

Supporting Information

Low-invasive sampling method with tape disc sampling for the taxonomic identification of archaeological and paleontological bones by proteomics

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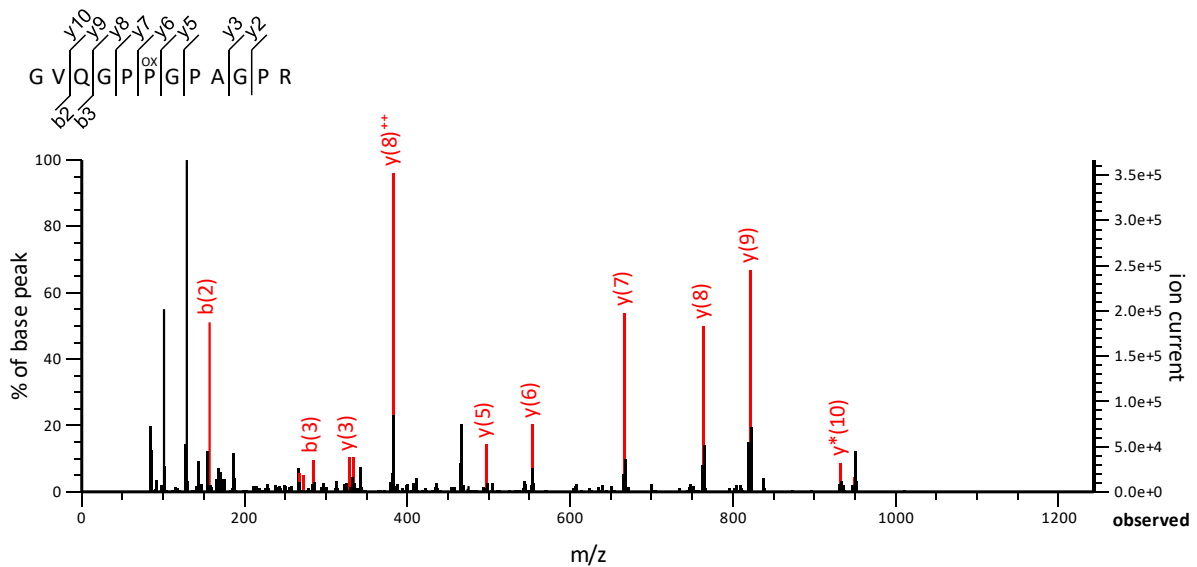
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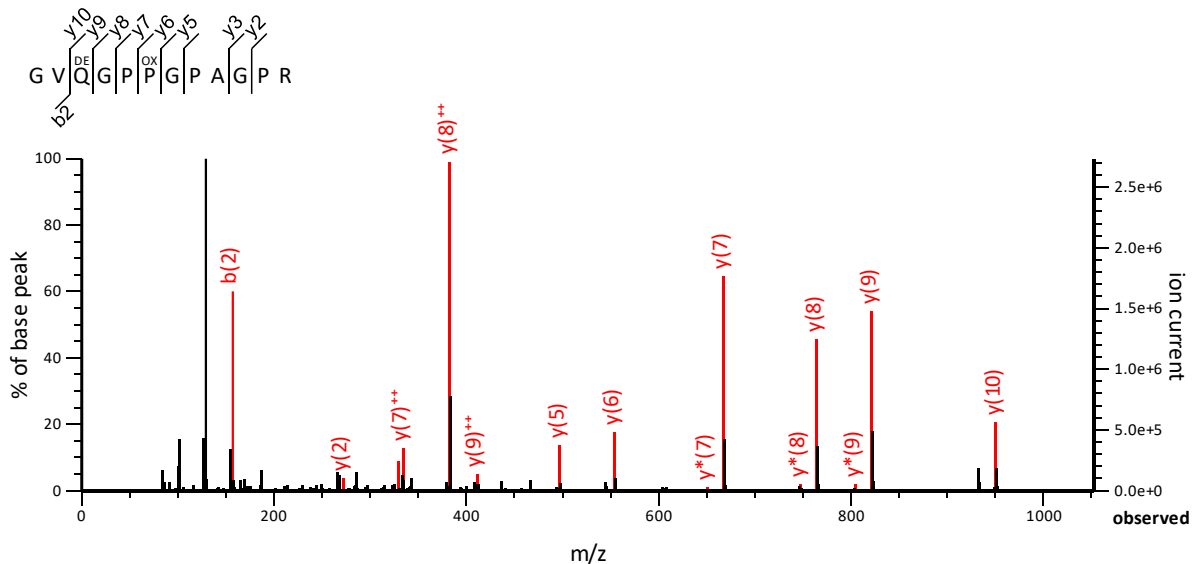


Supplementary Figure S1. MS/MS Fragmentation of GVQGGP^{ox}GPAGPR (peptide P1^m) found in entry AAI05185.1 of NCBI_Mamm, collagen alpha-1(I) chain precursor [*Bos taurus*] from sample Mod 1.

Match to Query 3580: 1104.568456 from (553.291504, 2⁺), intensity (3836956.9609), RT_in_seconds (2580.99978), index (6717)

Monoisotopic mass of neutral peptide Mr(calc): 1104.5676

Variable modifications: P6 Oxidation (P), Ion_Score: 39 Expected: 0.00075

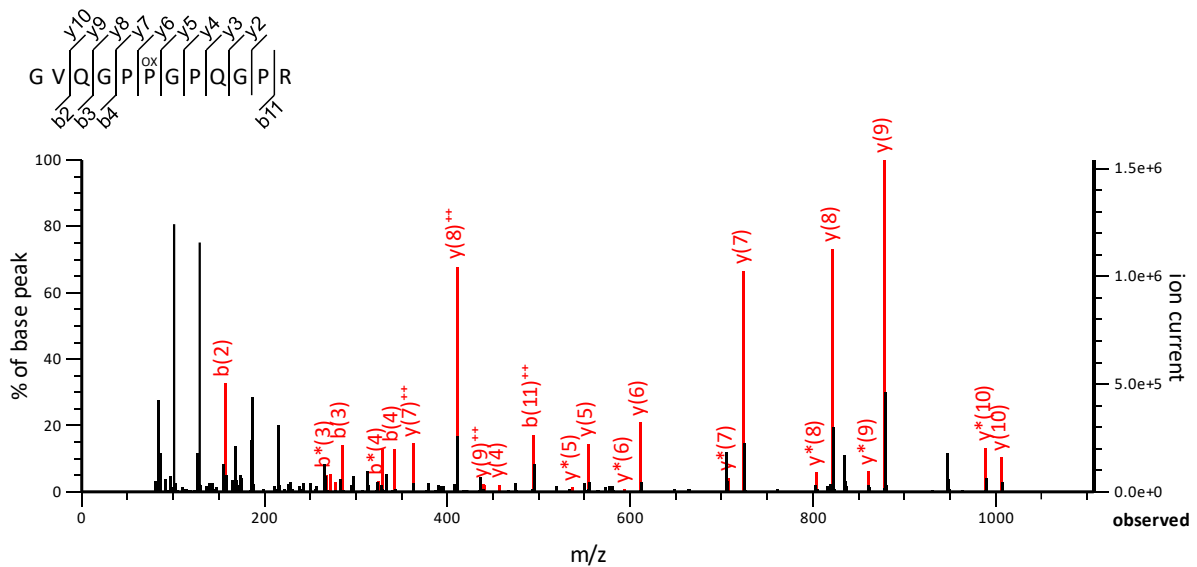


Supplementary Figure S2. MS/MS Fragmentation of GVQ^{dem}GPP^{ox}GPAGPR (peptide P1^m) found in entry AAI05185.1 of NCBI_Mamm, collagen alpha-1(I) chain precursor [*Bos taurus*] from sample Mod 1

Match to Query 3595: 1105.551718 from (553.783135, 2⁺), intensity (30251253.3555), RT_in_seconds (2559.30732), index (6606)

Monoisotopic mass of neutral peptide Mr(calc): 1105.5516

Variable modifications: Q3 Deamidated (NQ), P6 Oxidation (P), Ion_Score: 43 Expected: 0.0021

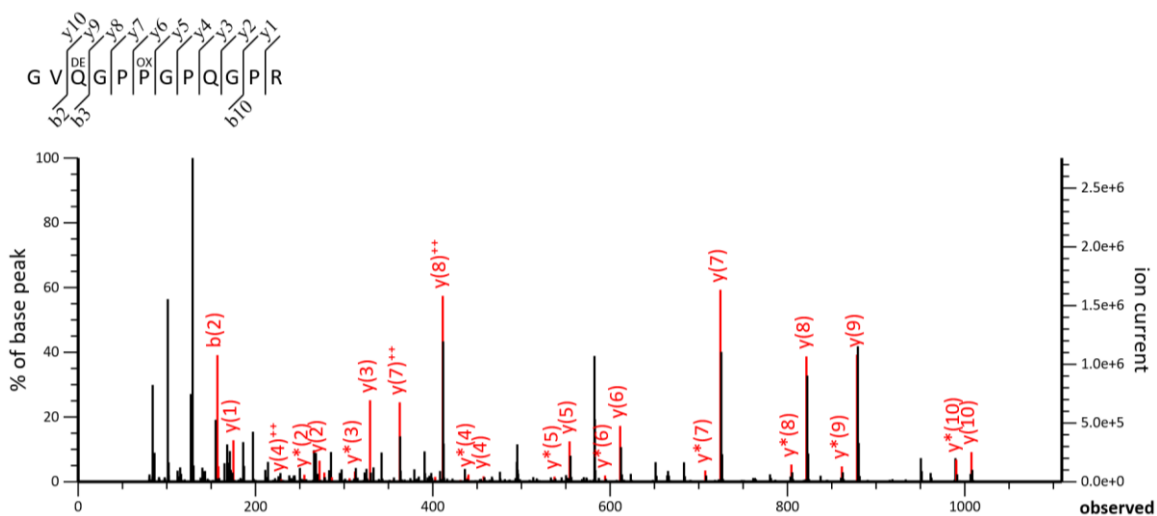


Supplementary Figure S3. MS/MS Fragmentation of GVQGGPP^{ox}GPQGPR (peptide P1^b) from entry XP_009685373.1 of NCBI_Aves, collagen alpha-1(I) chain precursor [*Struthio camelus*] from sample Mod 2.

Match to Query 7536: 1161.589458 from (581.802005, 2⁺), (49137275.2266), RT_in_seconds (1738.7082), index(4717)

Monoisotopic mass of neutral peptide Mr(calc): 1161.5891

Variable modifications: P6 Oxidation (P), Ion_Score: 37 Expected: 0.0036

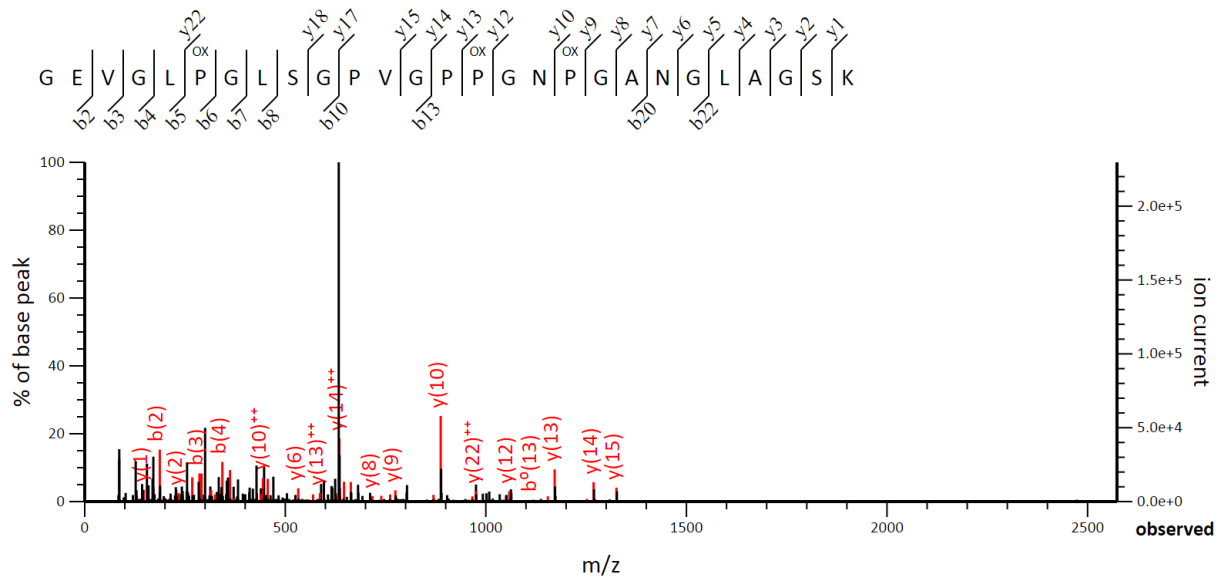


Supplementary Figure S4. MS/MS Fragmentation of GVQ^{dem}GPP^{ox}GPQGPR (peptide P1^b) from entry XP_009685373.1 of NCBI_Aves, collagen alpha-1(I) chain precursor [*Struthio camelus*] from sample Mod 2.

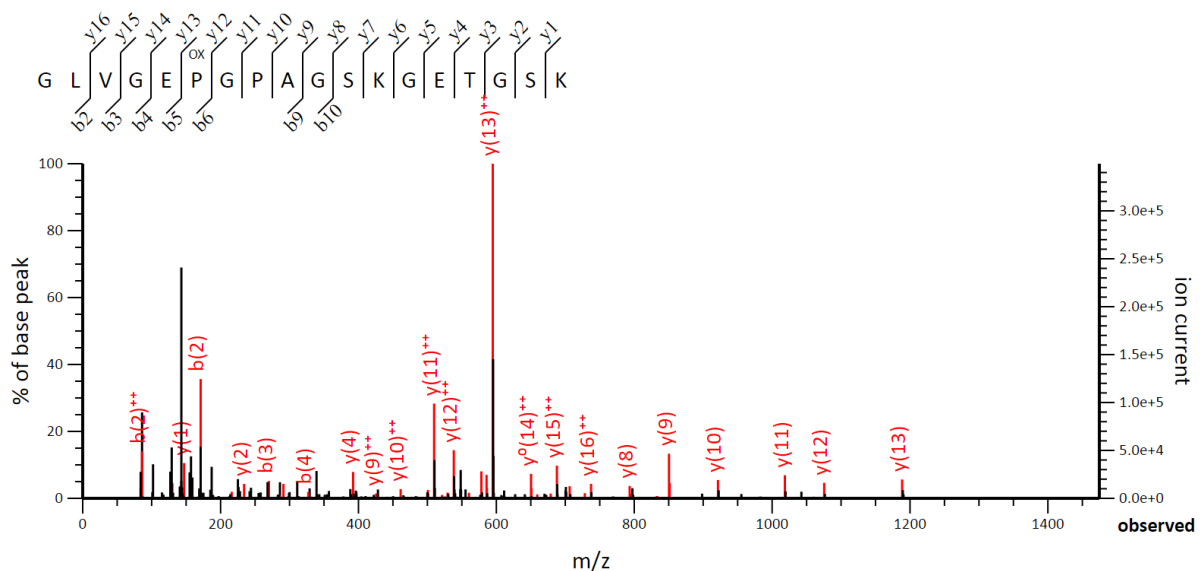
Match to Query 5086: 1044.445320 from (582.291334, 2⁺), intensity (993099.7197), RT_in_seconds (1202.8476), index (1341)

Monoisotopic mass of neutral peptide Mr(calc): 1162.5731

Variable modifications: Q3 Deamidated (NQ), P6 Oxidation (P), Ion_Score: 33, Expected: 0.0067

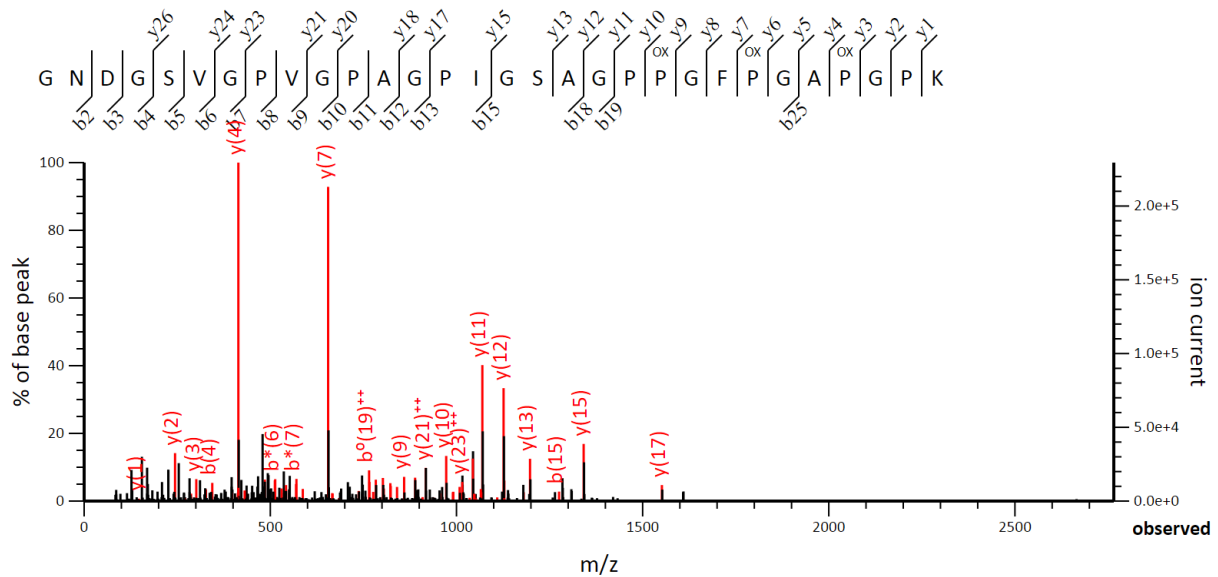


Supplementary Figure S5. MS/MS Fragmentation of GEVGLP^{ox}GLSGPVGPP^{ox}GNP^{ox}GANGLAGSK found in entry JAV39576.1 of NCBI_Mamm, collagen alpha-2(I) chain precursor [*Castor canadensis*] from sample Bou 4. Match to Query 23508: 2403.213642 from (802.078490, 3⁺), intensity (1371103.2500), RT_in_seconds (5108), scans (27653), index (22179) Monoisotopic mass of neutral peptide Mr(calc): 2403.2030 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: P6 Oxidation (P), P15 Oxidation (P), P18 Oxidation (P), Ion_Score: 42 Expected: 0.00049.

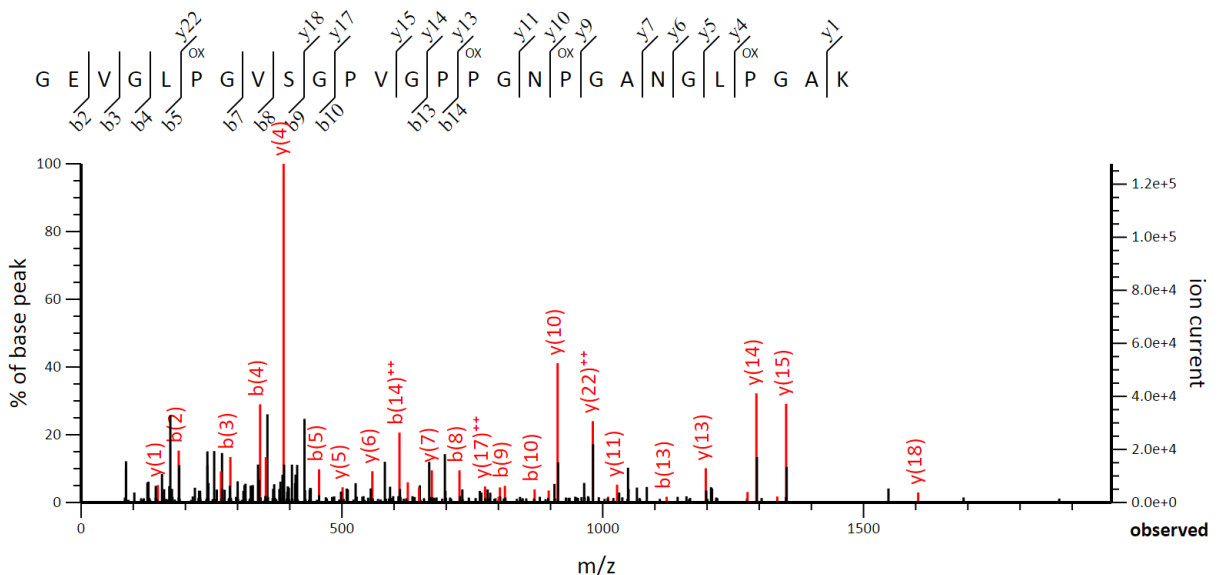


Supplementary Figure S6. MS/MS Fragmentation of GLVGEP^{ox}GPAGSKGETGSK found in entry JAV39576.1 of NCBI_Mamm, collagen alpha-2(I) chain precursor [*Castor canadensis*] from sample Bou 4. Match to Query 15633: 1642.817652 from (548.613160, 3⁺), intensity (2182462.0000), RT_in_seconds (2121), scans (8422), index (4468) Monoisotopic mass of neutral peptide Mr (calc): 1642.8162 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications: P6: Oxidation (P), Ion_Score: 53 Expected: 7.1e-005.

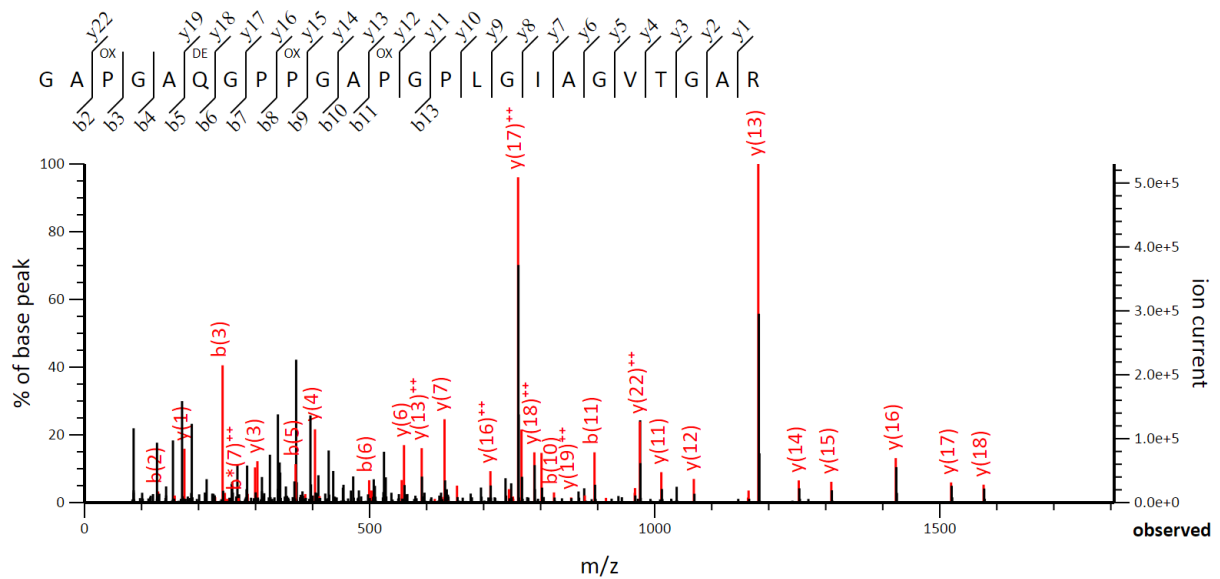


Supplementary Figure S7. MS/MS Fragmentation of GNDGSVGPVGPAGPIGSAGPP^{OX}GFP^{OX}GAP^{OX}GPK found in entry BAX02569.1 of NCBI_Mamm, alpha2 chain of type I collagen [*Sus scrofa domesticus*] from sample Bou 1. Match to Query 22044: 2615.284528 from (1308.649540, 2⁺), intensity (616256.3125), RT_in_seconds (4671), scans (24738), index (19359) Monoisotopic mass of neutral peptide Mr (calc): 2615.2617 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: P21 Oxidation (P), P24 Oxidation (P), P27 Oxidation (P), Ion_Score: 76 Expected: 1.9e-007



Supplementary Figure S8. MS/MS Fragmentation of GEVGLP^{OX}GVSGPVGPP^{OX}GNP^{OX}GANGLPGAK found in entry BAX02569.1 of NCBI_Mamm, alpha2 chain of type I collagen [*Sus scrofa domesticus*] from sample Bou 1. Match to Query 19705: 2415.210048 from (1208.612300, 2⁺), intensity (635233.9375), RT_in_seconds (4373), scans (22853), index (17734) Monoisotopic mass of neutral peptide Mr (calc): 2415.2031 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications: P6 Oxidation (P), P15 Oxidation (P), P18 Oxidation (P), P24 Oxidation (P), Ion_Score: 49 Expected: 2.8e-005



Supplementary Figure S9. MS/MS Fragmentation
of GAP^{ox}GAQ^{dem}GPP^{ox}GAP^{ox}GPLGIAGVTGAR found in entry XP_043343785.1 of NCBI_Mamm, collagen alpha-1(III) chain [*Cervus canadensis*] from sample Mod 4.

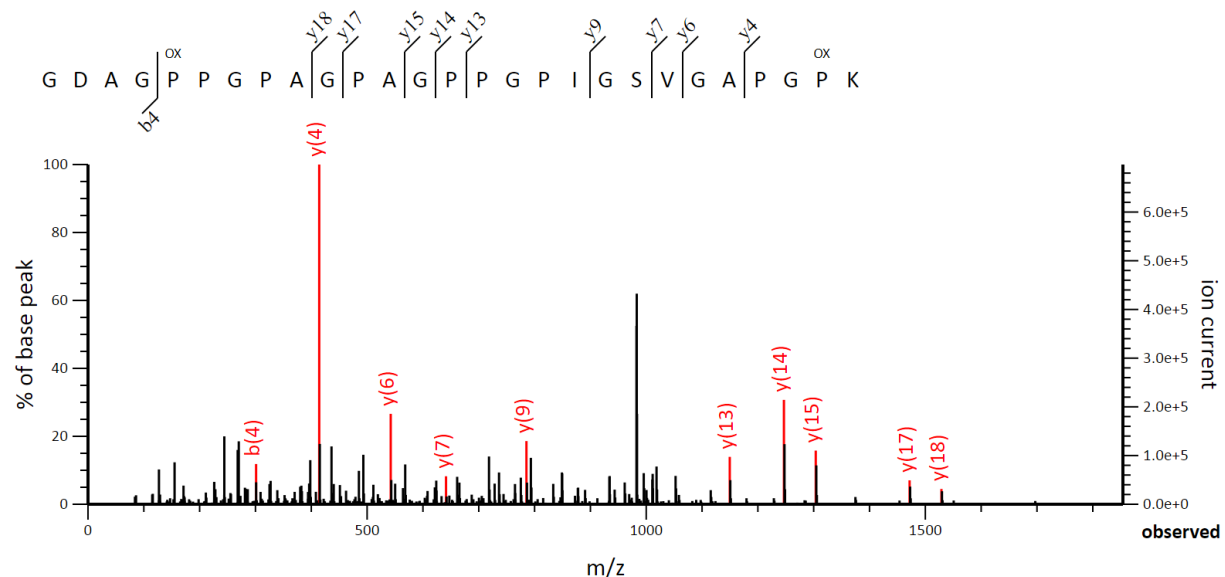
Match to Query 15178: 2074.051128 from (1038.032840, 2⁺), intensity (3587856.2500), RT_in_seconds (4777), scans (25815), index (20162)

Monoisotopic mass of neutral peptide Mr(calc): 2074.0444

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications: P3 Oxidation (P), Q6 Deamidated (NQ), P9 Oxidation (P)

P12 Oxidation (P), Ion_Score: 72 Expected: 1e-006



Supplementary Figure S10. MS/MS Fragmentation
of GDAGP^{ox}PGPAGPAGPPGPIGSVGVGAPGPO^{ox}K found in

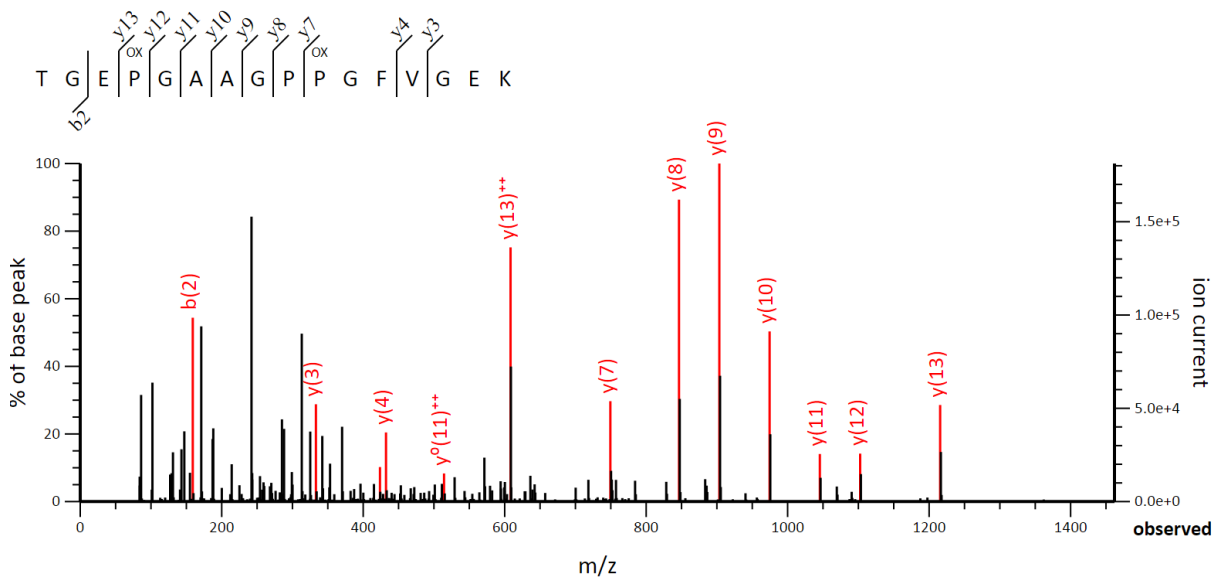
entry sp|C0HJN9.1|C01A1_EQUSP of NCBI_Mamm, RecName: Full=Collagen alpha-1(I) chain; AltName: Full=Alpha-1 type I collagen [*Equus caballus*] from sample Trem 1.

Match to Query 19001: 2263.124368 from (1132.569460, 2⁺), intensity (7975591.5000), RT_in_seconds (4346), scans (22744), index (17398)

Monoisotopic mass of neutral peptide Mr (calc): 2263.1234

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications: P5 Oxidation (P), P26 Oxidation (P), Ion_Score: 54 Expected: 1.8e-005



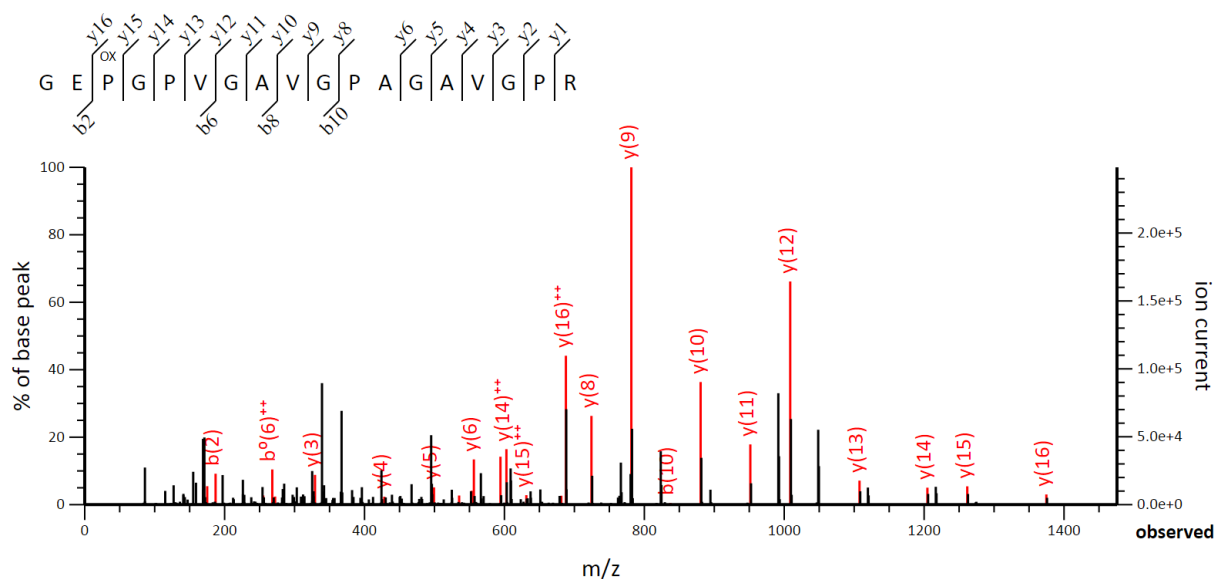
Supplementary Figure S11. MS/MS Fragmentation of TGE^{ox}P^{ox}GAA^{ox}GP^{ox}GFVGEK found in entry XP_004007775.1 of NCBI_Mamm, collagen alpha-2(I) chain [*Ovis aries*] from sample PE-F55.

Match to Query 18985: 1501.703648 from (751.859100, 2⁺), scans (17233), RT_in_seconds (3478.58544), index (12775)

Monoisotopic mass of neutral peptide Mr(calc): 1501.7049

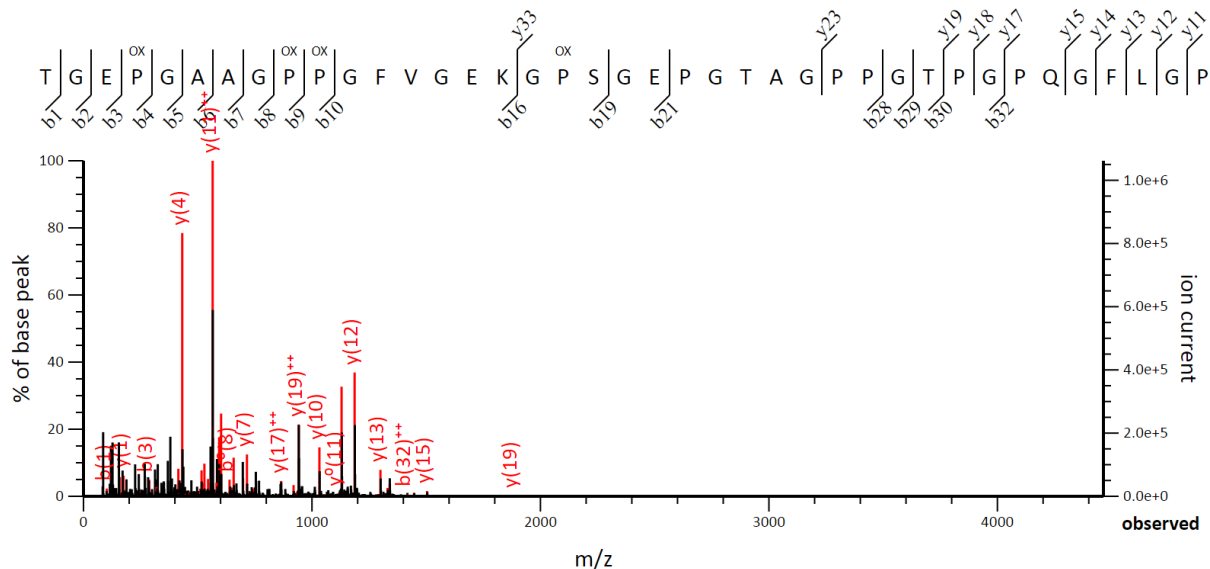
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications: P4 Oxidation (P), P10 Oxidation (P), Ion_Score: 55 Expected: 8.8e-005



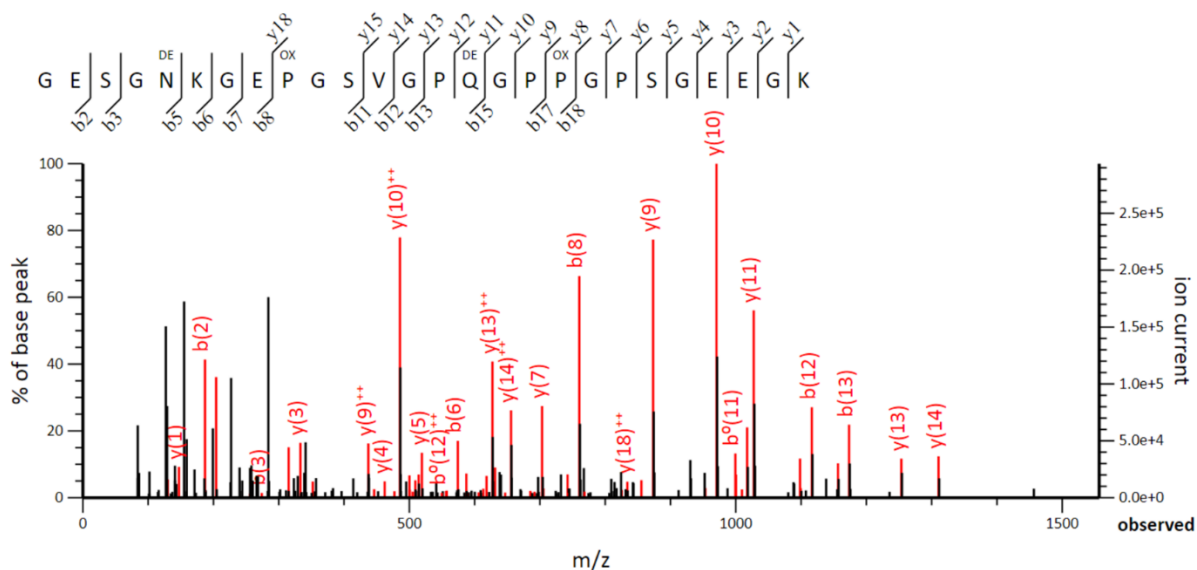
Supplementary Figure S12. MS/MS Fragmentation of GEP^{ox}GPVGA^{ox}VGPAGAVGPR found in entry XP_004007775.1 of NCBI_Mamm, collagen alpha-2(I) chain [*Ovis aries*] from sample PE-F55.

Match to Query 12588: 1434.702732 from (479.241520, 3⁺) intensity (9234155.0000)
 RT_in_seconds (2230) scans (11044) index (7752)
 Monoisotopic mass of neutral peptide Mr (calc): 1434.7004
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications: P9 Oxidation (P), Ion_Score: 38 Expected: 0.00048



Supplementary Figure S15. MS/MS Fragmentation
 of TGEPOXGAAGPPOXGFVGEKGPoxSGEPGTAGPPGTPGPQGFGLGPPoxGFLGLPoxGSR
 found in entry XP_005678993.1 of NCBI_Mamm, PREDICTED: collagen alpha-2(I) chain
 [*Capra hircus*] from sample PE-F21.

Match to Query 37849: 4560.212576 from (1141.060420, 4⁺) intensity (2038266.3750),
 RT_in_seconds (6806), scans (34309), index (26141)
 Monoisotopic mass of neutral peptide Mr(calc): 4560.1835
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications: P4 Oxidation (P), P9 Oxidation (P), P10 Oxidation (P), P18 Oxidation
 (P), P40 Oxidation (P), P46 Oxidation (P), Ion_Score: 55 Expected: 1.3e-005



Supplementary Figure S16. MS/MS Fragmentation of GESGN^{dem}KGEP^{ox}GSVGPQ^{dem}GPP^{ox}GPSGEEGK found in entry XP_008684476.1 of NCBI_Mamm, PREDICTED: collagen alpha-2(I) chain [*Ursus maritimus*] from sample Lov 11.

Match to Query 22640: 2425.050612 from (809.357480, 3⁺), intensity (24988886.0000), RT_in_seconds (2327), scans (9383), index (5089)

Monoisotopic mass of neutral peptide Mr(calc): 2425.0517

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications: N5 Deamidated (NQ), P9 Oxidation (P), Q15 Deamidated (NQ), P18 Oxidation (P), Ion_Score: 56 Expected: 0.00072