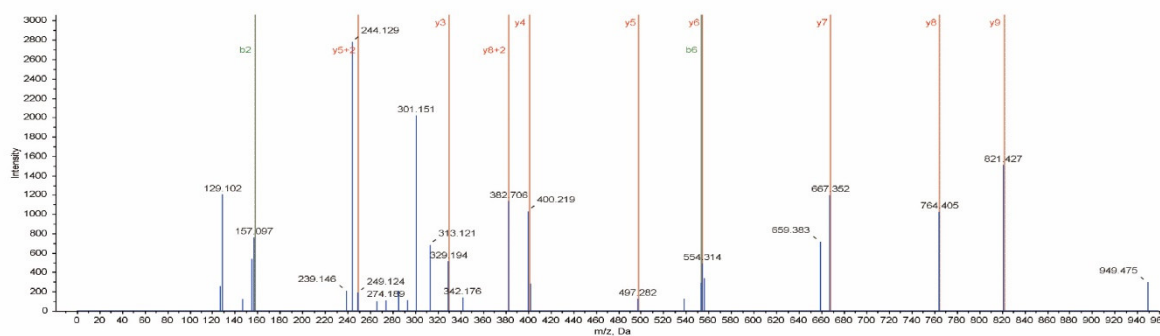


Supporting Information

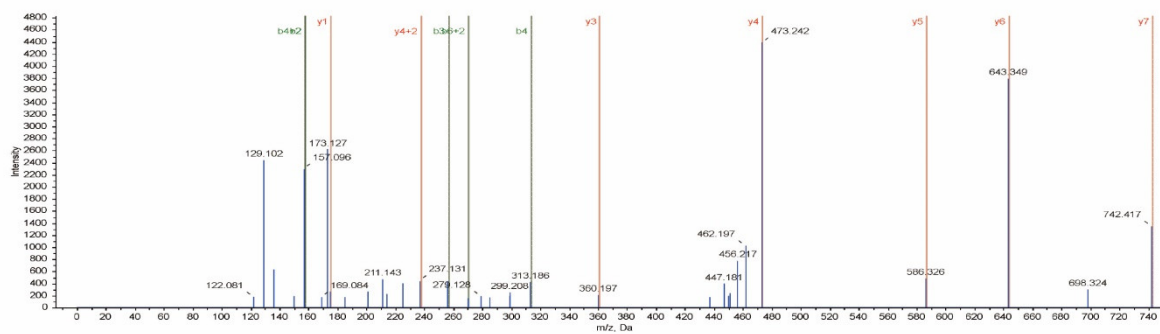
Organic Materials Used for Giant Buddhas and Wall Paintings in Bamiyan, Afghanistan

GVVGLPGQR



Residue	b	b+2	y	y+2
G	58.03	29.52	1106.56	553.78
V	157.10	79.05	1049.54	525.27
Q[Dea]	286.14	143.57	950.47	475.74
G	343.16	172.08	821.43	411.22
P	440.21	220.61	764.41	382.71
P[Oxi]	553.26	277.13	667.35	334.18
G	610.28	305.65	554.30	277.66
P	707.34	354.17	497.28	249.15
A	778.37	389.69	400.23	200.62
G	835.39	418.20	329.19	165.10
P	932.45	466.73	272.17	136.59
R	1088.55	544.78	175.12	88.06

GVQGGPPGAGPR



Residue	b	b+2	y	y+2
G	58.03	29.52	898.51	449.76
V	157.10	79.05	841.49	421.25
V	256.17	128.59	742.42	371.71
G	313.19	157.10	643.35	322.18
L	426.27	213.64	586.33	293.67
P[Oxi]	539.32	270.16	473.25	237.13
G	596.34	298.67	360.20	180.60
Q	724.40	362.70	303.18	152.09
R	880.50	440.75	175.12	88.06

Figure S1. MS/MS spectra of peptides identified for type I collagen α 1-chain in BMM194.

	Score	Mass	Matches	Sequences	emPAI							
4.1	CO1A2_BOVIN	147	128985	7 (7)	7 (7)	0.22						
Collagen alpha-2(I) chain OS=Bos taurus GN=COL1A2 PE=1 SV=2												
▼ 7 peptide matches (7 non-duplicate, 0 duplicate)												
Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Rank	U	Peptide			
4697	605.1700	1208.3254	1207.6673	0.6581	0	43	0.026	▶ ₁	U R.IGQPGAVGPGAGIR.G + Oxidation (P)			
4939	631.5900	1261.1654	1260.6211	0.5444	0	44	0.0017	▶ ₁	U R.GEAGPAGPAGPAGPR.G			
4954	634.5400	1267.0654	1266.6681	0.3974	0	45	0.0021	▶ ₁	U R.GIPGVPVGAAGATGAR.G + Oxidation (P)			
6054	791.2400	1580.4654	1579.7591	0.7064	0	64	0.00021	▶ ₁	U R.GPPGESGAAGPTGPIGSR.G + Oxidation (P)			
6161	809.1200	1616.2254	1615.7954	0.4300	0	35	0.01	▶ ₁	U K.GELGVPVGNPAGPAGPR.G + Deamidated (NQ); Oxidation (P)			
8160	1066.2800	2130.5454	2130.1070	0.4385	0	68	0.00092	▶ ₁	U R.GLPCVAGSVGEPGGLIAGPPGAR.G + 3 Oxidation (P)			
8648	1131.3700	2260.7254	2260.1237	0.6018	0	57	6.5e-005	▶ ₁	U R.GYPGNAGVPVGAAGAPGPGVPVVGK.H + 2 Oxidation (P)			
▶ 3 subsets and intersections (4 subset proteins in total)												
	Score	Mass	Matches	Sequences	emPAI							
6.1	CO1A1_BOVIN	115	138854	8 (8)	7 (7)	0.23						
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3												
6.2	CO1A1_HUMAN	91	138827	4 (4)	3 (3)	0.11						
Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=4												
6.3	CO1A1_CHICK	70	137670	2 (2)	2 (2)	0.05						
Collagen alpha-1(I) chain OS=Gallus gallus GN=COL1A1 PE=1 SV=3												
▼ 10 peptide matches (10 non-duplicate, 0 duplicate)												
Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Rank	U	1	2	3	Peptide
5007	641.6100	1281.2054	1280.6109	0.5945	0	46	0.0048	▶ ₁	U	■		K.GEAGPSGPGAGTGAR.G
5155	667.2000	1332.3854	1331.6470	0.7384	0	47	0.0066	▶ ₁	U	■		R.GPSGPGSPGPPGPK.G + Oxidation (P)
5488	718.4000	1434.7854	1434.6739	0.1115	0	61	0.00055	▶ ₁	U	■		R.GEPPAGLPGPPGER.G + 3 Oxidation (P)
5577	730.5500	1459.0854	1458.6852	0.4003	0	62	0.0036	▶ ₁	U	■	■	R.GSAGPPGATGPPGAAGR.V + 2 Oxidation (P)
5943	774.1300	1546.2454	1545.7900	0.4555	0	52	0.00051	▶ ₁	U	■		R.GETGPAGPAGPVPVVGAR.G
5999	781.2700	1560.5254	1559.8056	0.7198	0	40	0.013	▶ ₁	U	■		R.GETGPAGPAGPVPVVGAR.G
9833	903.0600	2706.1582	2705.2318	0.9264	0	54	0.028	▶ ₁	U	■	■	R.GFSGLGPPGPPGSPGEGQGPSGASGPAGPR.G + Deamidated (NQ); 3 Oxidation (P)
9834	903.5800	2707.7182	2706.2158	1.5024	0	53	0.0018	▶ ₁	U	■	■	R.GFSGLGPPGPPGAPGEGQGPSGASGPAGPR.G + 2 Deamidated (NQ); 4 Oxidation (P)
9834	903.5800	2707.7182	2706.2158	1.5024	0	51	0.0026	▶ ₂	U	■	■	R.GFSGLGPPGPPGSPGEGQGPSGASGPAGPR.G + 2 Deamidated (NQ); 3 Oxidation (P)
10168	951.9800	2852.9182	2852.4053	0.5128	1	45	0.049	▶ ₁	U	■		R.GLTGPIGPPGAPAGDKGEAGPSGPGTGAR.G + 2 Oxidation (P)
▶ 5 subsets and intersections (6 subset proteins in total)												
	Score	Mass	Matches	Sequences	emPAI							
9.1	CASA1_BOVIN	56	24513	3 (3)	2 (2)	0.33						
Alpha-S1-casein OS=Bos taurus GN=CSN1S1 PE=1 SV=2												
▶ 1 same set of CASA1_BOVIN												
▼ 3 peptide matches (2 non-duplicate, 1 duplicate)												
Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Rank	U	Peptide			
4960	▶ ₁	635.2600	1268.5054	1267.6812	0.8243	0	46	0.0094	▶ ₁	U R.YLGYLEQLLR.L + Deamidated (NQ)		
5339		692.9600	1383.9054	1383.7227	0.1827	0	43	0.0077	▶ ₁	U R.FFVAPFPEVFGK.E		
▶ 1 subset or intersection (2 subset proteins in total)												

Figure S2. The details of peptides identified by MASCOT search of proteins in BMM191. This figure corresponds to the list of peptides matched to those originated from CO1A1, CO1A2, and CASA1.

	Score	Mass	Matches	Sequences	emPAI				
5.1	CO1A1_BOVIN	134	138854	7 (7)	6 (6)	0.17			
Collagen alpha-1(I) chain OS= Bos taurus GN=COL1A1 PE= 1 SV=3									
7 peptide matches (6 non-duplicate, 1 duplicate)									
Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Rank	U	Peptide
<u>6164</u> >1	666.7400	1331.4654	1332.6310	1.1656	0	55	0.0091	>1	U R.GPSGPQGPPSGPPGPK.G + Deamidated (NQ) Oxidation (P)
<u>7115</u>	781.2500	1560.4854	1559.8056	0.6798	0	56	0.0022	>1	U R.GETGPAGPAGPIGFVGAR.G
<u>7574</u>	854.4600	1706.9054	1705.7656	1.1399	0	44	0.019	>1	U K.DGEAGAQQGPPGPPAGPAGER.G + Oxidation (P)
<u>7735</u>	880.7900	1759.5654	1758.7115	0.8539	0	42	0.033	>1	U K.GEPGSPGNGAPGQMGPR.G + Deamidated (NQ) Oxidation (P) Oxidation (M) 3
<u>8620</u>	659.6500	1975.9282	1974.9872	0.9410	1	40	0.017	>1	U K.SGDRGETGPAGPAGPIGFVGAR.G
<u>10097</u>	850.7600	2549.2582	2548.1831	1.0751	0	95	3.4e 007	>1	U R.GNDGATGAAGPPGPTGPPGPPG PGAVGAK.G + Deamidated (NQ) 3 Oxidation (P)
5 subsets and intersections (6 subset proteins in total)									
<hr/>									
6									
	Score	Mass	Matches	Sequences	emPAI				
6.1	CO1A2_BOVIN	119	128985	6 (6)	6 (6)	0.18			
Collagen alpha-2(I) chain OS= Bos taurus GN=COL1A2 PE= 1 SV=2									
6 peptide matches (6 non-duplicate, 0 duplicate)									
Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Rank	U	Peptide
<u>5739</u>	597.0800	1192.1454	1191.6724	0.4730	0	63	9.7e 005	>1	U R.IGQPGAVGPAGIR.G
<u>7184</u>	791.1300	1580.2454	1579.7591	0.4864	0	65	0.00023	>1	U R.GPPGESGAAGPTGPIGSR.G + Oxidation (P)
<u>7381</u>	825.3000	1648.5854	1647.8217	0.7638	0	51	0.0019	>1	U R.GSTGEIGPAGPPGPPGLR.G + 2 Oxidation (P)
<u>9165</u>	1066.8100	2131.6054	2130.1070	1.4985	0	48	0.0045	>1	U R.GLPGVAGSVGE PGLGIAGPPGAR.G + 3 Oxidation (P)
<u>9557</u>	1131.8000	2261.5854	2260.1237	1.4618	0	28	0.043	>1	U R.G PGNAGPVGAAGAPGPPGPPGPPGK. + 2 Oxidation (P)
<u>10482</u>	931.9900	2792.9482	2792.3002	0.6480	0	53	0.025	>1	U K.GEQGPAGPPG QGLPFPAGTAGEAGKPPGER.G + Deamidated (NQ) 3 Oxidation (P)
2 subsets and intersections (2 subset proteins in total)									

Figure S3. The details of peptides identified by MASCOT search of proteins in BMM199. This figure corresponds to the list of peptides matched to those originated from CO1A1 and CO1A2.

	Score	Mass	Matches	Sequences	emPAI
✓ 1.1 CO1A1_BOVIN	782	138854	60 (60)	32 (32)	2.34
Collagen alpha-1(I) chain OS=Bos taurus GN=COL1A1 PE=1 SV=3					
✓ 1.2 CO1A1_HUMAN	693	138827	49 (49)	25 (25)	1.64
Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=4					
✓ 1.3 CO1A1_RAT	393	137869	34 (34)	18 (18)	0.93
Collagen alpha-1(I) chain OS=Rattus norvegicus GN=Col1a1 PE=1 SV=5					
✓ 1.4 CO1A1_CHICK	311	137670	22 (22)	11 (11)	0.57
Collagen alpha-1(I) chain OS=Gallus gallus GN=COL1A1 PE=1 SV=3					
✓ 1.5 CO1A1_CYNPY	96	137479	4 (4)	3 (3)	0.11
Collagen alpha-1(I) chain OS=Cynops pyrrhogaster GN=COL1A1 PE=2 SV=1					
✓ 1.6 CO2A1_XENLA	56	142176	3 (3)	2 (2)	0.08
Collagen alpha-1(II) chain OS=Xenopus laevis GN=col2a1 PE=2 SV=2					

▼ 69 peptide matches (57 non-duplicate, 12 duplicate)

Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Rank	U	1	2	3	4	5	6	Peptide
7198	473.5100	945.0054	944.4312	0.5743	0	70	0.00027	▶ 1	U	■	■	■	■	■	K.QGPSGASGER.G
7866	544.8200	1087.6254	1087.5298	0.0956	0	48	0.034	▶ 1	U	■	■	■	■	■	R.GFPGADVAGPK.G + Oxidation (P)
7869	545.6500	1089.2854	1088.5727	0.7127	0	48	0.047	▶ 1	U	■	■	■	■	■	R.GVQPPGAPGPR.G
7887	548.3700	1094.7254	1094.5581	0.1673	0	49	0.028	▶ 1	U	■	■	■	■	■	R.GRPGAPGAPGAR.G + 2 Oxidation (P)
7959	558.7400	1115.4654	1115.4843	-0.0189	0	48	0.036	▶ 1	U	■	■	■	■	■	R.EGAPGAEQSPGR.D + 2 Oxidation (P)
7982	564.2700	1126.5254	1126.5731	-0.0476	1	29	0.044	▶ 1	U	■	■	■	■	■	R.GAAGLPQPKDR.G + 2 Oxidation (P)
8127	580.9800	1159.9454	1159.6350	0.3105	0	39	0.038	▶ 1	U	■	■	■	■	■	R.GVPPGAVGAPGK.D
8170	589.6300	1177.2454	1176.5598	0.6857	0	50	0.00079	▶ 1	U	■	■	■	■	■	R.GQAGVMGPPGPK.G + Oxidation (P); Oxidation (M)
8173	▶ 1	589.8000	1177.5854	1177.5438	0.0417	0	71	0.00021	▶ 1	U	■	■	■	■	R.GQAGVMGPPGPK.G + Deamidated (NQ); Oxidation (P); Oxidation (M)
8515	621.7000	1241.3854	1241.5888	-0.2034	0	53	0.0014	▶ 1	U	■	■	■	■	■	K.GLTGSPGSPGDK.T + Oxidation (P)
8581	630.0200	1258.0254	1257.5837	0.4417	0	58	0.0002	▶ 1	U	■	■	■	■	■	K.GLTGSPGSPGDK.T + 2 Oxidation (P)
8642	641.5900	1281.1654	1280.6109	0.5545	0	58	0.004	▶ 1	U	■	■	■	■	■	K.GEAGSPGAPGAGAR.G
8726	656.3800	1310.7454	1310.6215	0.1239	0	45	0.015	▶ 1	U	■	■	■	■	■	K.ETGSPGAPGAGAR.G
8765	665.1000	1328.1854	1327.6409	0.5446	0	51	0.013	▶ 1	U	■	■	■	■	■	R.GFFGLPGSPGPK.Q + 2 Oxidation (P)
8819	667.1800	1332.3454	1331.6470	0.6984	0	73	0.00012	▶ 1	U	■	■	■	■	■	R.GPSGQGPSGPPGPK.G + Oxidation (P)
8824	667.6200	1333.2254	1332.6310	0.5944	0	47	0.055	▶ 1	U	■	■	■	■	■	R.GPSGQGPSGPPGPK.G + Deamidated (NQ); Oxidation (P)
8880	672.7600	1343.5054	1343.6358	-0.1303	0	45	0.016	▶ 1	U	■	■	■	■	■	R.GFFGLPGSPGPK.Q + 3 Oxidation (P)
9268	718.4600	1434.9054	1434.6739	0.2315	0	45	0.04	▶ 1	U	■	■	■	■	■	R.GEPGAPLPGPPGER.G + 3 Oxidation (P)
9269	718.6400	1435.2654	1434.6739	0.5915	0	65	0.0009	▶ 1	U	■	■	■	■	■	R.GEPGAPLPGPPGER.G + 3 Oxidation (P)
9371	▶ 1	730.6000	1459.1854	1458.6852	0.5003	0	49	0.038	▶ 1	U	■	■	■	■	R.GSAGPPGATGPPGAGR.V + 2 Oxidation (P)
9797	▶ 1	774.2200	1546.4254	1545.7900	0.6355	0	45	0.0075	▶ 1	U	■	■	■	■	R.GETGAPGAPGPPGAGAR.G
9849	▶ 1	781.2500	1560.4854	1559.8056	0.6798	0	51	0.026	▶ 1	U	■	■	■	■	R.GETGAPGAPGPPGAGAR.G
9856	▶ 1	781.9000	1561.7854	1561.7737	0.0118	0	62	0.0022	▶ 1	U	■	■	■	■	K.DGLNGLPPIGPPGPR.G + Deamidated (NQ); 3 Oxidation (P)
9869	▶ 1	782.7500	1563.4854	1561.7737	1.7118	0	51	0.0043	▶ 1	U	■	■	■	■	K.DGLNGLPPIGPPGPR.G + Deamidated (NQ); 3 Oxidation (P)
9942	▶ 2	794.1600	1586.3054	1585.7485	0.5570	0	53	0.0028	▶ 1	U	■	■	■	■	K.GANGAPGIAGAPGPPGAGAR.G + Deamidated (NQ); 3 Oxidation (P)
10291	▶ 1	846.3100	1690.6054	1689.7707	0.8348	0	78	6.9e-006	▶ 1	U	■	■	■	■	K.DGEAGAPGPPGAPGAGAR.G
10351	▶ 1	854.7300	1707.4454	1706.7496	0.6958	0	53	0.016	▶ 1	U	■	■	■	■	K.DGEAGAPGPPGAPGAGAR.G + Deamidated (NQ); Oxidation (P)
10353	▶ 1	854.7700	1707.5254	1705.7656	1.7599	0	66	4.3e-005	▶ 1	U	■	■	■	■	K.DGEAGAPGPPGAPGAGAR.G + Oxidation (P)
10523	▶ 1	873.1400	1744.2654	1743.7660	0.4995	1	41	0.0073	▶ 1	U	■	■	■	■	R.EGAPGAEQSPGRDQSPGAK.G + 3 Oxidation (P)
10576	▶ 1	880.6900	1759.3654	1758.7115	0.6539	0	63	0.0019	▶ 1	U	■	■	■	■	K.GEPGSPGAPGPPGPPGAGAR.G + Deamidated (NQ); 3 Oxidation (P); Oxidation (M)
11030	▶ 2	916.8800	1831.7454	1831.8523	-0.1069	0	70	0.00037	▶ 1	U	■	■	■	■	R.GPPGFMGPPGLAGPPGESGR.E + 2 Oxidation (P); Oxidation (M)
11091	▶ 1	924.8400	1847.6654	1847.8472	-0.1818	0	54	0.015	▶ 1	U	■	■	■	■	R.GPPGFMGPPGLAGPPGESGR.E + 4 Oxidation (P); Oxidation (M)
11091	▶ 2	924.8400	1847.6654	1847.8472	-0.1818	0	48	0.054	▶ 2	U	■	■	■	■	R.GPPGFMGPPGLAGPPGESGR.E + 4 Oxidation (P)
11651	▶ 1	659.2600	1974.7582	1974.9872	-0.2290	1	36	0.058	▶ 1	U	■	■	■	■	K.SGDRGETGAPGAPGPPGAGAR.G
12170	▶ 1	1037.3100	2072.6054	2072.0036	0.6019	0	57	0.00016	▶ 1	U	■	■	■	■	K.GAPGADGAPGAPGTPGQGIAGQR.G + Oxidation (P)
12176	▶ 1	1037.8700	2073.7254	2072.9876	0.7379	0	39	0.012	▶ 1	U	■	■	■	■	K.GAPGADGAPGAPGTPGQGIAGQR.G + Deamidated (NQ); Oxidation (P)
12393	▶ 1	1059.9400	2117.8654	2116.9814	0.8840	0	43	0.0019	▶ 1	U	■	■	■	■	R.GEPGPPGAPGAPGPPGADGPPGAK.G + 2 Oxidation (P)
12442	▶ 1	1067.9000	2133.7854	2132.9763	0.8091	0	39	0.0036	▶ 1	U	■	■	■	■	R.GEPGPPGAPGAPGPPGADGPPGAK.G + 3 Oxidation (P)
12446	▶ 1	1068.2500	2134.4854	2133.9604	0.5251	0	33	0.047	▶ 1	U	■	■	■	■	R.GEPGPPGAPGAPGPPGADGPPGAK.G + Deamidated (NQ); 3 Oxidation (P)

	Score	Mass	Matches	Sequences	emPAI
5.1 CO3A1_BOVIN	268	93594	17 (17)	15 (15)	0.86
Collagen alpha-1(III) chain OS=Bos taurus GN=COL3A1 PE=1 SV=1					
5.2 CO3A1_RAT	120	138851	5 (5)	4 (4)	0.14
Collagen alpha-1(III) chain OS=Rattus norvegicus GN=Col3a1 PE=2 SV=3					

18 peptide matches (17 non-duplicate, 1 duplicate)

Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Rank	U	1	2	Peptide
7283	483.4400	964.8654	964.4978	0.3676	0	27	0.023	1	U	■	R.GPVGSPGPPGK.D + Oxidation (P)
7409	498.7800	995.5454	995.4672	0.0782	0	52	0.0052	1	U	■	R.GGAGPPGPEGGK.G + Oxidation (P)
7697	525.1500	1048.2854	1047.5098	0.7757	0	35	0.012	1	U	■	R.GPPGAGPPGPER.G + 2 Oxidation (P)
7856	543.0500	1084.0854	1083.5196	0.5658	0	42	0.0094	1	U	■	R.GPAGANLPGEK.G + Deamidated (NQ); Oxidation (P)
7987	564.8200	1127.6254	1127.5394	0.0861	0	56	0.0064	1	U	■	R.GLAGPPGMPGAR.G + 2 Oxidation (P); Oxidation (M)
8611	637.5200	1273.0254	1272.5847	0.4407	0	57	0.00086	1	U	■	R.GSPGGPGAAGFPGGR.G + 2 Oxidation (P)
8663	645.5500	1289.0854	1288.5797	0.5058	0	63	0.00049	1	U	■	R.GSPGGPGAAGFPGGR.G + 3 Oxidation (P)
9276	719.6700	1437.3254	1436.6532	0.6722	0	45	0.00066	1	U	■	R.GPPGPPGTNGVPGQR.G + 2 Deamidated (NQ); 3 Oxidation (P)
9767	770.6400	1539.2654	1537.7121	1.5533	0	56	0.0054	1	U	■	R.GETGPAGSPGAPGGR.G + Oxidation (P)
9972	800.2700	1598.5254	1598.7285	-0.2031	0	57	9.1e-005	1	U	■	K.GEVGPAGSPGSSGAPGQR.G + 2 Oxidation (P)
10155	827.1800	1652.3454	1651.8352	0.5103	0	70	0.00029	1	U	■	K.GEMGPAGIPGAPLIGAR.G + Oxidation (P); Oxidation (M)
11044	917.7300	1833.4454	1832.9017	0.5437	0	71	1.6e-005	1	U	■	R.GPPGQGLPGLAGTAGEPGR.D + 3 Oxidation (P)
12684	1098.9300	2195.8454	2194.9913	0.8541	0	51	0.03	1	U	■	K.GAAGPPPPGSAAGTGLQMPGER.G + 4 Oxidation (P); Oxidation (M)
12757	1107.8800	2213.7454	2212.0509	1.6945	0	31	0.031	1	U	■	K.GEGGPPGAAGPAGSGPAGPPGQGVK.G + 2 Oxidation (P)
13040	756.2000	2265.5782	2264.0458	1.5324	0	45	0.012	1	U	■	R.GENGSPGAPGAPGHPGPPGVPSPGK.N + Deamidated (NQ); 2 Oxidation (P)
13040	756.2000	2265.5782	2264.0458	1.5324	0	43	0.017	2	U	■	R.GENGSPGAPGAPGHPGPPGVPSPGK.S + Deamidated (NQ); 3 Oxidation (P)
14690	989.2200	2964.6382	2965.4530	-0.8149	1	43	0.017	1	U	■	R.GPTGPIPPGAPGQDKGESGAPGVGIAGPR.G + 4 Oxidation (P)

	Score	Mass	Matches	Sequences	emPAI
9.1 CASA1_BOVIN	64	24513	4 (4)	3 (3)	0.78
Alpha-S1-casein OS=Bos taurus GN=CSN1S1 PE=1 SV=2					

4 peptide matches (4 non-duplicate, 0 duplicate)

Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Rank	U	Peptide	
8602	634.6400	1267.2654	1266.6972	0.5683	0	54	0.0033	1	U	R.YLGYLEQLLR.L
8605	635.2100	1268.4054	1267.6812	0.7242	0	51	0.0095	1	U	R.YLGYLEQLLR.L + Deamidated (NQ)
9115	693.2200	1384.4254	1383.7227	0.7027	0	37	0.028	1	U	R.FFVAFFFEVFGK.E
9930	791.5700	1581.1254	1579.8206	1.3049	0	29	0.02	1	U	K.VPQLEIVNSAEER.L

2 subsets and intersections (3 subset proteins in total)

(b)

Figure S4. (a) The details of peptides identified by MASCOT search of proteins in BMM201. This figure corresponds to the list of peptides matched to those originated from CO1A1 and CO1A2. (b) The details of peptides identified by MASCOT search of proteins in BMM201. This figure corresponds to the list of peptides matched to those originated from CO1A3 and CASA1.

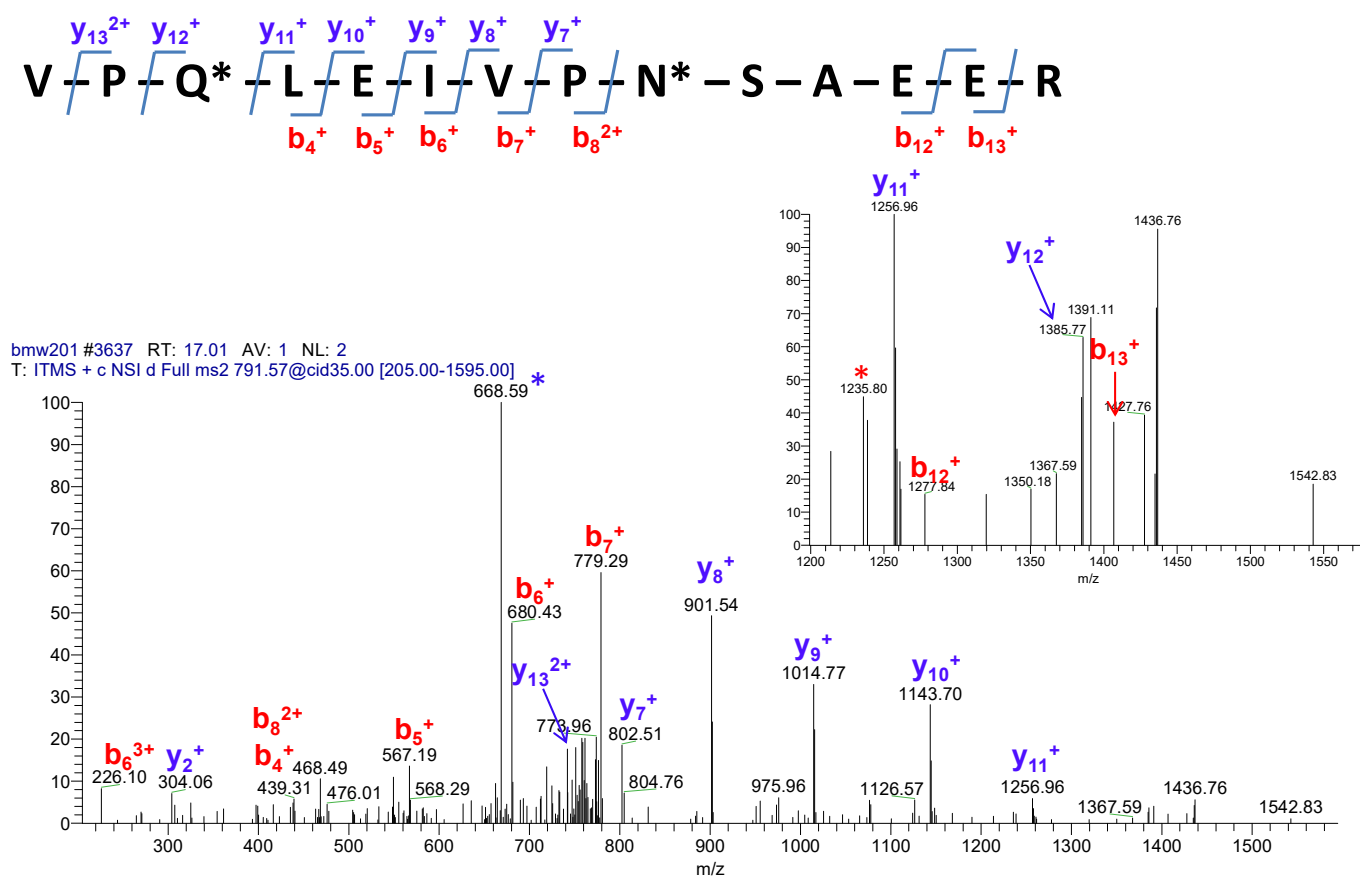


Figure S5. ESI-MS/MS spectrum of the precursor ion peak at m/z 791.6 ($z = 2$). This peptide was isolated by nano-LC of tryptic digest of a protein obtained from the specimen BMM201. In the sequence of VPQ*LEIVPN*SAEER, Gln (Q*) and Asn (N*) can be deamidated to Glu (E) and Asp (D), respectively, probably due to aging. Considering the existence of five COOH groups including those of Q* and N*, we assigned the base peak at m/z 668.6 ($z = 2$, indicated by an asterisk *) to the neutral loss of CO₂ from y_{12}^+ ion. The similar product ion peak at m/z 1235.8 ($z = 1$, indicated by an asterisk *) shown in the inset) could occur by neutral loss of CO₂ from b_{12}^+ ion. The amino acid sequence of this peptide differs from that of goat collagen VPQ*LEIVPKSAEER, in contrast to the peptide YGLYLEQ*LLR (the spectrum is shown in Figure 6 in the main text) commonly occurs in cattle and goat (Figure 5 in the main text).

Table S1. Details of Table 7: detected peptides from BMM061, 078 and 194.

BMM061						
N	Protein	Confidence	Sequence	Modifications	Cleavages	Δ Mass Prec MW z
1	Alpha-S1-casein	99	FFVAPFPEVF		cleaved F-G@C-term	0.0061 1198.6127 1
			FFVAPFPEVFGK			0.0064 1383.7291 2
		99	FVAPFPEVF		cleaved F-F@N-term; cleaved F-G@C-term	0.0043 1051.5416 1
			YLGYLEQLLR			0.0059 1266.7031 2
2	Beta-casein	99	AQTQSLVYFPFG- PIPN		cleaved F-A@N-term; cleaved N-S@C-term	0.0067 1727.8950 2
			LLYQEPVLGPVR		cleaved F-L@N-term	0.0084 1382.8007 2
		99	GPFPIIV			0.0023 741.4448 1
3	Alpha-S2-casein	99	NAVPIPTLNR			0.0064 1194.6785 2
BMM078						
N	Protein	Confidence	Sequence	Modifications	Cleavages	Δ Mass Prec MW z

1	Alpha-S1-casein	99	FFVAPFPEVF	cleaved F-G@C-term	0.0052	1198.6117	1	
		99	FFVAPFPEVFGK		0.0046	1383.7273	2	
		99	YLGYLEQLLR		Deami- dated(Q)@7	0.0076	1267.6888	2
2	ATP synthase subunit	98.9	LA- GNVMAGHAVIK	Oxidation(M)@6	-0.0974	1295.6046	2	
BMM194								
N	Protein	Confidence	Sequence	Modifications	Cleavages	Δ Mass	Prec MW	z
1	Collagen alpha-1(I) chain	99	GVVGLPGQR	Oxidation(P)@6		-0.0028	897.5005	2
		99	GVQGGPPGAGPR	Deami- dated(Q)@3; Ox- idation(P)@6		0.01	1105.5616	2

Confidence > 95%.

Table S2. MASCOT Search Results of Proteins in BMM191.

Description ^a	Score	Mass (Da)	Num. of Significant Matches	Num. of Significant Sequences	emPAI
Keratin, type II cytoskeletal 1 / <i>Homo sapiens</i>	341	65999	15	12	1.04
Keratin, type II cytoskeletal 6A / <i>Homo sapiens</i>	85	60008	3	3	0.2
Keratin, type II cytoskeletal 2 epidermal / <i>Homo sapiens</i>	76	65393	5	5	0.32
Keratin, type II cytoskeletal 1b / <i>Homo sapiens</i>	76	61650	1	1	0.06
Keratin, type I cytoskeletal 9 / <i>Homo sapiens</i>	194	62027	6	4	0.26
Keratin, type I cytoskeletal 10 / <i>Homo sapiens</i>	195	58792	10	10	0.85
Keratin, type I cytoskeletal 14 / <i>Homo sapiens</i>	124	51529	4	4	0.32
Keratin, type I cytoskeletal 16 / <i>Homo sapiens</i>	110	51236	4	4	0.32
Trypsin / <i>Sus scrofa</i>	142	24394	7	4	1.06
Collagen alpha-2(I) chain /<i>Bos taurus</i>	147	128985	7	7	0.22
Collagen alpha-1(I) chain /<i>Bos taurus</i>	115	138854	8	7	0.23
Collagen alpha-1(I) chain / <i>Homo sapiens</i>	91	138827	4	3	0.11
Collagen alpha-1(I) chain / <i>Gallus gallus</i>	70	137670	2	2	0.05
Calmodulin-like protein 5 / <i>Homo sapiens</i>	84	15883	1	1	0.25
Alpha-S1-casein /<i>Bos taurus</i>	56	24513	3	2	0.33
Cathepsin K / <i>Canis familiaris</i>	47	37037	1	1	0.1

^a Collagen and casein of cattle origin are highlighted on yellow background. Collagen originated from animal species other than cattle are printed on pale green background. Keratin and other proteins considered as contaminations are shown on pale blue background.

Table S3. MASCOT Search Results of Proteins in BMM199.

Description	Score	Mass (Da)	Num. of Significant Matches	Num. of Significant Sequences	emPAI
Keratin, type II cytoskeletal 1 / <i>Homo sapiens</i>	354	65999	14	13	1.15
Keratin, type II cytoskeletal 6A / <i>Homo sapiens</i>	118	60008	4	4	0.27
Keratin, type II cytoskeletal 1b / <i>Homo sapiens</i>	61	61650	1	1	0.06
Keratin, type I cytoskeletal 9 / <i>Homo sapiens</i>	394	62027	14	10	1.01
Keratin, type I cytoskeletal 10 / <i>Homo sapiens</i>	157	58792	5	5	0.36
Keratin, type I cytoskeletal 14 / <i>Homo sapiens</i>	95	51529	3	3	0.23
Trypsin / <i>Sus scrofa</i>	172	24394	9	3	2.19
Collagen alpha-2(I) chain /<i>Bos taurus</i>	119	128985	6	6	0.18
Collagen alpha-1(I) chain /<i>Bos taurus</i>	134	138854	7	6	0.17
Cystic fibrosis transmembrane conductance regulator / <i>Oryctolagus cuniculus</i>	48	167935	1	1	0.02
Dermcidin / <i>Homo sapiens</i>	60	11277	1	1	0.35
Cathepsin K / <i>Canis familiaris</i>	52	37037	1	1	0.1

^a Colour system of this Table is the same as that applied to Table S2.

Table S4. MASCOT Search Results of Proteins in BMM201.

Description ^a	Score	Mass (Da)	Num. of Significant Matches	Num. of Significant Sequences	emPAI
Keratin, type II cytoskeletal 1 / <i>Homo sapiens</i>	384	65999	19	9	1.04
Keratin, type II cytoskeletal 6A / <i>Homo sapiens</i>	105	60008	5	5	0.35
Keratin, type II cytoskeletal 2 epidermal / <i>Homo sapiens</i>	58	65393	3	3	0.18
Keratin, type II cytoskeletal 75 / <i>Rattus norvegicus</i>	121	58991	3	3	0.2
Collagen alpha-1(I) chain /<i>Bos taurus</i>	782	138854	60	32	2.34
Collagen alpha-1(I) chain / <i>Homo sapiens</i>	693	138827	49	25	1.64
Collagen alpha-1(I) chain / <i>Rattus norvegicus</i>	393	137869	34	18	0.93
Collagen alpha-1(I) chain / <i>Gallus gallus</i>	311	137670	22	11	0.57
Collagen alpha-1(I) chain / <i>Cynops pyrrhogaster</i>	96	137479	4	3	0.11
Collagen alpha-2(I) chain /<i>Bos taurus</i>	320	128985	20	15	0.53
Collagen alpha-2(I) chain / <i>Canis familiaris</i>	199	129321	8	6	0.18
Collagen alpha-2(I) chain / <i>Homo sapiens</i>	127	129209	5	5	0.15
Collagen alpha-2(I) chain / <i>Mus musculus</i>	102	129478	3	3	0.09
Collagen alpha-1(III) chain /<i>Bos taurus</i>	268	93594	17	15	0.86
Collagen alpha-1(III) chain / <i>Rattus norvegicus</i>	120	138851	5	4	0.14
Alpha-S1-casein /<i>Bos taurus</i>	64	24513	3	2	0.33

^a Colour system of this Table is the same as that applied to Table S2.

Table S5. MASCOT Scores of Proteins in Backgrounds of BMM191, BMM199, and BMM201.

Description	BMM191	BMM199	BMM201
	Score		
Keratin, type I cytoskeletal 9 / <i>Homo sapiens</i>	835	199	239
Keratin, type I cytoskeletal 10 / <i>Homo sapiens</i>	550	148	262
Keratin, type I cytoskeletal 14 / <i>Homo sapiens</i>	358	ND	73
Keratin, type I cytoskeletal 16 / <i>Homo sapiens</i>	260	ND	ND
Keratin, type I cytoskeletal 17 / <i>Homo sapiens</i>	ND	58	ND
Keratin, type I cytoskeletal 18 / <i>Rattus norvegicus</i>	ND	ND	60
Keratin, type I cytoskeletal 18 / <i>Scyliorhinus stellaris</i>	59	ND	ND
Keratin, type I cytoskeletal 79 / <i>Bos taurus</i>	71	ND	ND
Keratin, type I cuticular Ha4 / <i>Homo sapiens</i>	48	ND	ND
Keratin, type II cytoskeletal 1 / <i>Homo sapiens</i>	656	152	494
Keratin, type II cytoskeletal 1b / <i>Homo sapiens</i>	ND	61	100
Keratin, type II cytoskeletal 2 epidermal / <i>Homo sapiens</i>	404	ND	134
Keratin, type II cytoskeletal 5 / <i>Homo sapiens</i>	129	ND	87
Keratin, type II cytoskeletal 6A / <i>Rattus norvegicus</i>	188	ND	ND
Keratin, type II cytoskeletal 6B / <i>Homo sapiens</i>	212	ND	147
Keratin, type II cytoskeletal 75 / <i>Mus musculus</i>	133	ND	ND
Trypsin*1 / <i>Sus scrofa</i>	64	178	205
Cathepsin K / <i>Canis familiaris</i>	ND	60	ND
Dermcilin / <i>Homo sapiens</i>	ND	64	50
NACHT, LRP and PYD domains-containing Protein 6 / <i>Homo sapiens</i>	43	ND	ND
Glutamine-rich protein 2 / <i>Homo sapiens</i>	ND	ND	55
Advillin / <i>Mus musculus</i>	ND	ND	54
Cell surface glycoprotein MUC18 / <i>Rattus norvegicus</i>	54	ND	ND