	0	2468.1728	1	r.GDGGPPVSTYPGFGISGPPGPPGPAGK.e [3xOxidation]	0.0184
COL1A1	A0A1A8K041	[1160-1187]	1	2477.1692	1	r.GRSGETGPSGPPGNPGPPGPPGPPGPGI. [1xDeamidation; 2xOxidation]	0.0197
COL1A2	A0A6P3W0U2	[45-71]	0	2481.1681	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 1xOxidation]	0.0112
COL1A1	A0A1A8K041	[1133-1159]	1	2484.1936	1	r.GPPGPVGPAGKDGSNGMPGPIGPPGPR.g [4xOxidation]	0.0057
COL1A1	A0A1A8K041	[1133-1159]	1	2485.1776	1	r.GPPGPVGPAGKDGSNGMPGPIGPPGPR.g [1xDeamidation; 4xOxidation]	0.0171
COL1A2	A0A6P3W0U2	[45-71]	0	2497.163	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 2xOxidation]	-0.004
COL1A1	A0A452FHU9	[322-351]	0	2501.2055	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation]	-0.0196
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	-0.0002
COL1A3	A0A090AZH6	[304-333]	0	2563.1332	1	r.GNDGNSGAAGPPGPTGPAGPPGFPGGAGPK.g [2xDeamidation; 3xOxidation]	0.0049
COL1A1	A0A452FHU9	[1288-1309]	0	2578.1258	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 2xOxidation]	0.0125
COL1A3	A0A090AZH6	[304-333]	0	2579.1281	1	r.GNDGNSGAAGPPGPTGPAGPPGFPGGAGPK.g [2xDeamidation; 4xOxidation]	0.005
COL1A1	A0A3B5AFM4	[268-297]	0	2581.155	1	r.GNDGNTGAAGPPGPTGPAGPPGFPGGAGAK.g [5xOxidation]	-0.0035

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[322-351]	0	2597.175	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 6xOxidation]	0.0107
COL1A2	A0A6P3W0U2	[222-251]	0	2654.1965	1	r.GADGNTGPSGPAGPLGAAGPPGFPGAPGPK.g [8xOxidation]	-0.0064
COL1A2	A0A452G3V6	[535-564]	0	2677.2085	1	k.GENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [7xOxidation]	0.0065
COL1A1	A0A452FHU9	[984-1013]	1	2728.2744	1	k.QGPSGASGERGPPGPMGPPGLAGPPGESGR.e [1xDeamidation; 1xOxidation]	0.0037
COL1A2	A0A452G3V6	[711-740]	1	2750.2765	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [2xDeamidation; 5xOxidation]	-0.0111
COL1A2	A0A6P3W0U2	[1011-1040]	0	2751.2176	1	r.GHPGLQGMPGPNGPPGDSGPAGSTGHSGPR.g [2xDeamidation; 1xOxidation]	-0.0161
COL1A1	A0A3B5AFM4	[540-572]	1	2767.2765	1	r.GPAGAAGAVGAPGKDGDVGAPGSSGPAGPAGEK.g [5xOxidation]	-0.005
COL1A2	A0A6P3W0U2	[1115-1139]	1	2769.32	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [3xDeamidation; 1xOxidation]	-0.0136
COL1A2	A0A6P3W0U2	[1115-1139]	1	2784.3309	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [2xDeamidation; 2xOxidation]	-0.0186
COL1A2	A0A6P3W0U2	[1115-1139]	1	2785.3149	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [3xDeamidation; 2xOxidation]	-0.004
COL1A1	A0A452FHU9	[984-1013]	1	2792.254	1	k.QGPSGASGERGPPGPMGPPGLAGPPGESGR.e [1xDeamidation; 5xOxidation]	0.0178
COL1A2	A0A6P3W0U2	[609-641]	1	2867.3489	1	k.GEPGAVGPAGAPGHQGPAGMPGERGAGGTPGAK.g [1xDeamidation; 1xOxidation]	0.0138
COL1A2	A0A452G3V6	[532-564]	1	2879.4031	1	k.GPKGENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.018
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.0171
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0196
COL1A1	A0A6I9N4J7	[1248-1272]	1	2899.3542	1	k.MAHPEWKSDMFWVDPNQGSPLDAIK.v	0.0192
COL1A2	A0A6P3W0U2	[834-866]	0	2921.3773	1	k.GSPGESGPAGAPGTAGPQGQLGSQGFNGLPGGR.g [1xDeamidation]	-0.0194
COL1A2	A0A6P3W0U2	[834-866]	0	3001.3518	1	k.GSPGESGPAGAPGTAGPQGQLGSQGFNGLPGGR.g [1xDeamidation; 5xOxidation]	-0.0189

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A6P3W0U2	[663-695]	1	3002.2995	1	r.GAPGPSGPPGPAGANGEKGESGSYGPAGPAGPR.g [9xOxidation]	0.0116
COL1A3	A0A090AZH6	[691-723]	1	3018.3098	1	k.GEPGAAGAPGALGAPGMQGMPGERGAGGMPGAR.g [8xOxidation]	0.0034
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.005
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.0127
COL1A3	A0A090AZH6	[808-843]	1	3115.3948	1	k.GETGDTGPKGDAGAPGHAGPAGAAGPQGPAGNAGPK.g [1xDeamidation; 4xOxidation]	-0.0158
COL1A1	A0A1A8K041	[314-352]	1	3315.5261	1	r.GNDGAAGAAGPPGPTGPAGPPGFPGGPGSKGDVGAQGAR.g [2xDeamidation; 2xOxidation]	-0.0014
COL1A2	A0A452G3V6	[780-815]	1	3365.721	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [3xOxidation]	0.0115
COL1A2	A0A452G3V6	[780-815]	1	3366.705	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 3xOxidation]	0.0091
COL1A2	A0A452G3V6	[780-815]	1	3381.7159	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [4xOxidation]	0.0001
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	0.0055
COL1A1	A0A452FHU9	[322-360]	1	3397.6156	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPR.g [3xOxidation]	0.0197
COL1A1	A0A452FHU9	[1433-1463]	1	3397.6508	1	k.TSRLPIIDVAPLDVGAPDQEFGFDIGSVCFL. [1xCarbamidomethyl; 1xDeamidation; 3xOxidation]	-0.0156
COL1A1	A0A452FHU9	[322-360]	1	3413.6105	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPR.g [4xOxidation]	0.0111
COL1A1	A0A452FHU9	[237-243]	1	800.4009	1	k.PGRPGER.g [2xOxidation]	-0.0052
COL1A1	A0A452FHU9	[1310-1315]	0	810.4145	1	k.NWYISK.n	-0.0055
COL1A1	A0A3P9BC04	[373-381]	0	813.385	1	r.GEPGGAGPR.g [1xOxidation]	-0.0041
COL1A2	A0A3B4ZDV7	[152-160]	0	814.4054	1	k.GEPGAAGQK.g	-0.0095
COL2A1a	Q2I8Y0	[592-597]	0	821.3941	1	k.SWWTNK.s	-0.0167
COL2A1a	Q2I8Y0	[592-597]	0	822.3781	1	k.SWWTNK.s [1xDeamidation]	-0.0165

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0053
COL1A1	A0A3P9NHJ7	[177-185]	0	842.4115	1	r.GPSGPQGAR.g [1xOxidation]	-0.0057
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	-0.0071
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	-0.0071
COL1A2	A0A3B4ZDV7	[172-181]	0	856.4272	1	r.AGPAGPAGAR.g [2xOxidation]	0.0012
COL1A1	A0A3P9NHJ7	[177-185]	0	858.4064	1	r.GPSGPQGAR.g [2xOxidation]	0.0121
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.0104
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.0104
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.0104
COL1A1	A0A452FHU9	[1253-1259]	1	890.4261	1	k.NPARTCR.d [1xCarbamidomethyl; 1xOxidation]	-0.013
COL1A1	A0A452FHU9	[1253-1259]	1	891.4101	1	k.NPARTCR.d [1xCarbamidomethyl; 1xDeamidation; 1xOxidation]	-0.0022
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0193
COL1A1	A0A452FHU9	[361-369]	0	902.4326	1	r.GSEGPQGVR.g [1xOxidation]	0.0138
COL1A1	A0A3P9NHJ7	[892-901]	0	942.4275	1	k.PGPAGPGGER.g [3xOxidation]	-0.0081
COL1A1	A0A452FHU9	[564-573]	0	950.469	1	r.PGPPGPPGAR.g [3xOxidation]	0.0017
COL1A2	A0A452G3V6	[51-58]	0	953.4509	1	k.TSLSGMWR.n [1xOxidation]	0.0082
COL1A2	A0A3B4ZDV7	[361-370]	0	988.488	1	r.TGPIGMPGAR.g [2xOxidation]	0.0114
COL1A2	A0A3B4ZDV7	[1066-1074]	1	988.488	1	r.ADQPAMRAK.d [1xDeamidation]	0.0114
COL1A3	A0A3Q2CSU4	[670-681]	0	1006.5429	1	r.GAPGPVGPAGAR.g	0.0014
COL1A2	A0A452G3V6	[1-8]	0	1010.4975	1	.MLSFVDTR.t [1xAcetyl]	0.0026

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[299-308]	0	1010.5088	1	r.PGEPGLMGPR.g	-0.0086
COL1A3	A0A3Q2CSU4	[670-681]	0	1022.5378	1	r.GAPGPVGPAGAR.g [1xOxidation]	-0.0109
COL1A1	A0A452FHU9	[697-708]	0	1028.4756	1	r.GANGAPGNDGAK.g	0.0092
COL1A1	A0A6I9N4J7	[968-977]	0	1048.5058	1	k.QGPAGLFGER.g [1xDeamidation; 1xOxidation]	0.0188
COL1A1	A0A452FHU9	[121-131]	1	1050.5439	1	r.GPRGPAGPPGR.d [2xOxidation]	0.0087
COL1A2	A0A3B4ZDV7	[170-181]	1	1069.5497	1	r.GRAGPAGPAGAR.g [2xOxidation]	-0.0157
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	-0.0014
COL1A2	A0A3B4ZDV7	[290-301]	0	1085.5586	1	r.GLAGDPGAQGVK.g [1xOxidation]	0.0107
COL1A1	A0A452FHU9	[907-917]	1	1086.5287	1	k.GPRGETGPAGR.p [2xOxidation]	0.0079
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	0.0173
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.0097
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.0154
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0106
COL1A2	A0A3B4ZDV7	[1269-1277]	1	1124.5946	1	k.TVIEYRTNK.p [1xDeamidation]	-0.0102
COL1A1	A0A452FHU9	[733-744]	1	1127.5804	1	r.GAAGLPGPKGDR.g [2xOxidation]	-0.0021
COL1A2	A0A452G3V6	[323-334]	0	1138.5851	1	k.EGPAGLPGIDGR.p	-0.0155
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.0144
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0137
COL1A1	A0A3P9NHJ7	[1206-1214]	1	1183.5928	1	k.NWYMSKNIK.e	0.0054
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.012
COL1A1	A0A3P9NHJ7	[1133-1142]	0	1203.6216	1	k.SLSQQIEQIR.s [2xDeamidation]	-0.0011

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[881-891]	1	1229.6233	1	r.ADQPRSPASLR.p [2xOxidation]	-0.0055
COL1A2	A0A452G3V6	[214-228]	0	1251.6804	1	r.GIPGPVGAAGATGAR.g	-0.0175
COL1A2	A0A3B4ZDV7	[1073-1083]	1	1252.642	1	r.AKDYEVDATIK.s	0.0143
COL1A1	A0A3P9NHJ7	[333-347]	0	1258.6539	1	r.GPPGPQGAAGAPGPK.g	-0.0197
COL1A2	A0A452G3V6	[214-228]	0	1267.6753	1	r.GIPGPVGAAGATGAR.g [1xOxidation]	0.0109
COL1A1	A0A3P9NHJ7	[333-347]	0	1306.6386	1	r.GPPGPQGAAGAPGPK.g [3xOxidation]	0.0056
COL1A1	A0A3P9BC04	[671-685]	0	1307.6702	1	k.GEPGAVGVAGPSGPR.g	0.0181
COL1A1	A0A452FHU9	[1386-1398]	0	1457.7846	1	k.ALLLQGSNEIEIR.a [2xDeamidation]	0.0001
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.017
COL1A1	A0A452FHU9	[253-267]	1	1464.774	1	r.GLPGTAGLPGMKGHR.g [1xOxidation]	-0.0036
COL1A1	A0A3P9NHJ7	[877-891]	0	1473.6856	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation; 4xOxidation]	0.0021
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0134
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	0.0021
COL1A1	A0A3P9BC04	[1042-1057]	0	1500.7805	1	k.DGVNGLPGPIGPPGPR.g [1xDeamidation]	-0.0121
COL1A2	A0A452G3V6	[827-842]	1	1508.7928	1	k.DGRTGQPGAVGPAGIR.g	0.001
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	-0.0066
COL1A1	A0A452FHU9	[1152-1167]	0	1546.786	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	0.0199
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	0.0151
COL1A1	A0A3P9NHJ7	[431-447]	1	1568.8027	1	r.GAPGLVGPKGSTGEPGR.t [2xOxidation]	0.0101

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[397-414]	0	1569.7768	1	k.GANGAPGIAGAPGFPGAR.g [2xOxidation]	0.0102
COL1A1	A0A452FHU9	[397-414]	0	1570.7608	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 2xOxidation]	0.0174
COL1A2	A0A3B4ZDV7	[290-307]	1	1580.8027	1	r.GLAGDPGAQGVKGDGGPK.g	-0.0094
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0148
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0.0127
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	0.0087
COL1A1	A0A3P9BC04	[653-670]	0	1647.8701	1	r.GLTGPIGVPGPPGAQGEK.g [1xOxidation]	0.0008
COL1A1	A0A3P9BC04	[653-670]	0	1648.8541	1	r.GLTGPIGVPGPPGAQGEK.g [1xDeamidation; 1xOxidation]	-0.0123
COL1A1	A0A3P9BC04	[653-670]	0	1663.865	1	r.GLTGPIGVPGPPGAQGEK.g [2xOxidation]	0.0161
COL1A1	A0A452FHU9	[612-630]	0	1690.778	1	k.DGEAGAQGPPGPAGPAGER.g	0.0101
COL1A1	A0A452FHU9	[612-630]	0	1706.7729	1	k.DGEAGAQGPPGPAGPAGER.g [1xOxidation]	0.0124
COL1A1	A0A6I9N4J7	[866-886]	0	1779.9752	1	r.VGPPGPSGVGGPPGPLGPVGK.e	-0.0007
COL1A1	A0A3P9NHJ7	[874-891]	1	1782.8769	1	r.GERGFPGPPGPAQGEIGK.p [2xOxidation]	-0.0123
COL1A1	A0A452FHU9	[352-369]	1	1783.8318	1	k.GEAGPQGPRGSEGPQGVR.g [3xOxidation]	0.0057
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	-0.0075
COL2A1a	Q2I8Y0	[162-182]	0	1803.9137	1	r.VGPPGPNGNPGPPGPPGPGGK.d	-0.012
COL2A1a	Q2I8Y0	[162-182]	0	1804.8977	1	r.VGPPGPNGNPGPPGPPGPGGK.d [1xDeamidation]	0.0182
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	0.0069
COL2A1a	Q2I8Y0	[162-182]	0	1820.8926	1	r.VGPPGPNGNPGPPGPPGPGGK.d [1xDeamidation; 1xOxidation]	-0.0032
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	0.0039
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0026

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A3	A0A3Q2CSU4	[642-660]	0	1837.8675	1	k.PGEQGLPGEPGAVGPAGQR.g [4xOxidation]	0.016
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0005
COL1A2	A0A3B4ZDV7	[119-139]	1	2016.9808	1	r.GTPGTQGARGFPGTPGLPGMK.g [1xDeamidation; 2xOxidation]	-0.0127
COL1A2	A0A3B4ZDV7	[1231-1249]	1	2016.9833	1	k.AVVLQGSNDVELRAEGNSR.f [3xDeamidation]	-0.0152
COL1A2	A0A452G3V6	[323-344]	1	2028.0621	1	k.EGPAGLPGIDGRPGPIGPAGAR.g [1xOxidation]	-0.0111
COL1A1	A0A6I9N4J7	[1371-1389]	1	2056.0782	1	k.ALLLQGTNDVEIRAEGNSR.f	-0.0062
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0058
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.0082
COL1A1	A0A452FHU9	[934-957]	0	2073.9948	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 1xOxidation]	0.008
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	-0.0008
COL1A1	A0A452FHU9	[934-957]	0	2089.9897	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 2xOxidation]	0.0145
COL1A1	A0A452FHU9	[528-551]	1	2104.0669	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t	0.014
COL1A1	A0A3P9NHJ7	[484-505]	1	2105.0597	1	r.PGPPGPVGARGQPGVMGFPGPK.g [3xOxidation]	-0.0192
COL1A1	A0A452FHU9	[528-551]	1	2152.0517	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t [3xOxidation]	-0.0125
COL1A2	A0A3B4ZDV7	[742-766]	1	2179.0738	1	r.VGGAGPAGIVGPPGPAGAAGKDGPR.g [6xOxidation]	-0.0166
COL1A3	A0A3Q2CSU4	[513-536]	1	2180.0288	1	r.TGEPGLPGAKGMTGSPGNPGPDGK.m [1xDeamidation]	-0.009
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	0.0111
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.0013
COL1A1	A0A3P9BC04	[956-982]	1	2263.0698	1	r.GESGPSGPAGPSGPAGARGPSGPAGAK.g [2xOxidation]	0.0148
COL1A2	A0A452G3V6	[711-736]	0	2264.0942	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGK.h [1xDeamidation; 2xOxidation]	-0.0125
COL1A2	A0A452G3V6	[169-195]	0	2368.2143	1	r.GEVGLPGLSGPVGPPGNPGANGLPGAK.g [2xDeamidation]	0.0067

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[442-467]	1	2394.1056	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 2xOxidation]	0.0191
COL1A1	A0A452FHU9	[442-467]	1	2409.1165	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [3xOxidation]	0.0098
COL1A1	A0A452FHU9	[442-467]	1	2410.1005	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 3xOxidation]	0.0138
COL1A2	A0A3B4ZDV7	[767-793]	1	2461.1776	1	r.GLRGDVGPAGPSGEQGMVGPPGPAGDK.g [1xDeamidation]	0.0121
COL1A3	A0A3Q2CSU4	[307-336]	0	2481.1793	1	r.GNDGAAGAAGPPGPTGPAGPPGFPGGPGPK.g [1xDeamidation]	0.0021
COL1A1	A0A3P9BC04	[923-951]	1	2485.2066	1	k.GDRGETGLGGPPGPPGAPGAPGGVGPSGK.t [2xOxidation]	0.0043
COL1A3	A0A3Q2CSU4	[307-336]	0	2497.1742	1	r.GNDGAAGAAGPPGPTGPAGPPGFPGGPGPK.g [1xDeamidation; 1xOxidation]	-0.0104
COL1A1	A0A452FHU9	[322-351]	0	2501.2055	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation]	-0.0081
COL1A3	A0A3Q2CSU4	[307-336]	0	2513.1692	1	r.GNDGAAGAAGPPGPTGPAGPPGFPGGPGPK.g [1xDeamidation; 2xOxidation]	-0.0012
COL1A3	A0A3Q2CSU4	[1018-1046]	1	2563.1655	1	k.GDRGESGPAGAPGAPGPPGAPGPVGPAGK.t [8xOxidation]	-0.0097
COL1A1	A0A6I9N4J7	[819-848]	1	2580.1557	1	k.GDGGAPGPSGPVGGSGPQGPSGPSGPKGAR.g [1xDeamidation; 5xOxidation]	0.0049
COL1A1	A0A6I9N4J7	[819-848]	1	2595.1666	1	k.GDGGAPGPSGPVGGSGPQGPSGPSGPKGAR.g [6xOxidation]	-0.0165
COL1A1	A0A452FHU9	[322-351]	0	2597.175	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 6xOxidation]	0.0148
COL1A2	A0A3B4ZDV7	[972-1001]	0	2653.206	1	r.GHPGLQGMPGPSGPSGDTGAAGPNGPAGPR.g [2xDeamidation]	-0.0013
COL1A2	A0A452G3V6	[121-150]	0	2669.2325	1	r.GSDGSVGPVGPAGPIGSAGPPGFPGAPGPK.g [8xOxidation]	-0.0177
COL1A3	A0A3Q2CSU4	[781-810]	1	2681.2186	1	r.GAPGERGESGPPGPAGFAGAPGADGQPGAK.g [4xOxidation]	-0.0173
COL2A1a	Q2I8Y0	[316-345]	1	2686.2339	1	r.GENGSPGQPGAPGAPGAPGPVGPTGKNGER.g [3xDeamidation; 1xOxidation]	-0.0133
COL1A2	A0A452G3V6	[711-740]	1	2701.3077	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [1xDeamidation; 2xOxidation]	-0.0162
COL1A1	A0A452FHU9	[796-825]	1	2703.2394	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [4xOxidation]	-0.015
COL1A2	A0A452G3V6	[404-433]	1	2705.2398	1	r.GPPGESGAAGPTGPIGSRGPSGPPGPDGNK.g [5xOxidation]	-0.0113
COL2A1a	Q2I8Y0	[316-345]	1	2718.2238	1	r.GENGSPGQPGAPGAPGAPGPVGPTGKNGER.g [3xDeamidation; 3xOxidation]	-0.0039

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL2A1a	Q2I8Y0	[115-144]	1	2718.235	1	k.GDAGAPGPQGPAGSPGPQGPNGVPGPKGAR.g [1xDeamidation; 7xOxidation]	-0.0152
COL1A3	A0A3Q2CSU4	[1096-1125]	0	2727.1765	1	r.GFTGQQGPPGPPGPSGEAGPAGAAGPAGPR.g [2xDeamidation; 8xOxidation]	0.0086
COL1A1	A0A452FHU9	[796-825]	1	2735.2292	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [6xOxidation]	-0.0114
COL1A2	A0A452G3V6	[711-740]	1	2750.2765	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [2xDeamidation; 5xOxidation]	0.0051
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	0.008
COL1A3	A0A3Q2CSU4	[969-998]	1	2766.29	1	k.PGPAGPGGERGPPGPMGPPGLAGPPGEPGR.e [6xOxidation]	0.0063
COL1A2	A0A452G3V6	[532-564]	1	2879.4031	1	k.GPKGENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.0077
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	0.0047
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0061
COL1A1	A0A452FHU9	[709-741]	1	2883.4166	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g	-0.0094
COL1A1	A0A452FHU9	[763-795]	1	2883.4231	1	r.GLTGPIGPPGPAGAPGDKGETGPSGPAGPTGAR.g [2xOxidation]	-0.016
COL1A1	A0A452FHU9	[397-429]	1	2899.4082	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [4xOxidation]	-0.0104
COL1A1	A0A452FHU9	[709-741]	1	2899.4115	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g [1xOxidation]	-0.0138
COL1A1	A0A3P9NHJ7	[902-933]	1	3001.3341	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 5xOxidation]	0.0072
COL1A1	A0A3P9NHJ7	[902-933]	1	3002.3181	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 5xOxidation]	0.0191
COL1A1	A0A3P9NHJ7	[551-582]	1	3002.3471	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [1xDeamidation; 4xOxidation]	-0.0099
COL1A1	A0A3P9NHJ7	[551-582]	1	3017.358	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [5xOxidation]	0.0016
COL1A1	A0A3P9NHJ7	[902-933]	1	3018.313	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 6xOxidation]	0.0139
COL1A1	A0A3P9NHJ7	[551-582]	1	3018.342	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [1xDeamidation; 5xOxidation]	-0.0151
COL1A1	A0A3P9NHJ7	[617-649]	1	3049.428	1	k.GEPGAPGAPGAAGPPGLQGMPGERGAAGLPGLR.g [1xDeamidation; 8xOxidation]	0.0171
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.0146

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.0021
COL1A1	A0A452FHU9	[1108-1140]	1	3121.3842	1	k.GHRGFSGLQGPPGPPGSPGEQGPSGASGPAGPR.g [2xDeamidation; 7xOxidation]	-0.0023
COL1A2	A0A452G3V6	[422-457]	1	3227.52	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [4xOxidation]	0.01
COL1A1	A0A3P9NHJ7	[1070-1104]	0	3228.5306	1	r.SGEMGPAGPPGPPGPPGPPGAPGGGFDIGFITQEK.a [1xDeamidation]	0.0012
COL1A2	A0A452G3V6	[780-815]	1	3350.7101	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 2xOxidation]	-0.0181
COL1A2	A0A452G3V6	[780-815]	1	3365.721	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [3xOxidation]	-0.017
COL1A2	A0A3B4ZDV7	[1278-1308]	1	3366.7402	1	k.PNRLPLLDIAPLDIGGADQEFGLDIGPVCFK. [1xCarbamidomethyl; 1xOxidation]	-0.0145
COL1A2	A0A452G3V6	[780-815]	1	3381.7159	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [4xOxidation]	0.0156
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	0.0149
COL1A1	A0A452FHU9	[322-360]	1	3397.6156	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPR.g [3xOxidation]	0.0093
COL1A2	A0A452G3V6	[843-880]	0	3652.5524	1	r.GSQGSQGPAGPPGPPGPPGPPGPSGGGYDFGFDGDFYR.a [1xDeamidation; 4xOxidation]	0.0078
COL1A1	A0A452FHU9	[277-285]	0	801.3737	1	k.GDAGPAGPK.g [2xOxidation]	0.0011
COL1A1	A0A452FHU9	[826-834]	0	801.3737	1	k.GEPGDAGAK.g	0.0011
COL1A2	A0A452G3V6	[1082-1087]	1	805.4203	1	k.KTNEWK.k	-0.0118
COL1A2	A0A452G3V6	[1083-1088]	1	805.4203	1	k.TNEWKK.t	-0.0118
COL1A2	A0A452G3V6	[1082-1087]	1	806.4043	1	k.KTNEWK.k [1xDeamidation]	0.0126
COL1A2	A0A452G3V6	[1083-1088]	1	806.4043	1	k.TNEWKK.t [1xDeamidation]	0.0126
COL1A1	A0A3B5AFM4	[418-426]	0	813.385	1	r.GEPGGAGPR.g [1xOxidation]	0.0038

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A3B5AFM4	[298-306]	0	814.3802	1	k.GEGGPQGGR.g	-0.0038
COL1A3	A0A3Q2CSU4	[229-237]	0	827.4006	1	r.GPSGPQGAR.g [1xDeamidation]	0.0169
COL1A3	A0A3Q2CSU4	[346-354]	0	827.4006	1	r.GPEGPAGAR.g [1xOxidation]	0.0169
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0103
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	-0.0106
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	-0.0106
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.0184
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.0184
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.0184
COL1A1	A0A3B5AFM4	[506-515]	0	892.4635	1	r.PGPPGPSGAR.g	0.0071
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0132
COL1A2	A0A452G3V6	[272-281]	0	902.4513	1	r.AGVMGPAGSR.g	0.0095
COL1A1	A0A674DI56	[1368-1375]	0	943.419	1	k.NSVAYMDK.g [1xOxidation]	-0.0026
COL1A1	A0A452FHU9	[564-573]	0	950.469	1	r.PGPPGPPGAR.g [3xOxidation]	-0.0133
COL1A2	A0A452G3V6	[1-8]	0	1010.4975	1	.MLSFVDTR.t [1xAcetyl]	-0.0028
COL1A2	A0A452G3V6	[299-308]	0	1010.5088	1	r.PGEPGLMGPR.g	-0.014
COL1A2	A0A452G3V6	[968-976]	0	1013.515	1	r.AQPEDIPVK.n [1xDeamidation; 1xOxidation]	0.0091
COL1A1	A0A3B5AFM4	[1118-1126]	1	1017.5323	1	k.IRSPDGTQK.s [1xOxidation]	-0.0179
COL1A1	A0A452FHU9	[676-684]	1	1020.4857	1	r.GERGFPGER.g [1xOxidation]	0.0166
COL1A3	A0A3Q2CSU4	[670-681]	0	1022.5378	1	r.GAPGPVGPAGAR.g [1xOxidation]	0.0193

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A3B5AFM4	[624-635]	0	1027.4803	1	r.GAPGPAGNDGAK.g [1xOxidation]	0.0108
COL1A2	A0A452G3V6	[968-976]	0	1028.5259	1	r.AQPEDIPVK.n [2xOxidation]	0.0118
COL1A3	A0A3Q2CSU4	[1069-1080]	1	1069.5385	1	r.GPAGPAGARGDK.g [1xOxidation]	-0.0013
COL1A3	A0A3Q2CSU4	[295-306]	1	1069.5497	1	r.GRAGPPGAAGAR.g [2xOxidation]	-0.0125
COL1A3	A0A3Q2CSU4	[454-465]	1	1069.5497	1	r.GARGEPGAAGAR.g	-0.0125
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	-0.0016
COL1A2	A0A452G3V6	[109-120]	1	1081.5861	1	r.GRVGAPGPAGAR.g [1xOxidation]	-0.0087
COL1A3	A0A3Q2CSU4	[1069-1080]	1	1085.5334	1	r.GPAGPAGARGDK.g [2xOxidation]	-0.008
COL1A3	A0A3Q2CSU4	[454-465]	1	1085.5446	1	r.GARGEPGAAGAR.g [1xOxidation]	-0.0192
COL1A1	A0A452FHU9	[907-917]	1	1086.5287	1	k.GPRGETGPAGR.p [2xOxidation]	0.0068
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	0.0157
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.0082
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.0169
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0076
COL1A1	A0A452FHU9	[733-744]	1	1111.5854	1	r.GAAGLPGPKGDR.g [1xOxidation]	0.0147
COL1A1	A0A3B5AFM4	[540-553]	0	1112.5695	1	r.GPAGAAGAVGAPGK.d [2xOxidation]	0.0098
COL1A2	A0A452G3V6	[1089-1097]	1	1125.615	1	k.TIIEYKTNK.p [1xOxidation]	0.0043
COL1A1	A0A674DI56	[592-605]	0	1126.5851	1	r.GEAGAVGGVGAPGK.d	-0.0196
COL1A1	A0A3B5AFM4	[660-671]	1	1129.596	1	r.GAGGLPGVKGER.g [2xOxidation]	0.0011
COL1A1	A0A3B5AFM4	[1081-1090]	1	1133.5698	1	k.APDPLRGGYR.a [2xOxidation]	-0.001

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A3B5AFM4	[256-267]	0	1134.5902	1	r.PGPPGPSLQGAR.g [1xDeamidation]	0.0056
COL1A1	A0A452FHU9	[685-696]	0	1138.5487	1	r.GVQGPPGPAGPR.g [1xDeamidation; 3xOxidation]	0.0198
COL1A1	A0A452FHU9	[253-264]	0	1146.5823	1	r.GLPGTAGLPGMK.g [3xOxidation]	0.0184
COL1A2	A0A452G3V6	[323-334]	0	1154.58	1	k.EGPAGLPGIDGR.p [1xOxidation]	0.0141
COL1A1	A0A3B5AFM4	[197-208]	0	1156.6361	1	r.GFPGTPGLPGIK.g [1xOxidation]	0.0034
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.0158
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0121
COL1A3	A0A3Q2CSU4	[1292-1300]	1	1183.5994	1	k.NWYLSKNIK.d [2xDeamidation; 1xOxidation]	-0.007
COL1A2	A0A452G3V6	[759-770]	1	1185.5858	1	r.GPSGPQGIRGDK.g [1xDeamidation; 1xOxidation]	-0.0135
COL1A2	A0A452G3V6	[345-356]	0	1185.5899	1	r.GEPGNIGFPGPK.g [1xOxidation]	-0.0176
COL1A3	A0A3Q2CSU4	[583-596]	0	1186.5885	1	r.GVMGPTGPAGAAGK.d [1xOxidation]	0.0157
COL1A1	A0A452FHU9	[1236-1245]	0	1188.6219	1	k.SLSQQIENIR.s [1xDeamidation]	0.0088
COL1A1	A0A452FHU9	[598-611]	0	1192.6321	1	r.GVPGPPGAVGPAGK.d [2xOxidation]	0.0129
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.011
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	0.0156
COL1A3	A0A3Q2CSU4	[559-570]	0	1203.6191	1	r.GQPGVMGFPGLK.g [1xOxidation]	-0.001
COL1A3	A0A3Q2CSU4	[1218-1227]	0	1203.6216	1	k.SLSQQIEQIR.s [2xDeamidation]	-0.0035
COL1A2	A0A452G3V6	[881-891]	1	1214.6124	1	r.ADQPRSPASLR.p [1xDeamidation; 1xOxidation]	-0.0096
COL1A1	A0A674DI56	[234-246]	1	1240.6029	1	r.PGERGSAGPQGAR.g [1xDeamidation]	0.0095
COL1A1	A0A452FHU9	[958-969]	1	1241.6597	1	r.GVVGLPGQRGER.g [1xDeamidation; 1xOxidation]	-0.006
COL1A2	A0A452G3V6	[214-228]	0	1251.6804	1	r.GIPGPVGAAGATGAR.g	-0.0097

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[214-228]	0	1267.6753	1	r.GIPGPVGAAGATGAR.g [1xOxidation]	0.0083
COL1A1	A0A452FHU9	[781-795]	0	1311.6288	1	k.GETGPSGPAGPTGAR.g	0.016
COL1A1	A0A452FHU9	[415-429]	0	1316.6593	1	r.GPSGPQGPSGPPGPK.g	0.0165
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0113
COL1A3	A0A3Q2CSU4	[490-504]	1	1451.7601	1	k.GVNGERGVPGPVGPK.g [2xOxidation]	0.0021
COL1A1	A0A452FHU9	[918-933]	0	1458.7223	1	r.PGEVGPPGPPGPAGEK.g [1xOxidation]	0.0096
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.0109
COL1A1	A0A452FHU9	[253-267]	1	1464.774	1	r.GLPGTAGLPGMKGHR.g [1xOxidation]	-0.0103
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0094
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	-0.0018
COL1A1	A0A3B5AFM4	[1177-1188]	1	1501.7355	1	k.SSIPMKNWYLSK.n [3xOxidation]	0.0135
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	-0.0067
COL1A1	A0A452FHU9	[1152-1167]	0	1546.786	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	0.0159
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	0.0096
COL1A2	A0A452G3V6	[196-213]	0	1562.8285	1	k.GAAGLPGVAGAPGLPGPR.g [3xOxidation]	0.0002
COL1A2	A0A452G3V6	[59-72]	1	1567.7832	1	r.NSCLTHPKGLMGPR.g [1xCarbamidomethyl]	0.0054
COL1A1	A0A452FHU9	[397-414]	0	1570.7608	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 2xOxidation]	0.0141
COL1A2	A0A452G3V6	[404-421]	0	1580.7663	1	r.GPPGESGAAGPTGPIGSR.g [1xOxidation]	0.0182
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0081
COL1A1	A0A452FHU9	[397-414]	0	1586.7558	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 3xOxidation]	0.0168

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0.0187
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	0.0147
COL1A1	A0A452FHU9	[612-630]	0	1706.7729	1	k.DGEAGAQGPPGPAGPAGER.g [1xOxidation]	0.0069
COL1A1	A0A674DI56	[757-774]	0	1740.7857	1	r.GMTGPIGPPGPTGAHGEK.g [5xOxidation]	0.0053
COL1A1	A0A3B5AFM4	[789-808]	1	1745.8314	1	k.GARGGAGSPGATGFPGPAGR.v [3xOxidation]	0.0155
COL1A1	A0A452FHU9	[657-675]	0	1783.8093	1	k.PGEQGVPGDLGAPGPSGAR.g [1xDeamidation; 4xOxidation]	0.0099
COL1A1	A0A452FHU9	[352-369]	1	1783.8318	1	k.GEAGPQGPRGSEGPQGVR.g [3xOxidation]	-0.0126
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	-0.0059
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	0.0031
COL1A1	A0A3B5AFM4	[394-413]	0	1820.8661	1	k.GEPGPAGVQGLPGPSGEEGK.r [1xDeamidation]	0.0148
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	-0.0034
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0099
COL1A3	A0A3Q2CSU4	[642-660]	0	1837.8675	1	k.PGEQGLPGEPGAVGPAGQR.g [4xOxidation]	-0.0186
COL1A1	A0A452FHU9	[448-467]	0	1848.861	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 1xOxidation]	0.0171
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0026
COL1A1	A0A3B5AFM4	[612-635]	1	1997.9788	1	r.GGPGPVGPGGPRGAPGPAGNDGAK.g [1xDeamidation]	-0.0013
COL1A2	A0A452G3V6	[323-344]	1	2028.0621	1	k.EGPAGLPGIDGRPGPIGPAGAR.g [1xOxidation]	-0.0122
COL1A1	A0A3B5AFM4	[394-414]	1	2040.9469	1	k.GEPGPAGVQGLPGPSGEEGKR.g [1xDeamidation; 4xOxidation]	0.0053
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0111
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.0086

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A3B5AFM4	[187-208]	1	2082.0727	1	r.GAAGPQQGARGFPGTPGLPGIK.g [3xOxidation]	0.0195
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	0.0074
COL1A3	A0A3Q2CSU4	[919-942]	0	2106.021	1	k.GSAGSEGPAGAPGIPGPQGIAGQR.g [1xDeamidation; 1xOxidation]	0.0189
COL1A3	A0A3Q2CSU4	[513-536]	1	2179.0448	1	r.TGEPGLPGAKGMTGSPGNPGPDGK.m	0.0076
COL1A3	A0A3Q2CSU4	[513-536]	1	2180.0288	1	r.TGEPGLPGAKGMTGSPGNPGPDGK.m [1xDeamidation]	-0.0124
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	0.0147
COL1A1	A0A674DI56	[753-774]	1	2199.9757	1	k.DGMRGMTGPIGPPGPTGAHGEK.g [5xOxidation]	0.0064
COL1A1	A0A674DI56	[1030-1055]	0	2200.0014	1	r.GENGHAGSPGAPGPPGAPGPSGASGK.t [2xOxidation]	-0.0193
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.0117
COL1A2	A0A452G3V6	[711-736]	0	2263.1102	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGK.h [2xOxidation]	-0.0113
COL1A1	A0A452FHU9	[442-467]	1	2394.1056	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 2xOxidation]	0.0195
COL1A1	A0A452FHU9	[442-467]	1	2409.1165	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [3xOxidation]	0.0073
COL1A1	A0A452FHU9	[442-467]	1	2410.1005	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 3xOxidation]	0.0089
COL1A1	A0A674DI56	[961-987]	1	2445.1753	1	r.GPSGSPGVPGQAGEPGKQGPGGPVGER.g [2xOxidation]	0.0074
COL1A1	A0A674DI56	[961-987]	1	2461.1702	1	r.GPSGSPGVPGQAGEPGKQGPGGPVGER.g [3xOxidation]	0.0032
COL1A2	A0A452G3V6	[565-591]	0	2468.1728	1	r.GDGGPPVSTYPGFGISGPPGPPGPAGK.e [3xOxidation]	0.0173
COL1A1	A0A674DI56	[961-987]	1	2477.1651	1	r.GPSGSPGVPGQAGEPGKQGPGGPVGER.g [4xOxidation]	0.0173
COL1A3	A0A3Q2CSU4	[307-336]	0	2481.1793	1	r.GNDGAAGAAGPPGPTGPAGPPGFPGGPGPK.g [1xDeamidation]	-0.0028
COL1A1	A0A674DI56	[1135-1161]	1	2484.2048	1	r.GPHGSSGSTGKDGMNGLPGPIGPPGPR.g	0.002
COL1A1	A0A674DI56	[1135-1161]	1	2485.1888	1	r.GPHGSSGSTGKDGMNGLPGPIGPPGPR.g [1xDeamidation]	0.0114
COL1A3	A0A3Q2CSU4	[307-336]	0	2497.1742	1	r.GNDGAAGAAGPPGPTGPAGPPGFPGGPGPK.g [1xDeamidation; 1xOxidation]	-0.0174

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[683-707]	1	2501.1916	1	r.WATVSLSGNPGNDGPPGRDGQPGHK.g	-0.0192
COL1A3	A0A3Q2CSU4	[1270-1291]	1	2513.1357	1	k.VFCNMDTGETCVTPTQPEVAKK.n [2xCarbamidomethyl; 1xDeamidation]	0.0044
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	0.0124
COL1A3	A0A3Q2CSU4	[1018-1046]	1	2563.1655	1	k.GDRGESGPAGAPGAPGPPGAPGPVGPAGK.t [8xOxidation]	-0.0195
COL1A1	A0A452FHU9	[322-351]	0	2581.1801	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 5xOxidation]	-0.0036
COL1A2	A0A452G3V6	[535-564]	0	2597.2339	1	k.GENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	0.0031
COL1A2	A0A452G3V6	[535-564]	0	2678.1925	1	k.GENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [1xDeamidation; 7xOxidation]	0.013
COL1A2	A0A452G3V6	[711-740]	1	2702.2917	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [2xDeamidation; 2xOxidation]	-0.0012
COL1A2	A0A452G3V6	[404-433]	1	2705.2398	1	r.GPPGESGAAGPTGPIGSRGPSGPPGPDGNK.g [5xOxidation]	-0.0187
COL1A1	A0A3B5AFM4	[723-752]	1	2728.2081	1	r.GAPGERGETGPSGPAGFAGPPGADGQPGAK.g [1xDeamidation; 5xOxidation]	-0.0142
COL1A1	A0A3B5AFM4	[965-994]	1	2728.2115	1	r.GESGMSGPPGPPGTPGAPGAVGPSGKTGDR.g [6xOxidation]	-0.0176
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0132
COL1A3	A0A3Q2CSU4	[969-998]	1	2766.29	1	k.PGPAGPGGERGPPGPMGPPGLAGPPGEPGR.e [6xOxidation]	0.0084
COL1A1	A0A3B5AFM4	[540-572]	1	2767.2765	1	r.GPAGAAGAVGAPGKDGDVGAPGSSGPAGPAGEK.g [5xOxidation]	-0.0037
COL1A2	A0A452G3V6	[532-564]	1	2879.4031	1	k.GPKGENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.0128
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.0126
COL1A1	A0A452FHU9	[397-429]	1	2883.4132	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [3xOxidation]	-0.0173
COL1A1	A0A452FHU9	[397-429]	1	2899.4082	1	k.GANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK.g [4xOxidation]	0.013
COL1A1	A0A452FHU9	[709-741]	1	2899.4115	1	k.GDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPK.g [1xOxidation]	0.0096
COL1A1	A0A452FHU9	[763-795]	1	2899.4181	1	r.GLTGPIGPPGPAGAPGDKGETGPSGPAGPTGAR.g [3xOxidation]	0.0031

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A674DI56	[796-828]	1	3001.3307	1	r.GEHGAPGPAGFAGPPGADGQPGNKGEAGNNGPK.g [2xDeamidation; 2xOxidation]	-0.0143
COL1A1	A0A674DI56	[796-828]	1	3002.3147	1	r.GEHGAPGPAGFAGPPGADGQPGNKGEAGNNGPK.g [3xDeamidation; 2xOxidation]	0.0065
COL1A1	A0A674DI56	[796-828]	1	3017.3256	1	r.GEHGAPGPAGFAGPPGADGQPGNKGEAGNNGPK.g [2xDeamidation; 3xOxidation]	-0.01
COL1A1	A0A674DI56	[796-828]	1	3018.3096	1	r.GEHGAPGPAGFAGPPGADGQPGNKGEAGNNGPK.g [3xDeamidation; 3xOxidation]	-0.0019
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.0138
COL1A1	A0A674DI56	[820-855]	1	3084.4366	1	k.GEAGNNGPKGDAGAPGPGGPVGAPGPQGPAGNAGTK.g [3xOxidation]	0.0107
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.0131
COL1A2	A0A452G3V6	[422-457]	1	3212.5091	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [1xDeamidation; 3xOxidation]	-0.0148
COL1A1	A0A3B5AFM4	[268-306]	1	3315.4897	1	r.GNDGNTGAAGPPGPTGPAGPPGFPGGAGAKGEGGPQGGR.g [3xDeamidation; 1xOxidation]	-0.0185
COL1A2	A0A452G3V6	[780-815]	1	3365.721	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [3xOxidation]	0.0151
COL1A2	A0A452G3V6	[780-815]	1	3366.705	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 3xOxidation]	0.0068
COL1A2	A0A452G3V6	[780-815]	1	3381.7159	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [4xOxidation]	0.0061
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	0.0016
COL1A1	A0A452FHU9	[322-360]	1	3397.6156	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPR.g [3xOxidation]	0.0023
COL1A1	A0A452FHU9	[322-360]	1	3413.6105	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGPR.g [4xOxidation]	0.0101
Ovotransferrin	P02789	[352-360]	1	1089.5535	1	r.KDQLTPSPR.e [3xOxidation]	-0.0014
Ovalbumin	P01012	[371-382]	0	1345.7375	1	k.HIATNAVLFFGR.c	0.005
Ovalbumin-related protein Y	P01014	[373-384]	0	1412.7321	1	r.YNPTNAILFFGR.y	0.0047

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
Ovotransferrin	P02789	[141-154]	0	1534.8489	1	r.SAGWNIPIGTLLHR.g	-0.0007
Ovotransferrin	P02789	[602-616]	0	1709.8639	1	r.ECNLAEVPTHAVVVR.p [1xCarbamidomethyl; 1xOxidation]	-0.0167
Ovotransferrin	P02789	[602-616]	0	1710.8479	1	r.ECNLAEVPTHAVVVR.p [1xCarbamidomethyl; 1xDeamidation; 1xOxidation]	0.0113
Ovalbumin	P01012	[144-159]	0	1858.9658	1	r.ELINSWVESQTNGIIR.n	-0.0097
Ovalbumin	P01012	[144-159]	0	1859.9498	1	r.ELINSWVESQTNGIIR.n [1xDeamidation]	-0.0033
Serpin-Z1A	Q41593	[1-18]	1	2028.0543	1	.MATTLATDVRLSIAHQTR.f [1xAcetyl; 1xDeamidation]	-0.0131
Protein TENP	O42273	[51-71]	0	2271.0962	1	k.EPQTCSLAPWSPAGTELPAVK.v [1xCarbamidomethyl; 2xOxidation]	-0.002
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0082
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.0121
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.0121
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.0121
COL1A1	A0A3B5AFM4	[506-515]	0	892.4635	1	r.PGPPGPSGAR.g	0
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0151
COL1A1	A0A3B5AFM4	[612-623]	0	1068.5069	1	r.GGPGPVGPGGPR.g [4xOxidation]	0.0082
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.0006
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0009
COL1A1	A0A452FHU9	[733-744]	1	1111.5854	1	r.GAAGLPGPKGDR.g [1xOxidation]	0.0065
COL1A1	A0A3B5AFM4	[540-553]	0	1112.5695	1	r.GPAGAAGAVGAPGK.d [2xOxidation]	-0.0008
COL1A1	A0A452FHU9	[552-563]	0	1126.5123	1	k.TGPPGPAGQDGR.p [1xDeamidation; 1xOxidation]	0.0132
COL1A2	A0A452G3V6	[26-36]	0	1161.6296	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl]	-0.0198
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.0095

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0039
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	-0.0062
COL1A1	A0A452FHU9	[958-969]	1	1240.6757	1	r.GVVGLPGQRGER.g [1xOxidation]	0.0034
COL1A2	A0A452G3V6	[214-228]	0	1267.6753	1	r.GIPGPVGAAGATGAR.g [1xOxidation]	0.0106
COL1A1	A0A3B5AFM4	[183-196]	1	1383.6724	1	r.PGERGAAGPQQGAR.g [2xOxidation]	0.0078
COL1A1	A0A3B5AFM4	[708-722]	0	1383.6863	1	k.GEPGALGVAGPTGPR.g [3xOxidation]	-0.0061
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0058
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0142
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	0.003
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	-0.0003
COL1A2	A0A452G3V6	[196-213]	0	1562.8285	1	k.GAAGLPGVAGAPGLPGPR.g [3xOxidation]	-0.0052
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0032
COL1A1	A0A452FHU9	[397-414]	0	1586.7558	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 3xOxidation]	0.0081
COL1A1	A0A3P8W8U6	[490-507]	1	1647.8701	1	r.GPAGPPVISGPAGKEGPK.g [2xOxidation]	-0.0075
COL1A1	A0A3P8W8U6	[568-584]	1	1658.7955	1	r.GERGFPGMPGPSGEVGK.q	0.0158
COL1A1	A0A452FHU9	[493-510]	1	1671.8085	1	r.GFPGSDGVAGPKGPAGER.g [1xOxidation]	-0.0059
COL1A1	A0A452FHU9	[493-510]	1	1687.8034	1	r.GFPGSDGVAGPKGPAGER.g [2xOxidation]	-0.0087
COL1A1	A0A452FHU9	[657-675]	0	1719.8297	1	k.PGEQGVPGDLGAPGPSGAR.g [1xDeamidation]	-0.0144
COL1A2	A0A452G3V6	[1021-1035]	0	1769.8752	1	r.LLANHASQNITYHCK.n [1xCarbamidomethyl]	0.0051
COL1A1	A0A3B5AFM4	[394-413]	0	1820.8661	1	k.GEPGPAGVQGLPGPSGEEGK.r [1xDeamidation]	-0.008

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A3B5AFM4	[1144-1160]	0	1922.9065	1	k.SMYWVDPNQGSALDAIR.v	0.0129
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.013
COL1A2	A0A452G3V6	[737-758]	1	1998.0264	1	k.HGSRGEPGPVGAVGPAGAVGPR.g [1xOxidation]	-0.0158
COL1A1	A0A3B5AFM4	[394-414]	1	2040.9469	1	k.GEPGPAGVQGLPGPSGEEGKR.g [1xDeamidation; 4xOxidation]	0.0054
COL1A1	A0A452FHU9	[552-573]	1	2056.9795	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [4xOxidation]	0.0057
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	0.0141
COL1A1	A0A3B5AFM4	[187-208]	1	2082.0727	1	r.GAAGPQQGARGFPGTPGLPGIK.g [3xOxidation]	0.0053
COL1A1	A0A452FHU9	[657-678]	1	2093.9847	1	k.PGEQGVPGDLGAPGPSGARGER.g [1xDeamidation; 2xOxidation]	0.0173
COL1A1	A0A452FHU9	[564-585]	1	2094.0073	1	r.PGPPGPPGARGQAGVMGFPGPK.g [1xDeamidation; 4xOxidation]	-0.0053
COL1A1	A0A3B5AFM4	[187-208]	1	2098.0676	1	r.GAAGPQQGARGFPGTPGLPGIK.g [4xOxidation]	0.0142
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.0158
COL1A1	A0A452FHU9	[970-993]	1	2239.0738	1	r.GFPGLPGPSGEPGKQGPSGASGER.g [1xOxidation]	0.0062
COL1A1	A0A452FHU9	[970-993]	1	2255.0687	1	r.GFPGLPGPSGEPGKQGPSGASGER.g [2xOxidation]	-0.0037
COL1A1	A0A452FHU9	[882-906]	1	2263.0473	1	r.VGPPGPSGNAGPPGPPGPAGKEGSK.g [1xDeamidation; 6xOxidation]	0.0152
COL1A2	A0A452G3V6	[711-736]	0	2265.0782	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGK.h [2xDeamidation; 2xOxidation]	-0.0199
COL1A1	A0A452FHU9	[370-396]	0	2268.064	1	r.GEPGPPGPAGAAGPAGNPGADGQPGAK.g [1xOxidation]	-0.0196
COL1A1	A0A3B5AFM4	[897-920]	1	2284.1204	1	r.GFSGLPGPSGEPGKQGPSGLVGER.g [1xDeamidation; 1xOxidation]	0.0074
COL1A1	A0A452FHU9	[835-861]	0	2323.1313	1	k.GDAGPPGPAGPAGPPGPIGNVGAPGPK.g [4xOxidation]	-0.018
COL1A1	A0A3B5AFM4	[361-387]	1	2412.1175	1	r.GPAGAQGAIGAPGPKGNNGDHGNPGPK.g [3xDeamidation; 1xOxidation]	0.0112
COL1A1	A0A3B5AFM4	[361-387]	1	2427.1284	1	r.GPAGAQGAIGAPGPKGNNGDHGNPGPK.g [2xDeamidation; 2xOxidation]	0.0165
COL1A1	A0A452FHU9	[1141-1167]	1	2468.2528	1	r.GPPGSAGTPGKDGLNGLPGPIGPPGPR.g [3xOxidation]	-0.0195

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[277-303]	1	2494.0899	1	k.GDAGPAGPKGEPGSPGENGAPGQMGPR.g [1xDeamidation; 3xOxidation]	0.0112
COL1A1	A0A452FHU9	[1033-1061]	1	2497.2066	1	k.GDRGETGPAGPPGAPGAPGAPGPVGPAGK.s [3xOxidation]	0.0082
COL1A2	A0A452G3V6	[683-707]	1	2501.1916	1	r.WATVSLSGNPGNDGPPGRDGQPGHK.g	-0.0088
COL1A1	A0A452FHU9	[322-351]	0	2549.1903	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [1xDeamidation; 3xOxidation]	-0.0112
COL1A2	A0A452G3V6	[683-707]	1	2550.1604	1	r.WATVSLSGNPGNDGPPGRDGQPGHK.g [1xDeamidation; 3xOxidation]	0.0136
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	0.0175
COL1A1	A0A3B5AFM4	[1278-1300]	1	2563.1769	1	r.FTYSVSEDGCTSHTGSWGKTVIK.y [1xCarbamidomethyl; 1xOxidation]	-0.0157
COL1A1	A0A452FHU9	[1288-1309]	0	2578.1258	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 2xOxidation]	0.0174
COL1A1	A0A3B5AFM4	[962-990]	1	2579.1791	1	k.GDRGESGMSGPPGPPGTPGAPGAVGPSGK.t [3xOxidation]	-0.0004
COL1A3	A0A2D0SA79	[1130-1156]	1	2594.19	1	r.GPAGSTGVHGKDGMNGIPGPVGPPGPR.g [8xOxidation]	-0.0054
COL1A3	A0A2D0SA79	[785-814]	1	2670.2291	1	r.GGPGDRGEHGPPGPAGFAGPPGAAGQPGAK.g [1xDeamidation; 3xOxidation]	-0.0143
COL1A3	A0A2D0SA79	[785-814]	1	2685.24	1	r.GGPGDRGEHGPPGPAGFAGPPGAAGQPGAK.g [4xOxidation]	-0.0182
COL1A2	A0A452G3V6	[73-102]	0	2714.2441	1	r.GPPGASGAPGPQGFQGPPGEPGEPGQTGAR.g [2xDeamidation]	-0.0116
COL1A2	A0A452G3V6	[711-740]	1	2717.3026	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGKHGSR.g [1xDeamidation; 3xOxidation]	0.004
COL1A1	A0A452FHU9	[796-825]	1	2735.2292	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [6xOxidation]	-0.0134
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0193
COL1A1	A0A3P8W8U6	[702-732]	0	2767.2992	1	r.GFTGMQGPPGPSVGVSAPQPGPSGSAGSPGK.d [1xDeamidation; 1xOxidation]	0.0055
COL1A1	A0A3P8W8U6	[595-626]	1	2867.3489	1	r.GPPGPMGPPGLAGAPGEPGREGAPGNEGSSGR.d	0.0059
COL1A3	A0A2D0SA79	[983-1014]	1	3002.2929	1	r.GPPGPMGPPGLSGGPGEAGREGNPGHDGAPGR.d [1xDeamidation; 7xOxidation]	0.009

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1108-1140]	1	3009.4198	1	k.GHRGFSGLQGPPGPPGSPGEQGPSGASGPAGPR.g [2xDeamidation]	-0.0194
COL1A2	A0A452G3V6	[623-655]	0	3078.4803	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [1xDeamidation; 4xOxidation]	0.0007
COL1A2	A0A452G3V6	[623-655]	0	3093.4912	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [5xOxidation]	-0.0164
COL1A2	A0A452G3V6	[623-655]	0	3094.4752	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [1xDeamidation; 5xOxidation]	-0.0165
COL1A3	A0A2D0SA79	[815-850]	1	3100.3839	1	k.GEHGDTGPKGDAGPPGPSGPGGASGPQGPAGATGAK.g [1xDeamidation; 3xOxidation]	-0.0097
COL1A1	A0A452FHU9	[187-219]	0	3101.3905	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [1xDeamidation; 6xOxidation]	-0.019
COL1A2	A0A452G3V6	[623-655]	0	3158.4549	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [1xDeamidation; 9xOxidation]	0.0055
COL1A1	A0A452FHU9	[361-396]	1	3168.4577	1	r.GSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAK.g [1xDeamidation; 3xOxidation]	0.0048
COL1A1	A0A452FHU9	[361-396]	1	3183.4686	1	r.GSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAK.g [4xOxidation]	0.0195
COL1A1	A0A452FHU9	[361-396]	1	3185.4366	1	r.GSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAK.g [2xDeamidation; 4xOxidation]	-0.0065
COL1A1	A0A452FHU9	[697-732]	1	3194.4039	1	r.GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGER.g [2xDeamidation; 3xOxidation]	0.0075
COL1A1	A0A3B5AFM4	[1229-1257]	1	3265.4446	1	r.LMSNQASQNVTYHCKNSIAYMDSATGNLK.k [1xCarbamidomethyl; 3xDeamidation; 1xOxidation]	-0.0189
COL1A3	A0A2D0SA79	[311-349]	1	3317.5166	1	r.GNDGNSGPAGSPGPTGPAGPPGFPGGAGAKGETGPAGGR.g [2xOxidation]	-0.0158
COL1A2	A0A452G3V6	[780-815]	1	3350.7101	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 2xOxidation]	-0.0157
COL1A2	A0A452G3V6	[780-815]	1	3365.721	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [3xOxidation]	0.0081
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	0.018
COL1A1	A0A452FHU9	[1433-1463]	1	3397.6508	1	k.TSRLPIIDVAPLDVGAPDQEFGFDIGSVCFL. [1xCarbamidomethyl; 1xDeamidation; 3xOxidation]	-0.0086
COL1A2	A0A452G3V6	[623-658]	1	3435.6564	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSRGER.g [5xOxidation]	-0.0073

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
Ovalbumin-related protein Y	P01014	[153-182]	1	3381.7287	1	k.ETNGQIKDLLVSSSIDFGTTMVFINTIYFK.g	0.0113
Ovalbumin	P01012	[201-207]	0	821.3887	1	r.VTEQESK.p [1xDeamidation]	-0.0153
Ovalbumin	P01012	[86-93]	0	944.5411	1	r.DILNQITK.p	-0.0125
Ovalbumin	P01012	[86-93]	0	945.5251	1	r.DILNQITK.p [1xDeamidation]	-0.0083
Ovotransferrin	P02789	[447-458]	1	1295.7106	1	r.PASYFAVAVARK.d [1xOxidation]	-0.0195
Alpha-S2-casein	P02663	[129-140]	1	1383.7703	1	k.RNAVPITPTLNR.e [2xOxidation]	-0.0048
Alpha-S2-casein	P02663	[129-140]	1	1384.7543	1	k.RNAVPITPTLNR.e [1xDeamidation; 2xOxidation]	0.0186
Alpha-S2-casein	P02663	[129-140]	1	1385.7383	1	k.RNAVPITPTLNR.e [2xDeamidation; 2xOxidation]	-0.0026
Ovotransferrin	P02789	[316-327]	1	1425.7658	1	k.DLLFKDSAIMLK.r [2xOxidation]	-0.0199
Ovalbumin	P01012	[371-386]	1	1804.9163	1	k.HIATNAVLFFGRCVSP. [1xCarbamidomethyl; 1xOxidation]	-0.0021
Alpha-S2-casein	P02663	[107-128]	0	2714.3276	1	k.FPQYLQYLYQGPIVLNPWDQVK.r [5xDeamidation]	0.0096
COL1A1	A0A452FHU9	[237-243]	1	800.4009	1	k.PGRPGER.g [2xOxidation]	-0.0167
COL1A2	A0A452G3V6	[1082-1087]	1	805.4203	1	k.KTNEWK.k	-0.0177
COL1A2	A0A452G3V6	[1083-1088]	1	805.4203	1	k.TNEWKK.t	-0.0177
COL1A2	A0A452G3V6	[1082-1087]	1	806.4043	1	k.KTNEWK.k [1xDeamidation]	-0.0036
COL1A2	A0A452G3V6	[1083-1088]	1	806.4043	1	k.TNEWKK.t [1xDeamidation]	-0.0036
COL1A1	A0A452FHU9	[1310-1315]	0	811.3985	1	k.NWYISK.n [1xDeamidation]	-0.0177
COL1A2	A0A060N2D3	[461-469]	0	813.385	1	r.GEPGGSGPR.g	0.0116
COL1A2	A0A3P8VXI7	[181-189]	0	815.4258	1	k.GEPGAAGLK.g [1xOxidation]	0.0037

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A3P8VXI7	[208-215]	1	815.4482	1	r.GLAGERGR.p	-0.0187
COL1A1	A0A452FHU9	[244-252]	0	836.4373	1	r.GPPGPQGAR.g	-0.0176
COL1A1	A0A452FHU9	[1084-1092]	0	836.4373	1	r.GPAGPQGPR.g	-0.0176
COL1A2	A0A452G3V6	[393-399]	1	840.4574	1	r.GPLQHKK.t [1xDeamidation; 2xOxidation]	-0.0108
COL1A1	A0A3P9NHJ7	[177-185]	0	842.4115	1	r.GPSGPQGAR.g [1xOxidation]	-0.0061
COL1A1	A0A452FHU9	[268-276]	0	851.4258	1	r.GFSGLDGAK.g	0.0109
COL1A1	A0A452FHU9	[244-252]	0	852.4322	1	r.GPPGPQGAR.g [1xOxidation]	-0.0181
COL1A1	A0A452FHU9	[1084-1092]	0	852.4322	1	r.GPAGPQGPR.g [1xOxidation]	-0.0181
COL1A1	A0A452FHU9	[244-252]	0	868.4272	1	r.GPPGPQGAR.g [2xOxidation]	0.0163
COL1A1	A0A452FHU9	[352-360]	0	868.4272	1	k.GEAGPQGPR.g	0.0163
COL1A1	A0A452FHU9	[1084-1092]	0	868.4272	1	r.GPAGPQGPR.g [2xOxidation]	0.0163
COL1A1	A0A452FHU9	[958-966]	0	898.5105	1	r.GVVGLPGQR.g [1xOxidation]	-0.0163
COL1A2	A0A452G3V6	[272-281]	0	902.4513	1	r.AGVMGPAGSR.g	0.0058
COL1A2	A0A452G3V6	[335-344]	0	908.4948	1	r.PGPIGPAGAR.g [1xOxidation]	-0.0168
COL1A2	A0A452G3V6	[816-826]	0	909.4789	1	r.GPAGPTGPAGK.d	-0.0005
COL1A1	A0A452FHU9	[564-573]	0	918.4792	1	r.PGPPGPPGAR.g [1xOxidation]	-0.0142
COL1A2	A0A452G3V6	[335-344]	0	924.4898	1	r.PGPIGPAGAR.g [2xOxidation]	-0.003
COL1A2	A0A6P3W0U2	[464-473]	0	938.469	1	r.SGPPGPTGPR.g [1xOxidation]	0.0176
COL1A1	A0A452FHU9	[564-573]	0	950.469	1	r.PGPPGPPGAR.g [3xOxidation]	0.002
COL1A1	A0A3P9NHJ7	[484-493]	0	952.4847	1	r.PGPPGPVGAR.g [3xOxidation]	-0.0112
COL1A2	A0A452G3V6	[977-983]	1	968.4585	1	k.NWYRNSK.a [1xDeamidation]	0.0146

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A452G3V6	[1-8]	0	968.487	1	.MLSFVDTR.t	-0.0139
COL1A2	A0A060N2D3	[1015-1024]	1	969.4748	1	r.DGAPGPKGDR.g	0.0188
COL1A1	A0A452FHU9	[1141-1151]	0	973.4585	1	r.GPPGSAGTPGK.d [3xOxidation]	0.0051
COL1A2	A0A3P8VXI7	[405-414]	0	974.4724	1	r.SGPLGMPGAR.g [2xOxidation]	0.0164
COL1A2	A0A452G3V6	[1-8]	0	1010.4975	1	.MLSFVDTR.t [1xAcetyl]	0.016
COL1A2	A0A452G3V6	[299-308]	0	1010.5088	1	r.PGEPGLMGPR.g	0.0047
COL1A2	A0A452G3V6	[968-976]	0	1013.515	1	r.AQPEDIPVK.n [1xDeamidation; 1xOxidation]	0.0099
COL1A2	A0A452G3V6	[968-976]	0	1028.5259	1	r.AQPEDIPVK.n [2xOxidation]	0.0138
COL1A1	A0A452FHU9	[121-131]	1	1034.549	1	r.GPRGPAGPPGR.d [1xOxidation]	0.018
COL1A2	A0A060N2D3	[674-685]	0	1036.5534	1	r.GAPGIGGPTGPR.g	-0.0141
COL1A2	A0A3P8VXI7	[804-813]	1	1047.5582	1	r.PGIPGFKGAR.g [3xOxidation]	-0.0144
COL1A2	A0A452G3V6	[1120-1128]	0	1048.5496	1	r.LNIGPVCFK. [1xCarbamidomethyl; 1xDeamidation]	-0.019
COL1A1	A0A452FHU9	[121-131]	1	1050.5439	1	r.GPRGPAGPPGR.d [2xOxidation]	-0.0002
COL1A2	A0A060N2D3	[674-685]	0	1068.5432	1	r.GAPGIGGPTGPR.g [2xOxidation]	0.0013
COL1A2	A0A6P3W0U2	[210-221]	1	1069.5497	1	r.GRAGPSGPAGAR.g [1xOxidation]	-0.0102
COL1A1	A0A452FHU9	[310-321]	1	1079.5705	1	r.GRPGAPGPAGAR.g [1xOxidation]	0.0036
COL1A2	A0A452G3V6	[109-120]	1	1081.5861	1	r.GRVGAPGPAGAR.g [1xOxidation]	-0.0101
COL1A1	A0A3P9NHJ7	[472-483]	0	1085.5334	1	k.IGASGAPGQDGR.p	0.0001
COL1A1	A0A3P9NHJ7	[389-400]	1	1085.5446	1	r.GSRGEPGAAGAR.g	-0.0112
COL1A1	A0A3P9NHJ7	[814-824]	1	1087.5239	1	k.GNRGETGPAGR.p [1xOxidation]	0.0181
COL1A1	A0A452FHU9	[685-696]	0	1089.58	1	r.GVQGPPGPAGPR.g	0.0026

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[310-321]	1	1095.5654	1	r.GRPGAPGPAGAR.g [2xOxidation]	0.0102
COL1A1	A0A452FHU9	[733-744]	1	1095.5905	1	r.GAAGLPGPKGDR.g	-0.015
COL1A1	A0A452FHU9	[685-696]	0	1105.5749	1	r.GVQGPPGPAGPR.g [1xOxidation]	0.0101
COL1A1	A0A452FHU9	[733-744]	1	1111.5854	1	r.GAAGLPGPKGDR.g [1xOxidation]	0.0177
COL1A2	A0A6P3W0U2	[1310-1318]	1	1123.6106	1	k.TVIEYRTNK.p	-0.0009
COL1A2	A0A6P3W0U2	[1310-1318]	1	1124.5946	1	k.TVIEYRTNK.p [1xDeamidation]	0.0154
COL1A1	A0A452FHU9	[1084-1095]	1	1136.5807	1	r.GPAGPQGPRGDK.g	-0.013
COL1A1	A0A452FHU9	[685-696]	0	1138.5487	1	r.GVQGPPGPAGPR.g [1xDeamidation; 3xOxidation]	0.0193
COL1A2	A0A060N2D3	[587-600]	0	1142.58	1	r.GPAGATGSVGAPGK.d [1xOxidation]	-0.0144
COL1A2	A0A452G3V6	[323-334]	0	1154.58	1	k.EGPAGLPGIDGR.p [1xOxidation]	0.0087
COL1A1	A0A3P9NHJ7	[186-197]	0	1156.6361	1	r.GFPGTPGLPGIK.g [1xOxidation]	-0.0108
COL1A2	A0A452G3V6	[26-36]	0	1162.6136	1	k.CLQLVSGSLGK.r [1xCarbamidomethyl; 1xDeamidation]	-0.0098
COL1A2	A0A452G3V6	[830-842]	0	1180.6433	1	r.TGQPGAVGPAGIR.g	0.0097
COL1A1	A0A3P9NHJ7	[1206-1214]	1	1183.5928	1	k.NWYMSKNIK.e	0.0187
COL1A2	A0A452G3V6	[345-356]	0	1185.5899	1	r.GEPGNIGFPGPK.g [1xOxidation]	0.0183
COL1A1	A0A452FHU9	[1236-1245]	0	1188.6219	1	k.SLSQQIENIR.s [1xDeamidation]	0.0019
COL1A2	A0A060N2D3	[1299-1307]	1	1195.6106	1	k.NWYLSKNIR.e [2xDeamidation]	0.0013
COL1A2	A0A452G3V6	[830-842]	0	1196.6382	1	r.TGQPGAVGPAGIR.g [1xOxidation]	0.0139
COL1A2	A0A452G3V6	[759-770]	1	1200.5967	1	r.GPSGPQGIRGDK.g [2xOxidation]	0.0196

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[265-276]	1	1201.6072	1	k.GHRGFSGLDGAK.g	0.0042
COL1A1	A0A3P9NHJ7	[1133-1142]	0	1203.6216	1	k.SLSQQIEQIR.s [2xDeamidation]	0.0078
COL1A1	A0A3P9NHJ7	[1133-1142]	0	1204.6056	1	k.SLSQQIEQIR.s [3xDeamidation]	0.0147
COL1A2	A0A452G3V6	[881-891]	1	1229.6233	1	r.ADQPRSPASLR.p [2xOxidation]	-0.0109
COL1A2	A0A6P3W0U2	[1055-1067]	0	1249.6284	1	r.SGTQGPVGPVGHR.g [1xDeamidation]	-0.004
COL1A2	A0A452G3V6	[214-228]	0	1251.6804	1	r.GIPGPVGAAGATGAR.g	0.011
COL1A2	A0A060N2D3	[404-418]	0	1260.6695	1	r.GPAGAQGPVGAPGPK.g	-0.0061
COL1A2	A0A060N2D3	[404-418]	0	1261.6535	1	r.GPAGAQGPVGAPGPK.g [1xDeamidation]	0.002
COL1A2	A0A452G3V6	[892-902]	1	1278.6576	1	r.PKDYEVDATLK.s	-0.0182
COL1A1	A0A452FHU9	[240-252]	1	1292.6342	1	r.PGERGPPGPQGAR.g [1xDeamidation; 1xOxidation]	0.0094
COL1A1	A0A452FHU9	[472-486]	0	1435.6812	1	r.GEPGPAGLPGPPGER.g [3xOxidation]	0.0184
COL1A1	A0A452FHU9	[865-881]	0	1459.6924	1	r.GSAGPPGATGFPGAAGR.v [2xOxidation]	0.0148
COL1A1	A0A3P9NHJ7	[877-891]	0	1473.6856	1	r.GFPGPPGPAQGEIGK.p [1xDeamidation; 4xOxidation]	0.0065
COL1A1	A0A452FHU9	[171-186]	0	1496.7526	1	k.STGISVPGPMGPSGPR.g	0.0134
COL1A1	A0A452FHU9	[253-267]	1	1496.7638	1	r.GLPGTAGLPGMKGHR.g [3xOxidation]	0.0022
COL1A2	A0A452G3V6	[827-842]	1	1508.7928	1	k.DGRTGQPGAVGPAGIR.g	-0.0176
COL1A1	A0A452FHU9	[253-267]	1	1512.7587	1	r.GLPGTAGLPGMKGHR.g [4xOxidation]	0.0115
COL1A1	A0A3P9NHJ7	[431-447]	1	1536.8129	1	r.GAPGLVGPKGSTGEPGR.t	-0.0048
COL1A1	A0A452FHU9	[1152-1167]	0	1545.802	1	k.DGLNGLPGPIGPPGPR.g [2xOxidation]	-0.0074
COL1A1	A0A452FHU9	[1152-1167]	0	1546.786	1	k.DGLNGLPGPIGPPGPR.g [1xDeamidation; 2xOxidation]	0.0148

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[1066-1083]	0	1560.8129	1	r.GETGPAGPAGPIGPVGAR.g	0.013
COL1A2	A0A452G3V6	[196-213]	0	1562.8285	1	k.GAAGLPGVAGAPGLPGPR.g [3xOxidation]	0.0023
COL1A1	A0A3P9NHJ7	[514-531]	1	1583.7959	1	k.PGERGVMGPTGAAGAAGK.d	0.0067
COL1A1	A0A452FHU9	[397-414]	0	1585.7717	1	k.GANGAPGIAGAPGFPGAR.g [3xOxidation]	0.0121
COL1A1	A0A452FHU9	[397-414]	0	1586.7558	1	k.GANGAPGIAGAPGFPGAR.g [1xDeamidation; 3xOxidation]	0.0165
COL1A2	A0A6P3W0U2	[579-596]	0	1595.7772	1	r.GNPGPAGSVGSQGPIGAR.g [1xDeamidation; 1xOxidation]	0.0066
COL1A2	A0A6P3W0U2	[1303-1315]	1	1604.818	1	r.HTGQWSKTVIEYR.t	0.004
COL1A2	A0A452G3V6	[151-168]	0	1615.8187	1	k.GELGPVGNPGPAGPAGPR.g [1xOxidation]	0.0014
COL1A2	A0A452G3V6	[968-980]	1	1615.8227	1	r.AQPEDIPVKNWYR.n	-0.0026
COL1A2	A0A452G3V6	[968-980]	1	1617.7907	1	r.AQPEDIPVKNWYR.n [2xDeamidation]	0.0183
COL1A2	A0A6P3W0U2	[1303-1315]	1	1620.8129	1	r.HTGQWSKTVIEYR.t [1xOxidation]	0.0108
COL1A2	A0A3P8VXI7	[1061-1074]	1	1648.8224	1	r.ETCIHAHPESIARK.n [1xCarbamidomethyl]	0.0175
COL1A2	A0A3P8VXI7	[196-213]	1	1658.8205	1	r.GSNGSPGLAGSRGLAGER.g [1xOxidation]	0.0034
COL1A1	A0A452FHU9	[612-630]	0	1690.778	1	k.DGEAGAQGPPGPAGPAGER.g	0.0027
COL1A1	A0A452FHU9	[612-630]	0	1706.7729	1	k.DGEAGAQGPPGPAGPAGER.g [1xOxidation]	0.0098
COL1A2	A0A3P8VXI7	[561-579]	1	1740.8147	1	k.PGDRGIPGDQGAAGPAGAK.g [1xDeamidation; 3xOxidation]	-0.0055
COL1A2	A0A060N2D3	[851-870]	1	1745.8314	1	k.GARGGAGSPGATGFPGPAGR.v [3xOxidation]	-0.0015
COL1A1	A0A452FHU9	[1152-1169]	1	1759.9086	1	k.DGLNGLPGPIGPPGPRGR.t [1xDeamidation; 2xOxidation]	0.0045
COL1A1	A0A452FHU9	[352-369]	1	1783.8318	1	k.GEAGPQGPRGSEGPQGVR.g [3xOxidation]	0.0026
COL1A2	A0A3P8VXI7	[397-414]	1	1789.7956	1	r.GMPGPDGRSGPLGMPGAR.g [5xOxidation]	-0.0097

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[994-1013]	0	1800.8697	1	r.GPPGPMGPPGLAGPPGESGR.e [1xOxidation]	0.0109
COL1A1	A0A452FHU9	[994-1013]	0	1816.8647	1	r.GPPGPMGPPGLAGPPGESGR.e [2xOxidation]	0.0034
COL1A1	A0A452FHU9	[574-593]	1	1829.8851	1	r.GQAGVMGFPGPKGAAGEPGK.a [1xDeamidation; 1xOxidation]	0.0099
COL1A1	A0A452FHU9	[994-1013]	0	1832.8596	1	r.GPPGPMGPPGLAGPPGESGR.e [3xOxidation]	0.0028
COL1A1	A0A452FHU9	[448-467]	0	1832.8661	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation]	-0.0037
Ovalbumin	P01012	[21-47]	0	3066.4886	1	k.VHHANENIFYCPIAIMSALAMVYLGAK.d [1xCarbamidomethyl; 1xDeamidation; 2xOxidation]	-0.0017
COL1A1	A0A452FHU9	[994-1013]	0	1848.8545	1	r.GPPGPMGPPGLAGPPGESGR.e [4xOxidation]	0.016
COL1A1	A0A452FHU9	[448-467]	0	1848.861	1	k.GEPGPTGIQGPPGPAGEEGK.r [1xDeamidation; 1xOxidation]	0.0095
COL1A2	A0A6P3W0U2	[474-493]	1	1872.9086	1	r.GQPGTIGFPGPKGPGGEAGK.a [4xOxidation]	0.0197
COL1A2	A0A3P8VXI7	[792-810]	1	1884.8722	1	r.EGSPGNDGPPGRPGIPGFK.g [1xDeamidation; 3xOxidation]	-0.0108
COL1A2	A0A6P3W0U2	[474-493]	1	1888.9035	1	r.GQPGTIGFPGPKGPGGEAGK.a [5xOxidation]	0.0182
COL1A1	A0A452FHU9	[1062-1083]	1	1975.9944	1	k.SGDRGETGPAGPAGPIGPVGAR.g	-0.0049
COL1A1	A0A452FHU9	[448-468]	1	2019.973	1	k.GEPGPTGIQGPPGPAGEEGKR.g [2xOxidation]	0.0094
COL1A2	A0A452G3V6	[323-344]	1	2028.0621	1	k.EGPAGLPGIDGRPGPIGPAGAR.g [1xOxidation]	-0.0113
COL1A1	A0A452FHU9	[552-573]	1	2040.9846	1	k.TGPPGPAGQDGRPGPPGPPGAR.g [3xOxidation]	-0.015
COL1A1	A0A452FHU9	[934-957]	0	2057.0159	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g	-0.0161
COL1A1	A0A452FHU9	[934-957]	0	2073.0108	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xOxidation]	-0.0114
COL1A1	A0A452FHU9	[934-957]	0	2073.9948	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 1xOxidation]	0.0017
COL1A1	A0A452FHU9	[934-957]	0	2089.0057	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [2xOxidation]	0.0037

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A452FHU9	[934-957]	0	2089.9897	1	k.GAPGADGPAGAPGTPGPQGIAGQR.g [1xDeamidation; 2xOxidation]	0.0092
COL1A1	A0A452FHU9	[528-551]	1	2104.0669	1	r.PGEAGLPGAKGLTGSPGSPGPDGK.t	0.012
COL1A1	A0A3P9NHJ7	[484-505]	1	2106.0437	1	r.PGPPGPVGARGQPGVMGFPGPK.g [1xDeamidation; 3xOxidation]	-0.0108
COL1A2	A0A452G3V6	[434-457]	0	2151.0313	1	k.GEPGVVGAPGTAGPSGPSGLPGER.g [3xOxidation]	0.0124
COL1A1	A0A452FHU9	[1036-1061]	0	2153.0622	1	r.GETGPAGPPGAPGAPGAPGPVGPAGK.s [2xOxidation]	0.0092
COL1A1	A0A452FHU9	[709-732]	0	2198.9731	1	k.GDAGAPGAPGSQGAPGLQGMPGER.g [4xOxidation]	0.0065
COL1A1	A0A452FHU9	[910-933]	1	2216.0578	1	r.GETGPAGRPGEVGPPGPPGPAGEK.g [3xOxidation]	-0.0008
COL1A2	A0A3P8VXI7	[535-560]	0	2263.0626	1	k.GEQGPAGAPGFQGLPGPAGPGGEAGK.p [2xDeamidation]	0.0096
COL1A2	A0A452G3V6	[711-736]	0	2264.0942	1	r.GYPGNAGPVGAAGAPGPQGPVGPTGK.h [1xDeamidation; 2xOxidation]	-0.0172
COL1A2	A0A452G3V6	[599-622]	1	2285.0793	1	r.GDQGPVGRTGEPGAAGPPGFVGEK.g [3xOxidation]	0.0138
COL1A2	A0A452G3V6	[169-195]	0	2368.2143	1	r.GEVGLPGLSGPVGPPGNPGANGLPGAK.g [2xDeamidation]	-0.0113
COL1A1	A0A452FHU9	[442-467]	1	2409.1165	1	k.GDTGAKGEPGPTGIQGPPGPAGEEGK.r [3xOxidation]	0.015
COL1A2	A0A452G3V6	[502-528]	1	2410.1382	1	r.GEVGPAGPNGFAGPAGAAGQPGAKGER.g [1xDeamidation; 2xOxidation]	-0.0119
COL1A2	A0A6P3W0U2	[45-71]	0	2465.1732	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation]	0.0073
COL1A2	A0A6P3W0U2	[45-71]	0	2481.1681	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 1xOxidation]	0.0092
COL1A2	A0A6P3W0U2	[45-71]	0	2497.163	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 2xOxidation]	0.0006
COL1A2	A0A6P3W0U2	[45-71]	0	2513.1579	1	k.PGVDGPAGPPGPPGLGGNFAAQYDGAK.g [1xDeamidation; 3xOxidation]	-0.0081
COL1A1	A0A452FHU9	[1288-1309]	0	2562.1309	1	k.VFCNMETGETCVYPTQPSVAQK.n [2xCarbamidomethyl; 1xOxidation]	0.0078
COL1A1	A0A3P9NHJ7	[1184-1205]	1	2574.1521	1	k.VYCNMDTGETCITPTQPEVAKK.n [2xCarbamidomethyl; 2xOxidation]	0.0034
COL1A1	A0A452FHU9	[322-351]	0	2596.191	1	r.GNDGATGAAGPPGPTGPAGPPGFPGAVGAK.g [6xOxidation]	-0.0159
COL1A2	A0A3P8VXI7	[49-75]	0	2598.2107	1	k.PGLPGPPGPPGPPGLGGNFAAQYDGAK.g [7xOxidation]	-0.0129

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A2	A0A3P8VXI7	[583-612]	1	2653.1907	1	r.GNPGAAGATGSQGPMGVRGPSGPPGPDGGK.g [1xDeamidation; 4xOxidation]	0.0199
COL1A2	A0A6P3W0U2	[222-251]	0	2654.1965	1	r.GADGNTGPSGPAGPLGAAGPPGFPGAPGPK.g [8xOxidation]	0.0089
COL1A2	A0A3P8VXI7	[583-612]	1	2669.1856	1	r.GNPGAAGATGSQGPMGVRGPSGPPGPDGGK.g [1xDeamidation; 5xOxidation]	0.0141
COL1A1	A0A3P9NHJ7	[333-361]	1	2699.2696	1	r.GPPGPQGAAGAPGPKGNTFQGDVGAPGFK.g [1xDeamidation; 4xOxidation]	0.0163
COL1A1	A0A452FHU9	[796-825]	1	2703.2394	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [4xOxidation]	-0.0173
COL1A1	A0A452FHU9	[796-825]	1	2704.2234	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [1xDeamidation; 4xOxidation]	-0.0192
COL1A2	A0A060N2D3	[785-814]	1	2727.2241	1	r.GAPGERGETGPSGPAGFAGPPGADGQPGAK.g [5xOxidation]	0.0077
COL1A1	A0A452FHU9	[796-825]	1	2735.2292	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [6xOxidation]	0.0197
COL1A1	A0A452FHU9	[1111-1140]	0	2737.2448	1	r.GFSGLQGPPGPPGSPGEQGPSGASGPAGPR.g [5xOxidation]	0.0109
COL1A1	A0A452FHU9	[796-825]	1	2751.2241	1	r.GAPGDRGEPGPPGPAGFAGPPGADGQPGAK.g [7xOxidation]	-0.0069
COL1A1	A0A452FHU9	[1111-1140]	0	2753.2398	1	r.GFSGLQGPPGPPGSPGEQGPSGASGPAGPR.g [6xOxidation]	0.0089
COL1A2	A0A6P3W0U2	[1115-1139]	1	2769.32	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [3xDeamidation; 1xOxidation]	-0.0026
COL1A2	A0A6P3W0U2	[1115-1139]	1	2784.3309	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [2xDeamidation; 2xOxidation]	-0.0086
COL1A2	A0A6P3W0U2	[1115-1139]	1	2785.3149	1	k.DYEVDATLKSLNTQIDNLLSPEGSK.k [3xDeamidation; 2xOxidation]	-0.0022
COL1A1	A0A452FHU9	[598-630]	1	2864.3922	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [2xOxidation]	-0.0148
COL1A2	A0A452G3V6	[532-564]	1	2879.4031	1	k.GPKGENGPVGPTGPVGAAGPSGPNGPPGPAGSR.g [2xOxidation]	-0.0173
COL1A1	A0A452FHU9	[598-630]	1	2880.3871	1	r.GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGER.g [3xOxidation]	-0.017
COL1A2	A0A6P3W0U2	[834-866]	0	2922.3613	1	k.GSPGESGPAGAPGTAGPQGQLGSQGFNGLPGGR.g [2xDeamidation]	0.0064
COL1A1	A0A3P9NHJ7	[902-933]	1	3001.3341	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 5xOxidation]	0.0066
COL1A1	A0A3P9NHJ7	[902-933]	1	3002.3181	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 5xOxidation]	0.0051

Protein	Acc.	Slice	Mis.	m/z	z	Sequence	error
COL1A1	A0A3P9NHJ7	[902-933]	1	3017.329	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [1xDeamidation; 6xOxidation]	-0.0013
COL1A1	A0A3P9NHJ7	[902-933]	1	3018.313	1	r.GPPGPMGPPGLAGAPGEPGREGNPGNEGPSGR.d [2xDeamidation; 6xOxidation]	0.0101
COL1A1	A0A3P9NHJ7	[551-582]	1	3018.342	1	r.GEAGPSGSPGFQGLPGEPGAAGPAGSRNNSTR.r [1xDeamidation; 5xOxidation]	-0.0189
COL1A2	A0A452G3V6	[623-655]	0	3077.4963	1	k.GPSGEPGTAGPPGTPGPQGFLGPPGFLGLPGSR.g [4xOxidation]	0.0054
COL1A1	A0A452FHU9	[187-219]	0	3100.4065	1	r.GLPGPPGAPGPQGFQGPPGEPGEPGASGPMGPR.g [6xOxidation]	-0.0181
COL1A1	A0A3P9NHJ7	[279-314]	1	3110.4046	1	r.GPEGPAGARGEPGNPGPAGPAGPSGNPGTDGAPGAK.g [2xDeamidation; 2xOxidation]	0.0076
COL1A2	A0A452G3V6	[422-457]	1	3212.5091	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [1xDeamidation; 3xOxidation]	-0.015
COL1A2	A0A452G3V6	[422-457]	1	3227.52	1	r.GPSGPPGPDGNKGEPGVVGAPGTAGPSGPSGLPGER.g [4xOxidation]	-0.003
COL1A1	A0A3P9NHJ7	[1070-1104]	0	3228.5306	1	r.SGEMGPAGPPGPPGPPGPPGAPGGGFDIGFITQEK.a [1xDeamidation]	-0.0062
COL1A2	A0A452G3V6	[780-815]	1	3366.705	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 3xOxidation]	-0.0061
COL1A1	A0A452FHU9	[1433-1463]	1	3381.6559	1	k.TSRLPIIDVAPLDVGAPDQEFGFDIGSVCFL. [1xCarbamidomethyl; 1xDeamidation; 2xOxidation]	0.0129
COL1A2	A0A452G3V6	[780-815]	1	3382.6999	1	r.GLPGLKGHNGLQGLPGLAGHHGDQGAPGAVGPAGPR.g [1xDeamidation; 4xOxidation]	-0.0097
COL1A2	A0A452G3V6	[843-880]	0	3651.5684	1	r.GSQGSQGPAGPPGPPGPPGPPGPSGGGYDFGFDGDFYR.a [4xOxidation]	-0.0198
COL1A2	A0A452G3V6	[843-880]	0	3652.5524	1	r.GSQGSQGPAGPPGPPGPPGPPGPSGGGYDFGFDGDFYR.a [1xDeamidation; 4xOxidation]	-0.0029

Appendix B

File B1

>sp|P02453|CO1A1_BOVIN

MFSFVDLRLLLLLAATALLTHGQEEGQEEGQEEDIPPVTCVQNGLRYHDRDVWKPVPCQICVCDNGNVLCDDVICDELKD
CPNAKVPTDECCPVCPEGQESPTDQETTGVEGPKGDTGPRGPRGPAGPPGRDGICGQCGLCGPPGPPGPPGPPGPPGLGGN
FAPQLSYGYDEKSTGISVCGPMGPSGPRGLCGPPGACGPQGFQGPPGECGECGASGPMGPRGPPGPPGKNGDDGEAG
KCGRCGERGPPGPQGARGLCGTAGLCGMKGHRGFSGLDGAKGDAGPAGPKGECGSCGENGACGQMGPRGLCGERG
RCGACGPAGARGNDGATGAAGPPGPTGPAGPPGFCGAVGAKGEGGPQGPRGSEGPQGVRGECGPPGPAGAAGPAGN
CGADGQCGAKGANGACGIAGACGFCGARGPSGPQGPSGPPGPKGNSGECGACGSKGDTGAKGECGPTGIQGPPGPA
GEEGKRGARGECGPAGLCGPPGERGGCGSRGFCGADGVAGPKGPAGERGACGPAGPKGSCGEAGRCGEAGLCGAKGL
TGSCGSCGPDGKTGPPGPAGQDGRCGPPGPPGARGQAGVMGFCGPKGAAGECGKAGERGVCGPPGAVGPAGKDGEA
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VGFGSGGGSSSSVKFVSTTSSSRKSFKS

>sp|Q5XQN5|K2C5_BOVIN Keratin, type II cytoskeletal 5 OS=Bos taurus OX=9913 GN=KRT5 PE=1 SV=1

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FRNRFGAGAGGGYGFGGGAGSGFGFGGGAGGGGFGLGGGAGFGGGFGGPGFPVCPPGGIQEVTVNQSLLTPLNLQID
PTIQRVRTEEREQIKTLNNKFASFIDKVRFLEQQNKVLDTKWALLQEQGTKTVRQNLEPLLEQYINNLRRQLDGIVGERGRL
DSELRNMQDLVEDFKNKYEDEINKRTTAENEFVMLKKDVDAAYMNKVELEAKVDALMDEINFMKMFFDAELSQMQTHV
SDTSVVLSMDNNRSLDLDSIIAEVKAQYEDIANRSRTEAESWYQTKYEELQQTAGRHGDDLRNTKHEISEMNRMIQRLRSE
IDNVKKQCANLQNAIADAEQRGELALKDARSKLAELEDALQKAKQDMARLLREYQELMNTKLALDVEIATYRKLLEGEECR
LSGEGVGPVNISVVTNTVSSGYGGGSGFGGGLGGGLGGGLGGGLGGGLGGGLGSGLGGGGSSSFYSSSSGGVGLGGGL
SVGGSGFSASSGRSLGFGSGGGSSSSVKFVSTTSSSRKSFKS

>sp|A1L595|K1C17_BOVIN Keratin, type I cytoskeletal 17 OS=Bos taurus OX=9913 GN=KRT17 PE=2 SV=1

MTTTIRHFSSGSIKGSSGLAGGSSRSCRVSGSLGGGSCRLGSAGGLGSGLGGSSYSSCYSFGSGGGYGSGGYVSGGYGGG
FGGVDGLLVGGEKATMQNLNDRLASYLDKVRALEEANTELELKIRDWYQKQAPGPAPDYSSYFKTIEDLRNKIHTATVDNA
NLLLQIDNARLAADDFRTKFETEQALRVSVEADINGLRRVLDELTLARADLEMQIENLKEELAYLRKNHEEEMKALRGQVG
GEINVEMDAAPGVDLSRILNEMRDQYEKMAEKNRKDAEDWFFSKTEELNREVATNSELVQSGKSEISELRRTLQALEIELQS
QLSMKASLEGSLAETENRYCMQLSQIQGLIGSVEEQLAQLRCEMEQQNQEYKILLDVKTRLEQEIATYRRLLEGEDAHLTQ
YKTKEPVTTRQVRTIVEEVQDGRVISSREQVHQTSH

>sp|Q9QWL7|K1C17_MOUSE Keratin, type I cytoskeletal 17 OS=Mus musculus OX=10090 GN=Krt17 PE=1 SV=3

MTTTIRQFTSSSSIKGSSGLGGGSSRTSCRLSGSLGAGSCRLGSASGLGSALGSNSYSSCYSFGTGSGYGGNFGGVDGLLAG
GEKATMQNLNDRLASYLDKVRALEEANTELEVKIRDWYQKQAPGPARDYSAYYHTIEDLKNKILVATVDNASILLQIDNARL
AADDFRTKFETEQALRMSVEADINGLRRVLDELTLARADLEMQIENLKEELAYLKKNHEEEMNALRGQVGGEINVEMDAA
PGVDLSRILSEMRDQYEKMAEKNRKDAEDWFFSKTEELNREVATNSELVQSGKSEISELRRTMQALEIELQSQLSMKASLE
GSLAETENRYCVQLSQIQGLIGSVEEQLAQLRCEMEQQNQEYKILLDVKTRLEQEIATYRRLLEGEDAHLTQYKPKEPVTTR
QVRTIVEEVQDGKVISSREQVHQTTR

>sp|Q148H4|KRT81_BOVIN Keratin, type II cuticular Hb1 OS=Bos taurus OX=9913 GN=KRT81 PE=2 SV=1

MTCGSGFRGRAFSCVSACGPRPGRCCITAAPYRGISCYRGLTGGFGSRSICGGFRAGSFGRSFGYRSGGVGGLNPPCITTVS
VNESLLTPLNLEIDPNAQCVKQEEKEQIKCLNNRFAAFIDKVRFLEQQNKLLETKLQFYQNRQCCESNLEPLFNGYIETLRRE
AECVEADSGRLSSELNSLQEVLEGYKKKYEEEVALRATAENEFVALKKDVDCAYLRKSDLEANVEALIQEIDFLRRLYEEEIRVL
QAHISDTSVIVKMDNSRDLNMDNIVAEIKAQYDDIASRSRAEAESWYRSKCEEIKATVIRHGETLRRTKEEINELNRVIQRLTA
EVENAKCQNSKLEAAVTQAEQQGEAALNDAKCKLAGLEEALQKAKQDMACLLKEYQEVMNSKLGLDIEIATYRRLLEGEE
QRLCEGVGSVNVCVSSSRGGVVCGDLCVSGSRPVTGSVCSAPCSGNLAVSTGLCAPCGPPNSVTSCGLGGISSCGVGSCAS
VCRKC

>sp|O57611|K1C18_SCYST Keratin, type I cytoskeletal 18 OS=Scyliorhinus stellaris OX=68454 GN=krt18 PE=1 SV=1

MTYRGYTSLSSHSGPMSIRRSMPLQSSASSISGYGQRMAVSRISRVASLGSSSSSAAGIGMGGVGNQKETMQDLNDRLAT
YLEKVHSLETGNAKLELQIKEHLDARGPSFRDWSIYEKPLNELRKEVYDMTVDNARLILQIDNARLAADDFRVKWESELSIR
QSVENDINGLRKVIDDTNIGRLHLETEIESLKEELIYIRKNHDEEVKALRSQVADSSVHVEVDSAPGPDLSKVLAEIRKEYEGV
AQKNKDDAEIWYKNQMDGYKVEVKHNTDELCSAKVQVTELHRQIQSLEVELESLLSMKNSLEGTLRDTELRYEMELQTIN
GMIAKLEADLHQIRGDMQAQVREYEILLNIKMKLEAEIATYRRLLDGEDINTLVESTSGVTSQTIKKTIVTTQKVVDGKIVSDE
TVQIN

>sp|P19001|K1C19_MOUSE Keratin, type I cytoskeletal 19 OS=Mus musculus OX=10090 GN=Krt19 PE=1 SV=1

MTSYSYRQTSAMSSFGGTGGGSVRIGSGGVFRAPSIHGGSGGRGVSVSSTRFVTSSSGSYGGVRGGSFSGTLAVSDGLLSG
NEKITMQNLNDRLASYLDKVRALEQANGELEVKIRDWYQKQGPGPSRDYNHYFKTIEDLRDKILGATIDNSKIVLQIDNARL
AADDFRTKFETEHALRLSVEADINGLRRVLDELTLARTDLEMQIESLKEELAYLKKNHEEEITALRSQVGGQVSVEVDSTPGV
DLAKILSEMRSQYEIMAEKNRKDAEATYLARIEELNTQVAVHSEQIQISKTEVTDLRRTLQGLEIELQSQLSMKAALEGTLAET
EARYGVQLSQIQSVISGFEAQLSDVRADIERQNQEYKQLMDIKSRLEQEIATYRSLLEGQEAHYNNLPTPKAI

>sp|Q6EIY9|K2C1_CANLF Keratin, type II cytoskeletal 1 OS=Canis lupus familiaris OX=9615 GN=KRT1 PE=2 SV=1

MSRHFSSRSGFRSGGGFSSGSAGLVSFQRRTTSSSVRHSGGGGGRFSGGRCGGGGGGGAGGGGFGSRSLVNLGGSKSIS
ISVAGGGGGRGGFGGGYGGGGFGGGGFGGGSGGFGLGGGFGGGGFGGGGFGGGGFGGGGFGGGSFGPVCPPGGIQ
EVTINQSLLQPLNVEIDPEIQKVKTREREQIKSLNNQFASFIDKVRFLEQQNQVLQTKWELLQQVDTSTRTHSLEPYFENYIS
NLRRRVDQLKSDQSRMDSELKNMQDLVEDYRNKYEDEINKRTNAENEFVTIKKDVDAAFMNKVDLQAKVDNLQQEIDFL
TTLYQAELSQMQTQISETNVILSMDNNRSLDLDSIISEVKAQYEEIAQKSKAEAEALYQTKYEELQITAGKHGDNLKSTKMEI
SELNRVAQRLRSEIDSVKKQISALQQSISDAEQRGENALKDAQSKLAELEDALQKAKEDMARLLRDYQELMNTKLALDMEI
ATYRTLLEGEESRMSGECAPNVSVSVNTSHTTISGGGGRGGGGFGSVGGGGGYGGGSYGSGGGSYGSGGGGGGSYGSG
GGGGGGYGSSSSSGGHRGGSGGGSRSGGSSGGRGSSSGGIKTSSGSSSVKFVSTSYSRAVR

>sp|P02538|K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens OX=9606 GN=KRT6A PE=1 SV=3

MASTSTTIRSHSSSRRGFSANSARLPGVSRSGFSSVSVSRSRGSGGLGGACGGAGFGSRSLYGLGGSKRISIGGGSCAISGG
YGSRAGGSYGFGGAGSGFGFGGGAGIGFGLGGGAGLAGGFGGPGFPVCPPGGIQEVTVNQSLLTPLNLQIDPTIQRVRAE
EREQIKTLNNKFASFIDKVRFLEQQNKVLETKWTLLQEQGTKTVRQNLEPLFEQYINNLRRQLDSIVGERGRLDSELRGMQ
DLVEDFKNKYEDEINKRTAAENEFVTLKKDVDAAYMNKVELQAKADTLTDEINFLRALYDAELSQMQTHISDTSVVLSMDN
NRNLDLDSIIAEVKAQYEEIAQRSRAEAESWYQTKYEELQVTAGRHGDDLRNTKQEIAEINRMIQRLRSEIDHVKKQCANLQ
AAIADAEQRGEMALKDAKNKLEGLEDALQKAKQDLARLLKEYQELMNVKLALDVEIATYRKLLEGEECRLNGEGVGQVNIS
VVQSTVSSGYGGASGVGSGLGLGGGSSYSYGSGLGVGGGFSSSSGRAIGGGLSSVGGGSSTIKYTTTSSSSRKSYKH

>sp|Q497I4|KRT35_MOUSE Keratin, type I cuticular Ha5 OS=Mus musculus OX=10090 GN=Krt35 PE=1 SV=1

MASKCLKASFSSGSLKSPGKAGGGSTRVSNMYSSSSCKLPSPSRGARSFSVCSAGLGRGNYRVSSCLPALCLPTGGFATSYG
TGGGWFGEGILTGNEKETMQSLNDRLASYLEKVRQLEQENASLESRIREWCEQQVPYMCPDYQSYFRTMEELQKKTLCSK
AENARLVVQIDNAKLAADDFRTKYETEVSLRQLVEADINGLRRILDDLTLCKADLEAQVESLKEELLCLKKNHEEEVNSLRCQ
LGDRLNVEVDAAPPVDLNRVLDEMRCQYETLVENNRRDAEDWYDTQTEELNQQVVSSSEQLQSCQSDIIELRRTVNSLEIE
LQAQQSMRDALDSTLAETEGRYSSQLAQMQCMIGNVESQLGEIRADLERQNQEYQVLLDVRARLECEINTYRGLLESEDS
KLPCNPCAPDYSSSKSCLPCLPAVSCSTGAARTTCSPRPVCVPCPGGRF

>sp|O76013|KRT36_HUMAN Keratin, type I cuticular Ha6 OS=Homo sapiens OX=9606 GN=KRT36 PE=1 SV=1

MATQTCTPTFSTGSIKGLCGTAGGISRVSSIRSVGSCRVPSLAGAAGYISSARSGLSGLGSCLPGSYLSSECHTSGFVGSGGW
FCEGSFNGSEKETMQFLNDRLANYLEKVRQLERENAELESRIQEWYEFQIPYICPDYQSYFKTIEDFQQKILLTKSENARLVL
QIDNAKLAADDFRTKYETELSLRQLVEADINGLRRILDELTLCKADLEAQVESLKEELMCLKKNHEEEVSVLRCQLGDRLNVE
VDAAPPVDLNKILEDMRCQYEALVENNRRDVEAWFNTQTEELNQQVVSSSEQLQCCQTEIIELRRTVNALEIELQAQHSM
RNSLESTLAETEARYSSQLAQMQCLISNVEAQLSEIRCDLERQNQEYQVLLDVKARLEGEIATYRHLLEGEDCKLPPQPCAT
ACKPVIRVPSVPPVPCVPSVPCTPAPQVGTQIRTITEEIRDGKVISSREHVQSRPL

Table B1. PQI and Q2E values per sample. The standard deviation and standard error correspond to the PQI and Q2E, respectively.

Reference	PQI	PQI sd	Q2E	Q2E error
D1	1.41685855	0.093186826	1	0
D2	1.433123792	0.093154546	0.9985	0.0015
D3	1.351531998	0.091152775	0.9987	0.0013
D4	1.343558163	0.088696301	0.9829	0.0086
D5	1.155457515	0.093173171	0.9649	0.0178
D6	0.997352804	0.102014885	0.9175	0.0269
D7	0.925318957	0.092491109	0.9074	0.0225
P1	1.252963227	0.07478907	0.9657	0.0129
P2	1.102245248	0.089191943	1	0
P3	1.291519676	0.076646805	0.9939	0.0061
P4	1.252911361	0.081793518	0.9788	0.0207
P5	1.222818589	0.083604572	0.976	0.0091
P6	1.234775203	0.085584772	0.9974	0.0016
P7	1.23675444	0.089632911	0.973	0.0118
P8	1.167468168	0.100921436	0.9829	0.0099
P9	1.181049431	0.08784966	0.995	0.005
P10	1.28262269	0.081803703	0.9977	0.0023
P11	1.241195521	0.078613767	0.9914	0.0061
P12	1.228925056	0.105023548	1	0
AL0	1.393559966	0.090330023		
AL3	0.826877675	0.072801426	0.6238	0.3762
AL6	0.828035566	0.071825034	0.7458	0.1398
AL9	0.767843934	0.07741463	0.7466	0.2118
AL12	0.760460785	0.076212155	0.6911	0.1539
AG0	1.314250809	0.087208281		
AG1	1.009371171	0.079413054		
AG2	0.883356899	0.077986161	0.7574	0.2067
AG3	0.904555685	0.083097629		
AG4	0.784580182	0.09375503	0.6381	0.3619
AG5	0.859518287	0.090337972		
AG6	0.779933174	0.075864091	0.6616	0.2039

Reference	PQI	PQI sd	Q2E	Q2E error
AB0	1.115792437	0.083169764		
AB3	0.892319207	0.07665456		
AB6	1.093320253	0.070986304		
AC0	1.035523087	0.089291275	0.8746	0.0938
AC3	1.015293502	0.077295825		
AC6	0.978916284	0.087305677		
MF	1.505697165	0.094407329		
MF1826	0.808366299	0.101302943	0.4029	0.0209
MF1741	0.719872641	0.116842995	0.6722	0.0824
MF1664	0.566016582	0.101273767	0.6418	0.0326
MF1661	0.559152632	0.098392681	0.4697	0.1405
MF1550	0.493738382	0.104439311		
MR1	1.135457491	0.089378347	0.9292	0.0208
MR2	1.15313181	0.085967546	0.9589	0.0216

Table B2. Bulk deamidation values per sample. Showing reference (Ref.), relative remaining Q and N for CO1A1, CO1A2, and average, and the standard deviation of the average.

Ref.	Q (CO1A1)	Q (CO1A2)	Q	sd (Q)	N (CO1A1)	N (CO1A2)	N	sd (N)
D1	0.981534597	0.985439028	0.983486813	0.002760849	0.944778867	0.866923829	0.905851348	0.055051825
D2	0.97407578	0.936578004	0.955326892	0.026514932	0.714642144	0.827229834	0.770935989	0.079611519
D3	0.955842177	0.965234906	0.960538541	0.006641663	0.773513842	0.795895891	0.784704866	0.015826499
D4	0.957053923	0.910047241	0.933550582	0.033238744	0.231757682	0.411715576	0.321736629	0.127249447
D5	0.855189565	0.771132296	0.813160931	0.059437465	0.406681266	0.398432455	0.402556861	0.00583279
D6	0.860896544	0.622765576	0.74183106	0.168384022	0.287812203	0.275587479	0.281699841	0.008644185
D7	0.813377973	0.714224333	0.763801153	0.070112211	0.28121204	0.339752993	0.310482516	0.041394705
P1	0.940118563	0.833054127	0.886586345	0.075705989	0.572830328	0.449257224	0.511043776	0.08737938
P2	0.968520086	0.956768891	0.962644488	0.00830935	1	0.510125673	0.755062836	0.346393459
P3	0.944678555	0.802320514	0.873499535	0.100662336	0	0.388509639	0.194254819	0.2747178
P4	0.919503538	0.892689685	0.906096612	0.018960257		0.717997076	0.717997076	0
P5	0.961357891	0.831369137	0.896363514	0.091915929	1	0.561638348	0.780819174	0.309968497
P6	0.978437243	0.951731142	0.965084192	0.018884065	1	0.78211118	0.89105559	0.154070662
P7	0.957049751	0.900105606	0.928577678	0.040265591	1	0.521659347	0.760829674	0.338237919
P8	0.9774074	0.883480209	0.930443805	0.066416554	1	0.308912964	0.654456482	0.48867233
P9	0.941297187	0.801335173	0.87131618	0.09896809	0.847096132	0.478326611	0.662711371	0.260759429
P10	0.986417254	0.989338956	0.987878105	0.002065955	1	0.633951953	0.816975976	0.258835056
P11	0.956195418	0.868642974	0.912419196	0.061908927	1	0.526611566	0.763305783	0.334736172
P12	0.962014064	0.859669257	0.91084166	0.072368707		0.293482322	0.293482322	0
AL0	1	1	1	0	0.982664452	1	0.991332226	0.012258083
AL3	0.324826869	0.739002672	0.53191477	0.292866519	1	0.447748525	0.723874263	0.390500763

Ref.	Q (CO1A1)	Q (CO1A2)	Q	sd (Q)	N (CO1A1)	N (CO1A2)	N	sd (N)
AL6	0.228632844	0.279434365	0.254033605	0.035922101	0.041864921	0.560129258	0.30099709	0.366468227
AL9	0.023772843	0	0.011886422	0.016809939	0.0970961	0.520091797	0.308593948	0.299103126
AL12	0.013772895	0	0.006886448	0.009738908	0.008179748	0.280901972	0.14454086	0.192843734
AG0	0.965233183	1	0.982616592	0.024583852	1	0.86487405	0.932437025	0.095548476
AG1	0.637866067	1	0.818933034	0.25606736	1	0.74657788	0.87328894	0.1791965
AG2	0.158163339	0.865471932	0.511817636	0.500142703	0.040057984	0.325916447	0.182987215	0.202132458
AG3	0.159678547	1	0.579839273	0.594196998	0.442823605	0.289258547	0.366041076	0.108586894
AG4	0.047451702	0.192282399	0.11986705	0.102410767	0	0.110010216	0.055005108	0.07778897
AG5	0.038333963	0	0.019166982	0.027106205	0	0.236071386	0.118035693	0.166927678
AG6	0.100059402	0.015043104	0.057551253	0.060115601	0	0.034149539	0.01707477	0.024147371
AB0	0.764575671	0.735434214	0.750004943	0.020606122	0	0.416756398	0.208378199	0.294691275
AB3	0.099373983	0.003085493	0.051229738	0.068086244	0.003956471	0.052101617	0.028029044	0.034043759
AB6	0.004360155	0.002197606	0.003278881	0.001529153	0.007851814	0.151756787	0.079804301	0.101756182
AC0	0.871188058	0.728420661	0.79980436	0.100951795	0	0.61411797	0.307058985	0.434246981
AC3	0.123148437	0.026245608	0.074697023	0.068520647	0.011621329	0.058445823	0.035033576	0.033109917
AC6	0.102717618	0.030806139	0.066761878	0.050849095	0	0.487662617	0.243831308	0.344829543
MF	0.92404839	0.906107147	0.915077768	0.012686375	0.764450225	0.845081353	0.804765789	0.057014818
MF1826	0.277784156	0.22417472	0.250979438	0.037907595	0.003733761	0.096085227	0.049909494	0.065302348
MF1741	0.468836487	0.484592174	0.47671433	0.011140953	0.002378036	0.155327485	0.078852761	0.108151592
MF1664	0.443005345	0.402137442	0.422571393	0.028897971	0.001004772	0.151286929	0.076145851	0.106265532
MF1661	0.055940636	0.265373765	0.1606572	0.148091586	0.000995345	0.071927915	0.03646163	0.050156902
MF1550	0.224893163	0.020847997	0.12287058	0.144281721	0.001695503	0.045028263	0.023361883	0.030640888
MR1	0.83993974	0.832135267	0.836037504	0.005518596	0.01243196	0.47714632	0.24478914	0.328602675
MR2	0.911966719	0.996295443	0.954131081	0.059629413	0.084881538	0.290461836	0.187671687	0.145367223

Table B3. Site-specific deamidation values per sample for CO1A1 and CO1A2. Showing reference, half-time, relative remaining N and Q, size (intensity) and protein.

Ref	Half-time	RelNonDeam	Size	Protein
D1	-1	0.958534687	111.2571499	sp|P02465|CO1A2_BOVIN
D1	-1	0.814079731	119.2220378	sp|P02465|CO1A2_BOVIN
D1	-1	0.989930478	119.2220378	sp|P02465|CO1A2_BOVIN
D1	1	0.638576119	159.1465564	sp|P02465|CO1A2_BOVIN
D1	1.02	0.911733076	130.5820486	sp|P02465|CO1A2_BOVIN
D1	1.08	0.914313671	115.9185744	sp|P02465|CO1A2_BOVIN
D1	1.14	0.985770129	158.0835993	sp|P02465|CO1A2_BOVIN
D1	1.18	0.804039006	159.7237745	sp|P02465|CO1A2_BOVIN
D1	21.1	0.944716146	203.8055132	sp|P02453|CO1A1_BOVIN
D1	21.1	0.945341652	226.4545366	sp|P02465|CO1A2_BOVIN
D1	28	0.991392658	107.4752596	sp|P02465|CO1A2_BOVIN
D1	48.2	0.96911176	136.4757037	sp|P02465|CO1A2_BOVIN
D1	57.8	0.820578214	215.0524605	sp|P02465|CO1A2_BOVIN
D1	224	0.981492671	116.9756786	sp|P02465|CO1A2_BOVIN
D1	287	0.92478128	106.5324455	sp|P02465|CO1A2_BOVIN
D1	610	0.989363219	145.5771671	sp|P02453|CO1A1_BOVIN
D1	610	1	117.0672993	sp|P02465|CO1A2_BOVIN
D1	620	1	100.9968654	sp|P02453|CO1A1_BOVIN
D1	630	0.974684762	182.1382775	sp|P02453|CO1A1_BOVIN
D1	630	0.99025651	161.029003	sp|P02465|CO1A2_BOVIN
D1	640	1	381.6305293	sp|P02453|CO1A1_BOVIN
D1	640	0.984538829	115.4057423	sp|P02465|CO1A2_BOVIN
D1	660	1	141.6901341	sp|P02465|CO1A2_BOVIN
D1	670	1	101.9179911	sp|P02453|CO1A1_BOVIN
D1	670	0.966886769	127.2453477	sp|P02465|CO1A2_BOVIN
D1	700	1	107.3781321	sp|P02465|CO1A2_BOVIN
D1	750	1	106.4783942	sp|P02453|CO1A1_BOVIN
D1	750	0.98022137	158.9240986	sp|P02465|CO1A2_BOVIN
D1	800	0.985553212	136.8033693	sp|P02465|CO1A2_BOVIN
D1	5200	0.964609542	119.5782037	sp|P02465|CO1A2_BOVIN
D1	6800	1	101.8328514	sp|P02453|CO1A1_BOVIN
D1	7200	1	101.6472118	sp|P02453|CO1A1_BOVIN
D1	7600	0	105.2142057	sp|P02453|CO1A1_BOVIN
D1	8900	0.990243964	101.8328514	sp|P02453|CO1A1_BOVIN
D1	10000	0.98440207	125.477108	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
D2	-1	0.934791711	109.8224116	sp|P02465|CO1A2_BOVIN
D2	-1	0.74364017	116.639134	sp|P02465|CO1A2_BOVIN
D2	-1	0.962169779	116.639134	sp|P02465|CO1A2_BOVIN
D2	1	0.633150046	149.7797542	sp|P02465|CO1A2_BOVIN
D2	1.02	0.776816474	121.5015114	sp|P02465|CO1A2_BOVIN
D2	1.08	0.866204164	112.5124744	sp|P02465|CO1A2_BOVIN
D2	1.14	0.889169772	157.344998	sp|P02465|CO1A2_BOVIN
D2	1.18	0.790233474	161.4681728	sp|P02465|CO1A2_BOVIN
D2	21.1	0.712263824	165.388061	sp|P02453|CO1A1_BOVIN
D2	21.1	0.986566097	214.223728	sp|P02465|CO1A2_BOVIN
D2	28	1	103.2219344	sp|P02453|CO1A1_BOVIN
D2	28	0.941717602	104.5208031	sp|P02465|CO1A2_BOVIN
D2	48.2	0.916015779	138.9826626	sp|P02465|CO1A2_BOVIN
D2	57.8	0.845762212	185.8850751	sp|P02465|CO1A2_BOVIN
D2	64	1	120.5297459	sp|P02465|CO1A2_BOVIN
D2	224	0.961556033	113.1837661	sp|P02465|CO1A2_BOVIN
D2	287	0.74407037	130.5566216	sp|P02465|CO1A2_BOVIN
D2	610	0.983734308	130.9018763	sp|P02453|CO1A1_BOVIN
D2	610	1	115.6618006	sp|P02465|CO1A2_BOVIN
D2	620	1	101.0246843	sp|P02453|CO1A1_BOVIN
D2	630	0.966123435	151.0403216	sp|P02453|CO1A1_BOVIN
D2	630	0.98372422	149.4252056	sp|P02465|CO1A2_BOVIN
D2	640	1	115.6618006	sp|P02465|CO1A2_BOVIN
D2	660	0.978848783	153.4124794	sp|P02465|CO1A2_BOVIN
D2	670	1	100.8177881	sp|P02453|CO1A1_BOVIN
D2	670	0.963920655	119.9237019	sp|P02465|CO1A2_BOVIN
D2	700	1	105.6106967	sp|P02465|CO1A2_BOVIN
D2	750	0.994835035	103.0177619	sp|P02453|CO1A1_BOVIN
D2	750	0.093553932	162.5810848	sp|P02465|CO1A2_BOVIN
D2	800	0.999211993	121.0914966	sp|P02465|CO1A2_BOVIN
D2	5200	0.928098925	137.9633114	sp|P02465|CO1A2_BOVIN
D2	6800	1	102.0288357	sp|P02453|CO1A1_BOVIN
D2	7200	1	101.6529918	sp|P02453|CO1A1_BOVIN
D2	8900	0.99363617	102.0288357	sp|P02453|CO1A1_BOVIN
D2	10000	0.952768653	150.479973	sp|P02465|CO1A2_BOVIN
D3	-1	0.860210488	109.8134962	sp|P02465|CO1A2_BOVIN
D3	-1	0.716293525	113.3775559	sp|P02465|CO1A2_BOVIN
D3	-1	0.767981904	113.3775559	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
D3	1	0.671771831	158.345358	sp|P02465|CO1A2_BOVIN
D3	1.02	0.873308172	131.2511798	sp|P02465|CO1A2_BOVIN
D3	1.08	0.775396884	109.6321157	sp|P02465|CO1A2_BOVIN
D3	1.14	0.861207799	173.8228267	sp|P02465|CO1A2_BOVIN
D3	1.18	0.788024059	167.3872864	sp|P02465|CO1A2_BOVIN
D3	21.1	0.773253327	234.5069596	sp|P02453|CO1A1_BOVIN
D3	21.1	0.928131368	280.3947773	sp|P02465|CO1A2_BOVIN
D3	28	0.826957465	102.9170442	sp|P02465|CO1A2_BOVIN
D3	48.2	0.826693616	140.5097072	sp|P02465|CO1A2_BOVIN
D3	57.8	0.743289463	254.0224687	sp|P02465|CO1A2_BOVIN
D3	224	0.85722321	110.5064687	sp|P02465|CO1A2_BOVIN
D3	287	0.716325533	107.8087413	sp|P02465|CO1A2_BOVIN
D3	610	0.958946071	131.3804475	sp|P02453|CO1A1_BOVIN
D3	610	1	111.1683166	sp|P02465|CO1A2_BOVIN
D3	630	0.945162661	191.5982539	sp|P02453|CO1A1_BOVIN
D3	630	0.988050709	153.2866886	sp|P02465|CO1A2_BOVIN
D3	640	1	110.9453028	sp|P02465|CO1A2_BOVIN
D3	660	1	141.6176464	sp|P02465|CO1A2_BOVIN
D3	670	1	126.8244546	sp|P02465|CO1A2_BOVIN
D3	700	1	102.2349435	sp|P02465|CO1A2_BOVIN
D3	750	0.979116913	110.267375	sp|P02453|CO1A1_BOVIN
D3	750	1	150.5968715	sp|P02465|CO1A2_BOVIN
D3	800	0.962176679	130.7588114	sp|P02465|CO1A2_BOVIN
D3	5200	0.872994625	123.6333783	sp|P02465|CO1A2_BOVIN
D3	6800	1	101.5618383	sp|P02453|CO1A1_BOVIN
D3	7200	1	100.8534693	sp|P02453|CO1A1_BOVIN
D3	8900	0.942685628	101.5618383	sp|P02453|CO1A1_BOVIN
D3	10000	0.93182459	140.0714016	sp|P02465|CO1A2_BOVIN
D4	-1	0.865365849	105.3450758	sp|P02465|CO1A2_BOVIN
D4	-1	0.405934605	108.8638631	sp|P02465|CO1A2_BOVIN
D4	-1	0.233080752	108.8638631	sp|P02465|CO1A2_BOVIN
D4	1	0.20496025	154.3884715	sp|P02465|CO1A2_BOVIN
D4	1.02	0.138437831	113.7000621	sp|P02465|CO1A2_BOVIN
D4	1.08	0.328305399	105.0250956	sp|P02465|CO1A2_BOVIN
D4	1.14	0.440662479	134.8772751	sp|P02465|CO1A2_BOVIN
D4	1.18	0.220723461	127.1581656	sp|P02465|CO1A2_BOVIN
D4	21.1	0.228142198	144.1617902	sp|P02453|CO1A1_BOVIN
D4	21.1	0.63404227	195.9492776	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
D4	28	0	122.4808299	sp|P02453|CO1A1_BOVIN
D4	28	0.82269611	100.5518738	sp|P02465|CO1A2_BOVIN
D4	48.2	0.796532842	117.6847252	sp|P02465|CO1A2_BOVIN
D4	57.8	0.554284466	150.2784729	sp|P02465|CO1A2_BOVIN
D4	224	0.928613048	105.293612	sp|P02465|CO1A2_BOVIN
D4	287	0.540597685	126.1797569	sp|P02465|CO1A2_BOVIN
D4	610	0.921248223	107.9096713	sp|P02453|CO1A1_BOVIN
D4	610	0.966393173	106.329714	sp|P02465|CO1A2_BOVIN
D4	620	1	101.9572972	sp|P02453|CO1A1_BOVIN
D4	630	0.941463156	143.3975653	sp|P02453|CO1A1_BOVIN
D4	630	0.929919719	131.8171365	sp|P02465|CO1A2_BOVIN
D4	640	1	548.6429905	sp|P02453|CO1A1_BOVIN
D4	640	0.985074372	106.0364733	sp|P02465|CO1A2_BOVIN
D4	660	0.958894516	130.919417	sp|P02465|CO1A2_BOVIN
D4	670	1	102.2742927	sp|P02453|CO1A1_BOVIN
D4	670	0.987095036	111.9205081	sp|P02465|CO1A2_BOVIN
D4	700	0.989333293	104.7101833	sp|P02465|CO1A2_BOVIN
D4	750	0.703578143	104.4343485	sp|P02453|CO1A1_BOVIN
D4	750	0.995917291	137.8249629	sp|P02465|CO1A2_BOVIN
D4	800	0.994310892	110.0557661	sp|P02465|CO1A2_BOVIN
D4	5200	0.800781593	120.5733263	sp|P02465|CO1A2_BOVIN
D4	6800	1	101.0764971	sp|P02453|CO1A1_BOVIN
D4	7200	0.890537124	100.9199896	sp|P02453|CO1A1_BOVIN
D4	8900	0.937835075	100.9608097	sp|P02453|CO1A1_BOVIN
D4	10000	0.850661238	137.1965261	sp|P02465|CO1A2_BOVIN
D5	-1	0.767181781	105.4541241	sp|P02465|CO1A2_BOVIN
D5	-1	0.31976255	104.3147707	sp|P02465|CO1A2_BOVIN
D5	-1	0.132200746	104.3147707	sp|P02465|CO1A2_BOVIN
D5	1	0.304300494	156.4541453	sp|P02465|CO1A2_BOVIN
D5	1.02	0.249917483	121.6758102	sp|P02465|CO1A2_BOVIN
D5	1.08	0.286548697	102.960573	sp|P02465|CO1A2_BOVIN
D5	1.14	0.344494858	146.7255925	sp|P02465|CO1A2_BOVIN
D5	1.18	0.361718652	137.0368422	sp|P02465|CO1A2_BOVIN
D5	21.1	0.404978252	191.8109382	sp|P02453|CO1A1_BOVIN
D5	21.1	0.457632408	285.3125354	sp|P02465|CO1A2_BOVIN
D5	28	0.19129439	101.1890697	sp|P02465|CO1A2_BOVIN
D5	48.2	0.437187053	125.6264525	sp|P02465|CO1A2_BOVIN
D5	57.8	0.570139679	193.1149562	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
D5	224	0.624309429	103.6921715	sp|P02465|CO1A2_BOVIN
D5	287	0.404764618	126.981188	sp|P02465|CO1A2_BOVIN
D5	610	0.864054143	110.9136477	sp|P02453|CO1A1_BOVIN
D5	610	0.913953373	104.1999103	sp|P02465|CO1A2_BOVIN
D5	620	1	102.5067373	sp|P02453|CO1A1_BOVIN
D5	630	0.854411564	165.8584397	sp|P02453|CO1A1_BOVIN
D5	630	0.780495386	151.029596	sp|P02465|CO1A2_BOVIN
D5	640	1	103.8833174	sp|P02465|CO1A2_BOVIN
D5	660	0.876813009	121.5200463	sp|P02465|CO1A2_BOVIN
D5	670	1	100.924314	sp|P02453|CO1A1_BOVIN
D5	670	0.942447093	118.2469305	sp|P02465|CO1A2_BOVIN
D5	700	1	101.3964396	sp|P02465|CO1A2_BOVIN
D5	750	0.76059912	106.8751925	sp|P02453|CO1A1_BOVIN
D5	750	0.979899654	127.2369613	sp|P02465|CO1A2_BOVIN
D5	800	0.870550734	120.2185474	sp|P02465|CO1A2_BOVIN
D5	5200	0.587883626	115.599321	sp|P02465|CO1A2_BOVIN
D5	6800	1	100.8423817	sp|P02453|CO1A1_BOVIN
D5	7600	0.436714218	103.197918	sp|P02453|CO1A1_BOVIN
D5	8900	1	100.8423817	sp|P02453|CO1A1_BOVIN
D5	10000	0.627248363	138.4487387	sp|P02465|CO1A2_BOVIN
D6	-1	0.790376236	104.9176185	sp|P02465|CO1A2_BOVIN
D6	1	0.145175019	132.696064	sp|P02465|CO1A2_BOVIN
D6	1.02	0.224208659	109.2934406	sp|P02465|CO1A2_BOVIN
D6	1.08	0.452016128	101.2004563	sp|P02465|CO1A2_BOVIN
D6	1.14	0.031500014	120.5476934	sp|P02465|CO1A2_BOVIN
D6	1.18	0.179821768	121.8943614	sp|P02465|CO1A2_BOVIN
D6	11.8	0	100.2934004	sp|P02453|CO1A1_BOVIN
D6	21.1	0.283302494	145.7837312	sp|P02453|CO1A1_BOVIN
D6	21.1	0.404324185	173.2213159	sp|P02465|CO1A2_BOVIN
D6	28	0	100.4708047	sp|P02465|CO1A2_BOVIN
D6	48.2	0.647045226	110.5160545	sp|P02465|CO1A2_BOVIN
D6	57.8	0.15474095	223.8496553	sp|P02465|CO1A2_BOVIN
D6	224	0.190887898	101.2004563	sp|P02465|CO1A2_BOVIN
D6	287	0.477694796	121.7657408	sp|P02465|CO1A2_BOVIN
D6	610	0.60498571	102.3118521	sp|P02453|CO1A1_BOVIN
D6	610	1	100.9938821	sp|P02465|CO1A2_BOVIN
D6	630	0.797021069	141.065097	sp|P02453|CO1A1_BOVIN
D6	630	0.665933463	127.8797786	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
D6	640	1	550.4582878	sp|P02453|CO1A1_BOVIN
D6	640	1	100.8701125	sp|P02465|CO1A2_BOVIN
D6	660	0.894411034	107.5295918	sp|P02465|CO1A2_BOVIN
D6	670	1	100.6544119	sp|P02453|CO1A1_BOVIN
D6	670	0.887593716	108.3826288	sp|P02465|CO1A2_BOVIN
D6	700	1	100.1881057	sp|P02465|CO1A2_BOVIN
D6	750	0.861547154	111.103191	sp|P02453|CO1A1_BOVIN
D6	750	1	108.4208293	sp|P02465|CO1A2_BOVIN
D6	800	0.828371804	110.3706674	sp|P02465|CO1A2_BOVIN
D6	5200	0.431558721	109.8257693	sp|P02465|CO1A2_BOVIN
D6	6800	1	100.4699143	sp|P02453|CO1A1_BOVIN
D6	7200	1	100.8776406	sp|P02453|CO1A1_BOVIN
D6	7600	0	123.7964762	sp|P02453|CO1A1_BOVIN
D6	8900	1	100.4699143	sp|P02453|CO1A1_BOVIN
D6	10000	0.483975931	131.7139486	sp|P02465|CO1A2_BOVIN
D7	-1	0.780662799	103.2948357	sp|P02465|CO1A2_BOVIN
D7	-1	0	101.006395	sp|P02465|CO1A2_BOVIN
D7	-1	0	101.006395	sp|P02465|CO1A2_BOVIN
D7	1	0.248891519	121.8252389	sp|P02465|CO1A2_BOVIN
D7	1.02	0.313413823	105.8051122	sp|P02465|CO1A2_BOVIN
D7	1.08	0.626918829	103.7662917	sp|P02465|CO1A2_BOVIN
D7	1.14	0.354458938	113.9537822	sp|P02465|CO1A2_BOVIN
D7	1.18	0.268362119	117.662628	sp|P02465|CO1A2_BOVIN
D7	21.1	0.275121363	151.071492	sp|P02453|CO1A1_BOVIN
D7	21.1	0.465854359	164.4425878	sp|P02465|CO1A2_BOVIN
D7	28	0.473405253	102.6857279	sp|P02465|CO1A2_BOVIN
D7	48.2	0.530942657	109.3039039	sp|P02465|CO1A2_BOVIN
D7	57.8	0.225888086	150.8511167	sp|P02465|CO1A2_BOVIN
D7	224	0.605262445	103.3629416	sp|P02465|CO1A2_BOVIN
D7	287	0.441384667	112.7985113	sp|P02465|CO1A2_BOVIN
D7	610	0.763569408	109.6419971	sp|P02453|CO1A1_BOVIN
D7	610	1	101.006395	sp|P02465|CO1A2_BOVIN
D7	620	0.832654257	105.4487488	sp|P02453|CO1A1_BOVIN
D7	630	0.828833868	152.6328528	sp|P02453|CO1A1_BOVIN
D7	630	0.743008987	135.3046607	sp|P02465|CO1A2_BOVIN
D7	640	0.769248466	433.9449445	sp|P02453|CO1A1_BOVIN
D7	640	1	101.9461573	sp|P02465|CO1A2_BOVIN
D7	660	0.976294274	105.2903934	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
D7	670	1	102.1070815	sp|P02453|CO1A1_BOVIN
D7	670	1	105.3008145	sp|P02465|CO1A2_BOVIN
D7	700	1	100.3008369	sp|P02465|CO1A2_BOVIN
D7	750	0.76933046	110.2057097	sp|P02453|CO1A1_BOVIN
D7	750	1	110.6322251	sp|P02465|CO1A2_BOVIN
D7	800	0.968814405	115.7498982	sp|P02465|CO1A2_BOVIN
D7	5200	0.453268884	105.6720716	sp|P02465|CO1A2_BOVIN
D7	6800	1	100.4515344	sp|P02453|CO1A1_BOVIN
D7	7600	0	104.9319569	sp|P02453|CO1A1_BOVIN
D7	8900	1	100.4515344	sp|P02453|CO1A1_BOVIN
D7	10000	0.584021245	133.3851566	sp|P02465|CO1A2_BOVIN
P1	-1	0.769235784	104.1867708	sp|P02465|CO1A2_BOVIN
P1	1.08	1	101.5749283	sp|P02465|CO1A2_BOVIN
P1	21.1	0.540974142	106.0177262	sp|P02453|CO1A1_BOVIN
P1	48.2	0.959624887	114.7206005	sp|P02465|CO1A2_BOVIN
P1	224	1	101.5749283	sp|P02465|CO1A2_BOVIN
P1	287	0.017492938	133.06404	sp|P02465|CO1A2_BOVIN
P1	610	1	106.9700991	sp|P02453|CO1A1_BOVIN
P1	630	0.811975867	171.302558	sp|P02465|CO1A2_BOVIN
P1	630	0.925042551	228.6968876	sp|P02453|CO1A1_BOVIN
P1	640	1	185.5339994	sp|P02453|CO1A1_BOVIN
P1	800	1	190.1994905	sp|P02465|CO1A2_BOVIN
P1	7600	0.940937341	174.9403173	sp|P02453|CO1A1_BOVIN
P2	-1	0	110.9279739	sp|P02465|CO1A2_BOVIN
P2	1.08	1	110.9279739	sp|P02465|CO1A2_BOVIN
P2	1.18	0	105.3049353	sp|P02465|CO1A2_BOVIN
P2	21.1	1	138.2501848	sp|P02453|CO1A1_BOVIN
P2	48.2	1	124.4982405	sp|P02465|CO1A2_BOVIN
P2	224	1	110.9279739	sp|P02465|CO1A2_BOVIN
P2	287	0.359826553	149.4819367	sp|P02465|CO1A2_BOVIN
P2	610	1	139.0458447	sp|P02453|CO1A1_BOVIN
P2	630	0.956768891	299.2595142	sp|P02465|CO1A2_BOVIN
P2	630	0.958344548	360.7735805	sp|P02453|CO1A1_BOVIN
P2	640	1	534.814047	sp|P02453|CO1A1_BOVIN
P2	7600	1	171.916522	sp|P02453|CO1A1_BOVIN
P3	-1	0.493984616	107.8877596	sp|P02465|CO1A2_BOVIN
P3	1.08	1	107.9938823	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
P3	1.18	0	104.9344441	sp|P02465|CO1A2_BOVIN
P3	21.1	0	147.0863952	sp|P02453|CO1A1_BOVIN
P3	48.2	1	120.7363646	sp|P02465|CO1A2_BOVIN
P3	224	1	107.9938823	sp|P02465|CO1A2_BOVIN
P3	287	0.025675826	133.0586949	sp|P02465|CO1A2_BOVIN
P3	610	1	102.0945541	sp|P02453|CO1A1_BOVIN
P3	630	0.770504168	163.8344835	sp|P02465|CO1A2_BOVIN
P3	630	0.951363691	168.678983	sp|P02453|CO1A1_BOVIN
P3	640	0.90314407	192.5504451	sp|P02453|CO1A1_BOVIN
P3	800	1	192.8855265	sp|P02465|CO1A2_BOVIN
P3	7600	1	183.1680941	sp|P02453|CO1A1_BOVIN
P4	-1	0.845689367	106.2173397	sp|P02465|CO1A2_BOVIN
P4	1	1	113.8257147	sp|P02465|CO1A2_BOVIN
P4	1.02	1	103.3606001	sp|P02465|CO1A2_BOVIN
P4	1.08	1	104.5953168	sp|P02465|CO1A2_BOVIN
P4	1.18	0.872321186	282.1926005	sp|P02465|CO1A2_BOVIN
P4	28	0.436937488	105.9932829	sp|P02465|CO1A2_BOVIN
P4	48.2	0.945089254	113.8268085	sp|P02465|CO1A2_BOVIN
P4	224	0.261001456	104.5953168	sp|P02465|CO1A2_BOVIN
P4	287	0.02033673	152.8323074	sp|P02465|CO1A2_BOVIN
P4	610	1	108.6261523	sp|P02453|CO1A1_BOVIN
P4	630	0.818821972	141.3581437	sp|P02465|CO1A2_BOVIN
P4	630	0.909219669	239.7435071	sp|P02453|CO1A1_BOVIN
P4	640	0.937013812	170.5057748	sp|P02453|CO1A1_BOVIN
P4	800	1	317.7053704	sp|P02465|CO1A2_BOVIN
P4	10000	1	169.4722939	sp|P02465|CO1A2_BOVIN
P5	-1	0.534399947	105.8213887	sp|P02465|CO1A2_BOVIN
P5	1.08	1	104.1610492	sp|P02465|CO1A2_BOVIN
P5	1.14	1	119.6795277	sp|P02465|CO1A2_BOVIN
P5	1.18	1	119.6795277	sp|P02465|CO1A2_BOVIN
P5	21.1	1	109.3432909	sp|P02453|CO1A1_BOVIN
P5	48.2	0.974231894	113.4389417	sp|P02465|CO1A2_BOVIN
P5	224	1	104.1610492	sp|P02465|CO1A2_BOVIN
P5	287	0	213.0527434	sp|P02465|CO1A2_BOVIN
P5	610	1	109.083367	sp|P02453|CO1A1_BOVIN
P5	630	0.813790361	186.1606197	sp|P02465|CO1A2_BOVIN
P5	630	0.950548012	210.3827784	sp|P02453|CO1A1_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
P5	640	1	230.6446849	sp|P02453|CO1A1_BOVIN
P5	800	1	161.5192553	sp|P02465|CO1A2_BOVIN
P5	7600	0.931100558	136.1125195	sp|P02453|CO1A1_BOVIN
P5	10000	1	109.3777533	sp|P02465|CO1A2_BOVIN
P6	1.14	1	108.1993017	sp|P02465|CO1A2_BOVIN
P6	21.1	1	102.3047195	sp|P02453|CO1A1_BOVIN
P6	48.2	0.938905422	163.1182655	sp|P02465|CO1A2_BOVIN
P6	287	0.037133871	120.8129221	sp|P02465|CO1A2_BOVIN
P6	630	0.942390427	192.4381078	sp|P02465|CO1A2_BOVIN
P6	630	0.974893415	254.0556455	sp|P02453|CO1A1_BOVIN
P6	640	1	152.1762686	sp|P02453|CO1A1_BOVIN
P6	670	1	100.3547919	sp|P02453|CO1A1_BOVIN
P6	800	1	243.4233512	sp|P02465|CO1A2_BOVIN
P6	7600	1	259.9405246	sp|P02453|CO1A1_BOVIN
P7	-1	0.657022574	101.0661014	sp|P02465|CO1A2_BOVIN
P7	1.08	0.606503699	101.0661014	sp|P02465|CO1A2_BOVIN
P7	21.1	1	140.4512037	sp|P02453|CO1A1_BOVIN
P7	48.2	1	117.8412974	sp|P02465|CO1A2_BOVIN
P7	224	1	101.0661014	sp|P02465|CO1A2_BOVIN
P7	287	0.023053058	113.4262976	sp|P02465|CO1A2_BOVIN
P7	630	0.888599986	178.7325221	sp|P02465|CO1A2_BOVIN
P7	630	0.948953666	258.3781567	sp|P02453|CO1A1_BOVIN
P7	640	1	311.8100861	sp|P02453|CO1A1_BOVIN
P7	800	1	172.5065176	sp|P02465|CO1A2_BOVIN
P8	-1	1	101.5222474	sp|P02465|CO1A2_BOVIN
P8	1.08	1	101.5222474	sp|P02465|CO1A2_BOVIN
P8	1.18	1	119.7887902	sp|P02465|CO1A2_BOVIN
P8	21.1	1	128.5831499	sp|P02453|CO1A1_BOVIN
P8	48.2	1	114.0794256	sp|P02465|CO1A2_BOVIN
P8	224	1	101.5222474	sp|P02465|CO1A2_BOVIN
P8	287	0.014698422	163.6059591	sp|P02465|CO1A2_BOVIN
P8	630	0.860584907	147.6538283	sp|P02465|CO1A2_BOVIN
P8	630	0.973780141	258.8461073	sp|P02453|CO1A1_BOVIN
P8	640	1	182.4063881	sp|P02453|CO1A1_BOVIN
P8	800	1	193.9443114	sp|P02465|CO1A2_BOVIN
P8	7600	1	171.5009363	sp|P02453|CO1A1_BOVIN
P9	1.18	0.763907405	110.9503328	sp|P02465|CO1A2_BOVIN
P9	21.1	0.502563787	100.5694876	sp|P02453|CO1A1_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
P9	48.2	0.69714823	124.5442801	sp|P02465|CO1A2_BOVIN
P9	287	0.016780746	130.368759	sp|P02465|CO1A2_BOVIN
P9	610	1	100.3541039	sp|P02453|CO1A1_BOVIN
P9	620	1	102.4503041	sp|P02453|CO1A1_BOVIN
P9	630	0.758447786	162.14081	sp|P02465|CO1A2_BOVIN
P9	630	0.93197524	233.0184478	sp|P02453|CO1A1_BOVIN
P9	640	1	277.6320286	sp|P02453|CO1A1_BOVIN
P9	800	1	203.9640119	sp|P02465|CO1A2_BOVIN
P9	7600	0.841294179	188.938321	sp|P02453|CO1A1_BOVIN
P10	1.18	0.452936614	104.3673668	sp|P02465|CO1A2_BOVIN
P10	21.1	1	152.2880156	sp|P02453|CO1A1_BOVIN
P10	48.2	1	113.0032341	sp|P02465|CO1A2_BOVIN
P10	287	0.540994293	107.8201423	sp|P02465|CO1A2_BOVIN
P10	630	0.989338956	244.0833279	sp|P02465|CO1A2_BOVIN
P10	630	0.98795634	268.4140406	sp|P02453|CO1A1_BOVIN
P10	640	0.981915038	245.8022845	sp|P02453|CO1A1_BOVIN
P10	7600	1	138.3829174	sp|P02453|CO1A1_BOVIN
P11	-1	0.79630146	102.9475894	sp|P02465|CO1A2_BOVIN
P11	1.02	1	100.6003388	sp|P02465|CO1A2_BOVIN
P11	1.08	0.577012336	102.2942874	sp|P02465|CO1A2_BOVIN
P11	1.14	0.723574938	104.1711555	sp|P02465|CO1A2_BOVIN
P11	21.1	1	102.5124581	sp|P02453|CO1A1_BOVIN
P11	28	0.591159552	100.7175854	sp|P02465|CO1A2_BOVIN
P11	48.2	0.725632062	120.1258123	sp|P02465|CO1A2_BOVIN
P11	224	1	102.0479665	sp|P02465|CO1A2_BOVIN
P11	287	0.018094799	142.8580975	sp|P02465|CO1A2_BOVIN
P11	610	1	100.929973	sp|P02453|CO1A1_BOVIN
P11	620	1	102.0773288	sp|P02453|CO1A1_BOVIN
P11	630	0.817654491	140.0090325	sp|P02465|CO1A2_BOVIN
P11	630	0.969015535	212.7993132	sp|P02453|CO1A1_BOVIN
P11	640	0.934882578	124.5630835	sp|P02453|CO1A1_BOVIN
P11	660	1	119.4539854	sp|P02465|CO1A2_BOVIN
P11	750	1	110.2908809	sp|P02465|CO1A2_BOVIN
P11	800	1	219.9500136	sp|P02465|CO1A2_BOVIN
P11	7600	0.839390555	193.1656823	sp|P02453|CO1A1_BOVIN
P11	10000	0.921484741	100.8653782	sp|P02465|CO1A2_BOVIN
P12	1.18	0.23110521	105.8625832	sp|P02465|CO1A2_BOVIN
P12	48.2	0.961605607	105.040072	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
P12	287	0.018828789	117.0033038	sp|P02465|CO1A2_BOVIN
P12	630	0.846948004	187.1543627	sp|P02465|CO1A2_BOVIN
P12	630	0.963956423	184.3328318	sp|P02453|CO1A1_BOVIN
P12	640	0.953048993	180.6359673	sp|P02453|CO1A1_BOVIN
P12	800	1	147.2837854	sp|P02465|CO1A2_BOVIN
P12	7600	1	123.3128396	sp|P02453|CO1A1_BOVIN
AL0	-1	1	113.881314	sp|P02465|CO1A2_BOVIN
AL0	1.08	1	113.881314	sp|P02465|CO1A2_BOVIN
AL0	21.1	0.981935146	249.7398895	sp|P02453|CO1A1_BOVIN
AL0	224	1	113.881314	sp|P02465|CO1A2_BOVIN
AL0	287	1	305.7513572	sp|P02465|CO1A2_BOVIN
AL0	610	1	123.5126717	sp|P02453|CO1A1_BOVIN
AL0	630	1	140.0277389	sp|P02453|CO1A1_BOVIN
AL0	630	1	114.8368505	sp|P02465|CO1A2_BOVIN
AL0	640	1	346.4285044	sp|P02453|CO1A1_BOVIN
AL0	660	1	114.8368505	sp|P02465|CO1A2_BOVIN
AL0	700	1	104.4169992	sp|P02465|CO1A2_BOVIN
AL0	5200	1	114.8368505	sp|P02465|CO1A2_BOVIN
AL3	-1	0.73899767	170.0824846	sp|P02465|CO1A2_BOVIN
AL3	1	0.252959905	408.6621112	sp|P02465|CO1A2_BOVIN
AL3	1.08	0.371065287	109.5921137	sp|P02465|CO1A2_BOVIN
AL3	1.18	1	119.9394768	sp|P02465|CO1A2_BOVIN
AL3	48.2	1	296.3641126	sp|P02465|CO1A2_BOVIN
AL3	224	1	109.5921137	sp|P02465|CO1A2_BOVIN
AL3	287	0.035136978	458.7116532	sp|P02465|CO1A2_BOVIN
AL3	610	1	122.2654962	sp|P02453|CO1A1_BOVIN
AL3	630	0.176440568	118.4082357	sp|P02453|CO1A1_BOVIN
AL3	630	0.983337341	207.4598334	sp|P02465|CO1A2_BOVIN
AL3	640	0.321442761	243.4696604	sp|P02453|CO1A1_BOVIN
AL3	660	0	138.1714664	sp|P02465|CO1A2_BOVIN
AL3	750	1	138.1714664	sp|P02465|CO1A2_BOVIN
AL3	10000	0	119.9394768	sp|P02465|CO1A2_BOVIN
AL6	-1	0.588097847	167.4432751	sp|P02465|CO1A2_BOVIN
AL6	1	0.383765138	249.4514545	sp|P02465|CO1A2_BOVIN
AL6	1.08	0.3420727	111.2970356	sp|P02465|CO1A2_BOVIN
AL6	1.18	1	107.8257069	sp|P02465|CO1A2_BOVIN
AL6	21.1	0	281.6255328	sp|P02453|CO1A1_BOVIN
AL6	28	1	107.6142948	sp|P02453|CO1A1_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
AL6	48.2	1	131.4485856	sp|P02465|CO1A2_BOVIN
AL6	224	1	111.2970356	sp|P02465|CO1A2_BOVIN
AL6	287	1	110.1008115	sp|P02465|CO1A2_BOVIN
AL6	610	0.58065877	107.6828259	sp|P02453|CO1A1_BOVIN
AL6	630	0	124.0893107	sp|P02453|CO1A1_BOVIN
AL6	630	0.310757799	194.6274027	sp|P02465|CO1A2_BOVIN
AL6	640	0.287955093	162.6145396	sp|P02453|CO1A1_BOVIN
AL6	700	0	109.4733637	sp|P02465|CO1A2_BOVIN
AL6	10000	0	107.8257069	sp|P02465|CO1A2_BOVIN
AL9	-1	0.738180119	207.7747773	sp|P02465|CO1A2_BOVIN
AL9	1	0.271676626	257.0094173	sp|P02465|CO1A2_BOVIN
AL9	1.08	0	109.3054973	sp|P02465|CO1A2_BOVIN
AL9	1.18	1	113.0080534	sp|P02465|CO1A2_BOVIN
AL9	21.1	0	153.8508334	sp|P02453|CO1A1_BOVIN
AL9	28	1	109.4459754	sp|P02453|CO1A1_BOVIN
AL9	224	1	109.3054973	sp|P02465|CO1A2_BOVIN
AL9	610	1	110.063118	sp|P02453|CO1A1_BOVIN
AL9	630	0.076599425	127.3609235	sp|P02453|CO1A1_BOVIN
AL9	640	0	560.3137422	sp|P02453|CO1A1_BOVIN
AL9	700	0	104.8727859	sp|P02465|CO1A2_BOVIN
AL9	10000	0	113.0080534	sp|P02465|CO1A2_BOVIN
AL12	-1	0.642121544	104.844374	sp|P02465|CO1A2_BOVIN
AL12	1	1	102.7691625	sp|P02465|CO1A2_BOVIN
AL12	1.08	0.179267117	105.8819797	sp|P02465|CO1A2_BOVIN
AL12	1.18	0	105.8390187	sp|P02465|CO1A2_BOVIN
AL12	21.1	0	190.9244087	sp|P02453|CO1A1_BOVIN
AL12	28	1	104.2724618	sp|P02453|CO1A1_BOVIN
AL12	224	0	105.8819797	sp|P02465|CO1A2_BOVIN
AL12	610	0	107.6914189	sp|P02453|CO1A1_BOVIN
AL12	630	0.058063603	119.839584	sp|P02453|CO1A1_BOVIN
AL12	640	0.010018175	338.1759664	sp|P02453|CO1A1_BOVIN
AL12	700	0	110.7874103	sp|P02465|CO1A2_BOVIN
AL12	10000	0	109.2271927	sp|P02465|CO1A2_BOVIN
AG0	-1	1	106.6072011	sp|P02465|CO1A2_BOVIN
AG0	-1	1	106.6072011	sp|P02465|CO1A2_BOVIN
AG0	-1	0.954248392	130.7370611	sp|P02465|CO1A2_BOVIN
AG0	1.08	0.954248392	130.7370611	sp|P02465|CO1A2_BOVIN
AG0	1.14	1	114.1798427	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
AG0	21.1	1	229.0154824	sp|P02453|CO1A1_BOVIN
AG0	224	0.51980933	130.7370611	sp|P02465|CO1A2_BOVIN
AG0	287	1	225.8380726	sp|P02465|CO1A2_BOVIN
AG0	610	1	124.6882776	sp|P02453|CO1A1_BOVIN
AG0	610	1	106.6072011	sp|P02465|CO1A2_BOVIN
AG0	630	0.949594677	126.5197096	sp|P02453|CO1A1_BOVIN
AG0	630	1	263.8125196	sp|P02465|CO1A2_BOVIN
AG0	640	0.960369141	166.6185813	sp|P02453|CO1A1_BOVIN
AG0	640	1	106.6072011	sp|P02465|CO1A2_BOVIN
AG0	660	1	123.0921397	sp|P02465|CO1A2_BOVIN
AG0	670	1	106.6072011	sp|P02465|CO1A2_BOVIN
AG0	5200	1	120.121374	sp|P02465|CO1A2_BOVIN
AG1	-1	1	192.0299147	sp|P02465|CO1A2_BOVIN
AG1	1	0	293.8851046	sp|P02465|CO1A2_BOVIN
AG1	1.08	0.430927597	141.1023197	sp|P02465|CO1A2_BOVIN
AG1	21.1	1	560.8919752	sp|P02453|CO1A1_BOVIN
AG1	224	1	141.1023197	sp|P02465|CO1A2_BOVIN
AG1	287	1	409.641606	sp|P02465|CO1A2_BOVIN
AG1	610	1	127.4217265	sp|P02453|CO1A1_BOVIN
AG1	630	0.361215206	126.6508227	sp|P02453|CO1A1_BOVIN
AG1	630	1	201.3761523	sp|P02465|CO1A2_BOVIN
AG1	640	0.763529253	204.2724297	sp|P02453|CO1A1_BOVIN
AG2	-1	0.757365375	130.8373807	sp|P02465|CO1A2_BOVIN
AG2	1	0	212.7766451	sp|P02465|CO1A2_BOVIN
AG2	1.08	0.693885808	110.3525646	sp|P02465|CO1A2_BOVIN
AG2	21.1	0.040057984	407.1431585	sp|P02453|CO1A1_BOVIN
AG2	48.2	0	121.2661215	sp|P02465|CO1A2_BOVIN
AG2	224	1	110.3525646	sp|P02465|CO1A2_BOVIN
AG2	287	0	328.7222161	sp|P02465|CO1A2_BOVIN
AG2	610	0	110.5678624	sp|P02453|CO1A1_BOVIN
AG2	630	0.065070443	120.2238222	sp|P02453|CO1A1_BOVIN
AG2	630	1	185.3933434	sp|P02465|CO1A2_BOVIN
AG2	640	0.191658821	188.5812555	sp|P02453|CO1A1_BOVIN
AG2	700	0	105.1612007	sp|P02465|CO1A2_BOVIN
AG3	-1	0.641051379	145.7424805	sp|P02465|CO1A2_BOVIN
AG3	1	0	188.8623159	sp|P02465|CO1A2_BOVIN
AG3	1.08	1	134.0996469	sp|P02465|CO1A2_BOVIN
AG3	21.1	0.385326462	150.6938753	sp|P02453|CO1A1_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
AG3	224	1	134.0996469	sp|P02465|CO1A2_BOVIN
AG3	287	0	351.9502688	sp|P02465|CO1A2_BOVIN
AG3	630	0.063141794	130.5380688	sp|P02453|CO1A1_BOVIN
AG3	630	1	181.9529142	sp|P02465|CO1A2_BOVIN
AG3	640	0.174287033	307.2255585	sp|P02453|CO1A1_BOVIN
AG4	-1	1	128.9006617	sp|P02465|CO1A2_BOVIN
AG4	1	0	128.9006617	sp|P02465|CO1A2_BOVIN
AG4	21.1	0	233.403223	sp|P02453|CO1A1_BOVIN
AG4	48.2	0	143.4105452	sp|P02465|CO1A2_BOVIN
AG4	287	0	184.7245608	sp|P02465|CO1A2_BOVIN
AG4	610	0	103.2250269	sp|P02453|CO1A1_BOVIN
AG4	630	0	115.5407652	sp|P02453|CO1A1_BOVIN
AG4	630	0.255748719	137.0951103	sp|P02465|CO1A2_BOVIN
AG4	640	0.054725682	173.238026	sp|P02453|CO1A1_BOVIN
AG4	700	0	110.9414059	sp|P02465|CO1A2_BOVIN
AG5	-1	0.134750245	172.9543472	sp|P02465|CO1A2_BOVIN
AG5	1	1	261.1992325	sp|P02465|CO1A2_BOVIN
AG5	1.08	0	128.7136169	sp|P02465|CO1A2_BOVIN
AG5	1.18	0	135.9400219	sp|P02465|CO1A2_BOVIN
AG5	21.1	0	424.7962189	sp|P02453|CO1A1_BOVIN
AG5	224	0	128.7136169	sp|P02465|CO1A2_BOVIN
AG5	287	0	431.6591893	sp|P02465|CO1A2_BOVIN
AG5	610	0	117.6897206	sp|P02453|CO1A1_BOVIN
AG5	630	0	141.2338235	sp|P02453|CO1A1_BOVIN
AG5	640	0.052230393	285.9112595	sp|P02453|CO1A1_BOVIN
AG5	700	0	139.1061694	sp|P02465|CO1A2_BOVIN
AG6	-1	0.152577219	105.4658517	sp|P02465|CO1A2_BOVIN
AG6	1.08	0	102.6804767	sp|P02465|CO1A2_BOVIN
AG6	1.18	0	104.4366574	sp|P02465|CO1A2_BOVIN
AG6	21.1	0	188.2774722	sp|P02453|CO1A1_BOVIN
AG6	48.2	0	157.5072788	sp|P02465|CO1A2_BOVIN
AG6	224	0.58807982	102.6804767	sp|P02465|CO1A2_BOVIN
AG6	287	0	143.4888976	sp|P02465|CO1A2_BOVIN
AG6	630	0	109.8618889	sp|P02453|CO1A1_BOVIN
AG6	630	0.016376424	374.0525067	sp|P02465|CO1A2_BOVIN
AG6	640	0.107784814	237.3161612	sp|P02453|CO1A1_BOVIN
AG6	700	0	123.5592839	sp|P02465|CO1A2_BOVIN
AB0	-1	0.340533566	112.25063	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
AB0	1	1	116.4562238	sp|P02465|CO1A2_BOVIN
AB0	1.08	1	108.0450362	sp|P02465|CO1A2_BOVIN
AB0	21.1	0	119.4196865	sp|P02453|CO1A1_BOVIN
AB0	21.1	0	106.2181532	sp|P02465|CO1A2_BOVIN
AB0	48.2	1	119.0732898	sp|P02465|CO1A2_BOVIN
AB0	224	0	108.0450362	sp|P02465|CO1A2_BOVIN
AB0	287	0	143.0167183	sp|P02465|CO1A2_BOVIN
AB0	610	1	103.042979	sp|P02453|CO1A1_BOVIN
AB0	630	0.72651046	104.2769082	sp|P02453|CO1A1_BOVIN
AB0	630	0.7554631	110.7461191	sp|P02465|CO1A2_BOVIN
AB0	640	0.767663665	120.6061783	sp|P02453|CO1A1_BOVIN
AB0	660	1	106.9372307	sp|P02465|CO1A2_BOVIN
AB0	670	0	100.8389054	sp|P02453|CO1A1_BOVIN
AB0	700	1	104.7437537	sp|P02465|CO1A2_BOVIN
AB0	5200	0	106.9372307	sp|P02465|CO1A2_BOVIN
AB3	-1	0	104.9430905	sp|P02465|CO1A2_BOVIN
AB3	1.08	1	101.7748178	sp|P02465|CO1A2_BOVIN
AB3	1.18	0.566783553	100.800864	sp|P02465|CO1A2_BOVIN
AB3	11.8	0	100.9879114	sp|P02453|CO1A1_BOVIN
AB3	21.1	0	132.6696414	sp|P02453|CO1A1_BOVIN
AB3	21.1	0	110.3836467	sp|P02465|CO1A2_BOVIN
AB3	48.2	0	106.3609059	sp|P02465|CO1A2_BOVIN
AB3	224	0	100.3628178	sp|P02453|CO1A1_BOVIN
AB3	224	0.186403059	101.7748178	sp|P02465|CO1A2_BOVIN
AB3	287	0	114.4638287	sp|P02465|CO1A2_BOVIN
AB3	610	0	103.1160447	sp|P02453|CO1A1_BOVIN
AB3	630	0.040086442	117.3291905	sp|P02453|CO1A1_BOVIN
AB3	630	0.011571754	103.4083511	sp|P02465|CO1A2_BOVIN
AB3	640	0.119330791	242.7799018	sp|P02453|CO1A1_BOVIN
AB3	670	0	102.0742521	sp|P02453|CO1A1_BOVIN
AB3	700	0	104.135636	sp|P02465|CO1A2_BOVIN
AB3	6800	0	103.2695068	sp|P02453|CO1A1_BOVIN
AB3	7200	0	103.4475089	sp|P02453|CO1A1_BOVIN
AB3	8900	0	103.2695068	sp|P02453|CO1A1_BOVIN
AB3	10000	0	116.3886805	sp|P02465|CO1A2_BOVIN
AB6	-1	0.670398038	113.5318957	sp|P02465|CO1A2_BOVIN
AB6	1	0	111.5174631	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
AB6	1.08	1	102.8790716	sp|P02465|CO1A2_BOVIN
AB6	1.14	0	100.7689273	sp|P02465|CO1A2_BOVIN
AB6	1.18	0	101.9253506	sp|P02465|CO1A2_BOVIN
AB6	11.8	0.039990821	102.1307062	sp|P02453|CO1A1_BOVIN
AB6	21.1	0	141.4583623	sp|P02453|CO1A1_BOVIN
AB6	21.1	0	118.5848193	sp|P02465|CO1A2_BOVIN
AB6	48.2	0	107.1568339	sp|P02465|CO1A2_BOVIN
AB6	224	0	100.4531611	sp|P02453|CO1A1_BOVIN
AB6	224	0	101.7722182	sp|P02465|CO1A2_BOVIN
AB6	610	0	103.6411822	sp|P02453|CO1A1_BOVIN
AB6	620	0	105.1231658	sp|P02453|CO1A1_BOVIN
AB6	630	0.022964075	109.2952767	sp|P02453|CO1A1_BOVIN
AB6	630	0.004733171	125.9469753	sp|P02465|CO1A2_BOVIN
AB6	640	0	1000	sp|P02453|CO1A1_BOVIN
AB6	660	0	101.7445254	sp|P02465|CO1A2_BOVIN
AB6	670	0	101.1491926	sp|P02465|CO1A2_BOVIN
AB6	700	0	101.2636319	sp|P02465|CO1A2_BOVIN
AB6	750	0.218655528	101.7167338	sp|P02453|CO1A1_BOVIN
AB6	750	0	101.5534969	sp|P02465|CO1A2_BOVIN
AB6	5200	0	100.9320795	sp|P02465|CO1A2_BOVIN
AB6	10000	0	215.2475479	sp|P02465|CO1A2_BOVIN
AC0	-1	0.678121755	101.2397005	sp|P02465|CO1A2_BOVIN
AC0	-1	1	101.2397005	sp|P02465|CO1A2_BOVIN
AC0	-1	0.624094979	106.1804437	sp|P02465|CO1A2_BOVIN
AC0	1	0.065159635	109.2992369	sp|P02465|CO1A2_BOVIN
AC0	1.08	0.856644239	105.3072318	sp|P02465|CO1A2_BOVIN
AC0	21.1	0	138.170459	sp|P02453|CO1A1_BOVIN
AC0	21.1	1	108.6242078	sp|P02465|CO1A2_BOVIN
AC0	48.2	1	130.0212577	sp|P02465|CO1A2_BOVIN
AC0	224	1	105.3072318	sp|P02465|CO1A2_BOVIN
AC0	287	0	145.2768905	sp|P02465|CO1A2_BOVIN
AC0	610	1	108.6579896	sp|P02453|CO1A1_BOVIN
AC0	610	0	101.2397005	sp|P02465|CO1A2_BOVIN
AC0	630	0.742002321	109.1119745	sp|P02453|CO1A1_BOVIN
AC0	630	0.69333462	107.3846758	sp|P02465|CO1A2_BOVIN
AC0	640	0.901056642	143.4193815	sp|P02453|CO1A1_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
AC0	640	1	101.2397005	sp|P02465|CO1A2_BOVIN
AC0	660	1	112.4326575	sp|P02465|CO1A2_BOVIN
AC0	670	0.321878245	101.2397005	sp|P02465|CO1A2_BOVIN
AC0	700	0.807484275	107.4925747	sp|P02465|CO1A2_BOVIN
AC0	750	1	117.5355037	sp|P02465|CO1A2_BOVIN
AC0	5200	0.139526774	109.8812344	sp|P02465|CO1A2_BOVIN
AC3	-1	0.150198499	107.3530482	sp|P02465|CO1A2_BOVIN
AC3	1	0	101.3636739	sp|P02465|CO1A2_BOVIN
AC3	1.08	0.926241348	102.7687515	sp|P02465|CO1A2_BOVIN
AC3	1.14	0.31535482	100.7398739	sp|P02465|CO1A2_BOVIN
AC3	1.18	0	100.9579341	sp|P02465|CO1A2_BOVIN
AC3	11.8	0.084074458	105.2886023	sp|P02453|CO1A1_BOVIN
AC3	21.1	0.004095206	174.6670063	sp|P02453|CO1A1_BOVIN
AC3	21.1	0	111.9150795	sp|P02465|CO1A2_BOVIN
AC3	48.2	0	104.8279861	sp|P02465|CO1A2_BOVIN
AC3	224	0	100.5008279	sp|P02453|CO1A1_BOVIN
AC3	224	0	102.7687515	sp|P02465|CO1A2_BOVIN
AC3	287	0	187.5106563	sp|P02465|CO1A2_BOVIN
AC3	610	0	102.1296218	sp|P02453|CO1A1_BOVIN
AC3	630	0.031634041	115.0824048	sp|P02453|CO1A1_BOVIN
AC3	630	0.06101891	113.5245243	sp|P02465|CO1A2_BOVIN
AC3	640	0.151921116	453.7495452	sp|P02453|CO1A1_BOVIN
AC3	660	0	100.5645524	sp|P02465|CO1A2_BOVIN
AC3	700	0.227418811	102.6313118	sp|P02465|CO1A2_BOVIN
AC3	750	0.114978355	103.6211914	sp|P02453|CO1A1_BOVIN
AC3	750	0	100.254743	sp|P02465|CO1A2_BOVIN
AC3	5200	0	100.8418696	sp|P02465|CO1A2_BOVIN
AC3	7200	0	107.3451012	sp|P02453|CO1A1_BOVIN
AC3	10000	0	140.5460382	sp|P02465|CO1A2_BOVIN
AC6	-1	1	1000	sp|P02465|CO1A2_BOVIN
AC6	1.18	0	280.7673452	sp|P02465|CO1A2_BOVIN
AC6	11.8	0	108.5464567	sp|P02453|CO1A1_BOVIN
AC6	21.1	0	203.9409425	sp|P02453|CO1A1_BOVIN
AC6	48.2	0	106.7230128	sp|P02465|CO1A2_BOVIN
AC6	57.8	0	125.5051988	sp|P02465|CO1A2_BOVIN
AC6	287	0	155.7490324	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
AC6	610	0	135.6250896	sp|P02453|CO1A1_BOVIN
AC6	620	0	107.6472241	sp|P02453|CO1A1_BOVIN
AC6	630	0.230539458	142.4169573	sp|P02453|CO1A1_BOVIN
AC6	630	0.037438195	282.9234597	sp|P02465|CO1A2_BOVIN
AC6	660	0	154.423378	sp|P02465|CO1A2_BOVIN
AC6	700	0	146.0809436	sp|P02465|CO1A2_BOVIN
AC6	750	0.330029961	150.9706697	sp|P02453|CO1A1_BOVIN
AC6	10000	0	114.5930824	sp|P02465|CO1A2_BOVIN
MF	-1	1	101.4473842	sp|P02465|CO1A2_BOVIN
MF	-1	0	101.4473842	sp|P02465|CO1A2_BOVIN
MF	-1	0.948732812	105.2552462	sp|P02465|CO1A2_BOVIN
MF	1	0.931002795	131.7062428	sp|P02465|CO1A2_BOVIN
MF	1.08	0.849640673	102.045914	sp|P02465|CO1A2_BOVIN
MF	1.14	1	103.6220219	sp|P02465|CO1A2_BOVIN
MF	1.18	0.909522942	107.1428208	sp|P02465|CO1A2_BOVIN
MF	21.1	0	100.3676194	sp|P02465|CO1A2_BOVIN
MF	21.1	0.764405706	193.902087	sp|P02453|CO1A1_BOVIN
MF	28	1	102.1964546	sp|P02465|CO1A2_BOVIN
MF	48.2	0.803492519	120.9704586	sp|P02465|CO1A2_BOVIN
MF	57.8	0.741441868	108.7144533	sp|P02465|CO1A2_BOVIN
MF	224	1	102.045914	sp|P02465|CO1A2_BOVIN
MF	287	0.719817543	157.6606642	sp|P02465|CO1A2_BOVIN
MF	610	1	101.4473842	sp|P02465|CO1A2_BOVIN
MF	610	1	101.8546525	sp|P02453|CO1A1_BOVIN
MF	630	0.910853819	102.3431781	sp|P02465|CO1A2_BOVIN
MF	630	0.893565756	130.0399189	sp|P02453|CO1A1_BOVIN
MF	640	1	101.4473842	sp|P02465|CO1A2_BOVIN
MF	640	0.93301435	215.6701537	sp|P02453|CO1A1_BOVIN
MF	660	0.981344136	103.6666421	sp|P02465|CO1A2_BOVIN
MF	670	1	101.4473842	sp|P02465|CO1A2_BOVIN
MF	700	1	100.4158907	sp|P02465|CO1A2_BOVIN
MF	750	0.990413671	105.1665035	sp|P02465|CO1A2_BOVIN
MF	5200	0.87442882	102.9480128	sp|P02465|CO1A2_BOVIN
MF	10000	0.901779346	155.7454275	sp|P02465|CO1A2_BOVIN
MF1826	-1	0.475965615	111.1559455	sp|P02465|CO1A2_BOVIN
MF1826	1	1	107.0197949	sp|P02465|CO1A2_BOVIN
MF1826	1.08	0.224615486	107.8606281	sp|P02465|CO1A2_BOVIN
MF1826	1.14	0	108.1773031	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
MF1826	1.18	0.015733617	105.5614091	sp|P02465|CO1A2_BOVIN
MF1826	21.1	0	258.230497	sp|P02453|CO1A1_BOVIN
MF1826	48.2	0.113799948	133.3168129	sp|P02465|CO1A2_BOVIN
MF1826	224	0.013876125	107.8606281	sp|P02465|CO1A2_BOVIN
MF1826	224	1	101.4190544	sp|P02453|CO1A1_BOVIN
MF1826	287	0	427.5146153	sp|P02465|CO1A2_BOVIN
MF1826	610	0.248536577	106.4978958	sp|P02453|CO1A1_BOVIN
MF1826	630	0.125509244	144.4047756	sp|P02465|CO1A2_BOVIN
MF1826	630	0.199929799	175.9804805	sp|P02453|CO1A1_BOVIN
MF1826	640	0.325060478	240.0546179	sp|P02453|CO1A1_BOVIN
MF1826	660	0.595143783	109.0771879	sp|P02465|CO1A2_BOVIN
MF1826	750	1	107.2806347	sp|P02465|CO1A2_BOVIN
MF1826	5200	0	106.2266804	sp|P02465|CO1A2_BOVIN
MF1826	10000	0	102.1931861	sp|P02465|CO1A2_BOVIN
MF1741	-1	0.736840821	112.3570773	sp|P02465|CO1A2_BOVIN
MF1741	1	0.115876487	201.609355	sp|P02465|CO1A2_BOVIN
MF1741	1.02	0	105.8794194	sp|P02465|CO1A2_BOVIN
MF1741	1.08	0.036120011	113.6219748	sp|P02465|CO1A2_BOVIN
MF1741	1.14	0.418405222	103.0272683	sp|P02465|CO1A2_BOVIN
MF1741	1.18	0	102.5082309	sp|P02465|CO1A2_BOVIN
MF1741	21.1	0	283.994045	sp|P02453|CO1A1_BOVIN
MF1741	48.2	0	103.6340331	sp|P02465|CO1A2_BOVIN
MF1741	57.8	0.041451319	117.8387736	sp|P02465|CO1A2_BOVIN
MF1741	224	0.011426798	113.6219748	sp|P02465|CO1A2_BOVIN
MF1741	224	1	101.6025005	sp|P02453|CO1A1_BOVIN
MF1741	287	0	103.0447731	sp|P02465|CO1A2_BOVIN
MF1741	610	0.470140164	112.526085	sp|P02453|CO1A1_BOVIN
MF1741	630	0.066030651	116.6774156	sp|P02465|CO1A2_BOVIN
MF1741	630	0.360729943	226.7710217	sp|P02453|CO1A1_BOVIN
MF1741	640	0.532039842	339.6061383	sp|P02453|CO1A1_BOVIN
MF1741	670	0.112301757	105.8794194	sp|P02465|CO1A2_BOVIN
MF1741	700	0.5	104.8430849	sp|P02465|CO1A2_BOVIN
MF1741	800	0.811910489	104.2439258	sp|P02465|CO1A2_BOVIN
MF1741	5200	0	102.992564	sp|P02465|CO1A2_BOVIN
MF1741	10000	0.516406945	329.5467389	sp|P02465|CO1A2_BOVIN
MF1664	-1	0.227706143	109.6116509	sp|P02465|CO1A2_BOVIN
MF1664	1	0.625577431	107.2828238	sp|P02465|CO1A2_BOVIN
MF1664	1.02	0	103.4512074	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
MF1664	1.08	0.161711995	108.5429292	sp|P02465|CO1A2_BOVIN
MF1664	1.14	0.015606857	122.0548551	sp|P02465|CO1A2_BOVIN
MF1664	1.18	0.690626647	111.6513348	sp|P02465|CO1A2_BOVIN
MF1664	21.1	0	285.4625657	sp|P02453|CO1A1_BOVIN
MF1664	48.2	0	141.4727902	sp|P02465|CO1A2_BOVIN
MF1664	224	0.603622725	108.5429292	sp|P02465|CO1A2_BOVIN
MF1664	224	1	100.8012701	sp|P02453|CO1A1_BOVIN
MF1664	287	0	240.1466953	sp|P02465|CO1A2_BOVIN
MF1664	610	0.288509052	107.060786	sp|P02453|CO1A1_BOVIN
MF1664	630	0.064717674	110.295014	sp|P02465|CO1A2_BOVIN
MF1664	630	0.356637382	165.4114602	sp|P02453|CO1A1_BOVIN
MF1664	640	0.510186264	231.1885103	sp|P02453|CO1A1_BOVIN
MF1664	660	0.626320314	110.6157459	sp|P02465|CO1A2_BOVIN
MF1664	670	1	103.4512074	sp|P02465|CO1A2_BOVIN
MF1664	700	0.5	102.5279855	sp|P02465|CO1A2_BOVIN
MF1664	750	0.808587083	112.4023497	sp|P02465|CO1A2_BOVIN
MF1664	800	0.10793357	101.6301288	sp|P02465|CO1A2_BOVIN
MF1664	5200	0.759753098	105.7642577	sp|P02465|CO1A2_BOVIN
MF1664	7600	0	100.4851368	sp|P02453|CO1A1_BOVIN
MF1664	10000	0.038529836	104.473196	sp|P02465|CO1A2_BOVIN
MF1661	1.08	0.074211492	102.2523906	sp|P02465|CO1A2_BOVIN
MF1661	1.14	0.571952732	103.8503556	sp|P02465|CO1A2_BOVIN
MF1661	1.18	0.080805484	103.5488048	sp|P02465|CO1A2_BOVIN
MF1661	21.1	0.039955626	166.9789673	sp|P02465|CO1A2_BOVIN
MF1661	21.1	0	297.4607146	sp|P02453|CO1A1_BOVIN
MF1661	48.2	0.019005749	138.3856301	sp|P02465|CO1A2_BOVIN
MF1661	57.8	0	138.064297	sp|P02465|CO1A2_BOVIN
MF1661	224	0.043669798	102.2523906	sp|P02465|CO1A2_BOVIN
MF1661	224	1	100.8386713	sp|P02453|CO1A1_BOVIN
MF1661	287	0.009737098	214.8271838	sp|P02465|CO1A2_BOVIN
MF1661	610	0.283147954	105.4772807	sp|P02453|CO1A1_BOVIN
MF1661	630	0.109746968	117.8185269	sp|P02465|CO1A2_BOVIN
MF1661	630	0.010102754	138.6923913	sp|P02453|CO1A1_BOVIN
MF1661	640	0.0628551	261.9912626	sp|P02453|CO1A1_BOVIN
MF1661	660	0.919668161	105.8789214	sp|P02465|CO1A2_BOVIN
MF1661	670	0.657326947	102.2644725	sp|P02465|CO1A2_BOVIN
MF1661	700	0.383822953	101.7663023	sp|P02465|CO1A2_BOVIN
MF1661	750	1	107.8887395	sp|P02465|CO1A2_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
MF1661	800	0.333100593	101.67817	sp|P02465|CO1A2_BOVIN
MF1661	5200	0.07675246	103.9260086	sp|P02465|CO1A2_BOVIN
MF1661	10000	0.27011178	190.412072	sp|P02465|CO1A2_BOVIN
MR1	-1	0.725535586	104.1477681	sp|P02465|CO1A2_BOVIN
MR1	1	0.548027223	147.8233576	sp|P02465|CO1A2_BOVIN
MR1	1.08	0.344022125	105.6181303	sp|P02465|CO1A2_BOVIN
MR1	1.14	0.736495	102.0912444	sp|P02465|CO1A2_BOVIN
MR1	1.18	0.881176685	103.5173592	sp|P02465|CO1A2_BOVIN
MR1	11.8	0	100.1787197	sp|P02453|CO1A1_BOVIN
MR1	21.1	0.713377807	108.9803238	sp|P02465|CO1A2_BOVIN
MR1	21.1	0	153.5037711	sp|P02453|CO1A1_BOVIN
MR1	28	1	100.3286464	sp|P02465|CO1A2_BOVIN
MR1	48.2	0.324416839	114.7612931	sp|P02465|CO1A2_BOVIN
MR1	57.8	0	105.7975045	sp|P02465|CO1A2_BOVIN
MR1	64	1	104.0497055	sp|P02453|CO1A1_BOVIN
MR1	224	0.846914387	105.6181303	sp|P02465|CO1A2_BOVIN
MR1	287	0.001699538	140.6980264	sp|P02465|CO1A2_BOVIN
MR1	610	0.81411583	102.6051341	sp|P02453|CO1A1_BOVIN
MR1	630	0.863371648	109.7345361	sp|P02465|CO1A2_BOVIN
MR1	630	0.788807712	138.1187925	sp|P02453|CO1A1_BOVIN
MR1	640	0.857790269	232.370846	sp|P02453|CO1A1_BOVIN
MR1	660	0.913575362	108.4194622	sp|P02465|CO1A2_BOVIN
MR1	670	0	100.8659001	sp|P02465|CO1A2_BOVIN
MR1	700	0.762317629	101.5658389	sp|P02465|CO1A2_BOVIN
MR1	750	1	111.3084469	sp|P02465|CO1A2_BOVIN
MR1	800	0.620808006	100.7574559	sp|P02465|CO1A2_BOVIN
MR1	5200	0.328267318	108.3209453	sp|P02465|CO1A2_BOVIN
MR1	10000	0.851526847	161.6870193	sp|P02465|CO1A2_BOVIN
MR2	-1	1	105.9491937	sp|P02465|CO1A2_BOVIN
MR2	1	0.710159269	104.1361009	sp|P02465|CO1A2_BOVIN
MR2	1.18	0.702676852	101.4122697	sp|P02465|CO1A2_BOVIN
MR2	11.8	1	100.6151371	sp|P02453|CO1A1_BOVIN
MR2	21.1	0	102.7497896	sp|P02453|CO1A1_BOVIN
MR2	48.2	0.66977329	100.9541547	sp|P02465|CO1A2_BOVIN
MR2	287	0.173086535	158.7917006	sp|P02465|CO1A2_BOVIN
MR2	630	1	120.5226381	sp|P02465|CO1A2_BOVIN
MR2	630	0.411359879	113.7468931	sp|P02453|CO1A1_BOVIN
MR2	640	0.992446951	338.0089066	sp|P02453|CO1A1_BOVIN

Ref	Half-time	RelNonDeam	Size	Protein
MR2	660	0.897204107	101.5550884	sp|P02465|CO1A2_BOVIN
MR2	750	1	103.6606722	sp|P02465|CO1A2_BOVIN
MR2	10000	0.997182193	219.4036928	sp|P02465|CO1A2_BOVIN

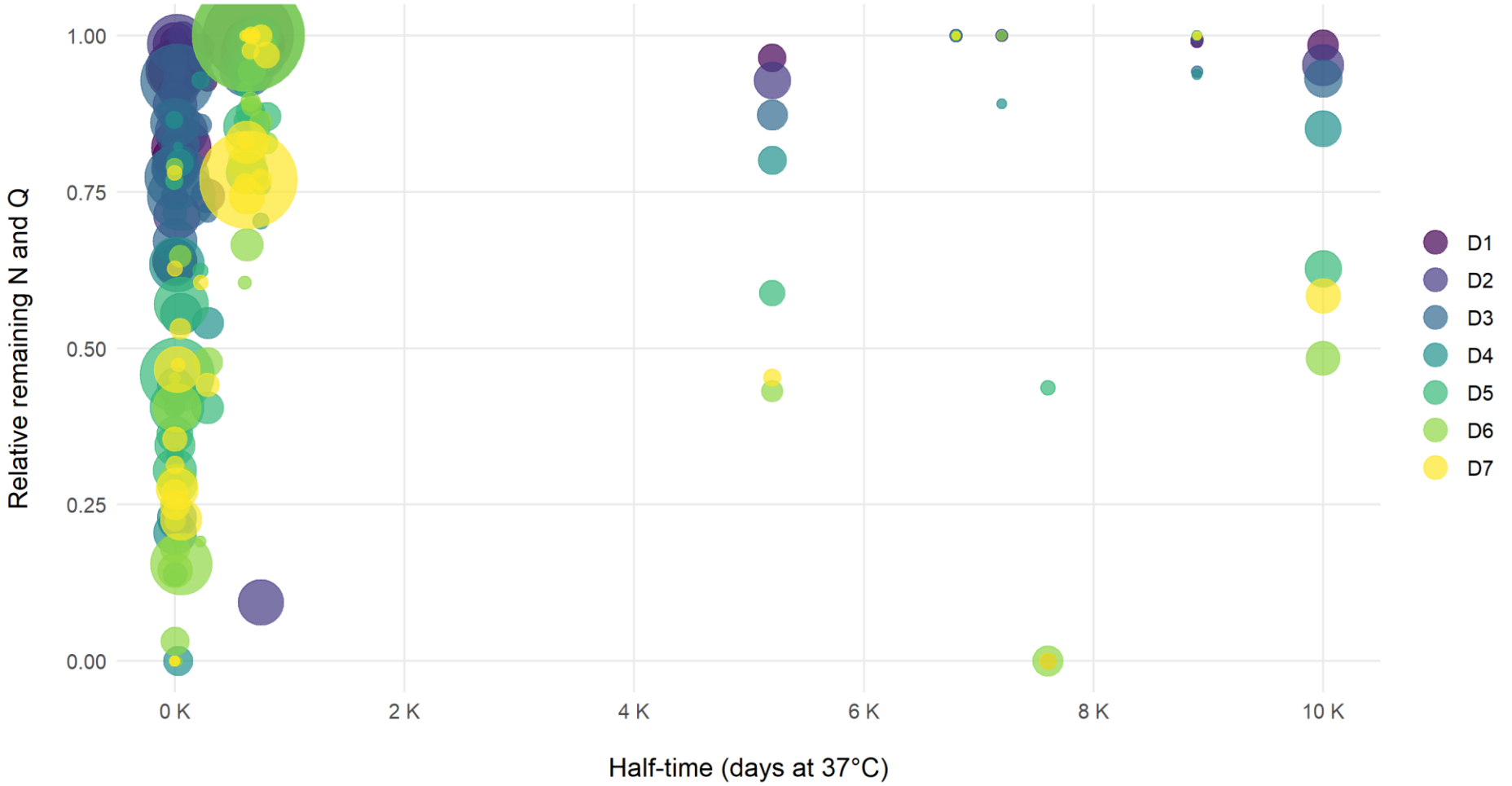

Figure B1. Site-specific deamidation of commercial collagen (Devro). Each point represents a specific three residue combination. The size of the point represents that site's intensity, relative to the total intensity of all peptides in the same sample

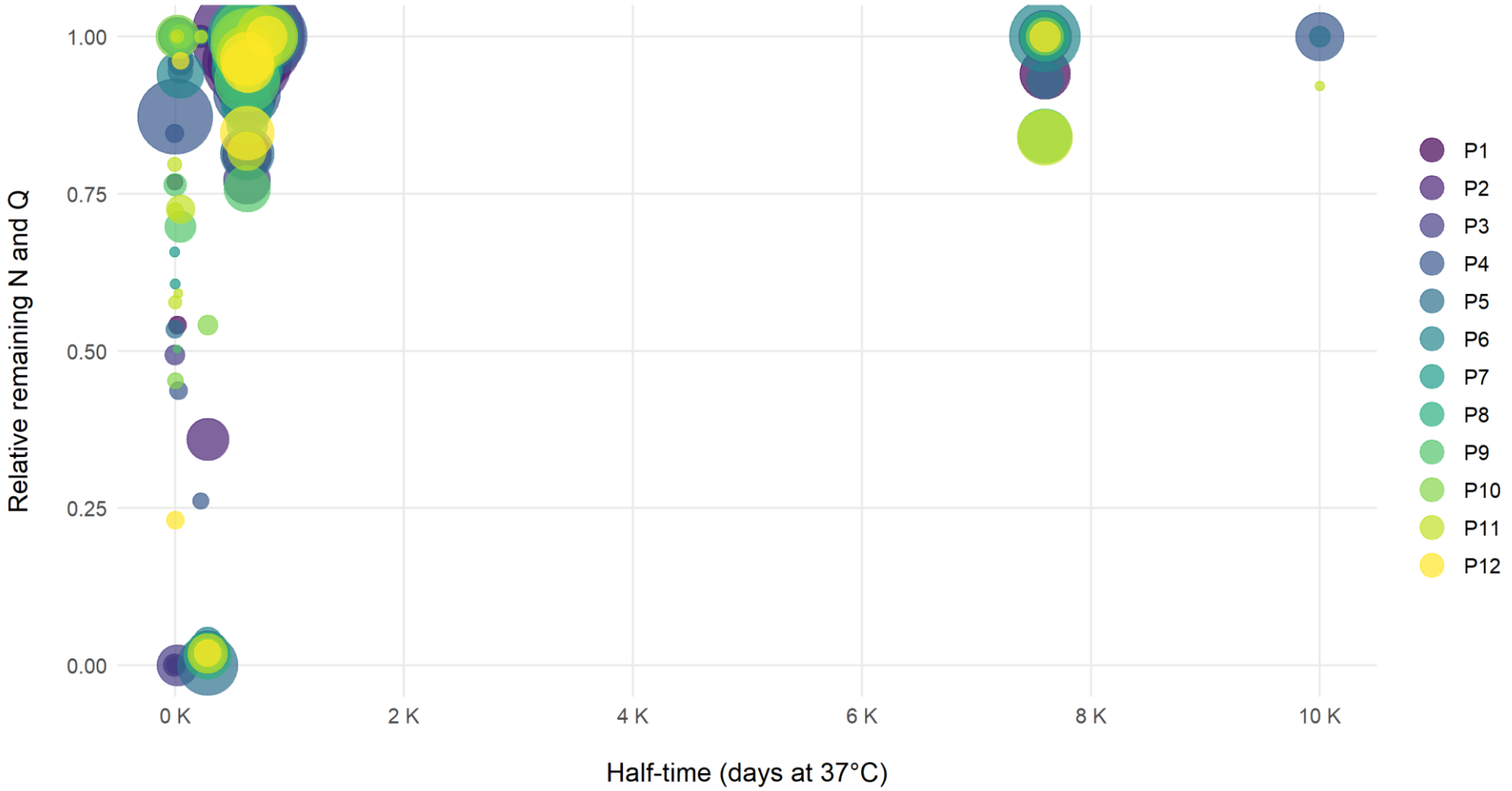

Figure B2. Site-specific deamidation of parchment samples. Each point represents a specific three residue combination. The size of the point represents that site's intensity, relative to the total intensity of all peptides in the same sample

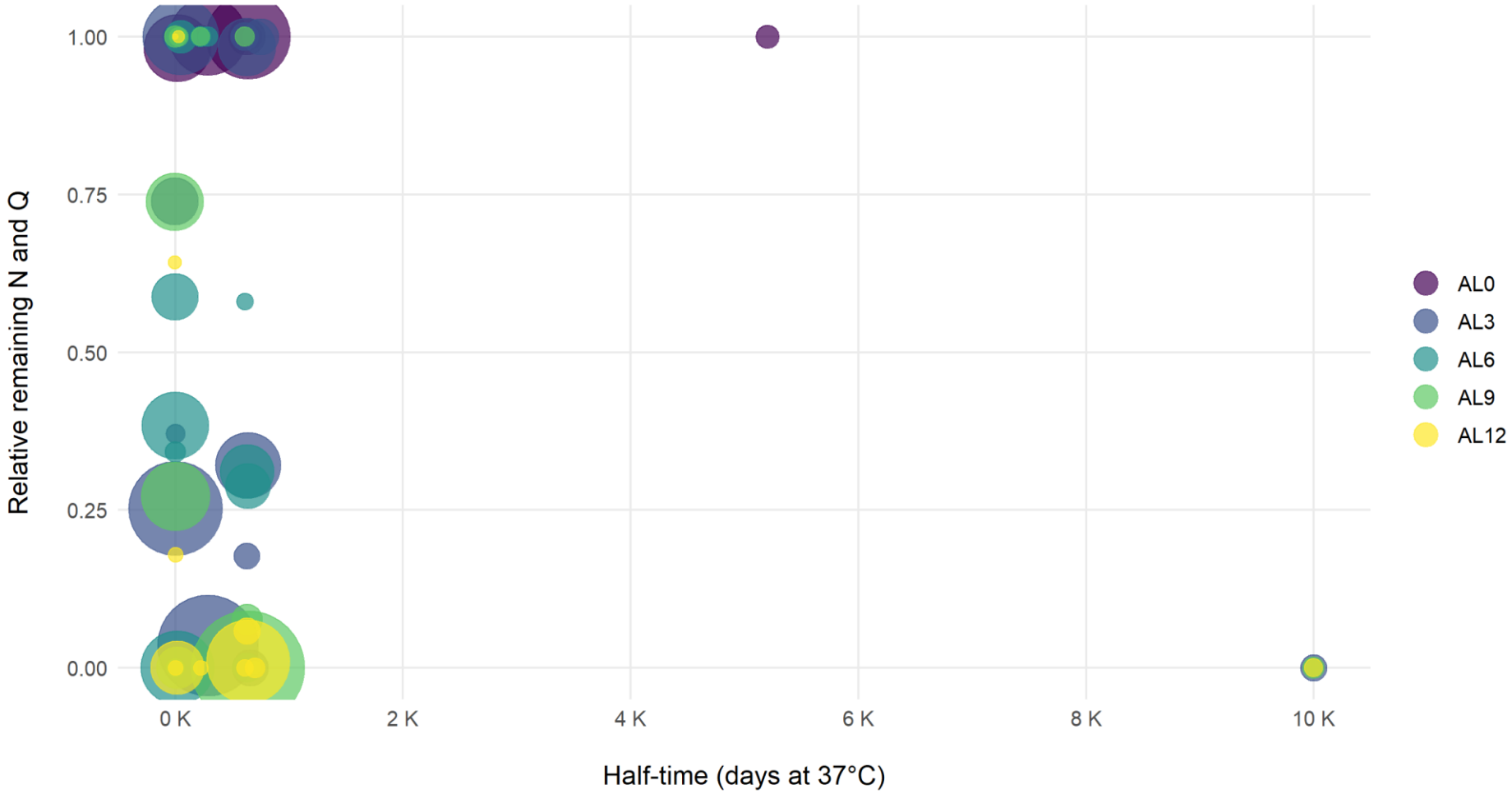

Figure B3. Site-specific deamidation of aged leather samples (goat) Each point represents a specific three residue combination. The size of the point represents that site's intensity, relative to the total intensity of all peptides in the same sample

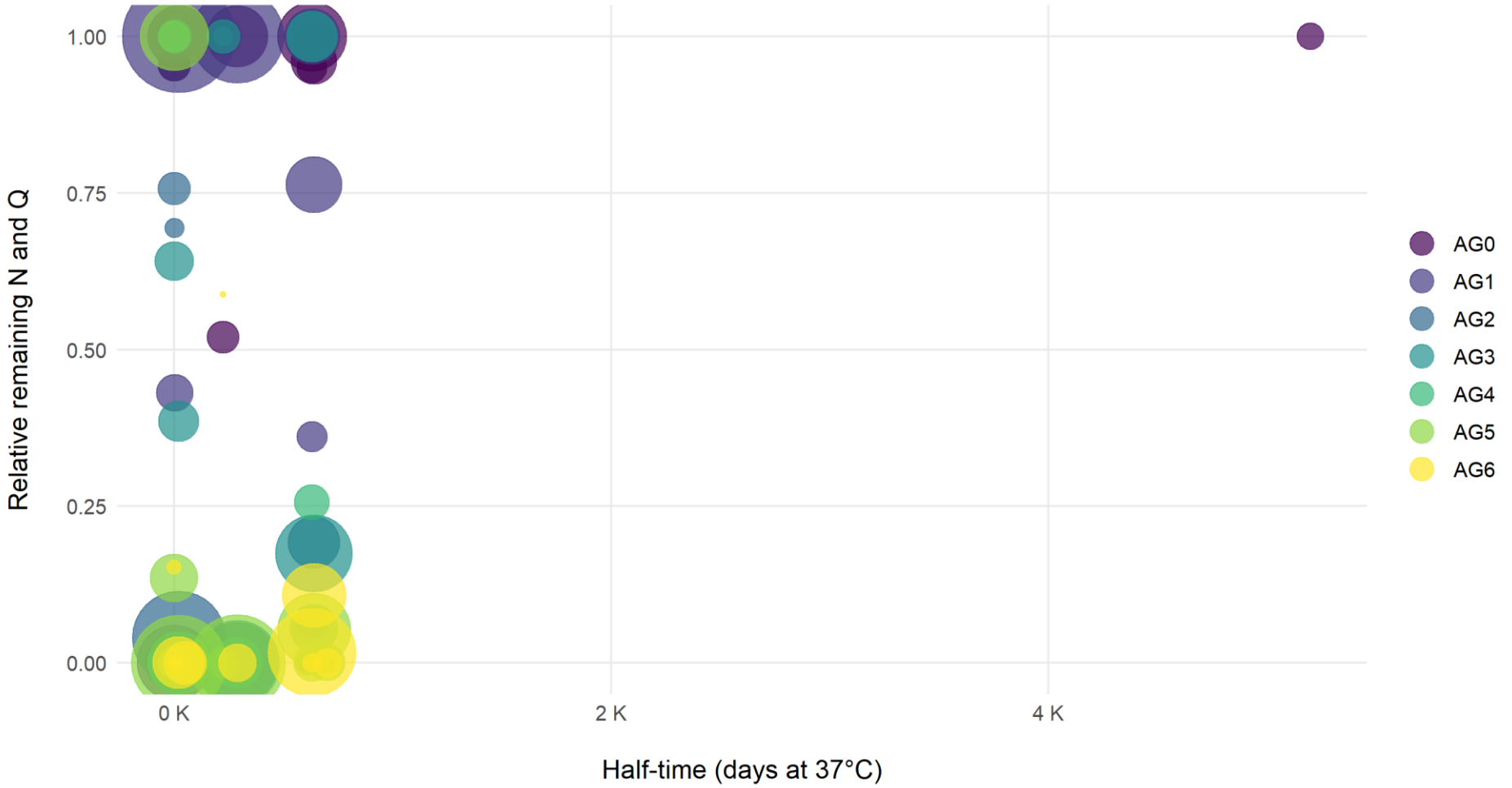

Figure B4. Site-specific deamidation of aged leather samples (unshaved goat) Each point represents a specific three residue combination. The size of the point represents that site's intensity, relative to the total intensity of all peptides in the same sample

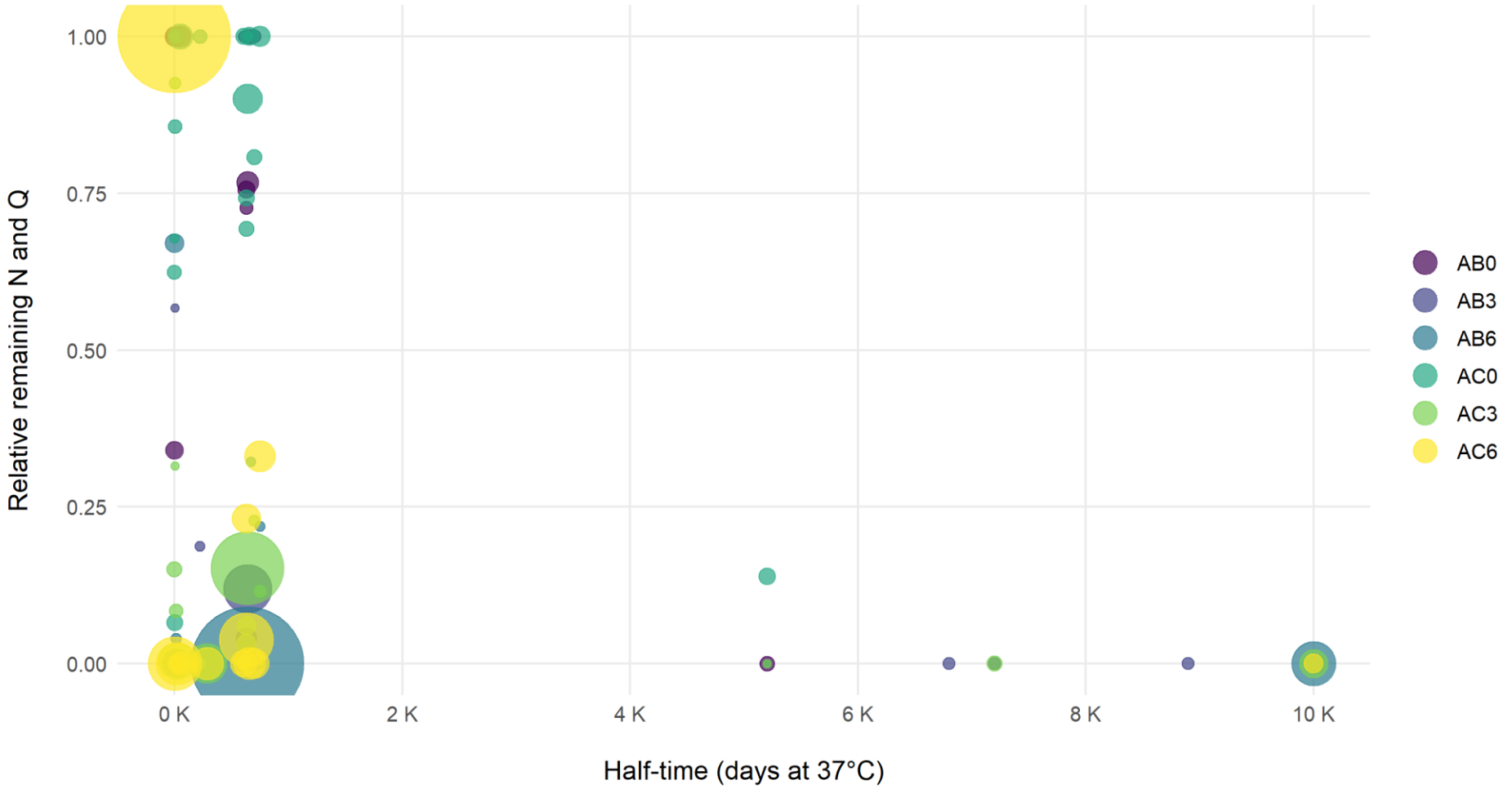

Figure B5. Site-specific deamidation of aged leather samples (buffalo and cow). Each point represents a specific three residue combination. The size of the point represents that site's intensity, relative to the total intensity of all peptides in the same sample.

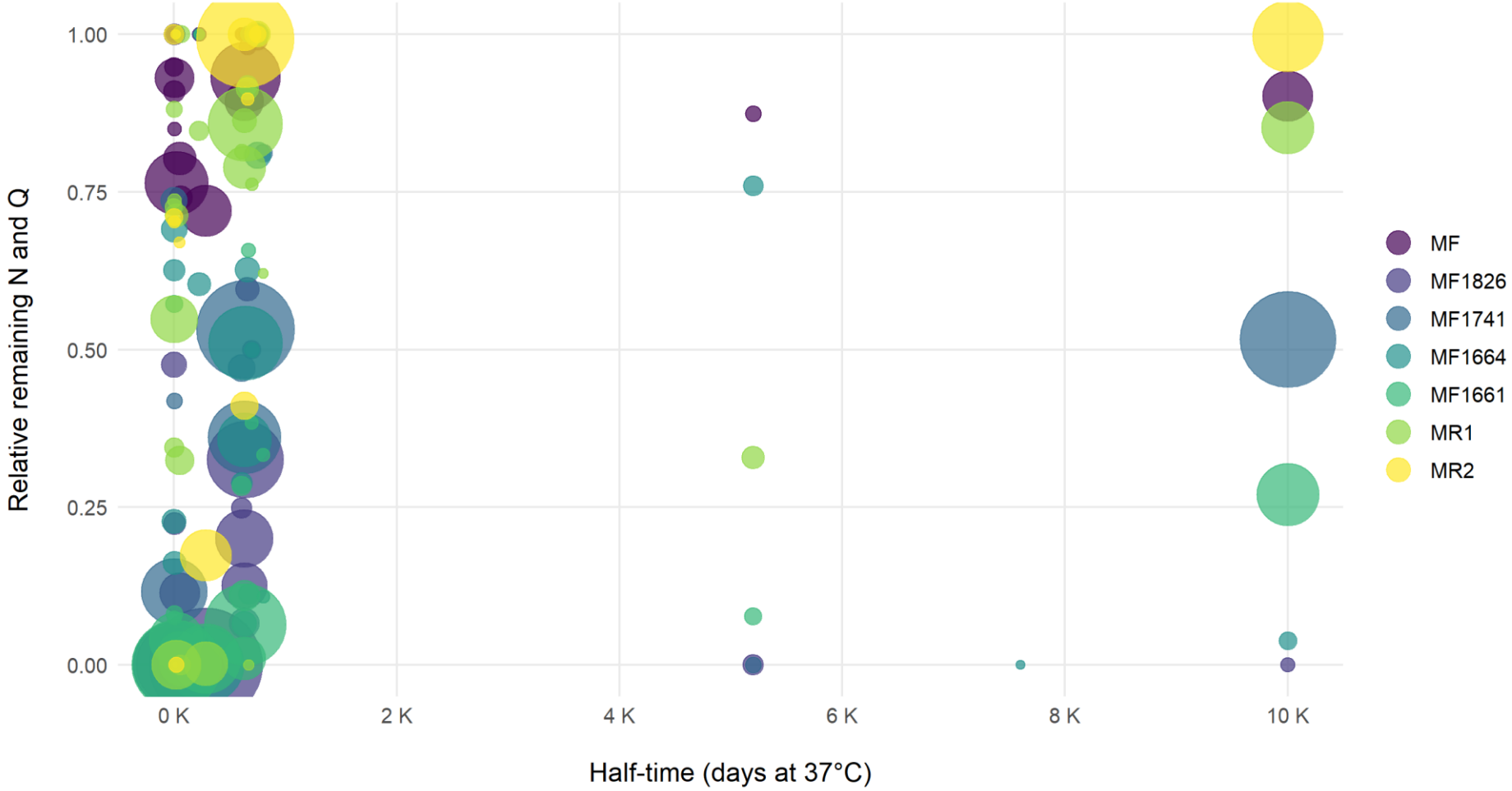

Figure B6. Site-specific deamidation of historical leather samples (Mafra and Mary Rose). Each point represents a specific three residue combination. The size of the point represents that site's intensity, relative to the total intensity of all peptides in the same sample.

Table B4. Collagen sequence coverage per sample.

Ref	CO1A1	CO1A2	CO3A1
D1	27.8%	74.6%	11.9%
D2	29.9%	75.4%	11.4%
D3	24.7%	75.6%	11.3%
D4	27.3%	75.7%	13.2%
D5	28.1%	75.6%	14.2%
D6	27.3%	73.7%	11.9%
D7	31.4%	74.5%	12.7%
P1	12.4%	39.0%	2.0%
P2	14.1%	50.4%	2.9%
P3	12.4%	41.0%	2.9%
P4	11.5%	30.4%	2.0%
P5	14.2%	47.3%	2.9%
P6	12.7%	34.7%	2.9%
P7	10.9%	31.4%	2.9%
P8	12.5%	35.5%	2.4%
P9	14.6%	43.9%	4.4%
P10	12.4%	39.9%	3.5%
P11	18.5%	54.3%	3.6%
P12	10.2%	37.5%	2.9%
AL0	11.4%	25.4%	1.6%
AL3	12.3%	39.4%	4.3%
AL6	13.1%	36.7%	3.3%
AL9	13.0%	28.0%	4.5%
AL12	13.7%	27.3%	3.2%
AG0	11.1%	34.1%	1.6%
AG1	9.9%	25.5%	0.7%
AG2	13.1%	32.4%	1.6%
AG3	11.8%	30.3%	1.6%
AG4	14.2%	35.6%	1.6%
AG5	10.9%	32.7%	2.5%
AG6	13.8%	40.4%	2.9%
AB0	13.6%	29.9%	3.1%
AB3	18.4%	36.4%	9.2%
AB6	17.8%	40.9%	9.4%
AC0	12.2%	33.9%	1.6%
AC3	19.8%	45.8%	7.7%

Ref	CO1A1	CO1A2	CO3A1
AC6	14.6%	34.8%	10.8%
MF	14.5%	61.6%	5.9%
MF1826	15.2%	39.6%	3.7%
MF1741	15.7%	40.2%	6.2%
MF1664	19.1%	53.7%	7.6%
MF1661	16.3%	53.4%	11.6%
MF1550	14.8%	49.6%	6.1%
MR1	15.3%	56.9%	7.3%
MR2	11.6%	30.9%	5.5%

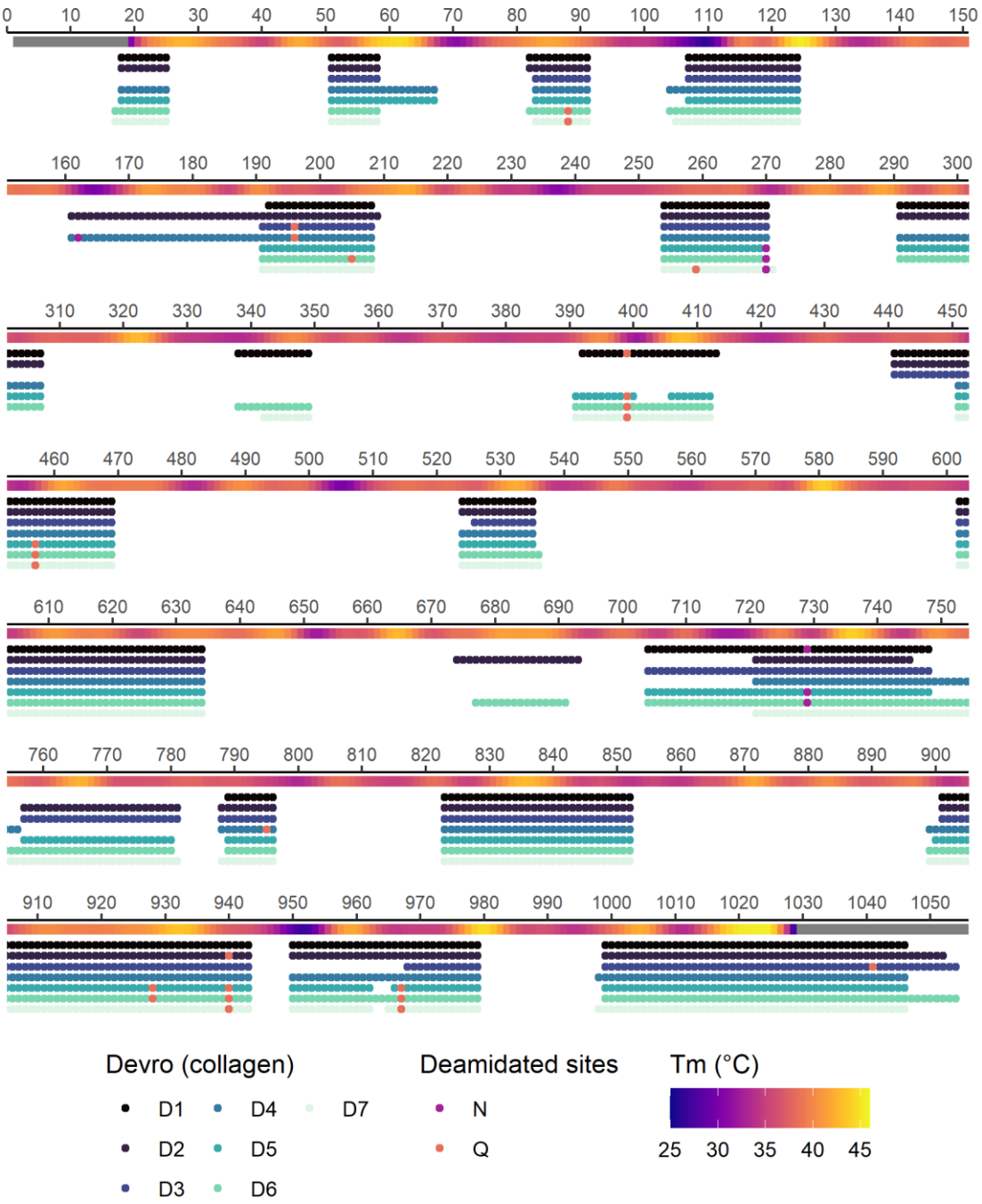

Figure B7. Collagen type I α1 from commercial collagen samples (Devro) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

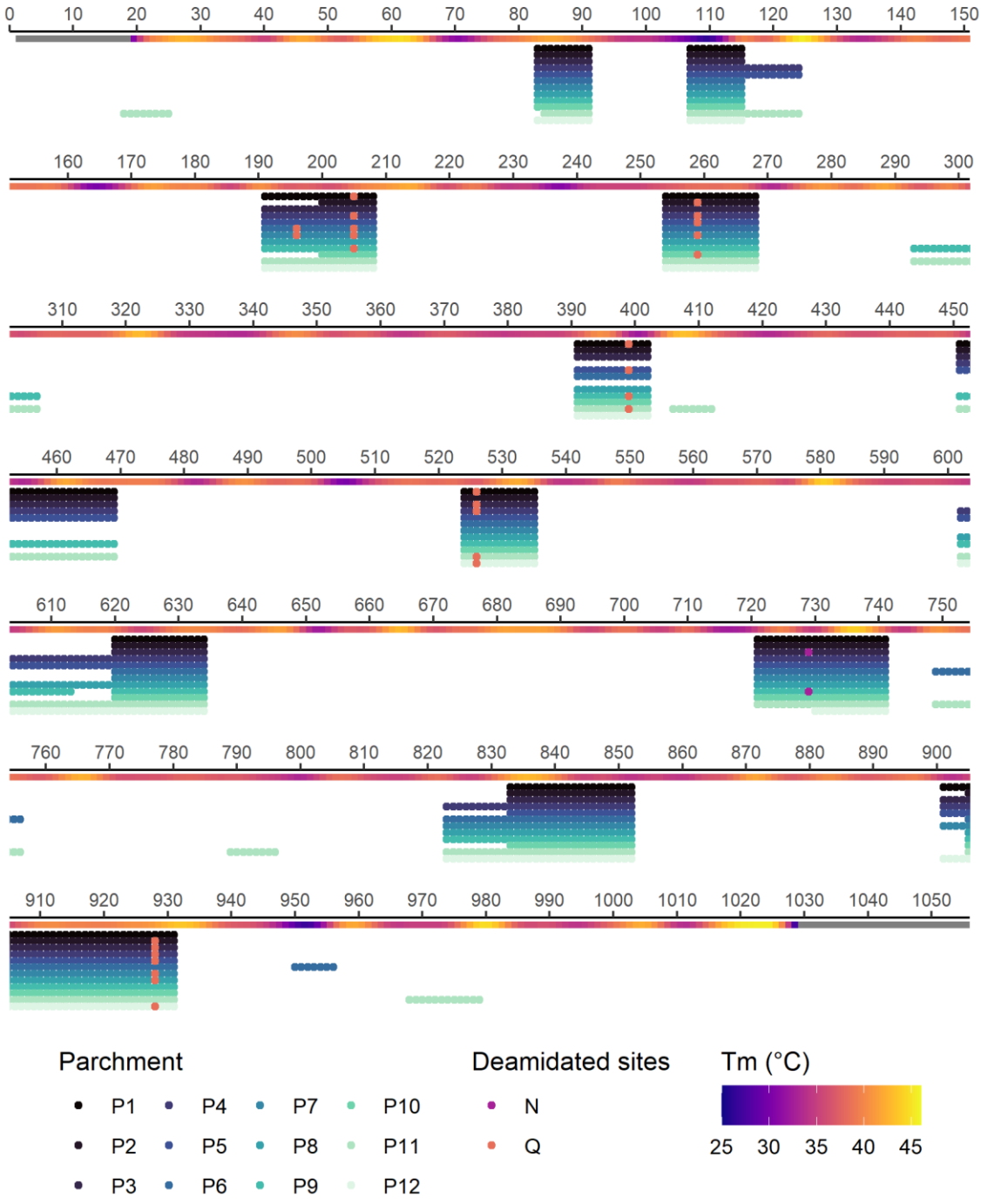

Figure B8. Collagen type I α1 from parchment samples identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

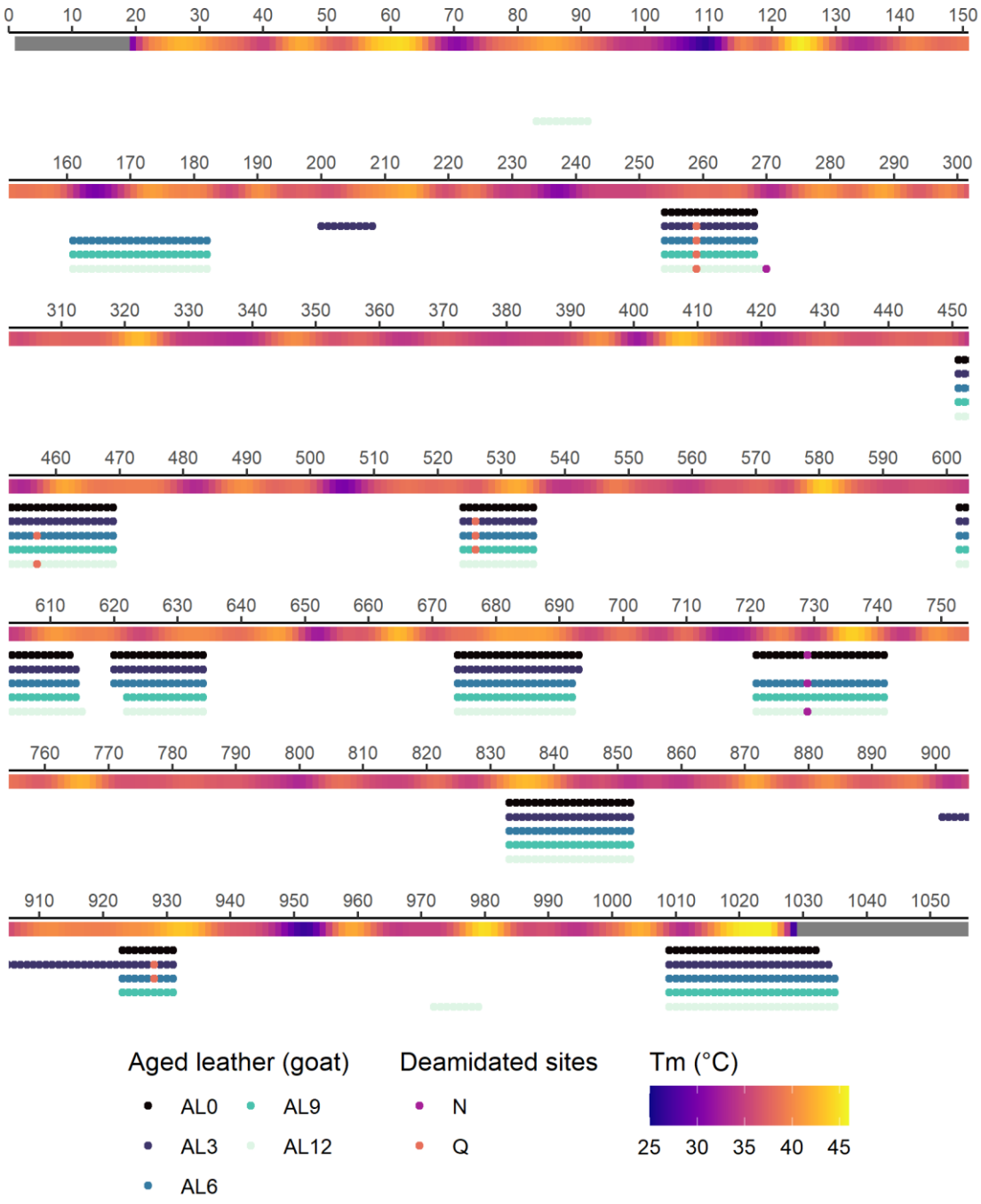

Figure B9. Collagen type I α1 from aged leather samples (goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

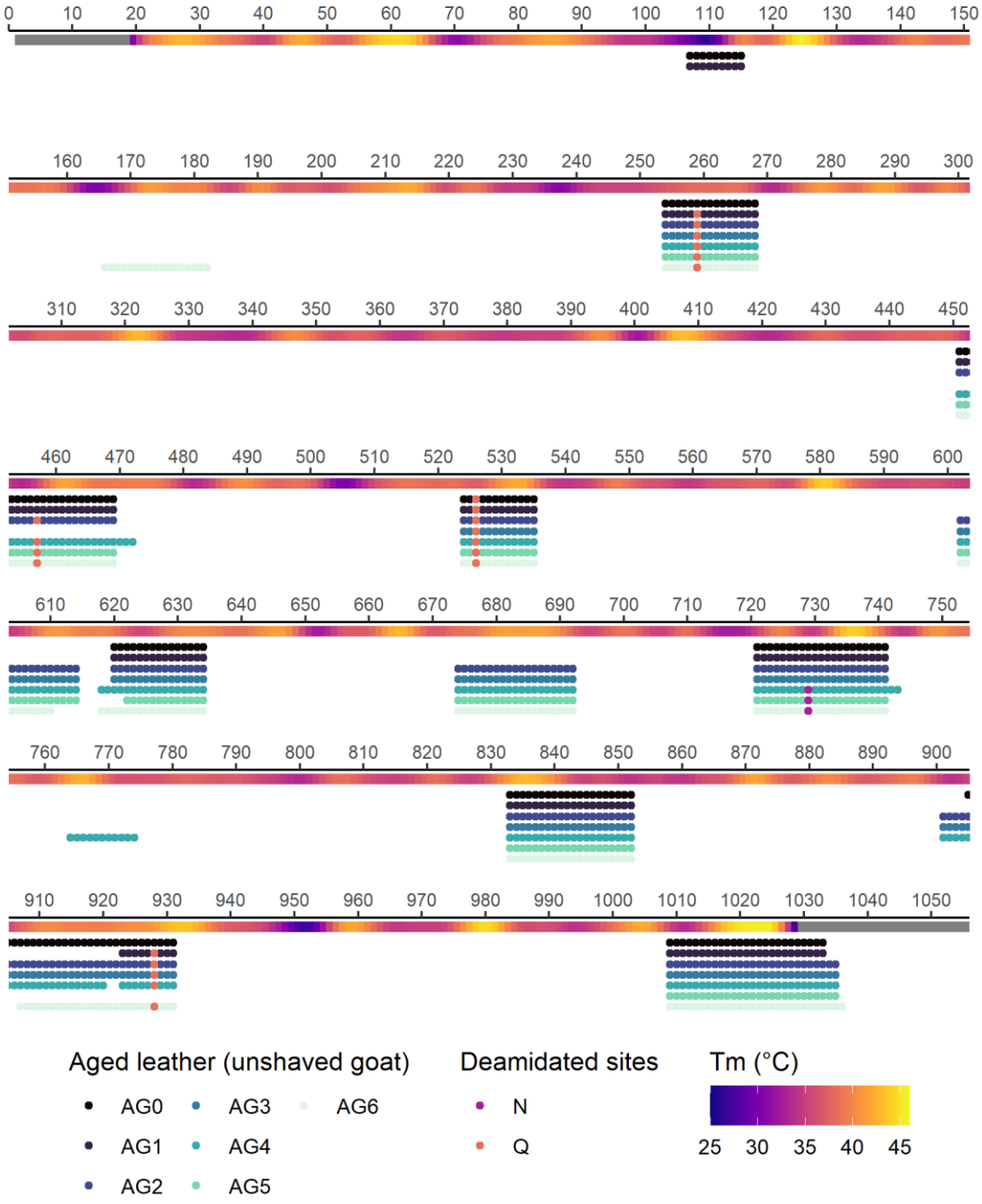

Figure B10. Collagen type I α1 from aged leather samples (unshaved goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

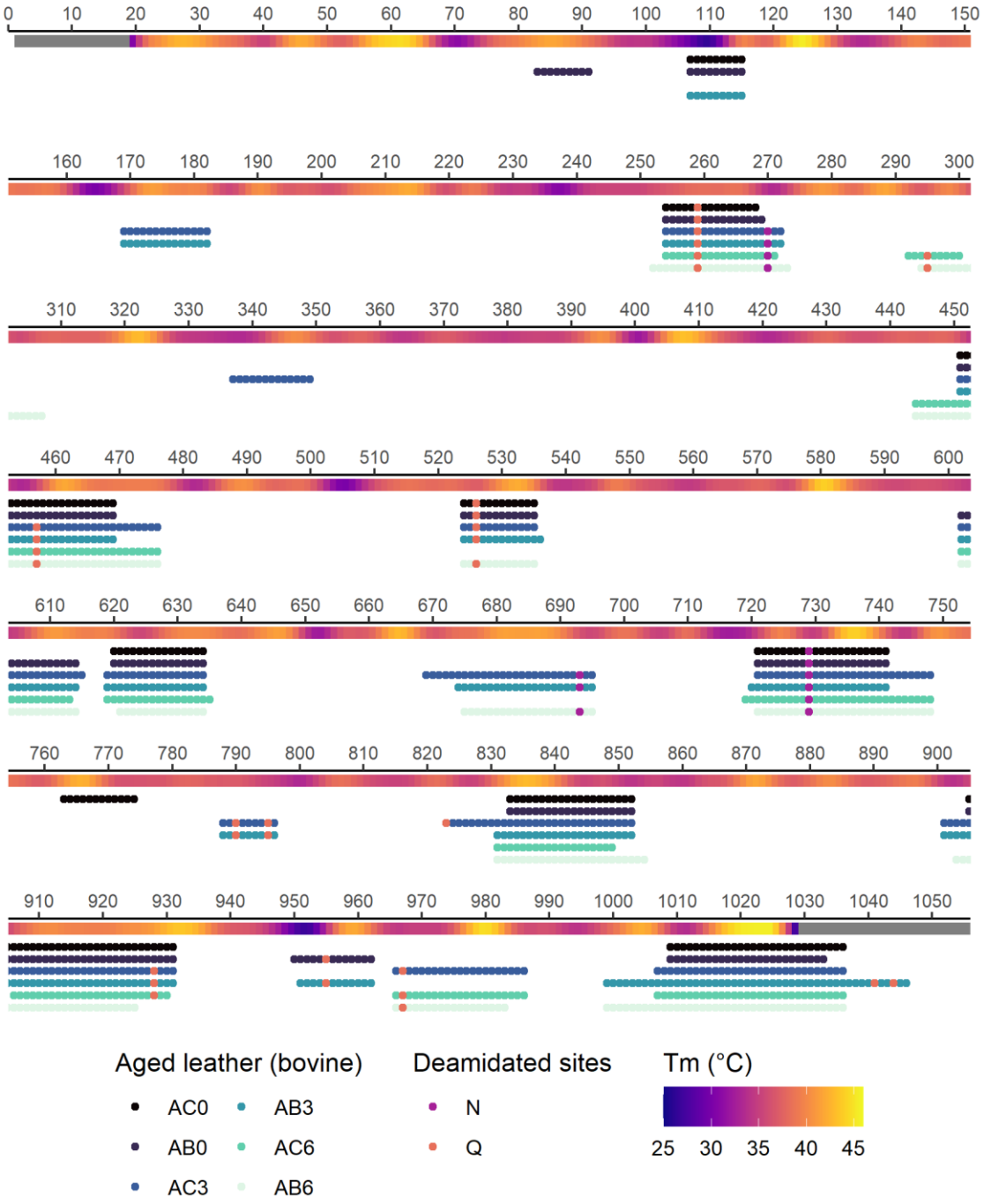

Figure B11. Collagen type I α1 from aged leather samples (buffalo and cow) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

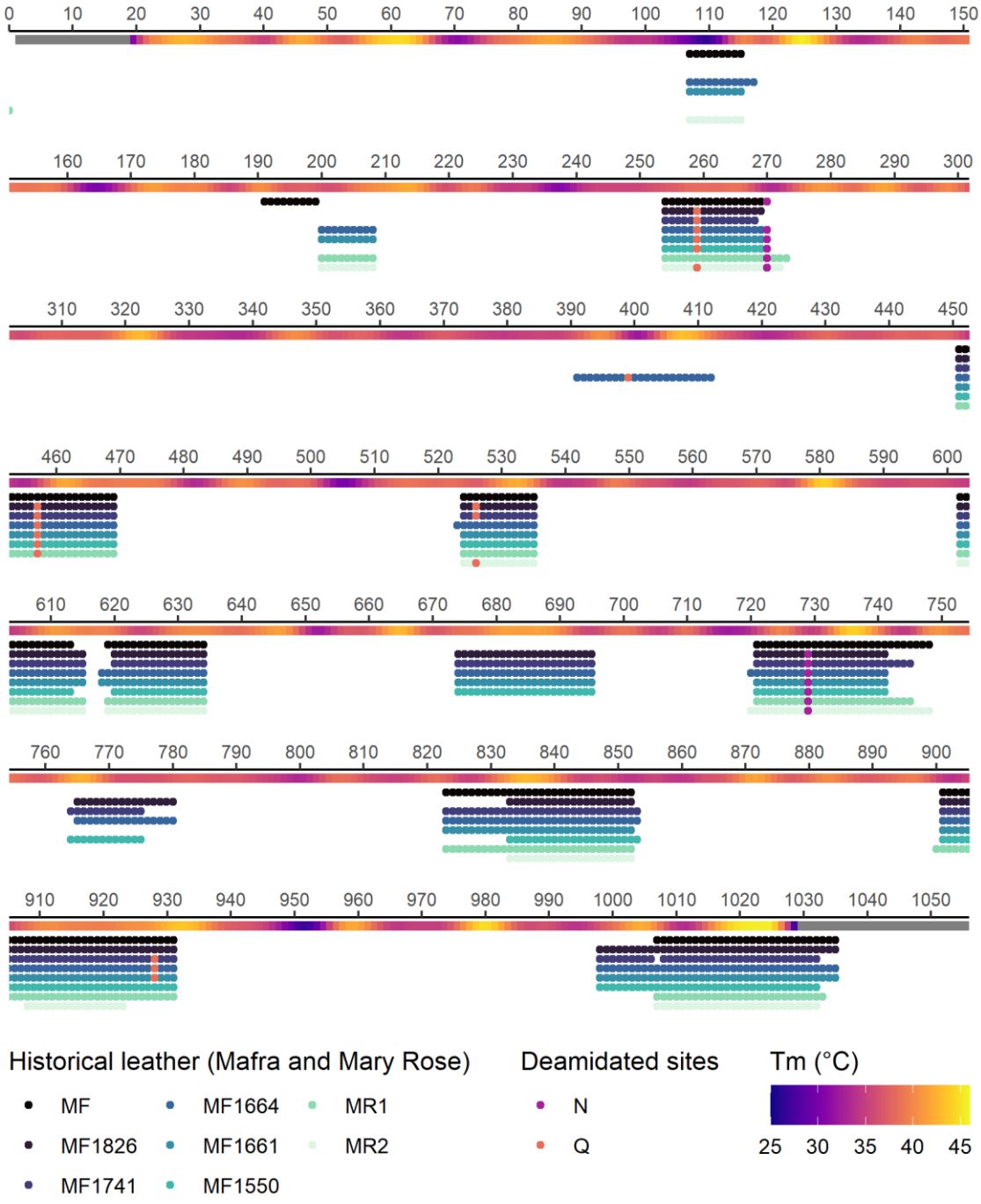

Figure B12. Collagen type I α1 from historical leather samples (Mafra and Mary Rose) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

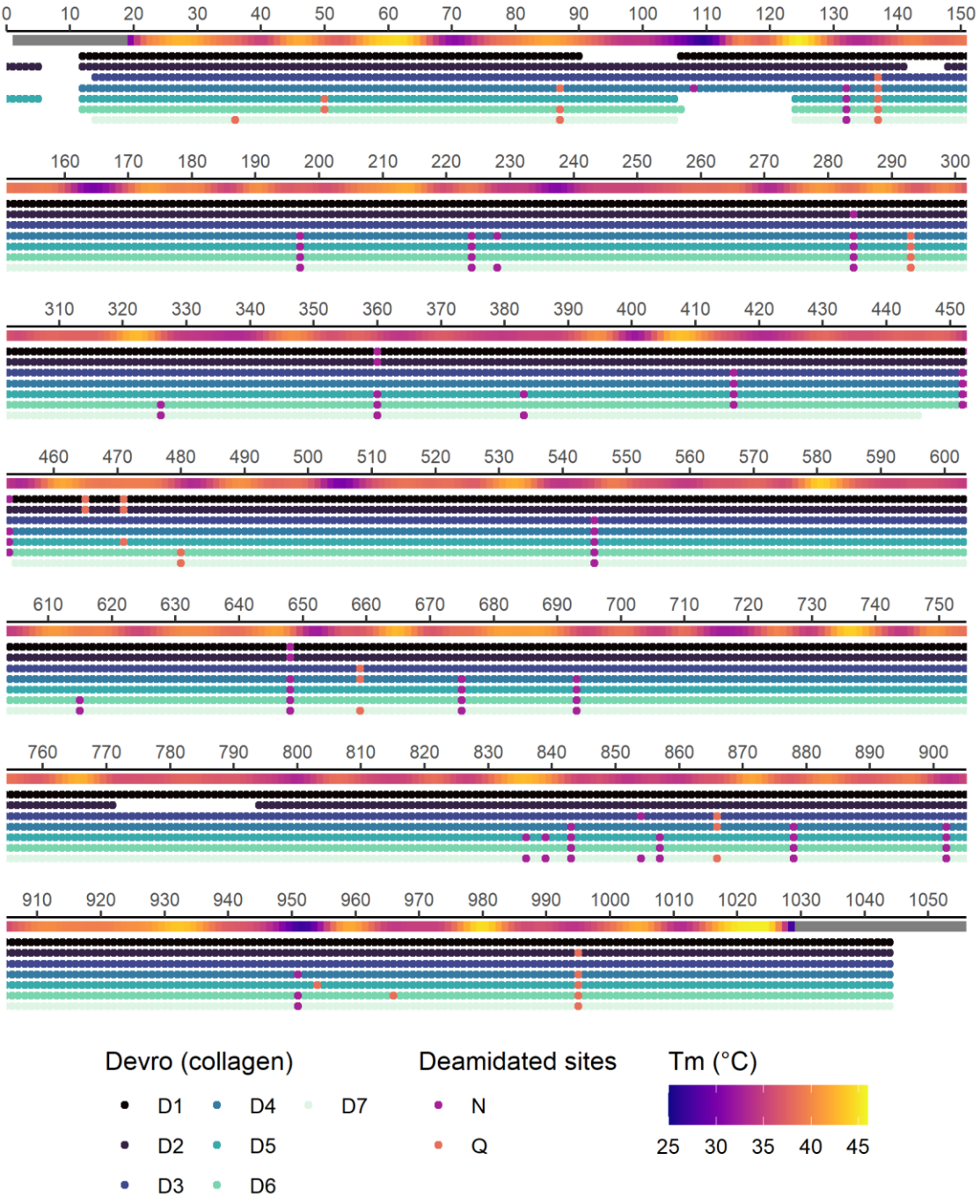

Figure B13. Collagen type I α2 from commercial collagen samples (Devro) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

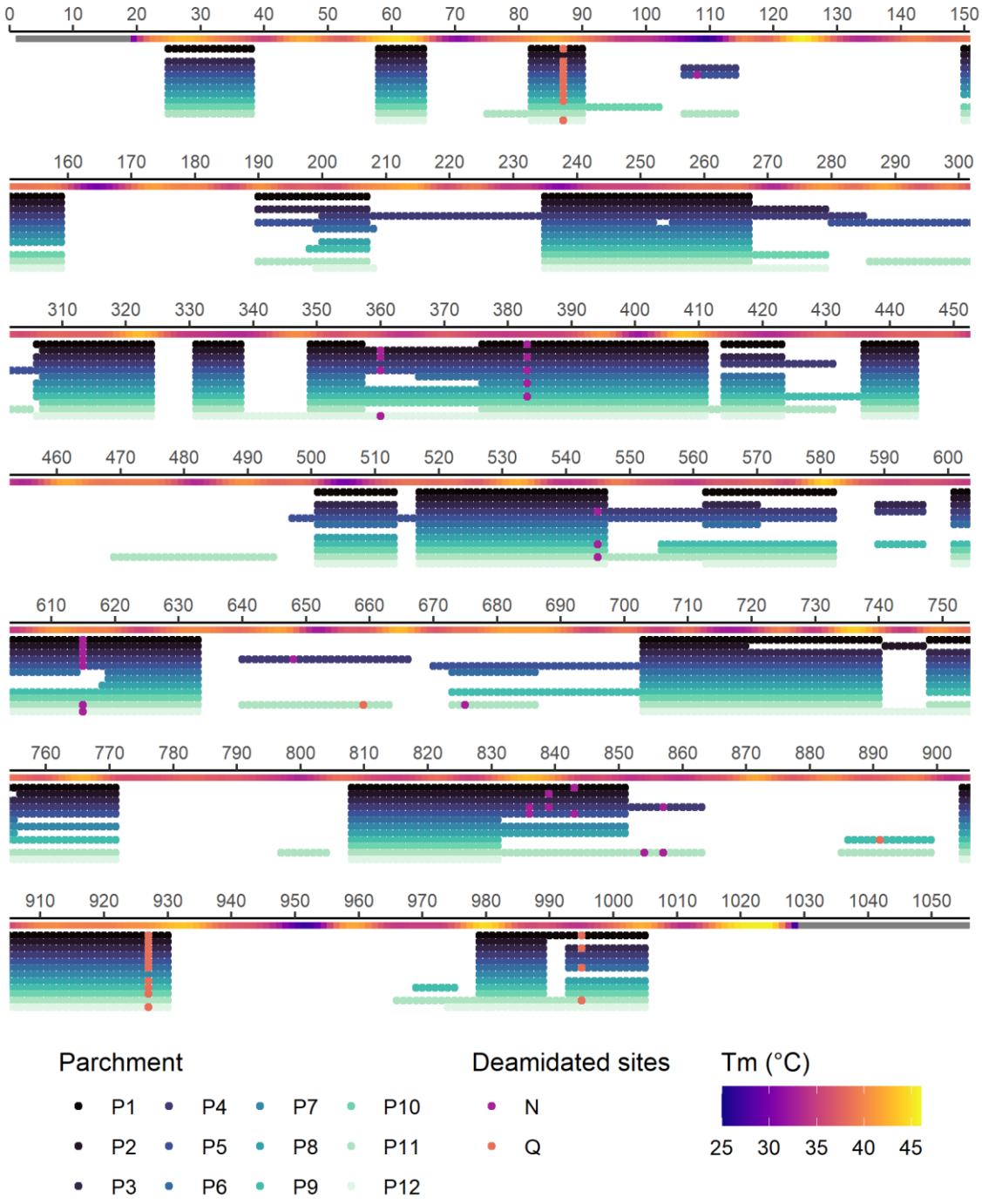

Figure B14. Collagen type I α2 from parchment samples identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

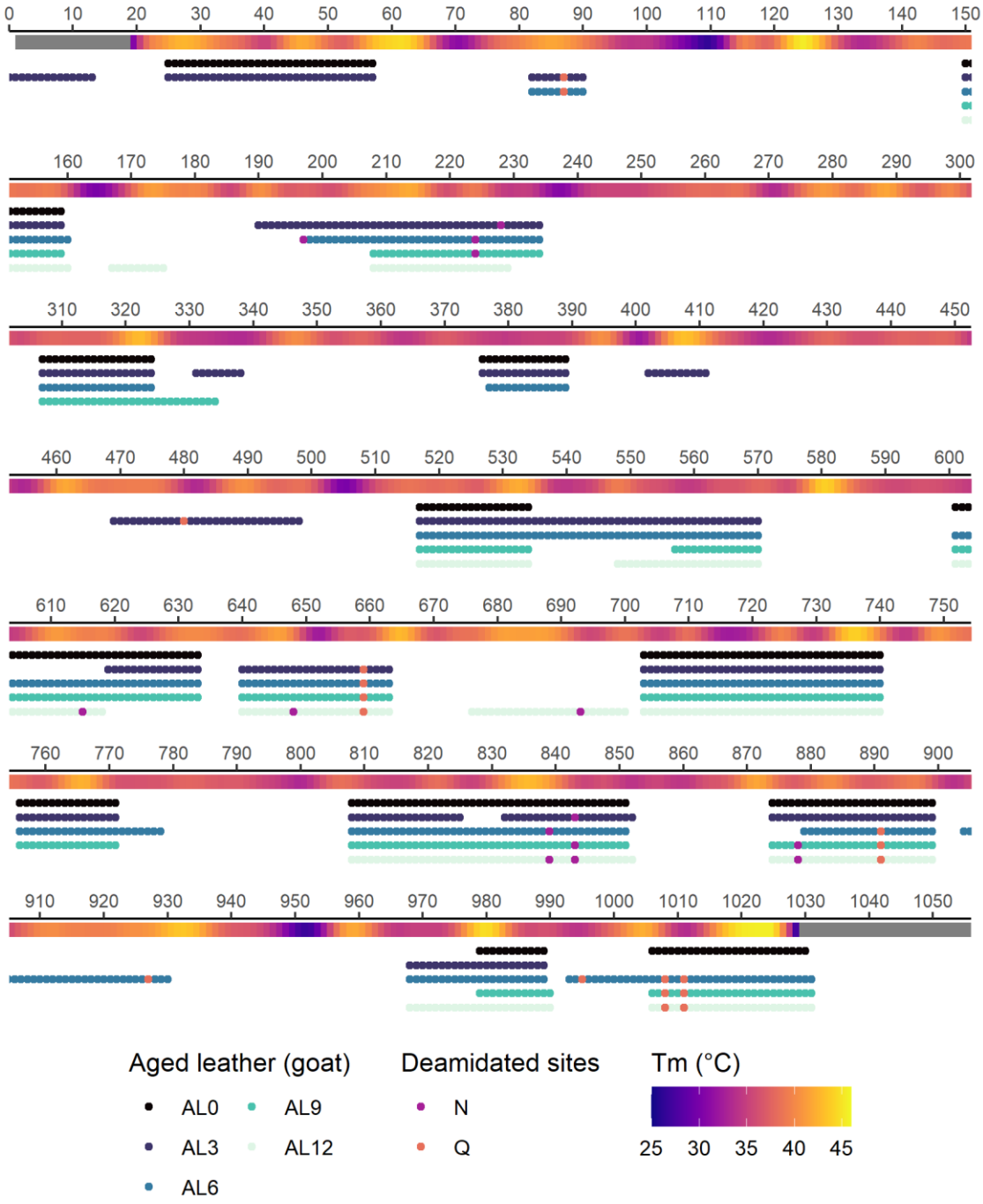

Figure B15. Collagen type I α2 from aged leather samples (goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

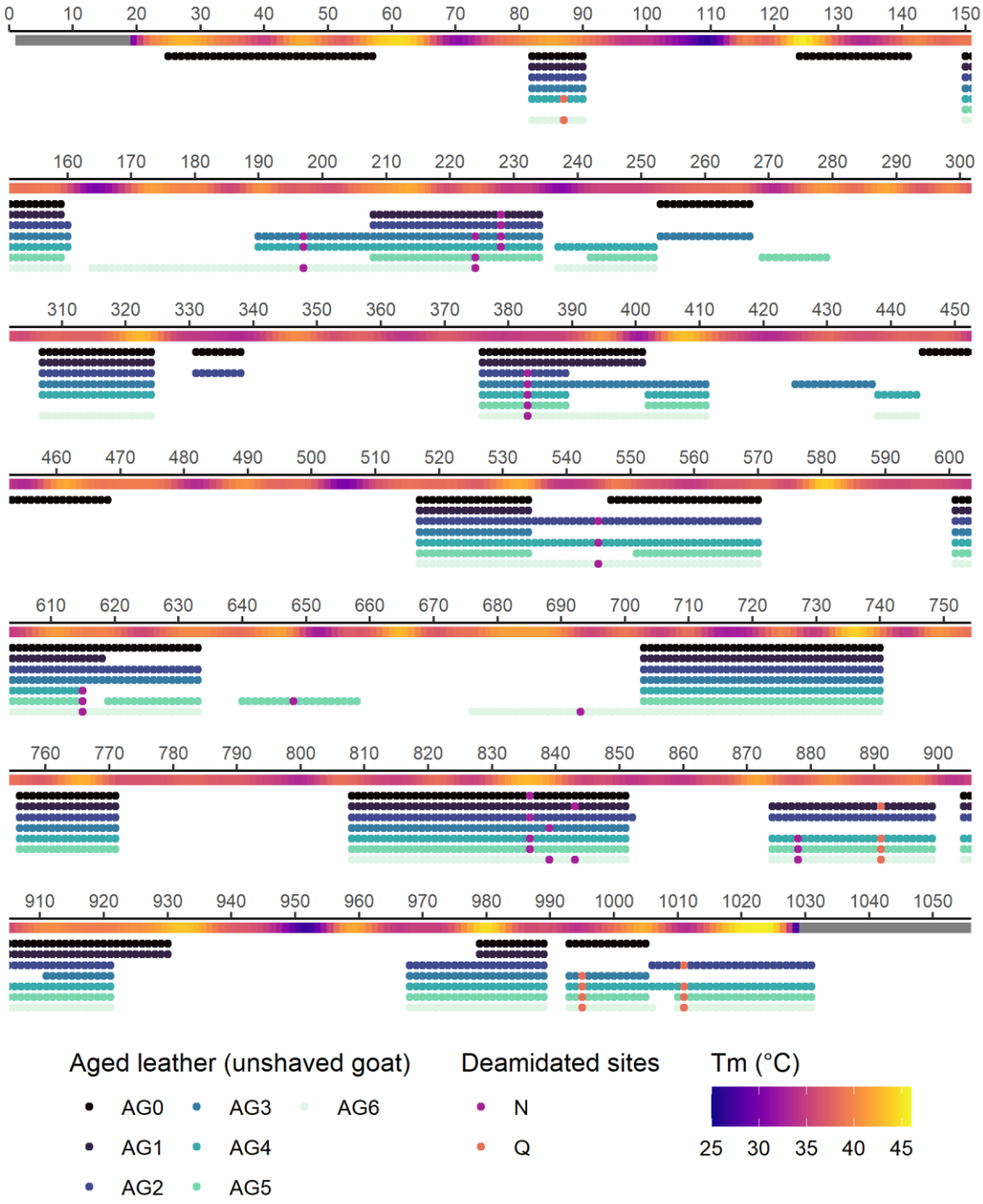

Figure B16. Collagen type I α2 from aged leather samples (unshave goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

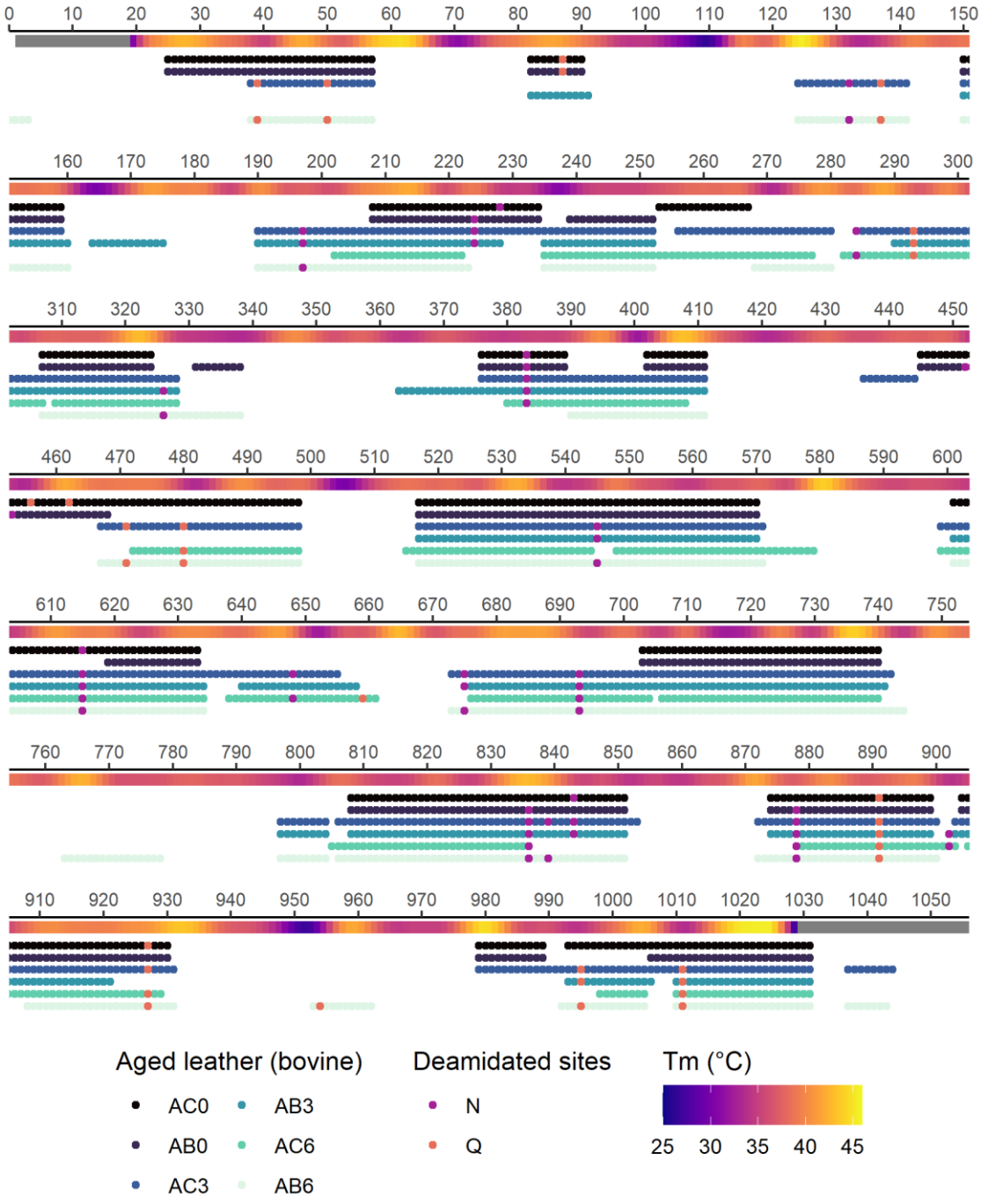

Figure B17. Collagen type I α2 from aged leather samples (buffalo and cow) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

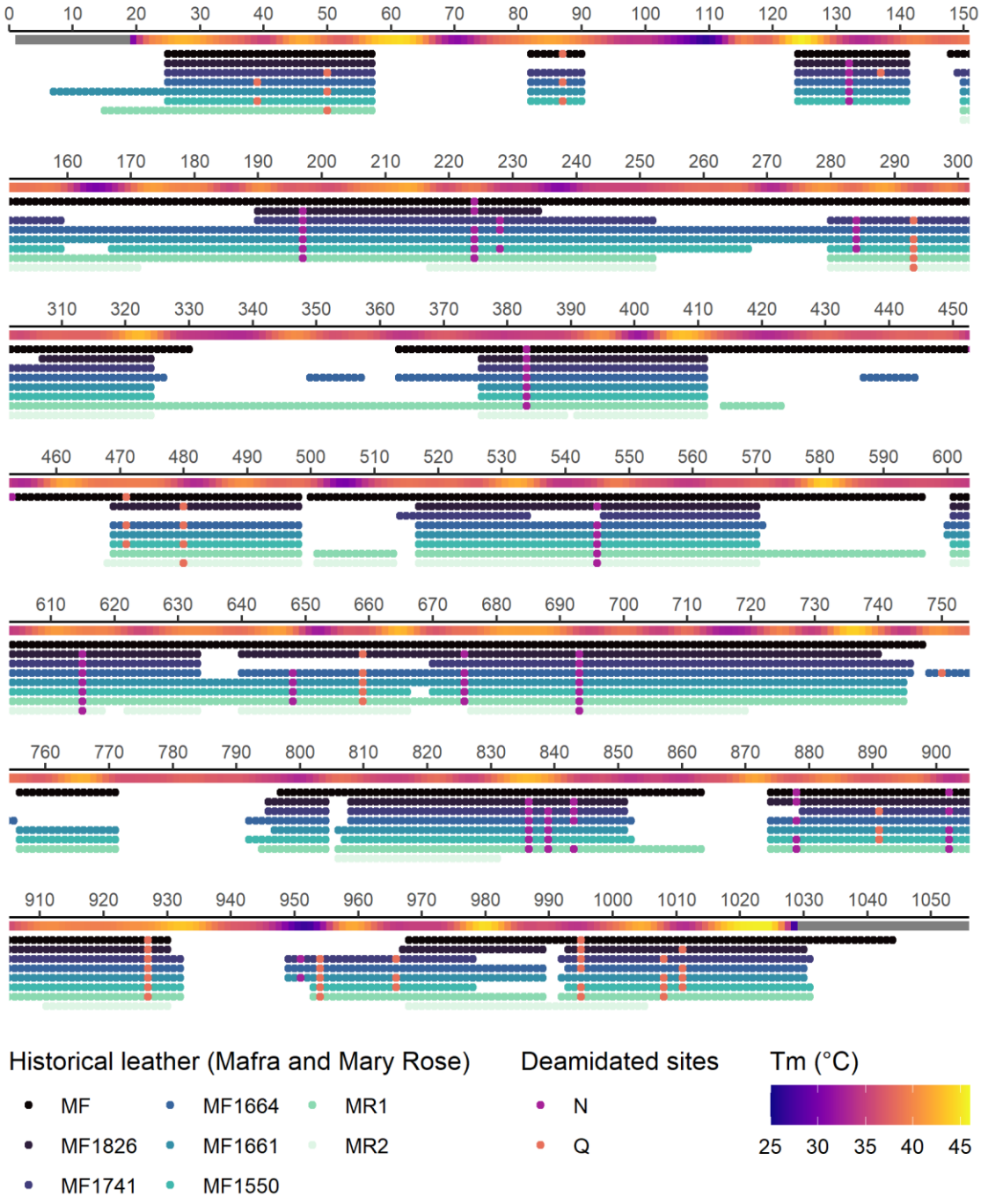

Figure B18. Collagen type I α2 from historical leather samples (Mafra and Mary Rose) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

Figure B19. Collagen type III α1 from commercial collagen samples (Devro) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

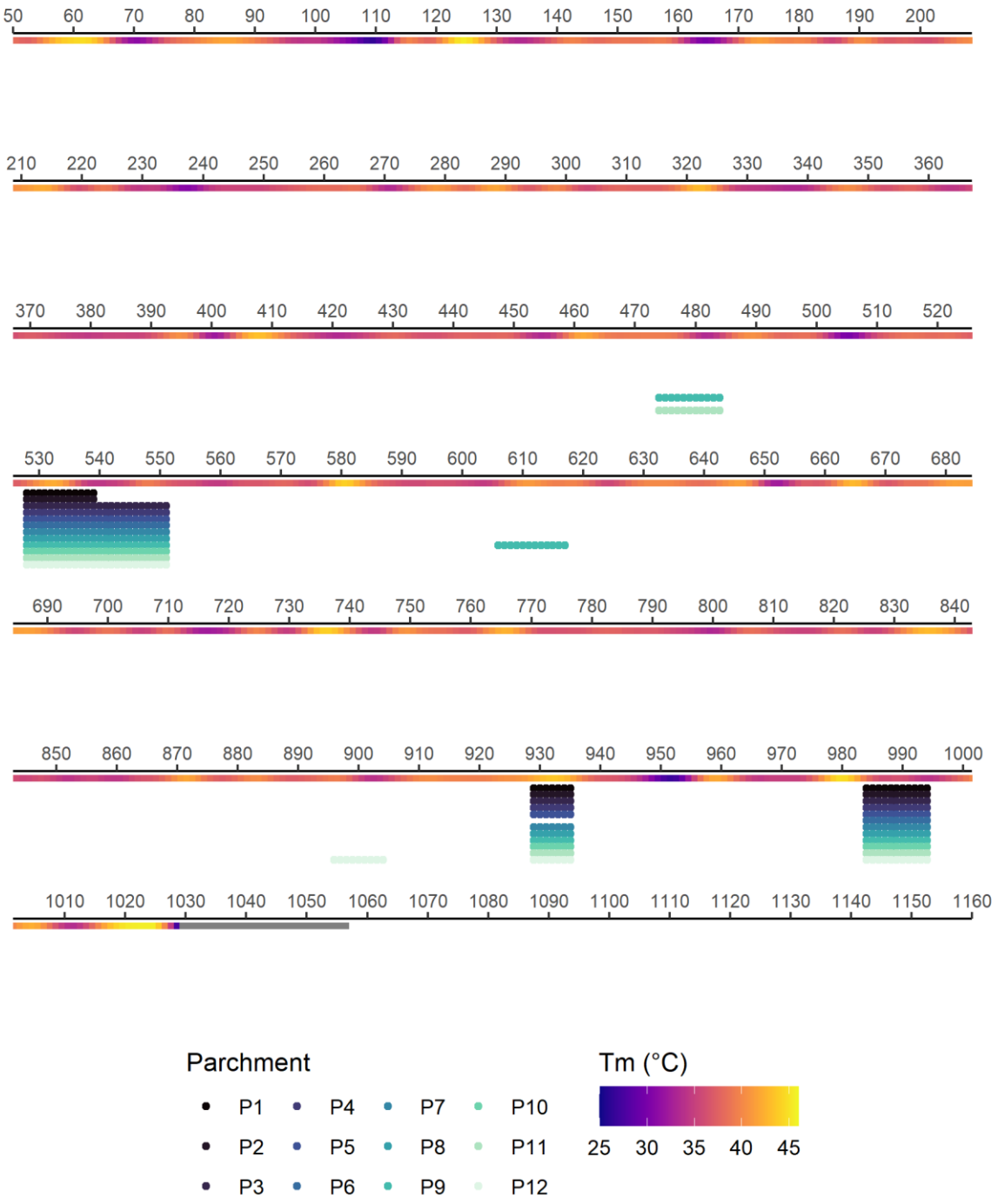

Figure B20. Collagen type III α1 from parchment samples identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

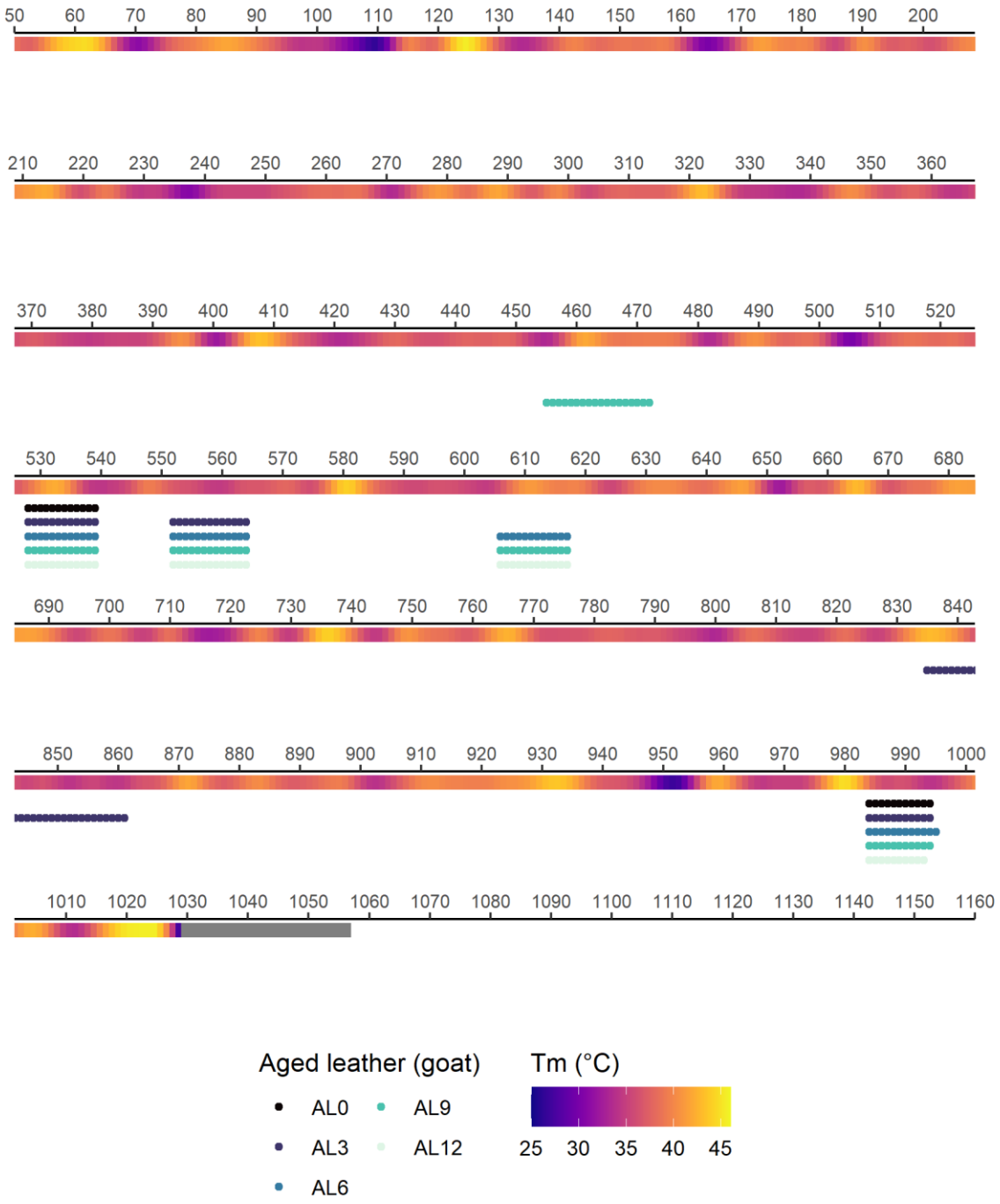

Figure B21. Collagen type III α1 from aged leather samples (goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

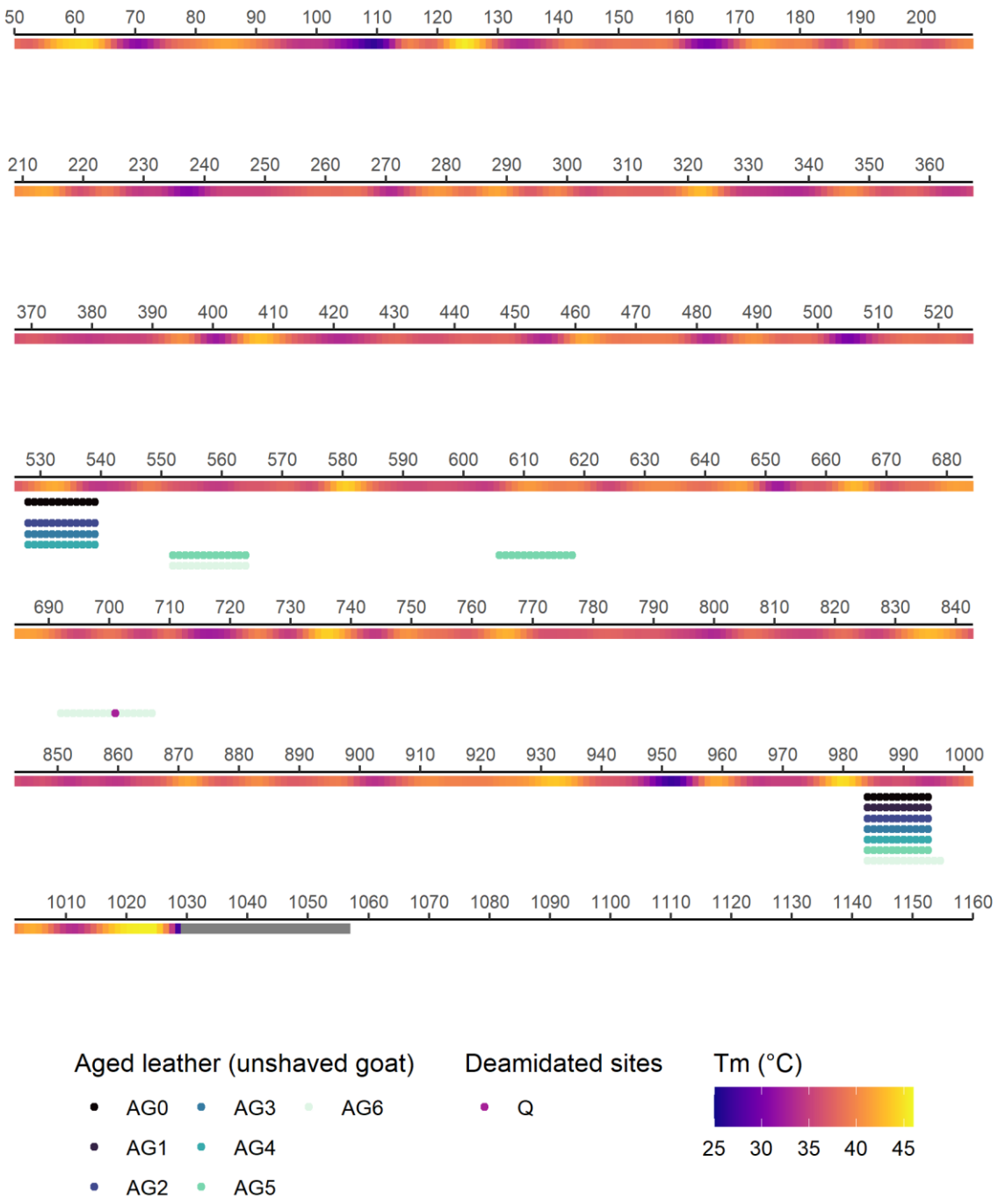

Figure B22. Collagen type III α1 from aged leather samples (unshaved goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

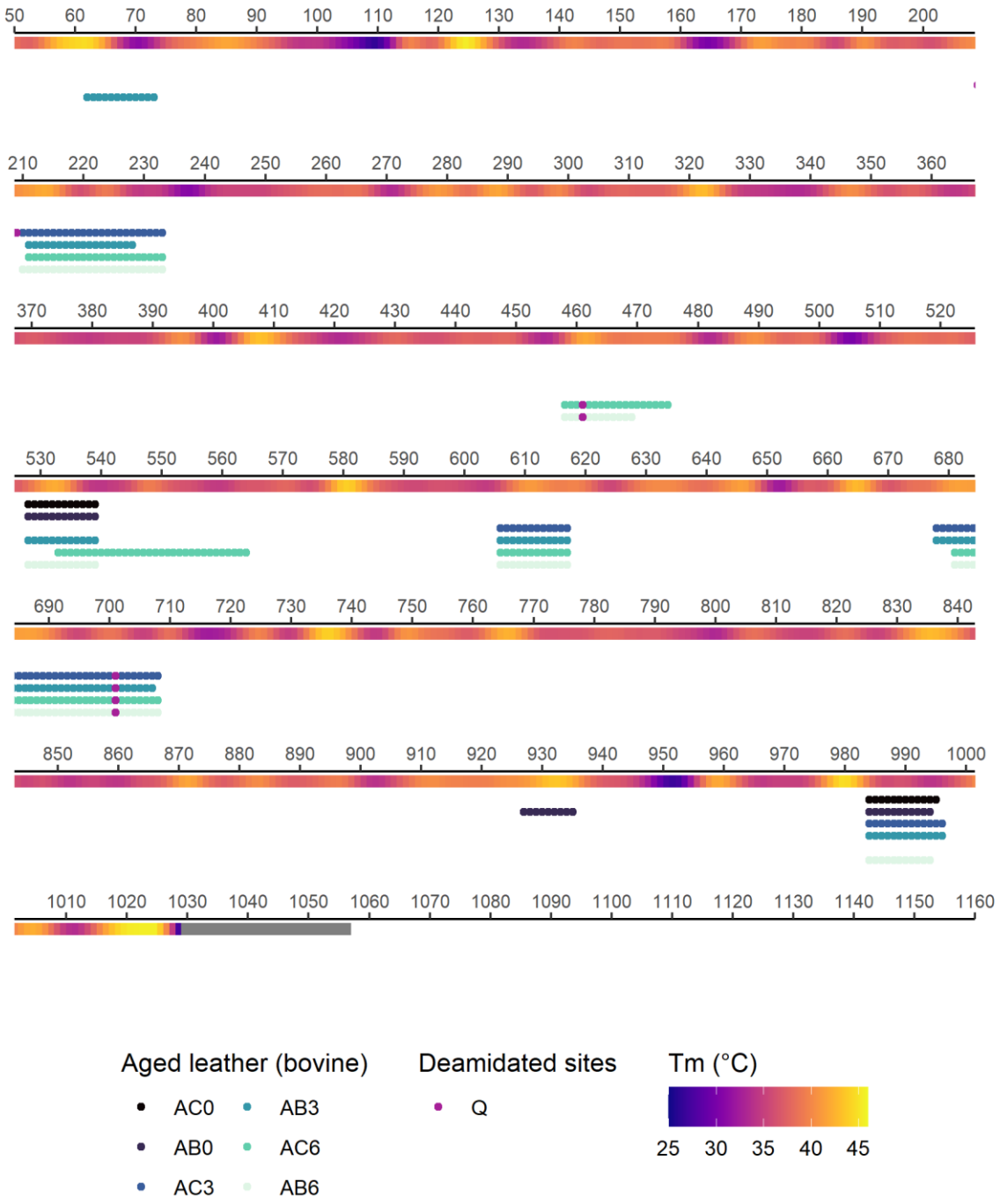

Figure B23. Collagen type III α1 from aged leather samples (buffalo and cow) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

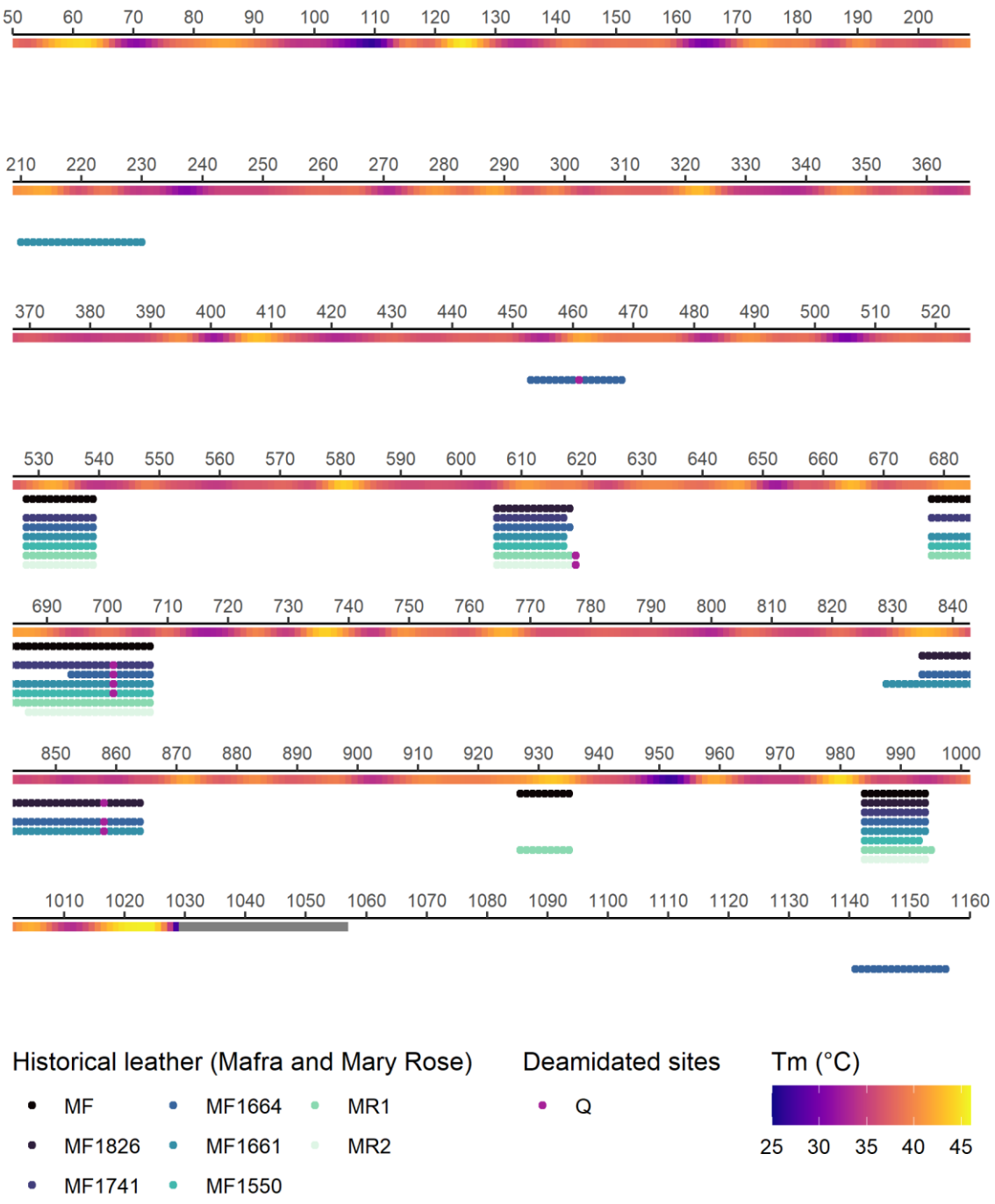

Figure B24. Collagen type III α1 from historical leather samples (Mafra and Mary Rose) identified by LC-MS/MS with collagen chain melting temperature (Tm) and deamidated asparagine (N) and glutamine (Q) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

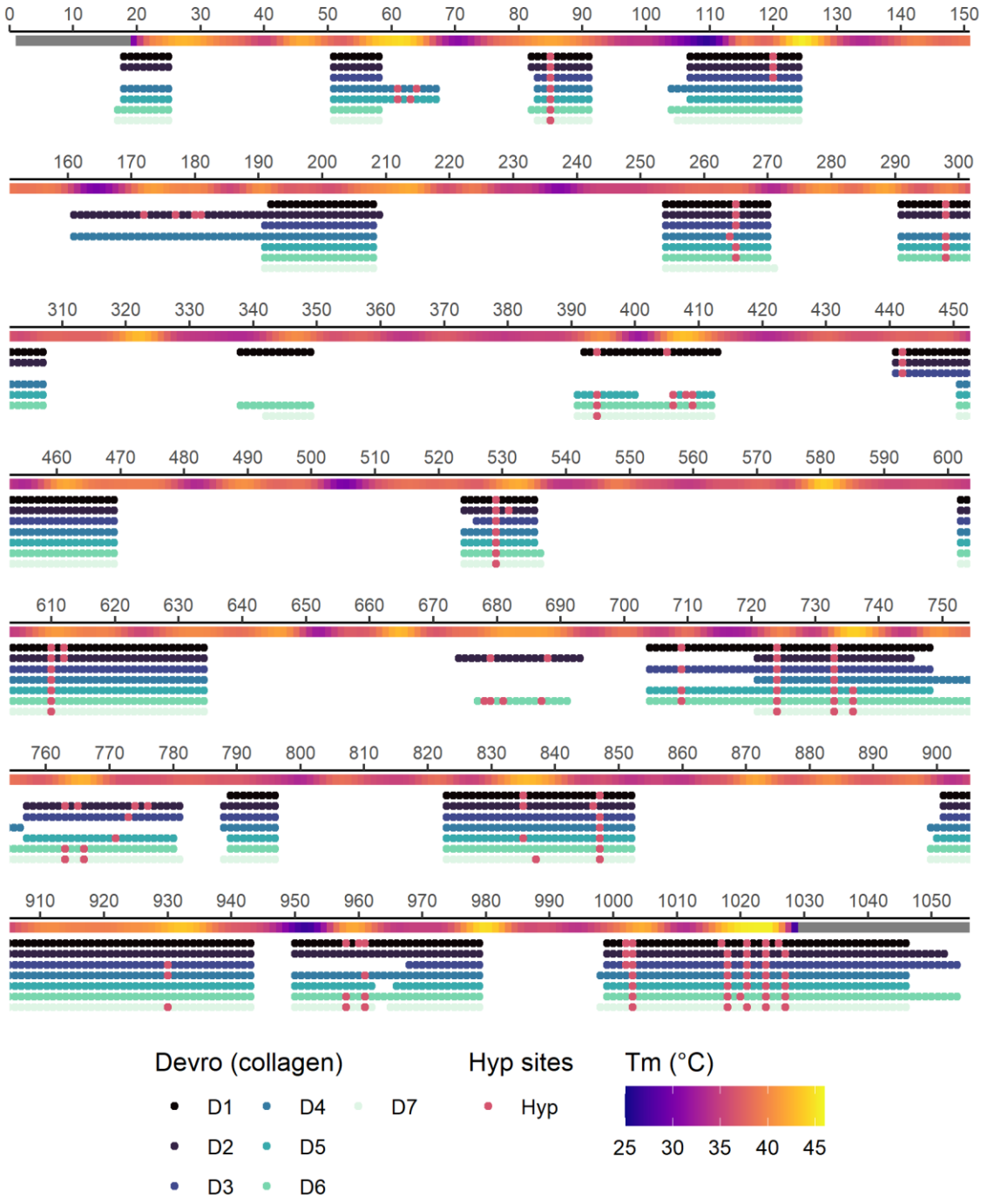

Figure B25. Collagen type I α1 from commercial collagen samples (Devro) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

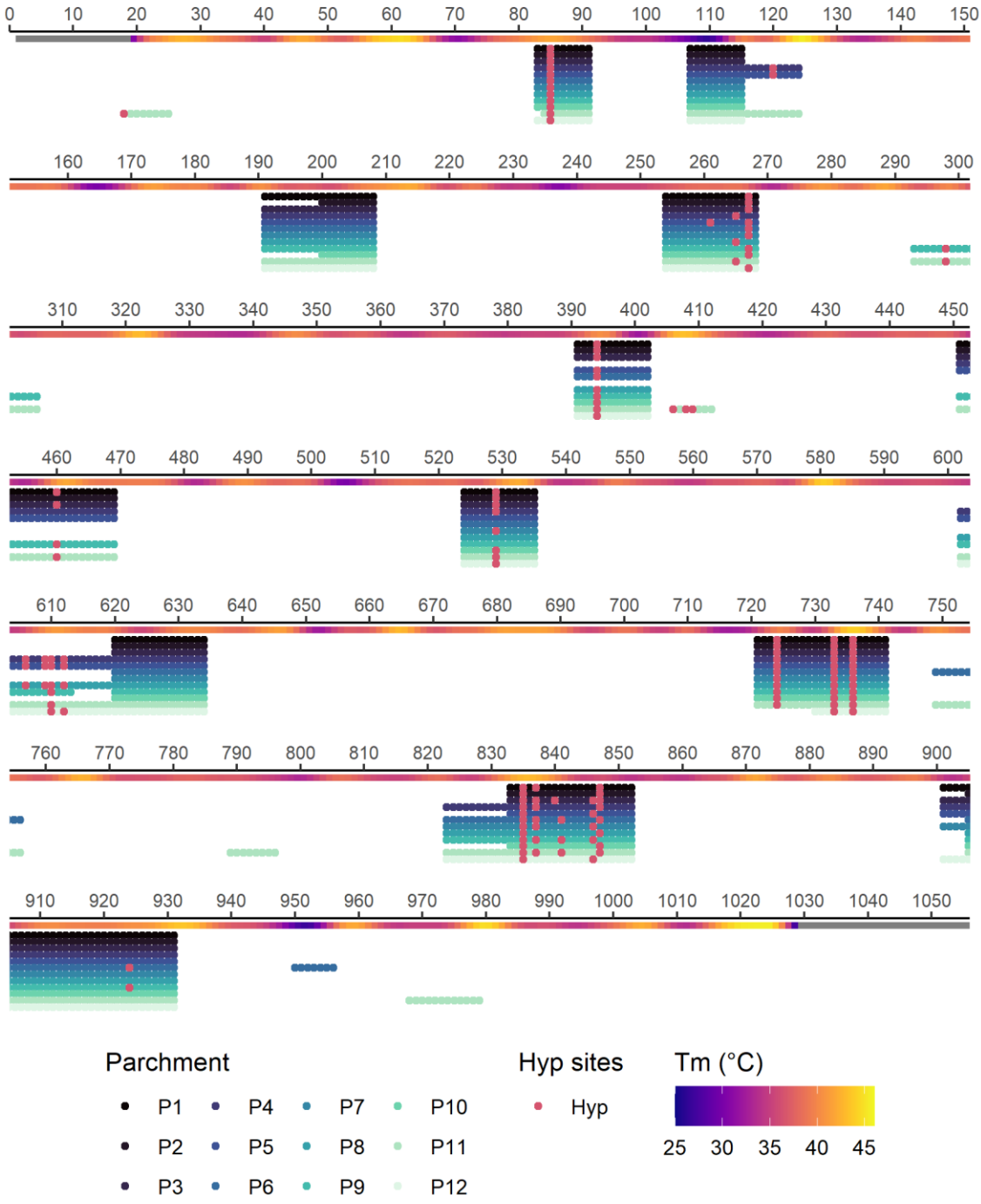

Figure B26. Collagen type I α1 from parchment samples identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

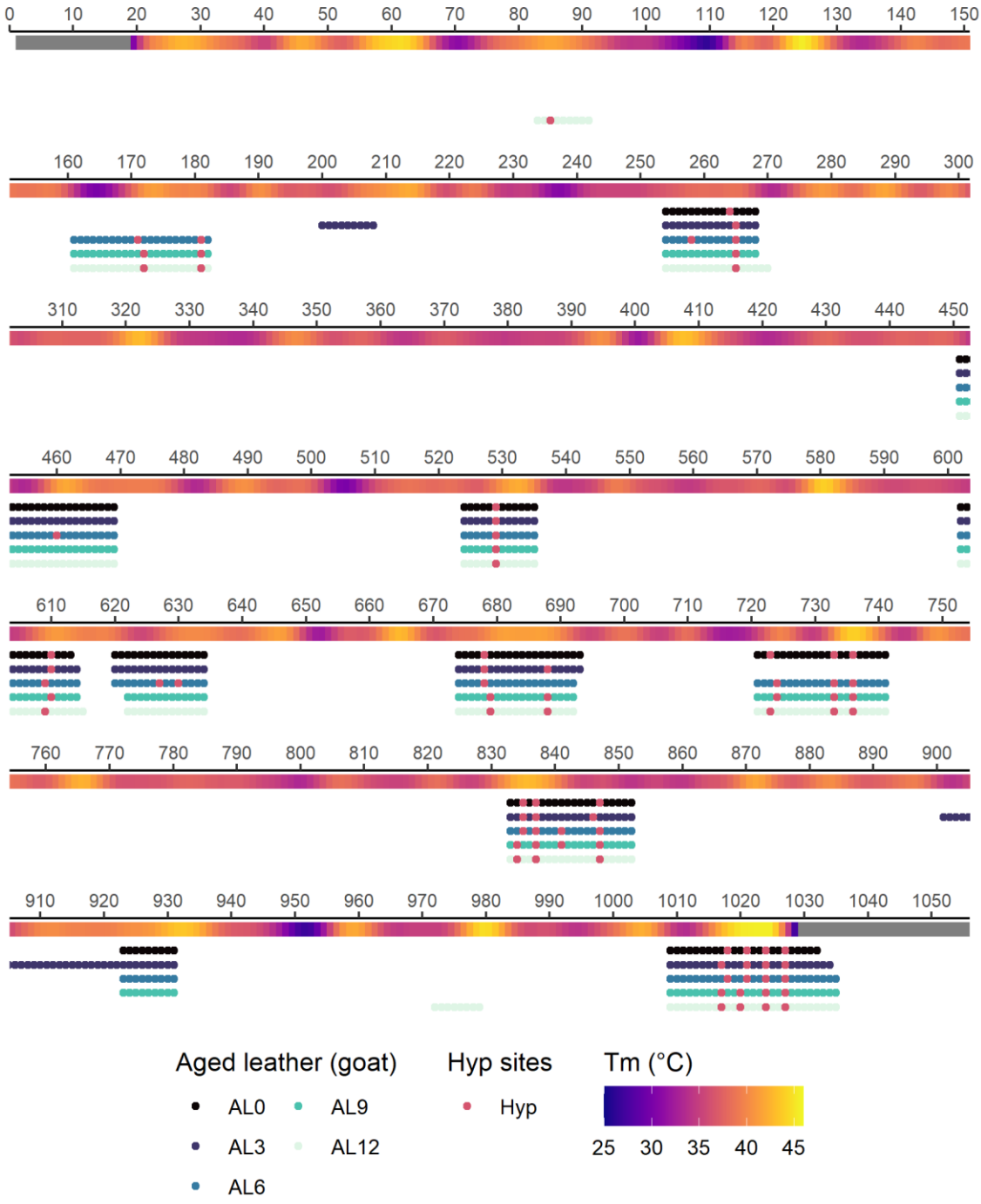

Figure B27. Collagen type I α1 from aged leather samples (goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

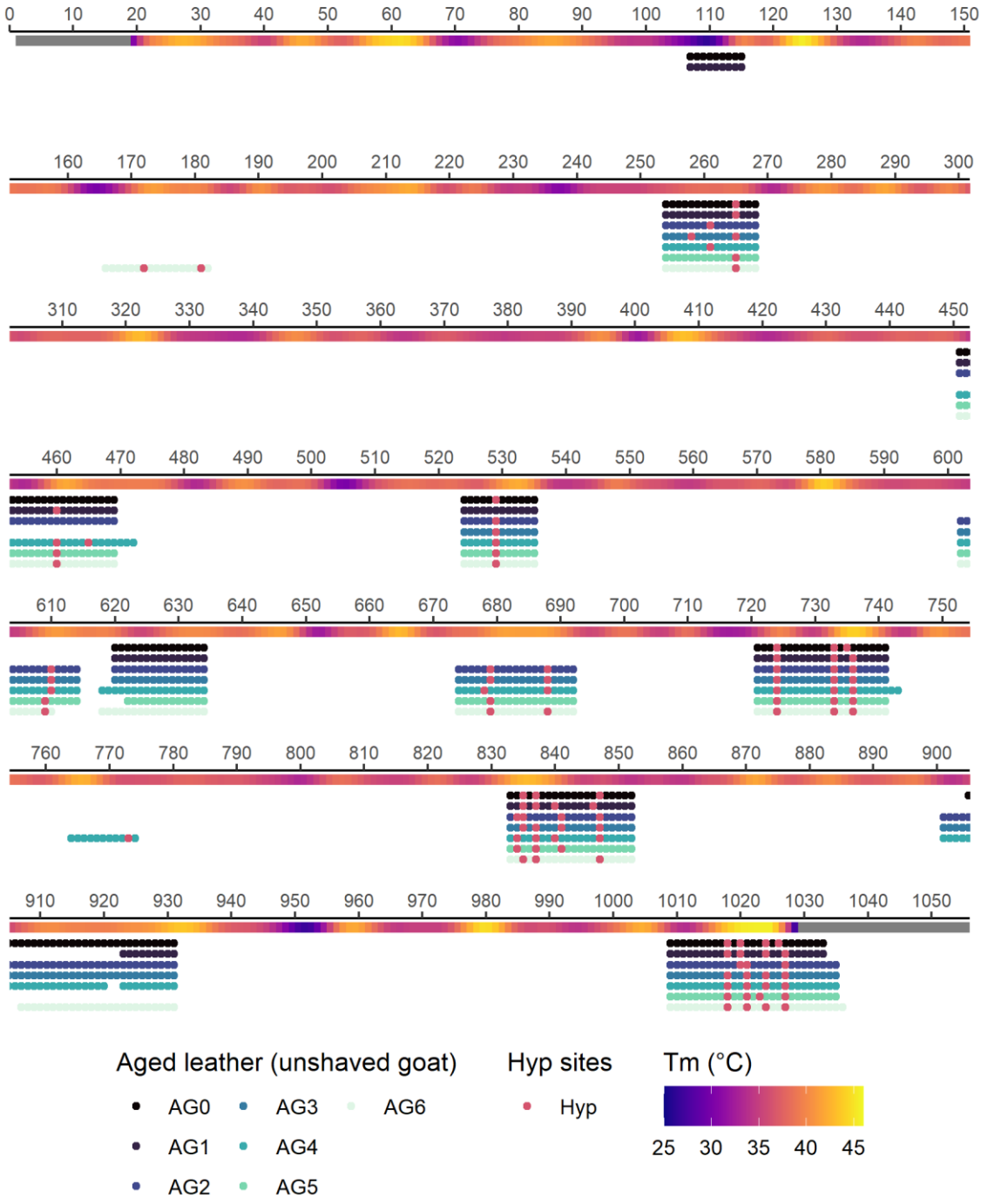

Figure B28. Collagen type I α1 from aged leather samples (unshaved goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

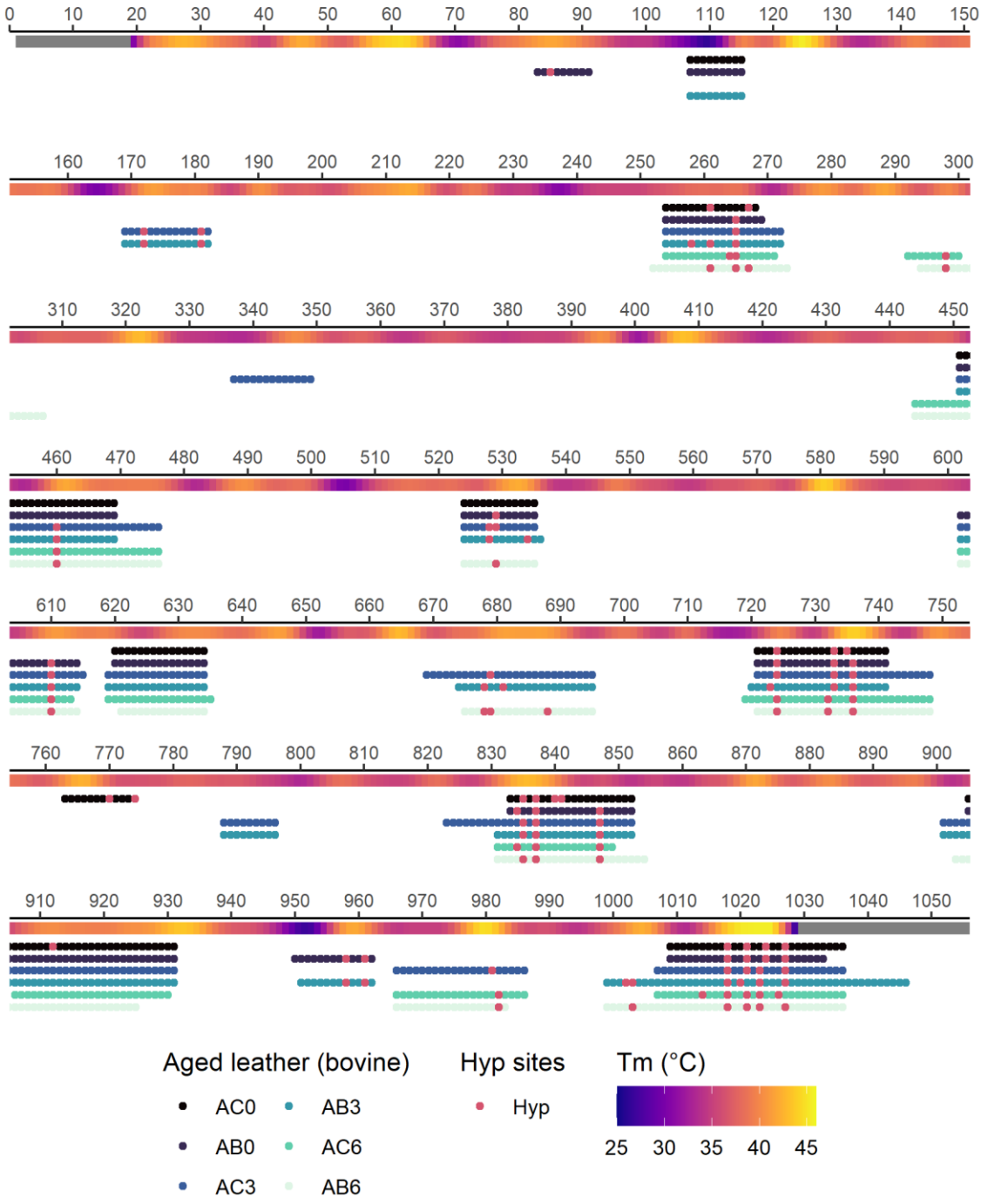

Figure B29. Collagen type I α1 from aged leather samples (buffalo and cow) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

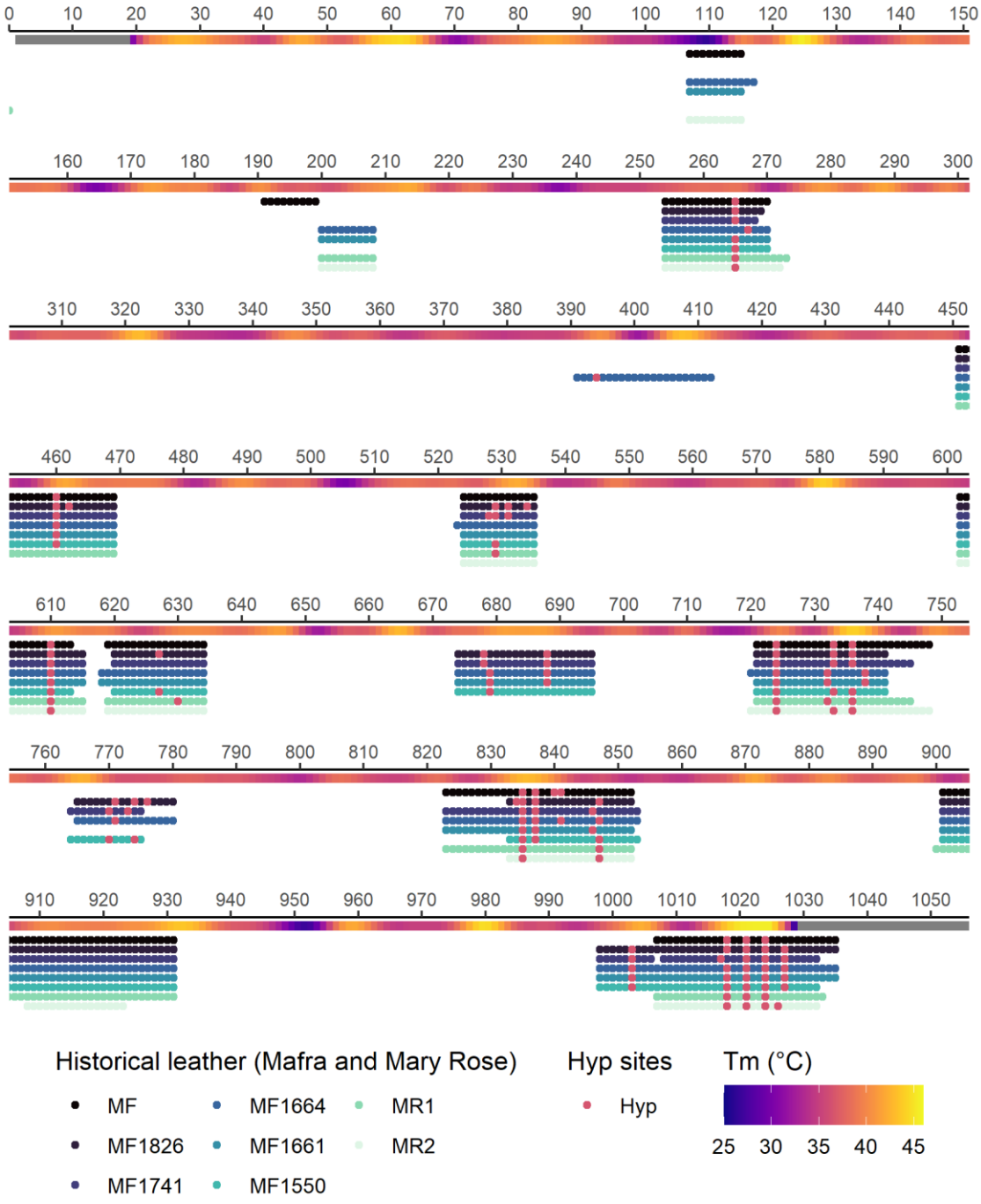

Figure B30. Collagen type I α1 from historical leather samples (Mafra and Mary Rose) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

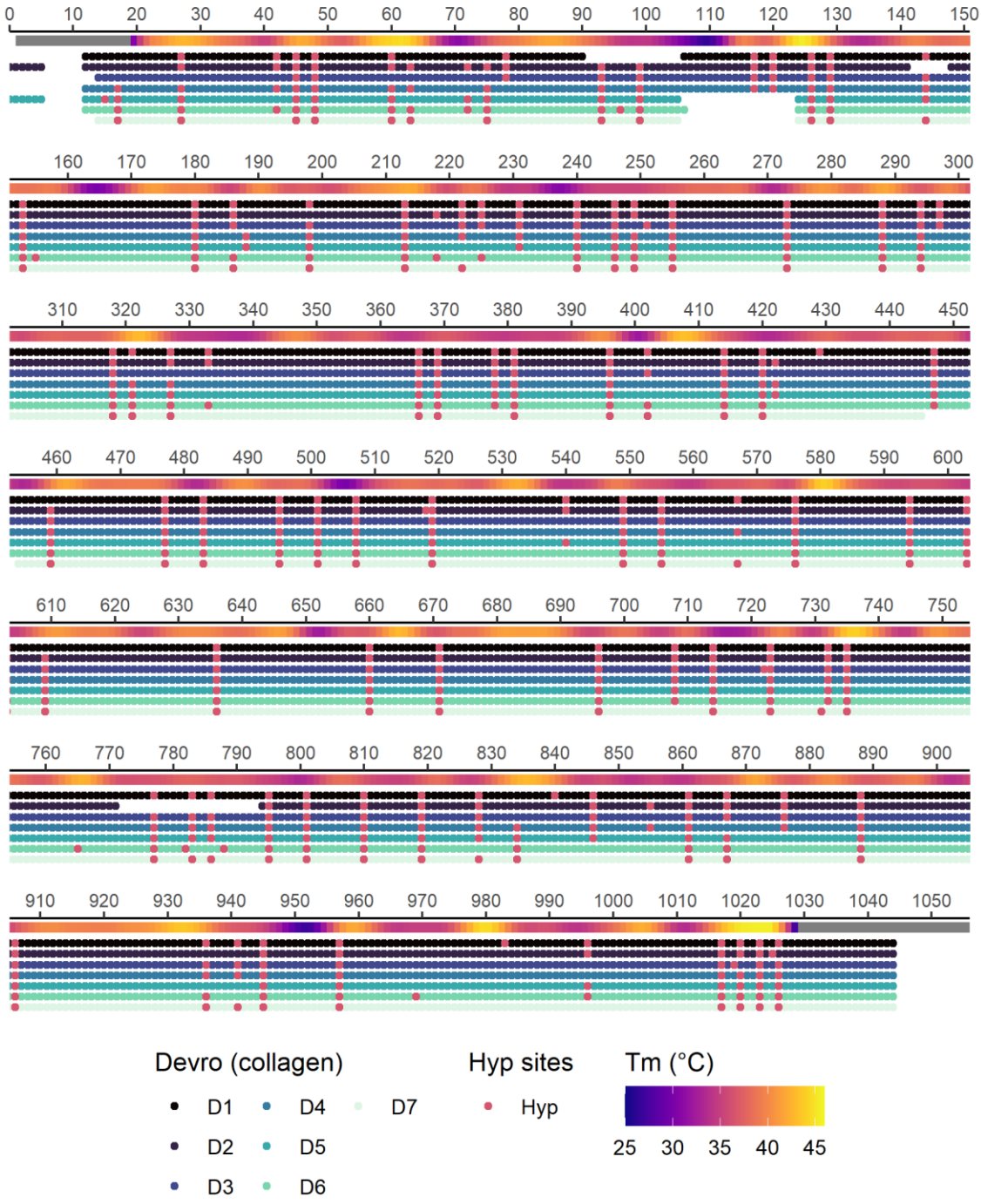

Figure B31. Collagen type I α2 from commercial collagen samples (Devro) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

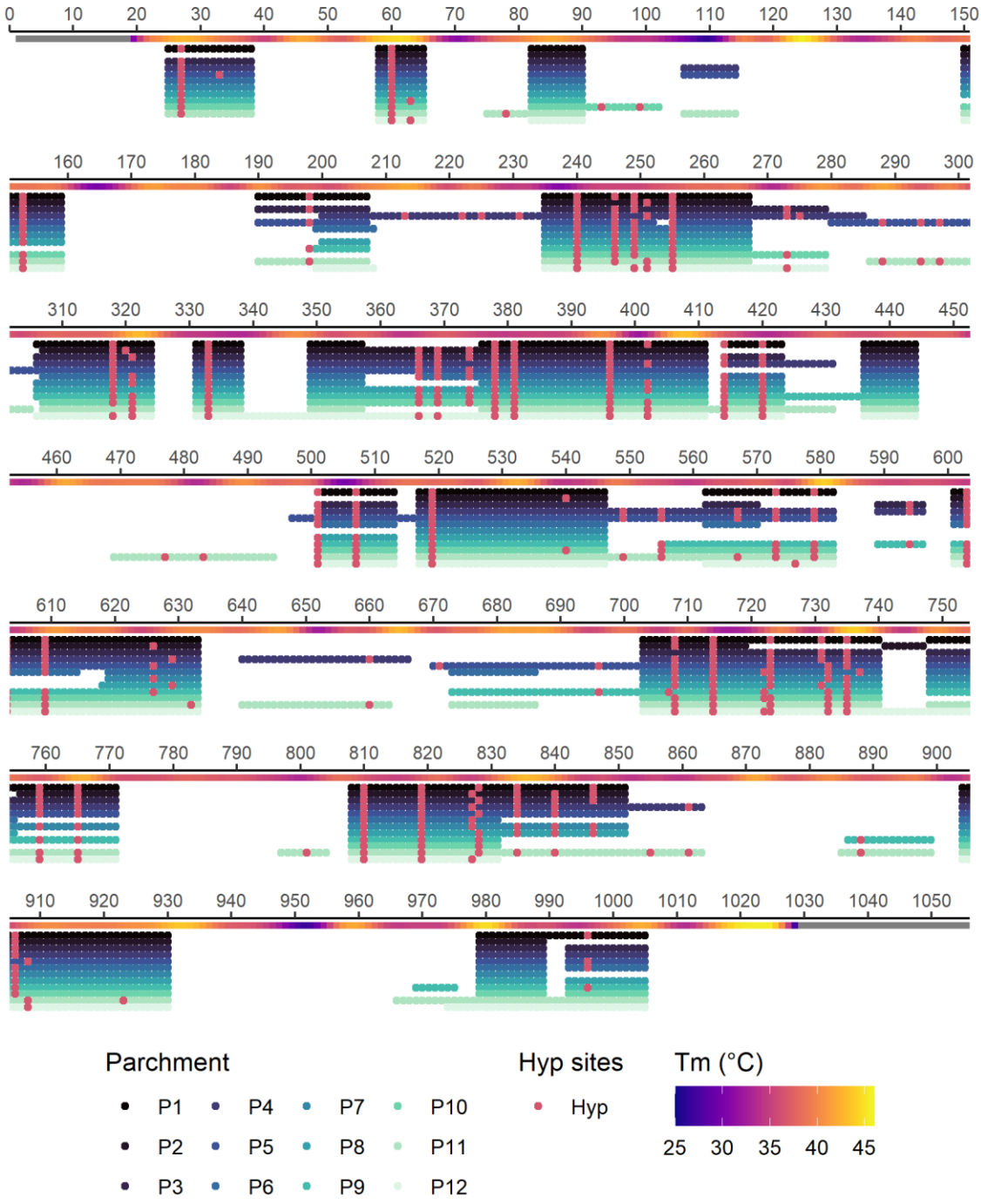

Figure B32. Collagen type I α2 from parchment samples identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

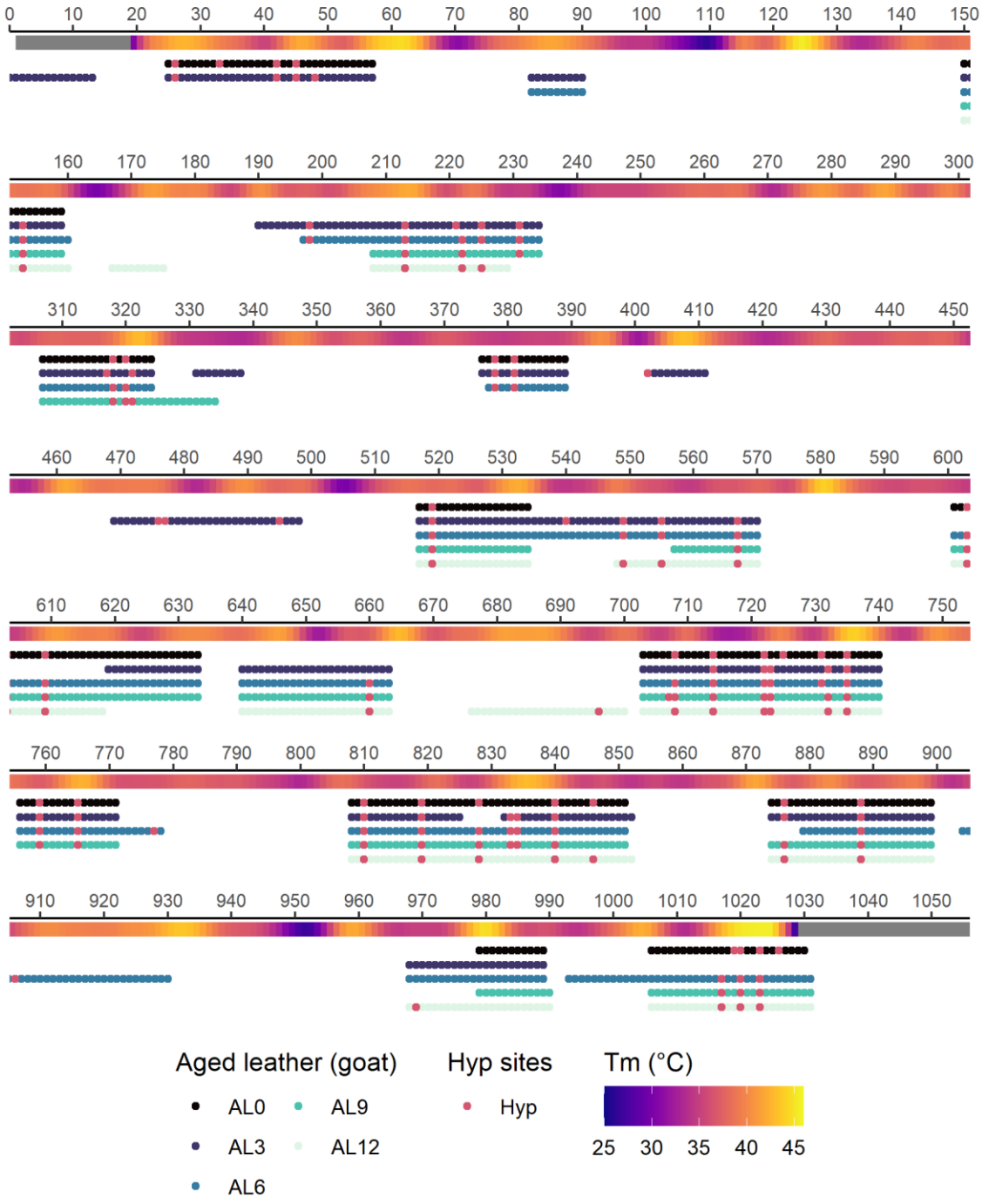

Figure B33. Collagen type I α2 from aged leather samples (goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

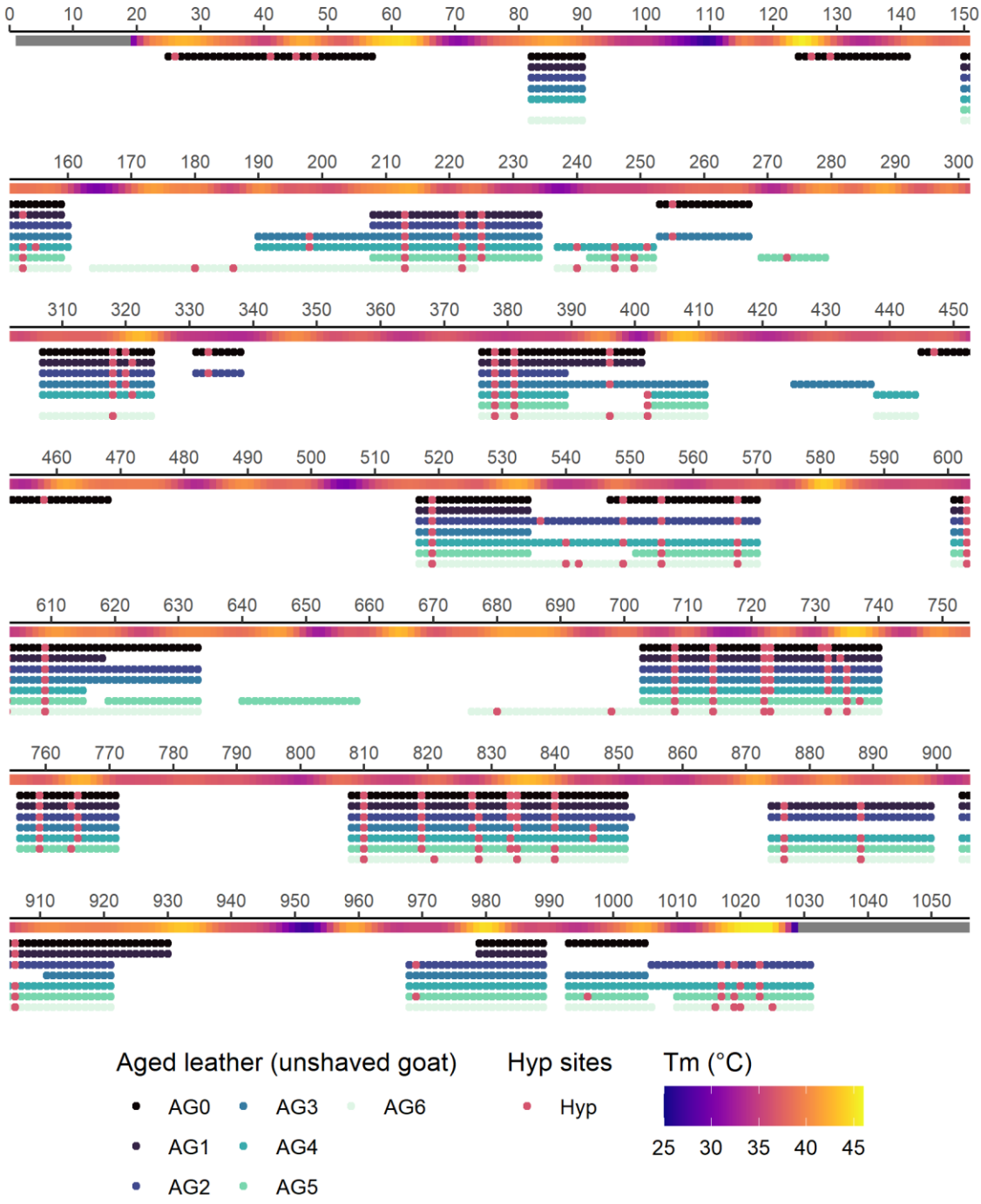

Figure B34. Collagen type I α2 from aged leather samples (unshaved goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

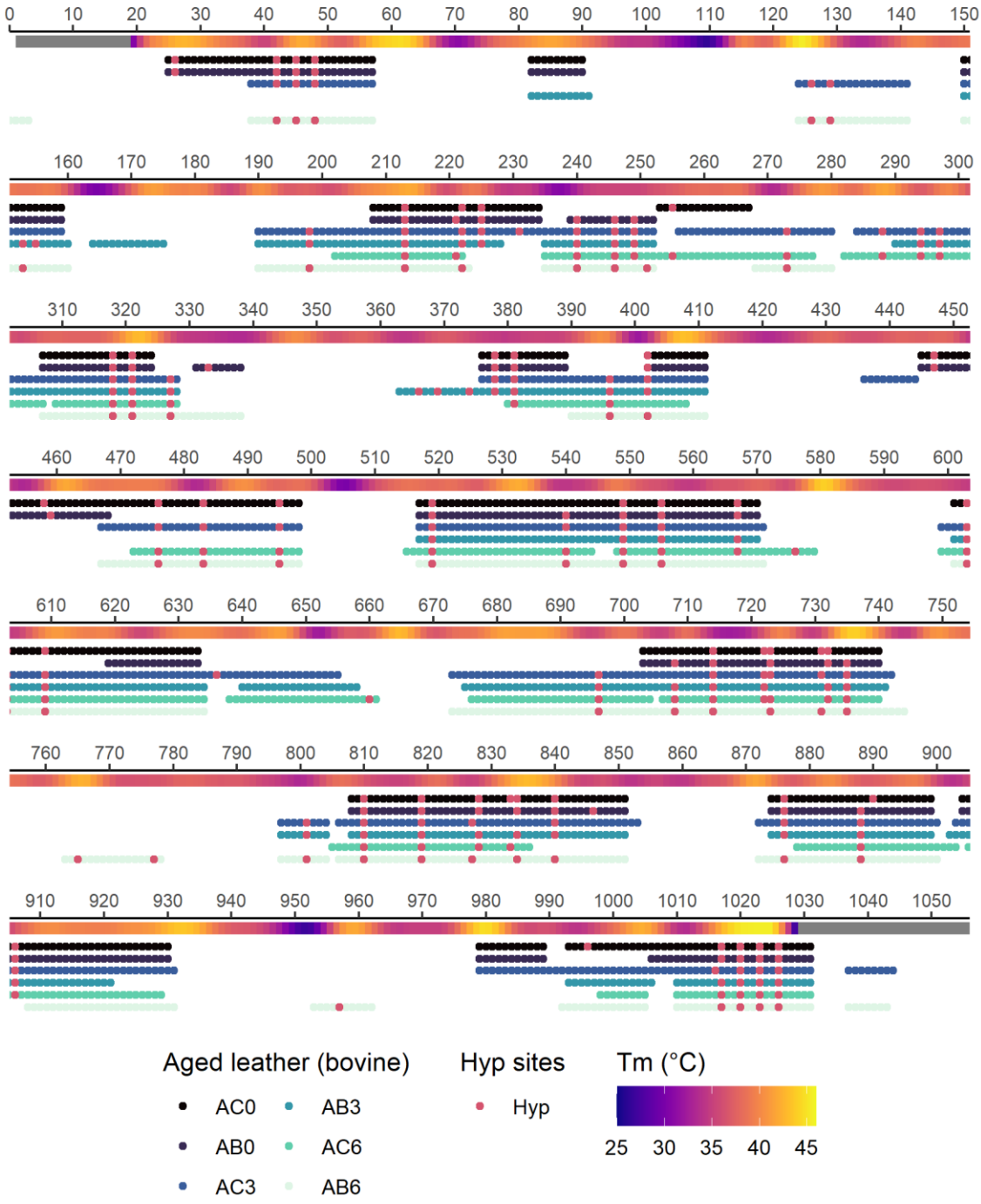

Figure B35. Collagen type I α2 from aged leather samples (buffalo and cow) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

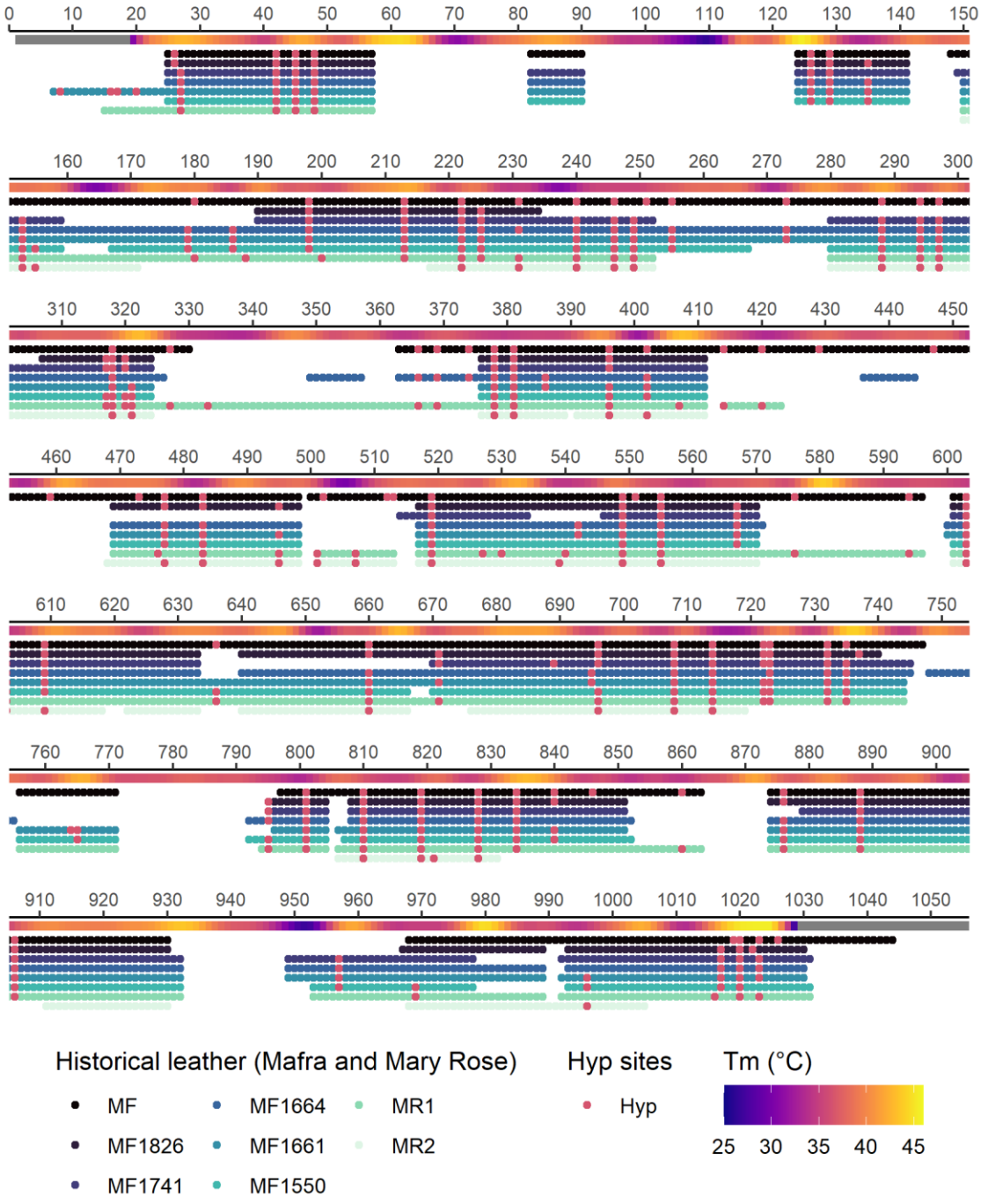

Figure B36. Collagen type I α2 from historical leather samples (Mafra and Mary Rose) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

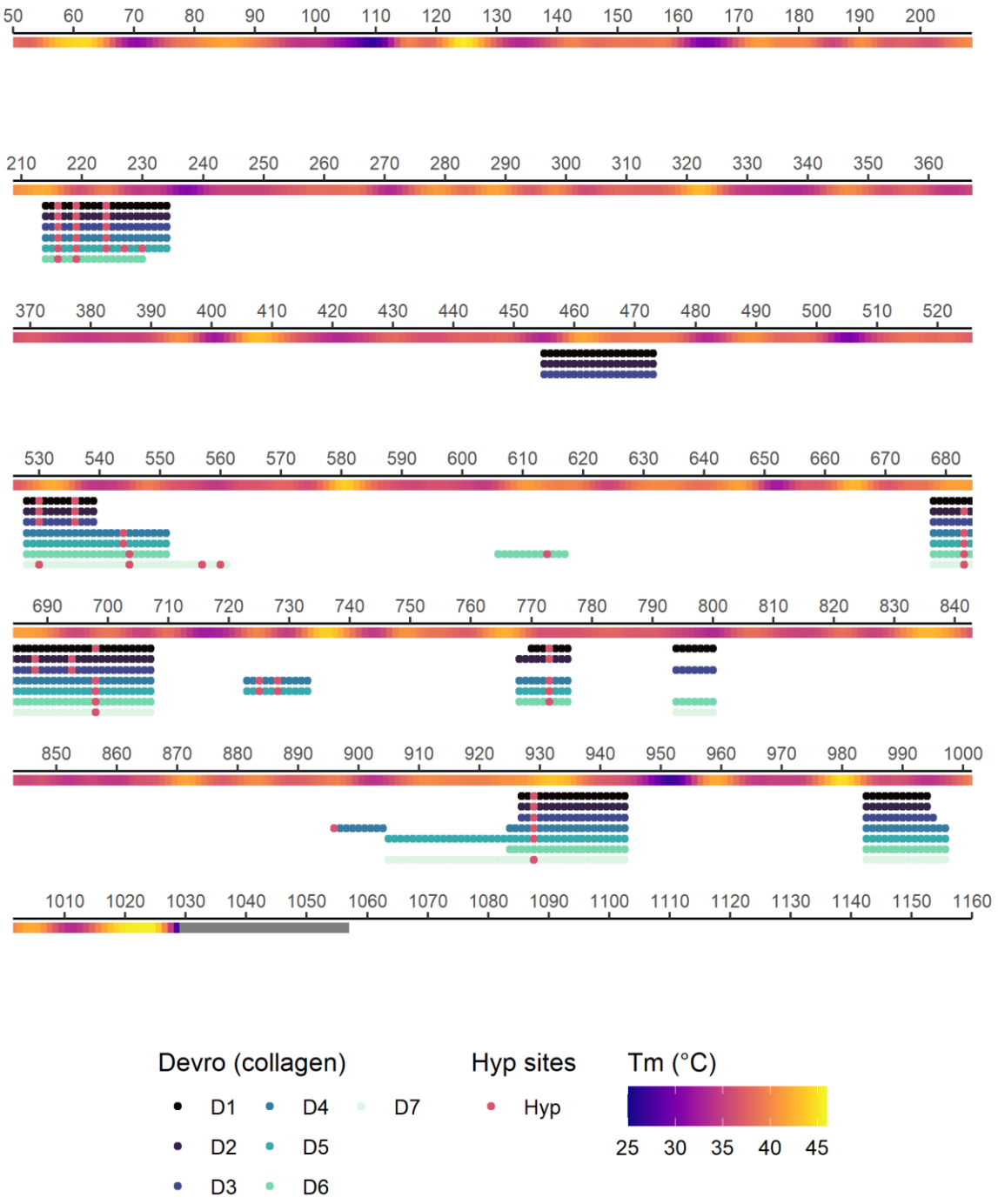

Figure B37. Collagen type III α1 from commercial collagen samples (Devro) identified by LC-MS/MS with collagen chain melting temperature (Tm) hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

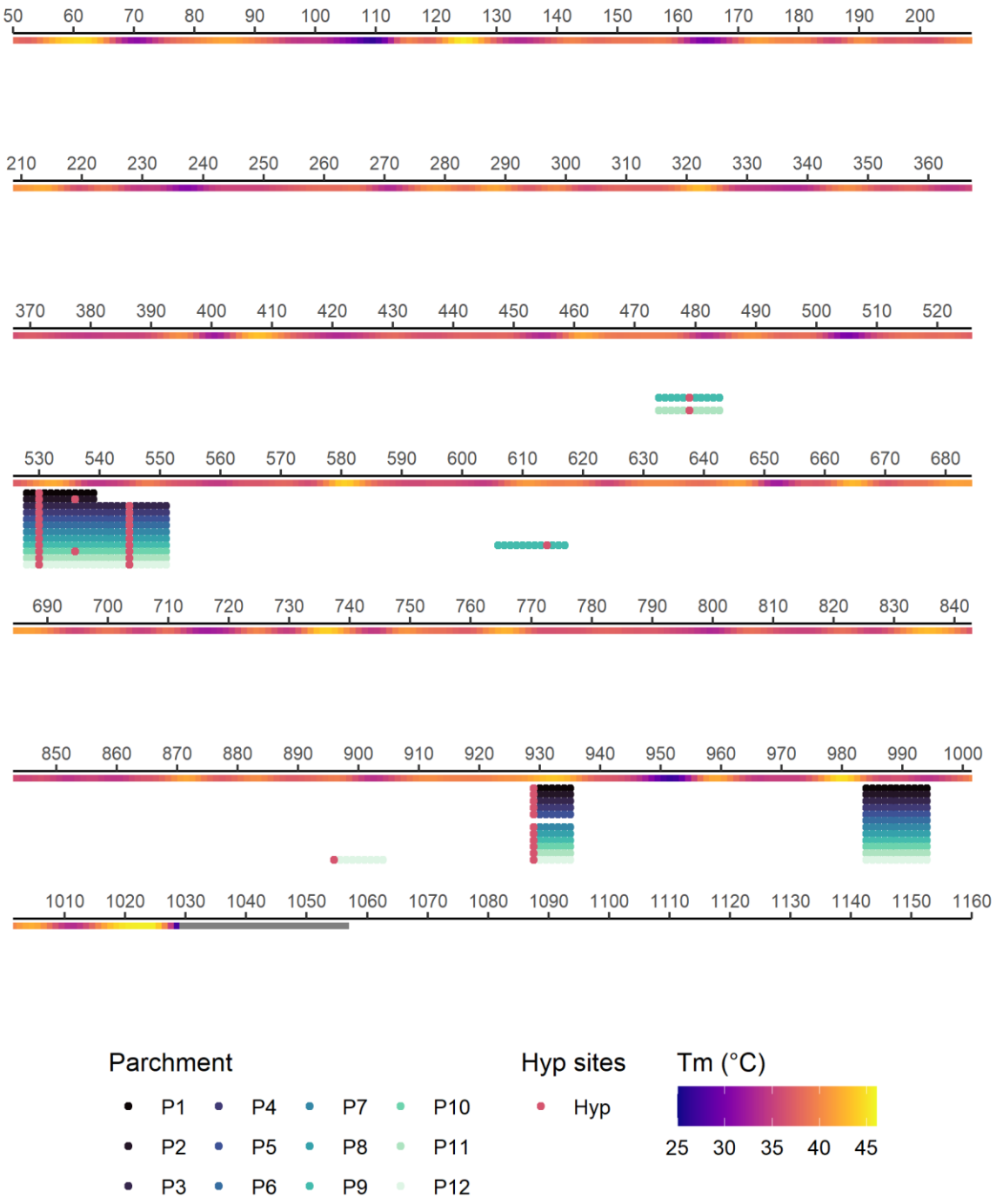

Figure B38. Collagen type III α1 from parchment samples identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

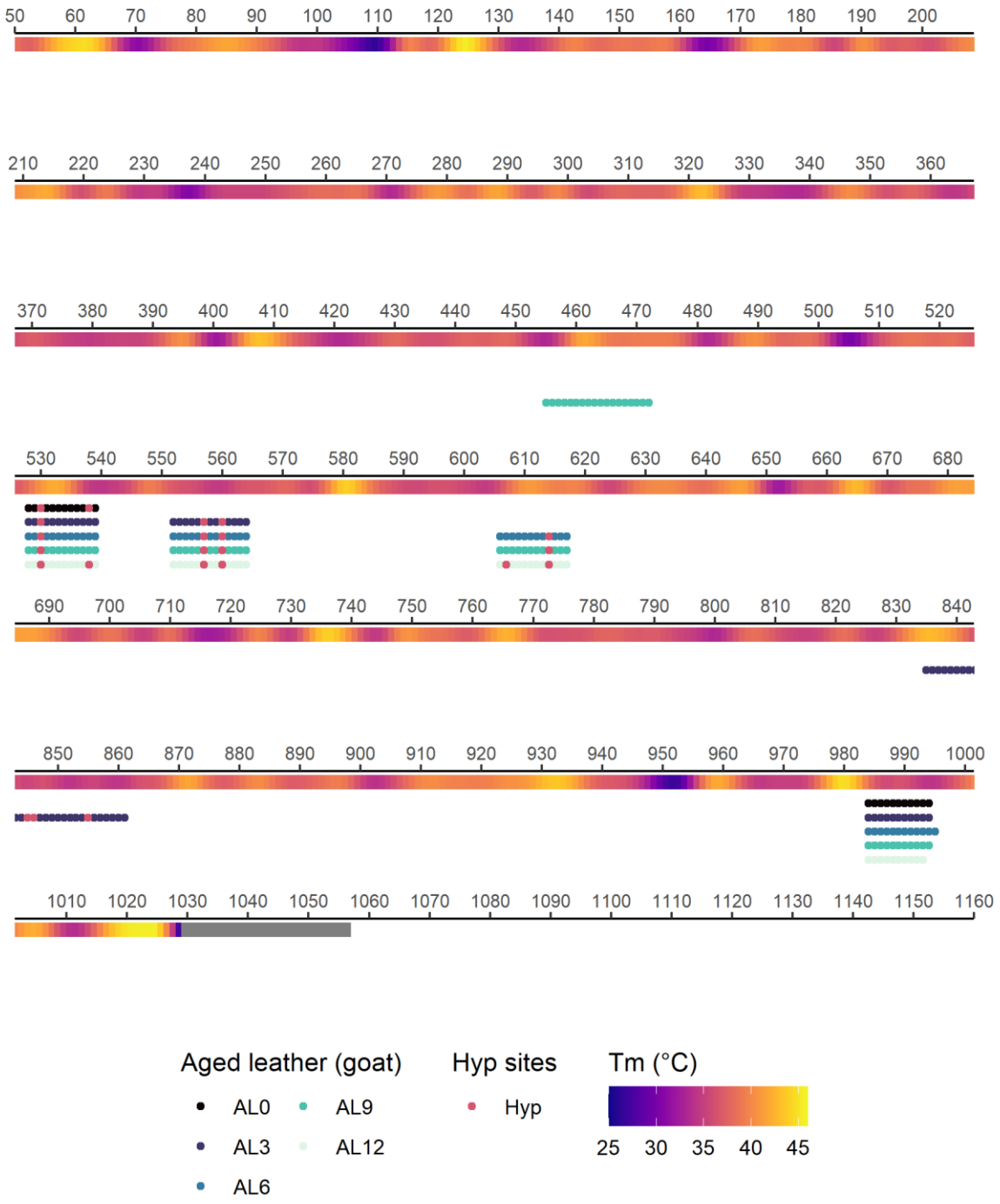

Figure B39. Collagen type III α1 from aged leather samples (goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

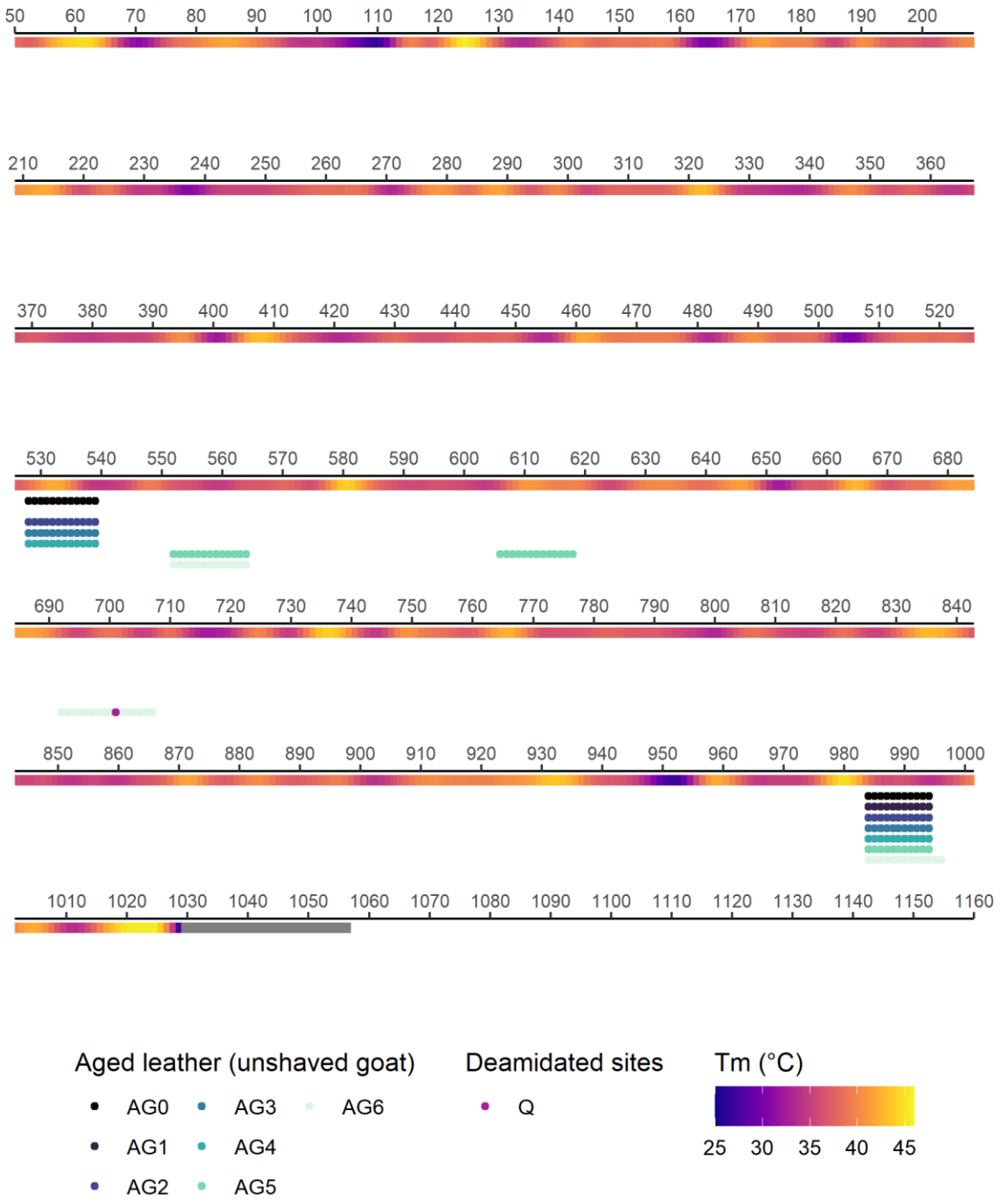

Figure B40. Collagen type III α1 from aged leather samples (unshaved goat) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

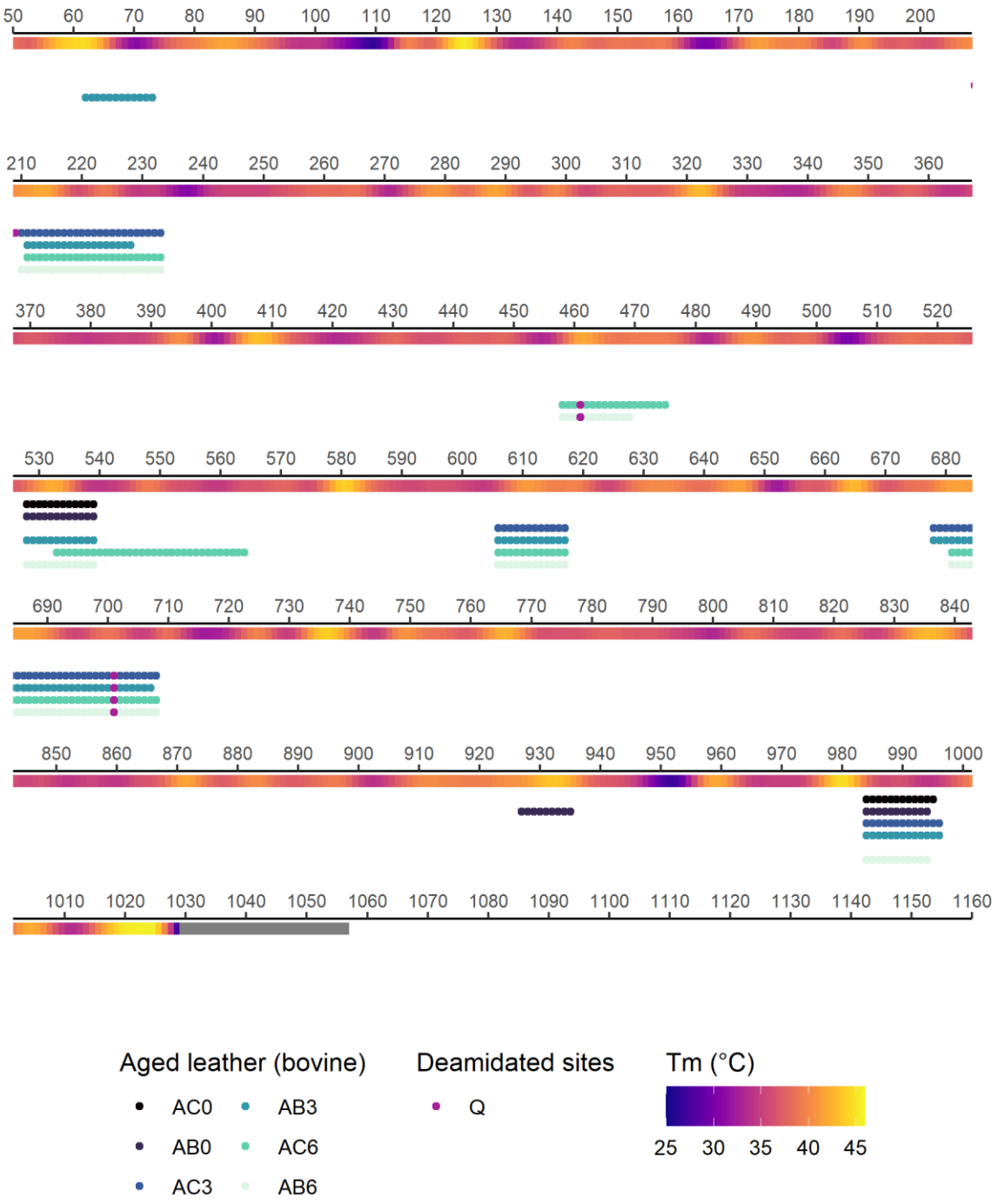

Figure B41. Collagen type III α1 from aged leather samples (buffalo and cow) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

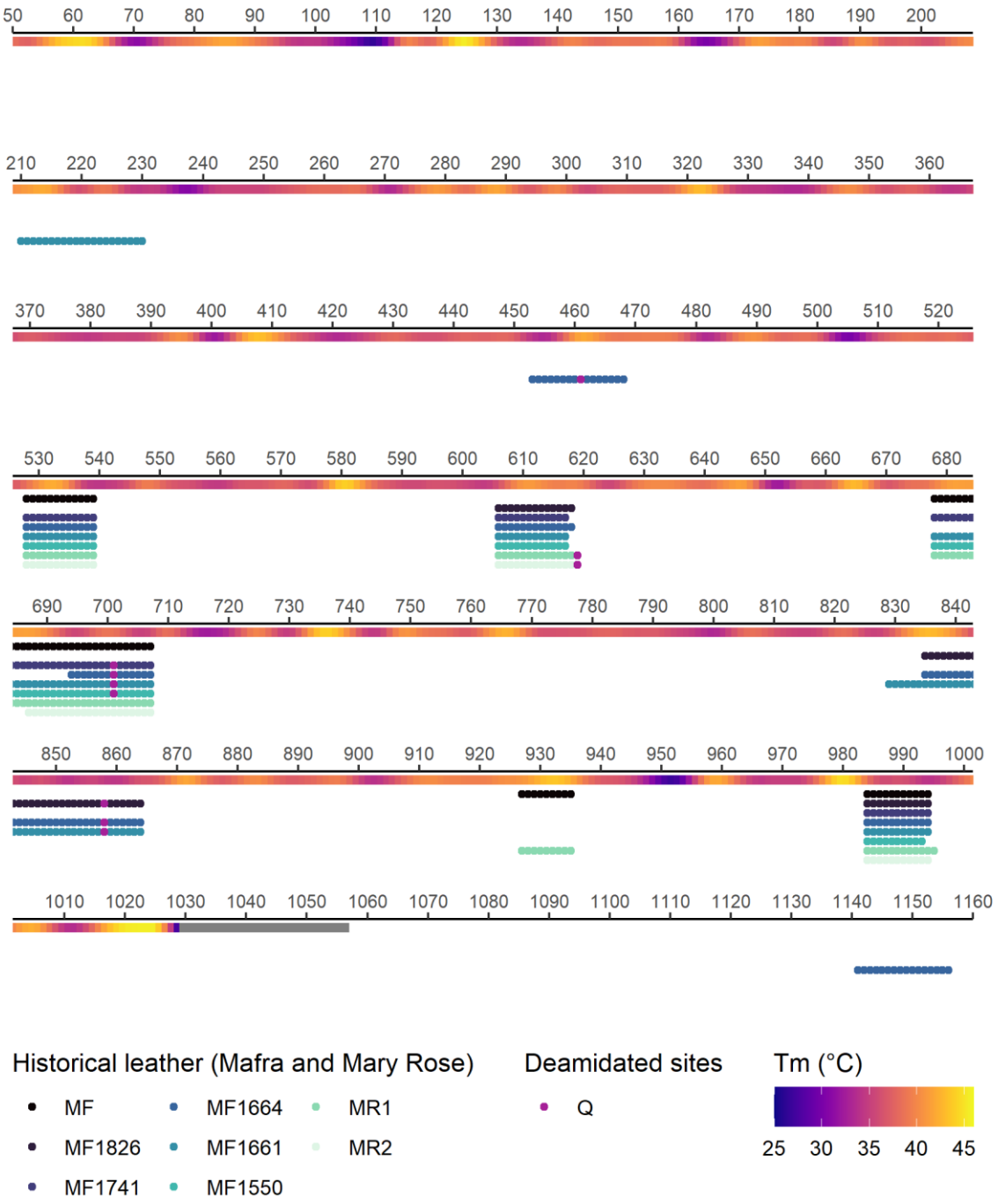

Figure B42. Collagen type III α1 from historical leather samples (Mafra and Mary Rose) identified by LC-MS/MS with collagen chain melting temperature (Tm) and hydroxyproline (Hyp) residues. The x-axis indicates position in the triple-helix. The melting temperature of collagen is directly correlated to the collagen chain stability and flexibility (Collins *et al.*, 1995; Rainey and Goh, 2004). In areas of the triple helix with a low melting temperature, deamidation of asparagine via succinimide (Asu) is more favourable and, under extreme pH conditions, it is possible that peptide cleavage occurs more readily in regions where the collagen chain is unstable and flexible (i.e. has a low Tm).

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