

Supplementary data for article:

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Identification of Protein Binders in Artworks by MALDI-TOF/TOF Tandem Mass Spectrometry.
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Electronic Supplementary Material 1

Identification of protein binders in artworks by MALDI-TOF/TOF tandem mass spectrometry

T. Tripković, C. Charvy, S. Alves, A.Đ. Lolić, R.M. Baošić, S.D. Nikolić-Mandić, J.C. Tabet

Electronic Supplementary Material 1 contains results obtained during Mascot search of SwissProt database for PMF and MS/MS spectra recorded for all reference materials and model samples considered in this research:

- Egg white
- Egg yolk
- Casein powder (Kremer Product No. 63200)
- Bovine quark cheese
- Bovine bone glue (Kremer Product No. 63000)
- Bovine hide glue (Product No. 63010)
- Rabbit skin glue, refined (Product No. 63025)
- Rabbit skin glue, raw (Product No. 63028)
- Technical gelatin from pig skin (Product No. 63040)
- Salianski isinglass (Product No. 63110)
- Egg white + Zinc white (9M11)
- Egg white + French Ochre (9M21)
- Egg yolk + Zinc white (10M11)
- Egg yolk + French Ochre (10M21)
- Bovine quark cheese + Zinc white (7M11)
- Bovine quark cheese + French Ochre (7M21)
- Rabbit skin glue (63025) + Zinc white (3M11)
- Rabbit skin glue (63025) + French Ochre (3M21)

Electronic Supplementary Material also contains results of SwissProt database search via Mascot obtained for PMF and MS/MS spectra of historical painting samples.

Full information about database search settings is provided in text (section Database Search). Ion series considered during database search were default for MALDI-TOF/TOF in Mascot. Ion series considered during database search were default for MALDI-TOF/TOF in Mascot.

Egg white

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Ovalbumin OVAL_CHICK P01012	Gallus gallus	149	71%	LYAEER	106 - 111	780.389	780.404	20	0	
				DEDTQAMPFR	191 - 200	1209.520	1209.518	-2	0	
				ADHPFLFCIK	361 - 370	1248.608	1248.608	0	0	8: Carboxymethyl (C)
				HIATNAVLFVGR	371 - 382	1345.738	1345.732	-4	0	
				YPILPEYLQCVK	112 - 123	1523.781	1523.806	16	0	10: Carboxymethyl (C)
				AFKDEDTQAMPFR	188 - 200	1555.721	1555.717	-2	1	
				LTEWTSSNVMEER	265 - 277	1581.721	1581.721	0	0	
				GGLPEINFQTAADQAR	128 - 143	1687.840	1687.830	-6	0	
				ISQAVHAAHAINEAGR	324 - 340	1773.899	1773.898	-1	0	
				GSIGAASMEFCFDVFK	2 - 17	1808.787	1808.778	-5	0	N-Term: Acetyl 11: Carboxymethyl (C)
				ELINSWVESQTNGIIR	144 - 159	1858.966	1858.953	-7	0	
				ELINSWVESQTNGIIR	144 - 159	1859.950	1859.941	-5	0	Deamidated (NQ)
				EVVGSAEAGVDAASVSEFR	341 - 360	2008.946	2009.000	27	0	
				DILNQITKPNDVYSFSLASR	86 - 105	2281.182	2281.199	7	0	
				VTEQESKPVQMMYQIGLFR	201 - 219	2284.146	2284.153	3	0	
				NVLQPSSVDSQTAMVLVNAIVFK	160 - 182	2460.317	2460.303	-5	0	
FDKLPGFGDSIEAQCGTSVNVHSSLR	60 - 85	2822.341	2822.356	5	1	15: Carboxymethyl (C)				
VHHANENIFYCPIAIMSALAMVYLGAKE	21 - 47	3034.499	3034.525	9	0	11: Carboxymethyl (C)				
ILELPPFASGTMSMLVLLPDEVSGLEQLSINFEK	230 - 264	3863.011	3863.011	0	0					
Ovotransferrin TRFE_CHICK P02789	Gallus gallus	64	32%	TCNWAR	260 - 265	808.341	808.371	37	0	2: Carboxymethyl (C)
				CLFKVR	662 - 667	823.449	823.431	-23	1	1: Carboxymethyl (C)
				VAAHAVVAR	266 - 274	893.532	893.551	22	0	
				RFGVNGSEK	633 - 641	994.495	994.401	-95	1	5: Deamidated (NQ)
				YFGYTGALR	540 - 548	1047.526	1047.535	8	0	
				FYTVISSLK	680 - 688	1057.593	1057.595	2	0	
				SDFHLFGPPGK	299 - 309	1201.600	1201.602	1	0	
				KDSNVNWNLLK	458 - 468	1331.670	1331.676	5	1	
				IQWCAVGDKEK	364 - 374	1334.641	1334.642	1	1	4: Carboxymethyl (C)
				DSNVNWNLLKGGK	459 - 470	1391.644	1391.680	26	1	3 Deamidations (NQ)
				ENRIQWCAVGGK	361 - 371	1403.674	1403.726	38	1	N-Term: Acetyl 7: Carboxymethyl (C)
				SAGWNIPIGTLHR	141 - 154	1534.849	1534.840	-6	0	
				TDERPASYFAVAVAR	443 - 457	1652.839	1652.833	-4	0	
				DDNKVEDIWSFLSK	275 - 288	1695.822	1695.824	1	1	
				GAIEWEGIESGSVEQAVAK	155 - 173	1959.966	1959.956	-5	0	
				ECNLAEVPTHAVVVRPEK	602 - 619	2049.043	2049.040	-2	0	2: Carboxymethyl (C)
TGTCNFDEYFSEGCAPGSPNSR	494 - 516	2551.998	2552.028	12	0	4: Carboxymethyl (C) 14: Carboxymethyl (C)				
GEADAVALDGGLVYTAGVCGLVPVMAER	406 - 433	2791.364	2791.374	4	0	19: Carboxymethyl (C)				
Lysozyme C LYSC_CHICK P00698	Gallus gallus	35	39%	WWCNDGR	80 - 86	994.384	994.390	7	0	3: Carboxymethyl (C)
				GTDVQAWIR	135 - 143	1045.543	1045.544	1	0	
				GYSLGNWVCAAK	40 - 51	1326.615	1326.593	-17	0	9: Carboxymethyl (C)
				CKGTDVQAWIR	133 - 143	1334.652	1334.652	0	1	1: Carboxymethyl (C)
				FESNFNTQATNR	52 - 63	1428.650	1428.655	4	0	
				IVSDGNGMNAVVAWR	116 - 130	1676.785	1676.776	-6	0	Deamidated (NQ)
Ovalbumin-related protein Y OVALY_CHICK P01014	Gallus gallus	26	11%	HSLELEEFR	354 - 362	1159.574	1159.569	-4	0	
				ADHPFLFFIR	363 - 372	1262.668	1262.663	-4	0	
				YNPTNAILFFGR	373 - 384	1412.732	1412.731	-1	0	11: Carboxymethyl (C)
				TFSVLPEYLSGAR	111 - 123	1543.746	1543.756	6	0	

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Ovalbumin OVAL_CHICK P01012	Gallus gallus	961	45%	LYAEER	106 - 111	780.389	780.340	-62	0	
				MYQIGLFR	212 - 219	1027.539	1027.544	4	0	
				DEDTQAMPFR	191 - 200	1209.520	1209.514	-6	0	
				ADHPFLFCIK	361 - 370	1248.608	1248.599	-7	0	8: Carboxymethyl (C)
				HIATNAVLFFGR	371 - 382	1345.738	1345.738	0	0	
				YPILPEYLQCVK	112 - 123	1523.781	1523.782	1	0	10: Carboxymethyl (C)
				AFKDEDTQAMPFR	188 - 200	1555.721	1555.721	0	1	
				LTEWTSSNVMEER	265 - 277	1581.721	1581.721	0	0	
				GGLEPINFQTAADQAR	128 - 143	1687.840	1687.842	1	0	
				GGLEPINFQTAADQAR	128 - 143	1709.822	1709.810	-7	0	4: Cation:Naili Mg[II](DE)
				ISQAVHAAHAEINEAGR	324 - 340	1773.899	1773.896	-2	0	
				ELINSWVESQTNGIIR	144 - 159	1858.966	1858.967	1	0	
				EVVGSAEAGVDAASVSEEFR	341 - 360	2008.946	2008.941	-2	0	
				DILNQITKPNDEVYFSLASR	86 - 105	2281.182	2281.182	0	0	
				VTEQESKPVQMMYQIGLFR	201 - 219	2284.146	2284.127	-8	0	
Ovotransferrin TRFE_CHICK P02789	Gallus gallus	177	18%	NVLQPSSVDSQTAMVLVNAIVFK	160 - 182	2460.317	2460.329	5	0	
				DLTQQERI	44 - 51	1045.516	1045.544	27	1	N-Term: Acetyl 4: Deamidated (NQ)
				YFGYTGALR	540 - 548	1047.526	1047.505	-20	0	
				FMMFESQNK	644 - 652	1161.507	1161.503	-3	0	
				SAGWNIPIGTLHR	141 - 154	1534.849	1534.826	-15	0	
				TDERPASYFAVAVAR	443 - 457	1652.839	1652.780	-36	0	
				GAIEWEGIESGSVEQAVAK	155 - 173	1959.966	1960.028	32	0	
				ECNLAEVPTHAVVVRPEK	602 - 619	2049.043	2049.010	-16	0	2: Carboxymethyl (C)
				TGTCNFDEYFSEGCAPGSPNSR	494 - 516	2551.998	2551.925	-28	0	4: Carboxymethyl (C) 14: Carboxymethyl (C)
				GEADAVALDGGLVYTAGVCGLVPVMAER	406 - 433	2791.364	2791.160	-73	0	19: Carboxymethyl (C)

Egg yolk

Proteins identified by PMF analysis with corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Vitellogenin-2 VIT2_CHICK P02845	Gallus gallus	110	23%	TKNPEQR	303 - 309	914.469	914.460	-10	1	N-Term: Acetyl
				ARCSVSYNK	1579 - 1587	1085.504	1085.498	-6	1	3: Carboxymethyl (C)
				ADTYFDNYR	633 - 641	1164.496	1164.479	-15	0	
				WKLCADASVR	1424 - 1433	1248.604	1248.488	-93	1	N-Term: Acetyl 4: Carboxymethyl (C)
				FDIDPGFNSRR	18 - 28	1365.655	1365.610	-33	1	N-Term: Acetyl
				IANADNLESIWR	342 - 353	1401.712	1401.573	-99	0	
				DASFIQNTYLHK	1008 - 1019	1436.717	1436.584	-93	0	
				VGATGEIFVVNSPR	642 - 655	1445.775	1445.637	-95	0	
				AVAYVKWGWDCR	1438 - 1449	1511.710	1511.656	-36	1	11: Carboxymethyl (C)
				MHHIGCQLCFSR	993 - 1004	1547.655	1547.517	-89	0	6: Carboxymethyl (C) 9: Carboxymethyl (C)
				SPQVEEYNGVWPR	74 - 86	1560.744	1560.622	-78	0	
				IVLMPVHTDADIDK	1028 - 1041	1566.820	1566.684	-87	0	
				GSAPDVPMQNYGSLR	272 - 286	1591.753	1591.631	-77	0	
				EALQPIHDLADEAISR	456 - 471	1777.908	1777.745	-92	0	
				LMANSAGSVADLVEVGIR	666 - 683	1801.948	1801.783	-91	0	

				LPFMYNISSACNIALK	599 - 614	1842.913	1842.819	-51	0	11: Carboxymethyl (C)
				VRSPQVEEYNGVWPR	72 - 86	1857.924	1857.823	-55	1	N-Term: Acetyl
				IETNPCEEETEIVVGR	895 - 910	1902.923	1902.775	-78	1	6: Carboxymethyl (C)
				TGGLQLVVYADTDSVRPR	1393 - 1410	1947.029	1946.876	-79	0	
				NAVSFGHSWILEEAPCR	1740 - 1756	1973.917	1973.776	-72	0	16: Carboxymethyl (C)
				NPVLQQVACLGYSSVVNR	428 - 445	2005.017	2004.864	-76	0	9: Carboxymethyl (C)
				SYLYNYESGMLNGLQDR	29 - 45	2022.923	2022.772	-74	0	
				SQNVYELQEAGIGGICHAR	147 - 165	2102.992	2102.832	-76	0	16: Carboxymethyl (C)
				QVYQISPFNEPTGVAVMEAR	240 - 259	2236.107	2235.926	-81	0	
				QVYQISPFNEPTGVAVMEAR	240 - 259	2278.117	2277.985	-58	0	N-Term: Acetyl
				YVVPSCGLPLEYGSYTTALAR	791 - 812	2431.221	2430.993	-94	0	6: Carboxymethyl (C)
				IVLMPVHTDADIDKIQLEIQAGSR	1028 - 1051	2662.423	2662.176	-93	1	
				Ovalbumin OVAL_CHICK P01012	Gallus gallus	56	32%	DSTRTOINK	48 - 56	1104.564
ADHPFLFCIK	361 - 370	1248.608	1248.602					-5	0	8: Carboxymethyl (C)
HIATNAVLFFGR	371 - 382	1345.738	1345.758					15	0	
AFKDEDTQAMPFR	188 - 200	1555.721	1555.736					10	1	
LTEWTSSNVMEER	265 - 277	1581.721	1581.752					19	0	
GGLEPINFQTAADQAR	128 - 143	1687.840	1687.882					25	0	
ISQAVHAAHAINEAGR	324 - 340	1773.899	1773.954					31	0	
ELINSWVESQTNGIIR	144 - 159	1858.966	1858.979					7	0	
DILNQITKPNQVYVYSLASR	86 - 105	2281.182	2281.205					10	0	
VTEQESKPVQMMYQIGLFR	201 - 219	2284.146	2284.115					-14	0	

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Vitellogenin-2 VIT2_CHICK P02845	Gallus gallus	305	10%	LPLSLPVGPR	1543 - 1552	1048.651	1048.612	-38	0	
				FLEVVLQCR	333 - 341	1164.608	1164.576	-28	0	8: Carboxymethyl (C)
				FDIDPGFNSR	18 - 27	1167.543	1167.526	-14	0	
				IANADNLESIWR	342 - 353	1401.712	1401.650	-45	0	
				LSQLESTMQIR	831 - 842	1418.767	1418.710	-40	0	
				VGATGEIFVNSPR	642 - 655	1445.775	1445.637	-95	0	
				SPQVEEYNGVWPR	74 - 86	1560.744	1560.683	-39	0	
				SPQVEEYNGVWPR	74 - 86	1561.728	1561.585	-92	0	8: Deamidated (NQ)
				LMANSAGSVADLVEVGIR	666 - 683	1801.948	1801.783	-91	0	
				ELLQQVMKTVVEPADR	746 - 761	1899.973	1899.805	-89	1	N-Term: Acetyl (N-term) 4: Deamidated (NQ) 5: Deamidated (NQ)
				NSIAGQWTQPVWMGELR	774 - 790	1972.970	1972.910	-30	0	
				NSIAGQWTQPVWMGELR	774 - 790	1973.954	1973.776	-90	0	6: Deamidated (NQ)
				IGNIYAPEDCPDLCVNIVR	116 - 134	2220.031	2219.855	-79	0	10: Carboxymethyl (C) 14: Carboxymethyl (C)
QVYQISPFNEPTGVAVMEAR	240 - 259	2236.107	2235.926	-81	0					
YVVPSCGLPLEYGSYTTALAR	791 - 812	2431.221	2430.993	-94	0	6: Carboxymethyl (C)				
Apovitellenin-1 APOV1_CHICK P02659	Gallus gallus	88	44%	NFLINETAR	75 - 83	1077.569	1077.446	-114	0	
				AGQFLLDVSTTVVSGIR	57 - 74	1891.028	1890.878	-80	0	
				RDWLVIPDAAAAYIYEAVNK	33 - 52	2278.187	2277.985	-88	1	
Lysozyme C LYSC_CHICK P00698	Gallus gallus	75	14%	GTDVQAWIR	135 - 143	1045.543	1045.552	9	0	
				FESNFNTQATNR	52 - 63	1428.650	1428.600	-35	0	
Ovalbumin OVAL_CHICK P01012	Gallus gallus	74	11%	HIATNAVLFFGR	371 - 382	1345.738	1345.600	-102	0	
				GGLEPINFQTAADQAR	128 - 143	1687.840	1687.686	-91	0	
				ELINSWVESQTNGIIR	144 - 159	1858.966	1858.979	7	0	
				ELINSWVESQTNGIIR	144-159	1859.950	1859.806	-77	0	12: Deamidated (NQ)

Casein powder (63200)

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Alpha-S2-casein CASA2_BOVIN P02663	Bos taurus	60	39%	TVYQHQQ	197 - 203	903.468	903.504	40	0	
				FALPQYLK	189 - 196	979.561	979.584	24	0	
				LTEEEKNR	168 - 175	1018.516	1018.534	17	1	
				AMKPWIQPK	204 - 212	1098.613	1098.617	4	0	
				NAVPTPTLNR	130 - 140	1195.679	1195.665	-12	0	
				ITVDDKHYQK	86 - 95	1246.643	1246.636	-6	1	
				EQLSTSEENSK	141 - 151	1251.570	1251.695	100	0	
				FPQYLQYLYQGPIVLNPWDQVK	107 - 128	2709.408	2709.572	61	0	
Alpha-S1-casein CASA1_BOVIN P02662	Bos taurus	59	42%	EGIHAQQK	140 - 147	910.474	910.502	30	0	
				YLGYLEQLLR	106 - 115	1267.704	1267.717	10	0	
				HIQKEDVPSEK	95 - 105	1337.681	1337.672	-7	1	
				FFVAPFPEVFGK	38 - 49	1384.730	1384.725	-4	0	
				HQGLPQEVLENLLR	23 - 37	1759.945	1759.931	-8	0	
				YKVPQLEIVPNSAEER	119 - 134	1951.952	1951.917	-18	1	12: Phospho (ST)
				EPMIGVNQELAYFYPELFR	148 - 166	2316.137	2316.171	15	0	

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Alpha-S1-casein CASA1_BOVIN P02662	Bos taurus	463	46%	YLGYLEQLLR	106 - 115	1267.704	1267.695	-7	0	
				HIQKEDVPSEK	95 - 105	1337.681	1337.672	-7	1	
				FFVAPFPEVFGK	38 - 49	1384.730	1384.722	-6	0	
				HQGLPQEVLENLLR	23 - 37	1759.945	1759.932	-7	0	
				YKVPQLEIVPNSAEER	119 - 134	1951.952	1951.743	-107	1	12: Phospho (ST)
				IGVNQELAYFYPELFR	151 - 166	1959.001	1958.787	-109	0	
				EPMIGVNQELAYFYPELFR	148 - 166	2316.137	2316.134	-1	0	
Beta-casein CASB_BOVIN P02666	Bos taurus	124	8%	DMPIQAFLLYQEPVLPVVR	199 - 217	2186.168	2186.181	6	0	
Alpha-S2-casein CASA2_BOVIN P02663	Bos taurus	23	3%	TVYQHQQ	197 - 203	903.468	903.504	40	0	

Bovine quark cheese

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Alpha-S2-casein CASA2_BOVIN	Bos taurus	76	40%	VIPYVR	215 - 220	746.456	746.442	-19	0	
				LTEEEK	168 - 173	748.372	748.345	-36	0	

P02663				ITVDDK	86 - 91	770.333	770.346	17	0	2: Phospho (ST)
				TVYQHQQ	197 - 203	903.468	903.515	51	0	
				FALPQYLK	189 - 196	979.561	979.478	-85	0	
				LTEEEKNR	168 - 175	1098.483	1098.518	32	1	2: Phospho (ST)
				TKLTEEEK	166 - 173	1137.448	1137.476	25	1	1: Phospho (ST) 4: Phospho (ST)
				NAVPIPTLNR	130 - 140	1195.679	1195.608	-60	0	
				EQLSTSEENSK	141 - 151	1251.570	1251.641	57	0	
				ALNEINQFYQK	96 - 106	1367.695	1367.669	-19	0	7: Phospho (ST)
Alpha-S1-casein CASA1_BOVIN P02662	Bos taurus	60	41%	NMAINPSKENLCSTFCK	40 - 56	1979.842	1979.843	0	1	
				TTMPLW	209 - 214	748.370	748.371	2	0	
				EDVPSEER	99 - 105	831.384	831.382	-3	0	
				YLGYLEQLLR	106 - 115	1267.704	1267.694	-8	0	
				HIQKEDVPSEER	95 - 105	1337.681	1337.689	6	1	
				FFVAPFPEVFGK	38 - 49	1384.730	1384.748	13	0	
				VPQLEIVPNSAEER	121 - 134	1660.794	1660.762	-19	0	10: Phospho (ST)
				HQGLPQEVLENENLLR	23 - 37	1759.945	1759.950	3	0	
Beta-lactoglobulin LACB_BOVIN P02754	Bos taurus	48	57%	YKVPQLEIVPNSAEER	119 - 134	1951.952	1951.969	8	1	12: Phospho (ST)
				EPMIGVNOELAYFYPELFR	148 - 166	2316.137	2316.133	-2	0	
				ALPMHIR	158 - 164	837.476	837.438	-46	0	
				TKIPAVFK	92 - 99	903.566	903.515	-57	1	
				VLVLDTDYKK	108 - 117	1193.678	1193.603	-63	1	
				TPEVDDEALEK	141 - 151	1325.551	1325.671	91	0	1: Phospho (ST)
				TPEVDDEALEK	141 - 151	1367.561	1367.675	83	0	N-Term: Acetyl (N-term) 1: Phospho (ST)
				TPEVDDEALEKFDK	141 - 154	1635.775	1635.808	20	1	
Beta-casein CASB_BOVIN P02666	Bos taurus	30	17%	LSFNPTQLEEQCHI	165 - 178	1716.790	1716.816	15	0	12: Carboxymethyl (C)
				YLLFCMENSAAPEQSLACQCLVR	118 - 140	2843.180	2842.916	-93	0	5: Carboxymethyl (C) 18: Carboxymethyl (C); + Phospho (ST)
				VAGTWYSLAMAASDISLLDAQSAPLR	31 - 56	2707.376	2707.319	-21	0	
AVPYRQR	192 - 198	830.452	830.433	-23	0					
DMPIQAFLLYQEPVLPVVR	199 - 217	2186.168	2186.177	4	0					

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Alpha-S1-casein CASA2_BOVIN P02662	Bos taurus	433	43%	EGIHAQQK	140 - 147	910.474	910.493	21	0	
				YLGYLEQLLR	106 - 115	1267.704	1267.694	-8	0	
				HIQKEDVPSEER	95 - 105	1337.681	1337.689	6	1	
				FFVAPFPEVFGK	38 - 49	1384.730	1384.748	13	0	
				HQGLPQEVLENENLLR	23 - 37	1759.945	1759.950	3	0	
				YKVPQLEIVPNSAEER	119 - 134	1951.952	1951.969	8	1	12: Phospho (ST)
				EPMIGVNOELAYFYPELFR	148 - 166	2316.137	2316.133	-2	0	
Beta-lactoglobulin LACB_BOVIN P02754	Bos taurus	205	26%	ALPMHIR	158 - 164	837.476	837.487	13	0	
				LSFNPTQLEEQCHI	165 - 178	1716.790	1716.780	-6	0	12: Carboxymethyl (C)
				VAGTWYSLAMAASDISLLDAQSAPLR	31 - 56	2707.376	2707.470	35	0	
Alpha-S2-casein CASA2_BOVIN P02663	Bos taurus	93	18%	FALPQYLK	189 - 196	979.561	979.529	-32	0	
				AMKPWIQPK	204 - 212	1098.613	1098.518	-87	0	
				NAVPIPTLNR	130 - 140	1195.679	1195.658	-18	0	
				ALNEINQFYQK	96 - 106	1367.695	1367.675	-15	0	
Beta-casein	Bos taurus	63	12%	GPFPIIV	218 - 224	742.450	742.426	-32	0	

CASB_BOVIN P02666				DMPIQAFLLYQEPVLPVLR	199 - 217	2186.168	2186.177	4	0	
Kappa-casein CASK_BOVIN P02668	Bos taurus	41	5%	YIPIQYVLSR	46 - 55	1251.710	1251.668	-33	0	

Bovine bone glue (63000)

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	72	28%	GPAGPQGPR	1084 - 1092	836.437	836.449	14	0	
				GPAGPQGPR	1084 - 1092	852.432	852.435	3	0	Oxidation (P)
				GEGGPQGPR	352 - 360	854.412	854.408	-4	0	
				GPAGPQGPR	1084 - 1092	868.427	868.459	36	0	2 Oxidation (P)
				GDRGDAGPK	742 - 750	872.422	872.441	22	1	
				GSEGPQGV	361 - 369	886.438	886.435	-3	0	
				GVVGLPGQR	958 - 966	898.511	898.524	15	0	Oxidation (P)
				GDTGPRGPR	115 - 123	944.454	944.494	42	1	2 Oxidation (P)
				GFPADGVAGPK	493 - 504	1088.537	1088.557	18	0	Oxidation (P)
				GVQPPGPAGPR	685 - 696	1105.575	1105.590	14	0	Oxidation (P)
				GVQPPGPAGPR	685 - 696	1121.570	1121.572	2	0	2 Oxidation (P)
				GQAGVMGFPGPK	574 - 585	1161.572	1161.579	6	0	Oxidation (P)
				GQAGVMGFPGPK	574 - 585	1177.567	1177.560	-6	0	2 Oxidation (P)
				GHRGFSGLDGAK	265 - 276	1201.607	1201.587	-17	1	
				GFPGLPGSPGEPGK	970 - 983	1328.648	1328.642	-5	0	2 Oxidation (P)
				GPSGQPSGPPGPK	415 - 429	1332.654	1332.641	-10	0	Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1427.703	1427.732	21	0	
				GEPGAGLPGPPGER	472 - 486	1435.681	1435.702	15	0	3 Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1459.692	1459.707	10	0	2 Oxidation (P)
				GETGPAGPAGPIGPVGAR	1066 - 1083	1560.813	1560.814	1	0	
				GNSGEPGAPGSKGDTGAK	430 - 447	1586.741	1586.752	8	1	
				GFPADGVAGPKGPAGER	493 - 510	1655.814	1655.828	8	1	Oxidation (P)
				DGLNLGPIGPPGPRGR	1152 - 1169	1726.935	1726.882	-31	1	
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1816.865	1816.875	5	0	Oxidation (P)
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1832.860	1832.876	9	0	3 Oxidation (P)
				GAPGADGPAGAPGTPGPGIAGQR	934 - 957	2057.016	2057.032	8	0	
				GAPGADGPAGAPGTPGPGIAGQR	934 - 957	2105.001	2105.038	18	0	3 Oxidation (P)
				GVQPPGPAGPRGANGAPGNDGAK	685 - 708	2131.028	2131.152	58	1	2 Oxidation (P)
				GFSGLQGGPPGSPGEPGQPSGASGPAGPR	1111 - 1140	2689.260	2689.310	18	0	2 Oxidation (P)
				GFSGLQGGPPGSPGEPGQPSGASGPAGPR	1111 - 1140	2705.255	2705.277	8	0	3 Oxidation (P)
				GAPGDRGEPGPPGAGFAGPPGADGQPGAK+	796 - 825	2719.234	2719.258	9	1	5 Oxidation (P)
				GDAGAPGAPGSQGA PGLQGM PGERGAAGLPGPK	709 - 741	2883.417	2883.415	-1	1	
GLPPPGAPGPGQFQGGPGEPEGASGPMGPR	187 - 219	3084.412	3084.389	-7	0	5 Oxidation (P)				
GLPPPGAPGPGQFQGGPGEPEGASGPMGPR	187 - 219	3100.407	3100.364	-14	0	6 Oxidation (P)				
GLPGERGR	215 - 222	857.459	857.410	-57	1	Oxidation (P)				
GPSGDRGPR	33 - 41	898.449	898.479	34	1					
GFPGTPGLPGFK	164 - 175	1206.615	1206.518	-81	0	2 Oxidation (P)				
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	33	14%							

				GFPGTPGLPGFK	164 - 175	1222.610	1222.519	-75	0	3 Oxidation (P)
				GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.641	-61	0	2 Oxidation (P)
				GAAGLPGVAGAPGLPGPR	308 - 325	1562.829	1562.716	-72	0	3 Oxidation (P)
				HGNRGEPPAGAVGPAGAVGPR	973 - 994	2028.996	2028.910	-42	1	3 Oxidation (P)
				GEPGAVGQPPGPSGEEGKR	359 - 379	2055.921	2055.922	0	1	6 Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2130.950	-77	0	3 Oxidation (P)
				GPPGESGAAGPTGPIGSRGPSGPPGPDGNK	590 - 619	2705.240	2705.016	-83	1	5 Oxidation (P)
				GPPGASGAPGPQGFQPPGEPGEPGQTGPAGAR	98 - 130	3033.357	3033.131	-74	0	6 Oxidation (P)

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_CANFA O46392	Canis familiaris	209	4%	GLPGEFGLPGPAGPR	574 - 588	1453.743	1453.644	-68	0	2 Oxidation (P)
				GAAGLPGVAGAPGLPGPR	310 - 327	1562.829	1562.716	-72	0	3 Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	883 - 906	2131.114	2130.950	-77	0	3 Oxidation (P)
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	178	6%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.641	-61	0	2 Oxidation (P)
				GAAGLPGVAGAPGLPGPR	308 - 325	1562.829	1562.716	-72	0	3 Oxidation (P)
				EGPVGLPGIDGRPGPIGPAGAR	463 - 484	2056.093	2055.922	-83	0	Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2130.950	-77	0	3 Oxidation (P)
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	96	5%	GPAGPQGPR	1084 - 1092	836.437	836.449	14	0	
				GEGGPQGPR	352 - 360	854.412	854.408	-4	0	
				GEPGSPGENGAPGQMGR	286 - 303	1726.745	1726.882	79	0	2 Oxidation (P)
				GFSGLQGPPGPPGSPGEGQGPSGASGPAGPR	1111 - 1140	2705.255	2705.335	30	0	3 Oxidation (P)
Collagen alpha-1(III) chain CO3A1_MOUSE P08121	Mus musculus	49	2%	GPAGPQGPR	1082 - 1090	836.437	836.449	14	0	
				GLPGPPGNNGNPGLPGSPGAPGK	878 - 900	2056.968	2057.032	31	0	4 Oxidation (P)
Collagen alpha-1(II) chain CO2A1_BOVIN P02459	Bos taurus	32	1%	GPPGPQGAR	267 - 275	836.437	836.449	14	0	

Bovine hide glue (63010)

Proteins identified by PMS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	87	22%	NPARTCR	1253 - 1259	817.410	817.430	25	1	
				GPAGPQGPR	1084 - 1092	836.437	836.358	-95	0	
				GFSGLDGAK	268 - 276	851.426	851.346	-93	0	
				GPAGPQGPR	1084 - 1092	852.432	852.347	-101	0	Oxidation (P)
				GEGGPQGPR	352 - 360	854.412	854.334	-91	0	
				GPAGPQGPR	1084 - 1092	868.427	868.380	-54	0	2 Oxidation (P)
				GDRGDAGPK	742 - 750	872.422	872.331	-104	1	
				GVVGLPGQR	958 - 966	882.516	882.580	73	0	
				GEGGPQGPR	352 - 360	886.401	886.352	-56	0	2Oxidation (P)
				GVVGLPGQR	958 - 966	898.511	898.427	-93	0	Oxidation (P)
				QGSPGASGER	984 - 993	945.438	945.346	-97	0	
				GFPGADGVAGPK	493 - 504	1088.537	1088.427	-101	0	Oxidation (P)
				GRPGAPGPAGAR	310 - 321	1095.565	1095.465	-92	0	2 Oxidation (P)
				GAAGEPGKAGER	586 - 597	1099.549	1099.429	-109	1	
				GNSGEPGAPGSK	430 - 441	1105.476	1105.452	-21	0	3 Oxidation
				GQAGVMGFPGPK	574 - 585	1177.567	1177.441	-107	0	2 Oxidation (P)
				GVPGPPGAVGPAGK	598 - 611	1192.632	1192.710	65	0	2 Oxidation (P)
				GHRGFSGLDGAK	265 - 276	1201.607	1201.468	-116	1	
				GVPGPPGAVGPAGK	598 - 611	1208.627	1208.548	-65	0	3 Oxidation (P)
				GDKGETGEQDR	1093 - 1104	1264.540	1264.422	-94	1	Oxidation (K)
				GPSGPQGPSGPPGPK	415 - 429	1332.654	1332.521	-100	0	Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1427.703	1427.612	-63	0	
				GEPGPAGLPGPPGER	472 - 486	1435.681	1435.561	-84	0	3 Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1459.692	1459.577	-79	0	2 Oxidation (P)
				GNSGEPGAPGSKGDTGAK	430 - 447	1586.741	1586.646	-60	1	
				GSPGEAGRPGEAGLPGAK	520 - 537	1655.798	1655.684	-69	0	3 Oxidation (P)
				GEPGSPGENGAPGQMGP	286 - 303	1710.750	1710.756	4	0	Oxidation (P)
				GEPGSPGENGAPGQMGP	286 - 303	1726.745	1726.754	5	0	2 Oxidation (P)
				SGDRGETGPAGPAGPIGPVGAR	1062 - 1083	1975.994	1975.980	-7	1	
				TGPPGPAQDGRPGPPGPPGAR	552 - 573	2056.980	2056.922	-28	0	4 Oxidation (P)
GVQPPGPAGPRGANGAPGNDGAK	685 - 708	2131.028	2131.013	-7	1	2 Oxidation (P)				
GETGPAGRPGEVPPGPPPAGEK	910 - 933	2216.058	2215.909	-67	0	3 Oxidation (P)				

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	323	12%	GHAGLAGAR	509 - 517	809.438	809.366	-89	0	
				NPARTCR	1156 - 1162	817.410	817.430	25	1	
				GPSGPGQIR	995 - 1003	868.464	868.380	-96	0	
				GPSGPPGPDGNK	608 - 619	1095.507	1095.465	-38	0	Oxidation (P)
				IGQP GAVGPAGIR	1066 - 1078	1192.680	1192.585	-79	0	
				GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.590	-97	0	2 Oxidation (P)
				GAAGLPGVAGAPGLPGPR	308 - 325	1562.829	1562.700	-82	0	3 Oxidation (P)
				EGPVGLPGIDGRPGPIGPAGAR	463 - 484	2056.093	2055.924	-83	0	Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2099.124	2098.920	-97	0	Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2130.937	-83	0	3 Oxidation (P)
GPSGEPGTAGPPGTPGPGQLL GAGPFLGLPGSR	845 - 877	3017.496	3017.146	-116	0	4 Oxidation (P)				
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	137	6%	NPARTCR	1253 - 1259	817.410	817.430	25	1	
				GPAGPQGPR	1084 - 1092	836.437	836.358	-95	0	
				GPAGPQGPR	1084 - 1092	852.432	852.347	-101	0	Oxidation (P)
				GEGGPQGPR	352 - 360	854.412	854.334	-91	0	
				GPAGPQGPR	1084 - 1092	868.427	868.380	-54	0	2 Oxidation (P)
				GSEGPQGVR	361 - 369	886.438	886.352	-97	0	
				GVVGLPGQR	958 - 966	898.511	898.427	-93	0	6: Oxidation (P)
				GRPGAPGPAGAR	310 - 321	1095.565	1095.465	-92	0	2Oxidation (P)
				GADGAPGKDGVR	751 - 762	1099.549	1099.429	-109	1	
				TGPPGPAGQDGRPGPPPPGAR	552 - 573	2056.980	2056.922	-28	0	4 Oxidation (P)
Collagen alpha-2(I) chain (Fragment) CO1A2_RABIT Q28668	Oryctolagus cuniculus	38	8%	GEPGPAGSIGPVGAAGPR	139 - 156	1562.792	1562.700	-59	0	Oxidation (P)
				GLPGVAGALGEPGLGIAGPPGAR	43 - 66	2097.145	2096.917	-109	0	Oxidation (P)

Rabbit skin glue, refined (63025)

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	50	20%	GPAGPQGPR	1084 - 1092	836.437	836.465	33	0	
				GFSGLDGAK	268 - 276	851.426	851.464	45	0	
				GPAGPQGPR	1084 - 1092	868.427	868.491	74	0	2 Oxidation (P)
				GVVGLPQQR	958 - 966	898.511	898.549	42	0	Oxidation (P)
				GFPGADGVAGPK	493 - 504	1088.537	1088.584	43	0	Oxidation (P)
				GVQGGPPGAPR	685 - 696	1105.575	1105.620	41	0	Oxidation (P)
				GVPGGPGAVGPAGK	598 - 611	1192.632	1192.721	74	0	2 Oxidation (P)
				GVPGGPGAVGPAGK	598 - 611	1208.627	1208.711	70	0	3 Oxidation (P)
				GFPGLPGSPGEPK	970 - 983	1312.653	1312.686	25	0	Oxidation (P)
				GFPGLPGSPGEPK	970 - 983	1328.648	1328.694	34	0	2 Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1427.703	1427.777	52	0	
				GEPGAPGLPDPGER	472 - 486	1435.681	1435.737	39	0	3 Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1459.692	1459.737	30	0	2 Oxidation (P)
				GETGPAGPAGPIGPVGR	1066 - 1083	1560.813	1560.876	40	0	
				GNSGEPGAPGSKGDTGAK	430 - 447	1586.741	1586.806	41	1	
				DGLNGLPGPIGPPGPRGR	1152 - 1169	1726.935	1726.932	-1	1	
				SGRGETGPAGPAGPIGPVGR	1062 - 1083	1975.994	1976.060	33	1	
				DGVRGLTPIGPPGAPAGPDK	759 - 780	2082.010	2082.156	70	1	6 Oxidation
				GVQGGPGAPRGANGAPGNDGAK	685 - 708	2131.028	2131.179	71	1	2 Oxidation (P)
				GFSGLQGPPGPPGSPGEGQGPSGASGPAGPR	1111 - 1140	2689.260	2689.322	23	0	2 Oxidation (P)
GFSGLQGPPGPPGSPGEGQGPSGASGPAGPR	1111 - 1140	2705.255	2705.336	30	0	3 Oxidation (P)				
GLTGPVGGPAGAPGDKGEAGPSGPAGPTGAR	763 - 795	2853.413	2853.487	26	1	2 Oxidation (P)				
GNDGATGAAGPPGPTGPAGPPGFPAGVAGAKGEGGPQGPR	322 - 360	3383.600	3383.794	57	1	3 Oxidation (P)				
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	44	18%	IGQPGAVGPAGIR	1066 - 1078	1192.680	1192.681	1	0	
				GIPGPVGAAGATGAR	326 - 340	1267.675	1267.666	-7	0	Oxidation (P)
				GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.733	4	0	2 Oxidation (P)
				GAAGLPGVAGAPGLPGPR	308 - 325	1562.829	1562.831	2	0	3 Oxidation (P)
				GSTGEIGPAGPPGPPGLR	380 - 397	1648.829	1648.831	1	0	2 Oxidation (P)
				GEPGAVGQPPGPPGSGEEGKR	359 - 379	1975.947	1975.987	21	1	Oxidation (P)
				EGPVGLPGIDGRPGPIGPAGAR	463 - 484	2056.093	2056.090	-2	0	Oxidation (P)
				EGPVGLPGIDGRPGPIGPAGAR	463 - 484	2072.088	2072.064	-12	0	2 Oxidation (P)
				KAVILQGSNDVELVAEGNSR	1286 - 1305	2115.104	2115.094	-5	1	Oxidation
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2131.106	-4	0	3 Oxidation (P)
				GPPGESGAAGPTGPIGSRGPPGPDGNK	590 - 619	2705.240	2705.238	-1	1	5 Oxidation (P)
				GPSGEPGTAGPPGTPGQGLLGAPGFLGLPGSR	845 - 877	3033.491	3033.510	6	0	5 Oxidation (P)

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	233	7%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.606	-85	0	2 Oxidation (P)
				GAAGLPGVAGAPGLPGPR	308 - 325	1562.829	1562.699	-83	0	3 Oxidation (P)
				GSTGEIGPAGPPGPPGLR	380 - 397	1648.829	1648.720	-66	0	2 Oxidation (P)
				EGPVGLPGIDGRPGPIGPAGAR	463 - 484	2056.093	2056.114	10	0	Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2115.119	2115.094	-12	0	2 Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2131.179	30	0	3 Oxidation (P)
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	38	2%	GFSGLQGPSPGSPGEGQGPSGASGPAGPR	1111 - 1140	2705.255	2705.238	-6	0	3 Oxidation (P)
Collagen alpha-1(III) chain CO3A1_MOUSE P08121	Mus musculus	35	3%	DGTSGHPPGIPPPGPR	1150 - 1165	1562.719	1562.699	-13	0	4 Oxidation (P)
				GPPGAQGPSPGSPGLGIAGLTGAR	932 - 955	2098.104	2098.210	51	0	Oxidation (P)

Rabbit skin glue, raw (63028)

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	46	19%	GVVGLPGQR	958 - 966	898.511	898.468	-47	0	Oxidation (P)
				GVQGGPPGAGPR	685 - 696	1105.575	1105.530	-41	0	Oxidation (P)
				GVPGGPGAVGPAGK	598 - 611	1192.632	1192.593	-33	0	2 Oxidation (P)
				GVPGGPGAVGPAGK	598 - 611	1208.627	1208.628	1	0	3 Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1427.703	1427.660	-30	0	
				GEPGPAGLPGPPGER	472 - 486	1435.681	1435.606	-52	0	3 Oxidation (P)
				ALLLQGSNEIEIR	1386 - 1398	1455.817	1455.692	-86	0	
				STGISVPGPMGPPGPR	171 - 186	1560.732	1560.727	-3	0	4 Oxidation (P)
				GNSGEPGAPGSKGDTGAK	430 - 447	1586.741	1586.684	-36	1	
				GEPGSPGENGAPGQMGR	286 - 303	1710.750	1710.789	23	0	Oxidation (P)
				GEPGSPGENGAPGQMGR	286 - 303	1726.745	1726.787	25	0	2 Oxidation (P)
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1816.865	1816.758	-59	0	2 Oxidation (P)
				SGDRGETGPAGPAGPIGPVGAR	1062 - 1083	1975.994	1975.890	-53	1	
				DGVRGLTGPIPPGAPAGPGDK	759 - 780	2082.010	2081.998	-6	1	6 Oxidation
				FTYSVTYDGCTSHTGAWGK	1405 - 1423	2096.902	2097.020	57	0	Oxidation (K)
				GVQGGPPGAPPRGANGAPNDGAK	685 - 708	2131.028	2130.995	-16	1	2 Oxidation (P)
				GFSGLQGPSPGSPGEGQGPSGASGPAGPR	1111 - 1140	2705.255	2705.079	-65	0	3 Oxidation (P)
				GLPGPPGAPGPFQGGPPGEPGEPGASGPMGPR	187 - 219	3084.412	3084.237	-57	0	5 Oxidation (P)
GLPGPPGAPGPFQGGPPGEPGEPGASGPMGPR	187 - 219	3100.407	3100.233	-56	0	6 Oxidation (P)				

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	216	4%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.668	-42	0	2 Oxidation (P)
				EGPVGLPGIDGRPGPIGPAGAR	463 - 484	2056.093	2056.044	-24	0	Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2130.995	-56	0	3 Oxidation (P)
Collagen alpha-2(I) chain (Fragments) CO1A2_CHICK P02467	Gallus gallus	37	2%	GLPGIAGATGEPGLGVSGPPGAR	881 - 904	2133.094	2133.074	-9	0	3 Oxidation (P)

Technical gelatin from pig skin (63040)

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_CANFA O46392	Canis familiaris	193	3%	GLPGEFGLPGPAGPR	574 - 588	1453.743	1453.609	-92	0	2 Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	883 - 906	2131.114	2130.984	-61	0	3 Oxidation (P)
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	37	4%	GFSGLQGPPGPPGSPGEGQPSGASGPAGPR	1111 - 1140	2689.260	2689.395	50	0	2 Oxidation (P)
				GLPGLGPPGAPGPGQFGPPGEPGEPGASGPMGPR	187 - 219	3084.412	3084.580	54	0	5 Oxidation (P)
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	34	4%	GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2131.212	46	0	3 Oxidation (P)
				GPSGEPGTAGPPGTPGPGQLLGLGAPGFLGLPGSR	845 - 877	3017.496	3017.630	44	0	4 Oxidation (P)

Salianski isinglass (63110)

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_CYNPY Q9YIB4	Cynops pyrrhogaster	103	2%	GAAGPPGATGFPGAAGR	852 - 868	1443.698	1443.702	3	0	2 Oxidation (P)
				GFPGSDGASGPKGAPGER	480 - 497	1691.762	1691.770	5	1	3 Oxidation
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	64	1%	GSAGPPGATGFPGAAGR	865 - 881	1443.698	1443.702	3	0	Oxidation (P)
Collagen alpha-2(I) chain CO1A2_ONCMY O93484	Oncorhynchus mykiss	51	2%	GQPGNIGFPGPK	481 - 492	1200.601	1200.594	-6	0	2 Oxidation (P)
				GAAGLPGVAGAPGFPGPR	304 - 321	1612.808	1612.603	-127	0	3 Oxidation (P)
Collagen alpha-1(II) chain CO2A1_HUMAN P02458	Homo sapiens	50	1%	GIVGLPGQR	981 - 989	912.526	912.515	-12	0	Oxidation (P)
Collagen alpha-1(II) chain CO2A1_BOVIN P02459	Bos taurus	12	1%	GEPGGAGPAGPPGER	495 - 509	1353.603	1353.518	-63	12	3 Oxidation (P)

Egg white + Zinc white (9M11)

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Ovalbumin OVAL_CHICK P01012	Gallus gallus	72	32%	LYAEER	106-111	780.389	780.392	4	0	
				DEDTQAMPFR	191-200	1209.520	1209.467	-44	0	
				ADHPFLFCIK	361-370	1248.608	1248.595	-10	0	
				HIATNAVLFFGR	371-382	1345.738	1345.822	63	0	
				YPILPEYLQCVK	112-123	1523.781	1523.874	61	0	
				AFKDEDTQAMPFR	188-200	1555.721	1555.799	50	1	
				LTEWTSSNVMEER	265-277	1581.721	1581.765	28	0	
				GGLEPINFQTAADQAR	128-143	1687.840	1687.713	-75	0	
				LTEWTSSNVMEERK	265-278	1709.816	1709.640	-103	1	
				DILNQITKPNDVYSFSLASR	86-105	2281.182	2281.276	41	0	
VTEQESKPVQMMYQIGLFR	201-219	2285.130	2285.087	-19	0	Deamidated (NQ)				

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Ovalbumin OVAL_CHICK P01012	Gallus gallus	584	33%	LYAEER	106-111	780.389	780.392	4	0	
				DEDTQAMPFR	191-200	1209.52	1209.467	-44	0	
				HIATNAVLFFGR	371-382	1345.738	1345.822	63	0	
				AFKDEDTQAMPFR	188-200	1555.721	1555.799	50	1	
				LTEWTSSNVMEER	265-277	1581.721	1581.765	28	0	
				GGLEPINFQTAADQAR	128-143	1687.840	1687.713	-75	0	
				EVVGSAAEAGVDAASVSEEFR	341-360	2088.912	2089.021	52	0	5: Phospho (ST)
				DILNQITKPNDVYSFSLASR	86-105	2281.182	2281.276	41	0	
				VTEQESKPVQMMYQIGLFR	201-219	2286.114	2286.242	56	0	2 Deamidated (NQ)

Egg white + French Ochre (9M21)

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Ovalbumin OVAL_CHICK P01012	Gallus gallus	73	31%	LYAEER	106-111	780.389	780.392	4	0	
				DEDTQAMPFR	191 - 200	1209.520	1209.463	-47	0	
				HIATNAVLFFGR	371 - 382	1345.738	1345.796	43	0	
				AFKDEDTQAMPFR	188 - 200	1555.721	1555.695	-16	1	
				AFKDEDTQAMPFR)	188 - 200	1571.716	1571.659	-36	1	10: Oxidation (M
				LTEWTSSNVMEER	265 - 277	1581.721	1581.659	-40	0	
				LTEWTSSNVMEER	265 - 277	1597.716	1597.614	-64	0	10: Oxidation (M)
				ELINSWVESQTNGIIR	144 - 159	1858.966	1859.134	90	0	
				EVVGSAEAGVDAASVSEEF	341-360	2008.946	2009.046	50	0	
				DILNQITKPNVDVYSFSLASR	86 - 105	2281.182	2281.307	55	0	
				DILNQITKPNVDVYSFSLASR	86 - 105	2283.150	2283.095	-24	0	4, 5: Deamidated (NQ)
VTEQESKPVQMMYQIGLFR	201-219	2281.146	2284.263	51	0					

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Ovalbumin OVAL_CHICK P01012	Gallus gallus	490	26%	LYAEER	106 - 111	780.389	780.392	4	0	
				DEDTQAMPFR	191 - 200	1209.520	1209.463	-47	0	
				HIATNAVLFFGR	371 - 382	1345.738	1345.796	43	0	
				AFKDEDTQAMPFR	188 - 200	1555.721	1555.695	-16	1	
				LTEWTSSNVMEER	265 - 277	1581.721	1581.659	-40	0	
				ELINSWVESQTNGIIR	144 - 159	1858.966	1859.134	90	0	
				EVVGSAEAGVDAASVSEEF	341 - 360	2008.946	2009.046	50	0	
				EVVGSAEAGVDAASVSEEF	341 - 360	2088.912	2089.053	67	0	5: Phospho (ST)
				DILNQITKPNVDVYSFSLASR	86 - 105	2281.182	2281.307	55	0	
				SAGWNIPIGTLLHR	141-154	1534.849	1534.834	-10	0	
Ovotransferrin TRFE_CHICK P02789	Gallus gallus	38	4%	TDERPASYFAVAVAR	443-457	1652.839	1652.605	-142	0	
Lysozyme C LYSC_CHICK P00698	Gallus gallus	21	8%	FESNFNTQATNR	52-63	1427.643	1428.731	56	0	

Egg yolk + Zinc white (10M11)

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Vitellogenin-2 VIT2_CHICK P02845	Gallus gallus	149	3%	LPLSLPVGPR	1543 - 1552	1048.651	1048.665	13	0	
				NIPFAEYPTYK	695 - 705	1342.668	1342.719	38	0	
				DASFIQNTYLHK	1008 - 1019	1436.717	1436.765	34	0	
				VGATGEIFVVNSPR	642 - 655	1445.775	1445.823	33	0	
				SPQVEEYNGVWPR	74 - 86	1560.744	1560.790	29	0	
Ovalbumin OVAL_CHICK P01012	Gallus gallus	86	8%	GGLPEINFQTAADQAR	128 - 143	1687.840	1687.892	31	0	
				ELINSWVESQTNGIIR	144 - 159	1859.950	1860.003	28	0	12: Deamidated (NQ)
Apovitellenin-1 APOV1_CHICK P02659	Gallus gallus	78	25%	NFLINETAR	75 - 83	1077.569	1077.577	7	0	
				AGQFLLDVVSQTIVVSGIR	57 - 74	1891.028	1891.003	-13	0	

Egg yolk + French Ochre (10M21)

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Vitellogenin-2 VIT2_CHICK P02845	Gallus gallus	59	11%	LPLSLPVGPR	1543 - 1552	1048.651	1048.646	-5	0	
				QQLTLVEVR	260 - 268	1085.631	1085.641	9	0	
				MTPPLTGDFR	821-830	1150.556	1150.543	-11	0	1: Oxidation (M)
				TVDLNNCQEK	182 - 191	1164.520	1164.518	-2	0	Deamidated (NQ)
				LEWPKVPSNVR	1472 - 1482	1324.737	1324.723	-11	1	
				NIPFAEYPTYK	695 - 705	1342.668	1342.708	30	0	
				IANADNLESIWR	342 - 353	1401.712	1401.709	-2	0	
				LSQLLESTMQIR	831-842	1418.767	1418.782	10	0	
				LSQLLESTMQIR	831 - 842	1434.762	1434.817	38	0	9: Oxidation (M)
				ILGIDSMFKVANK	1083 - 1095	1436.782	1436.766	-11	1	12: Deamidated (NQ)
				VGATGEIFVNSPR	642 - 655	1445.775	1445.737	-26	0	
				TVDLNNCQEKVQK	182 - 194	1560.769	1560.791	15	1	N-Term: Acetyl
				TVDLNNCQEKVQK	182 - 194	1561.753	1561.756	2	1	N-Term: Acetyl + Deamidated (NQ)
				LALKCIGNMGEPASLK	479-494	1687.876	1687.892	10	1	N-term: Acetyl 8: Deamidated (NQ)
				EALQPIHDLADEAISR	456 - 471	1777.908	1777.912	2	0	
LMANSAGSVADLVEVGIR	666 - 683	1859.953	1859.997	24	0	N-Term: Acetyl 2: Oxidation (M)				
NSIAGQWTQPVWMGELR	774 - 790	1988.965	1988.936	-14	0	13: Oxidation (M)				
SYLYNYEGSMLNGLQDR	29 - 45	2022.923	2022.926	2	0					
QVYQISPFNEPTGVAVMEAR	240 - 259	2236.107	2236.093	-6	0					

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Vitellogenin-2 VIT2_CHICK P02845	Gallus gallus	247	6%	LPLSLPVGPR	1543 - 1552	1048.651	1048.646	-5	0	
				QQLTLVEVR	260 - 268	1085.631	1085.641	9	0	
				MTPPLTGDFR	821 - 830	1150.556	1150.543	-11	0	1: Oxidation (M)
				ADTYFDNYR	633 - 641	1164.496	1164.518	19	0	
				NIPFAEYPTYK	695 - 705	1342.668	1342.708	30	0	
				IANADNLESIWR	342 - 353	1401.712	1401.709	-2	0	
				DASFIQNTYLHK	1008 - 1019	1436.717	1436.766	34	0	
				SPQVEEYNGVWPR	74 - 86	1560.744	1560.791	30	0	
				EALQPIHDLADEAISR	456 - 471	1777.908	1777.912	2	0	
				QVYQISPFNEPTGVAVMEAR	240 - 259	2236.107	2236.093	-6	0	
Ovalbumin OVAL_CHICK P01012	Gallus gallus	91	8%	GGLEPINFQTAADQAR	128 - 143	1687.840	1687.734	-63	0	
				ELINSWVESQTNGIIR	144 - 159	1859.950	1859.997	25	0	12: Deamidated (NQ)
Apovitellenin-1 APOV1_CHICK P02659	Gallus gallus	60	25%	NFLINETAR	75 - 83	1077.569	1077.554	-14	0	
				AGQFLLDVVSQTTVVSGIR	57 - 74	1891.028	1890.944	-45	0	

Bovine quark cheese + Zinc white (7M11)

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Alpha-S1-casein CASA1_BOVIN P02662	Bos taurus	68	41%	YLGYLEQLLR	106 - 115	1267.704	1267.764	47	0	
				FFVAPFPEVFGK	38 - 49	1384.730	1384.815	62	0	
				VPQLEIVPNSAEER	121 - 134	1660.794	1660.888	57	0	10: Phospho (ST)
				HQGLPQEVLENENLLR	23 - 37	1759.945	1760.039	54	0	
				DIGSESTEDQAMEDIK	58 - 73	1927.692	1927.790	51	0	4, 6: Phospho (ST)
				YKVPQLEIVPNSAEER	119 - 134	1951.952	1952.047	48	1	12: Phospho (ST)
				EPMIGVYNQELAYFYPELFR	148 - 166	2316.137	2316.310	75	0	
Beta-lactoglobulin LACB_BOVIN P02754	Bos taurus	34	17%	ALPMHIR	158 - 164	837.476	837.494	21	0	
				VLVLDTDYKK	108 - 117	1193.678	1193.706	24	1	
				TPEVDDEALEK	141 - 151	1245.584	1245.628	35	0	
				TPEVDDEALEKFDK	141 - 154	1635.775	1635.864	54	1	

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Alpha-S1-casein CASA1_BOVIN P02662	Bos taurus	595	41%	YLGYLEQLLR	106 - 115	1267.704	1267.764	47	0	
				FFVAPFPEVFGK	38 - 49	1384.730	1384.815	62	0	
				VPQLEIVPNSAEER	121 - 134	1660.794	1660.888	57	0	10: Phospho (ST)
				HQGLPQEVLENENLLR	23 - 37	1759.945	1760.039	54	0	
				DIGSESTEDQAMEDIK	58-73	1927.692	1927.790	51	0	4, 6: Phospho (ST)
				YKVPQLEIVPNSAEER	119 - 134	1951.952	1952.047	48	1	12: Phospho (ST)
				EPMIGVYNQELAYFYPELFR	148 - 166	2316.137	2316.310	75	0	
Alpha-S2-casein CASA2_BOVIN P02663	Bos taurus	64	8%	FALPQYLK	189 - 196	979.561	979.604	43	0	
				NAVPIPTLNR	130 - 140	1195.679	1195.730	43	0	
Beta-casein CASB_BOVIN P02666	Bos taurus	57	14%	GPFPIIV	218 - 224	742.450	742.486	49	0	
				VLPVPQK	185 - 191	780.498	780.517	25	0	
				DMPIQAFLLYQEPVLPVVR	199 - 217	2186.168	2186.312	70	0	
Beta-lactoglobulin LACB_BOVIN P02754	Bos taurus	39	10%	ALPMHIR	158 - 164	837.476	837.494	21	0	
				VLVLDTDYKK	108 - 117	1193.678	1193.706	24	1	
Kappa-casein CASK_BOVIN P02668	Bos taurus	33	5%	YIPIQYVLSR	46-55	1251.709	1251.750	32	0	

Bovine quark cheese + French Ochre (7M21)

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Alpha-S1-casein CASA1_BOVIN P02662	Bos taurus	46	34%	YLGYLEQLLR	106 - 115	1267.704	1267.704	0	0	
				FFVAPFPEVFGK	38 - 49	1384.730	1384.730	0	0	
				HQGLPQEVLNENLLR	23 - 37	1759.945	1759.945	0	0	
				YKVPQLEIVPNSAEER	119 - 134	1951.952	1951.952	0	1	12: Phospho (ST)
				EPMIGVNQELAYFYPELFR	148 - 166	2316.137	2316.137	0	0	
Beta-lactoglobulin LACB_BOVIN P02754	Bos taurus	35	38%	VLVLDTDYKK	108 - 117	1193.678	1193.651	-22	1	
				TPEVDDEALEK	141 - 151	1325.551	1325.682	99	0	1: Phospho (ST)
				VYVEELKPTPEGDLEILLQK	57 - 76	2313.259	2313.240	-8	0	
				VAGTWYSLAMAASDISLLDAQSAPLR	31 - 56	2707.376	2707.265	-41	0	

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Alpha-S1-casein CASA1_BOVIN P02662	Bos taurus	412	36%	TTMPLW	209-214	748.370	748.391	28	0	
				YLGYLEQLLR	106 - 115	1267.704	1267.704	0	0	
				FFVAPFPEVFGK	38 - 49	1384.730	1384.730	0	0	
				HQGLPQEVLNENLLR	23 - 37	1759.945	1759.945	0	0	
				YKVPQLEIVPNSAEER	119 - 134	1951.952	1951.952	0	1	12: Phospho (ST)
				EPMIGVNQELAYFYPELFR	148 - 166	2316.137	2316.137	0	0	
Alpha-S2-casein CASA2_BOVIN P02663	Bos taurus	21	4%	ALNEINQFYQK	96-106	1367.695	1367.629	-48	0	
Kappa-casein CASK_BOVIN P02668	Bos taurus	33	5%	YIPIQYVLSR	46-55	1251.709	1251.686	-19	0	

Rabbit skin glue, refined (63025) + Zinc white (3M11)

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	144	6%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.749	15	0	2 Oxidation (P)
				GAAGLPGVAGAPGLPGPR	308 - 325	1562.829	1562.799	-19	0	3 Oxidation (P)
				EGPVGLPGIDGRPGPIGPAGAR	463 - 484	2056.093	2056.027	-32	0	Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2099.124	2099.076	-23	0	Oxidation (P)
Collagen alpha-2(I) chain (Fragments) CO1A2_CHICK P02467	Gallus gallus	37	3%	GAAGLPGVAGAPGLPGPR	308 - 325	1562.829	1562.799	-19	0	3 Oxidation (P)
				GLPGIAGATGEPGLVSGPPGAR	881-904	2133.094	2133.063	-14	0	3 Oxidation (P)

Rabbit skin glue, refined (63025) + French ochre (3M21)

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	163	6%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.681	-33	0	2 Oxidation (P)
				GAAGLPGVAGAPGLPGPR	308 - 325	1562.829	1562.760	-44	0	3 Oxidation (P)
				EGPVGLPGIDGRPGPIGPAGAR	463 - 484	2056.093	2056.047	-22	0	Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2130.958	-73	0	3 Oxidation (P)
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	53	4%	GEPGPAGLPGPPGER	472-486	1435.681	1435.520	-112	0	3 Oxidation (P)
				SGBRGETGPAGPAGPIGPVGAR	1062 - 1083	1975.994	1975.920	-38	1	
				GEPGPTGIQGGPPGAGEEGKR	448-468	2019.973	2019.800	-86	1	2 Oxidation (P)
Collagen alpha-2(I) chain (Fragments) CO1A2_CHICK P02467	Gallus gallus	43	3%	GAAGLPGVAGAPGLPGPR	308-325	1562.829	1562.760	-44	0	3 Oxidation (P)
				GLPGIAGATGEPGLVSGPPGAR	881-904	2133.093	2133.081	-6	0	3 Oxidation (P)

Samples from the iconostasis of the church of Holy Virgin in Barič

Sample B4 from the Icon of Jesus Christ

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	24	2%	GSAGPPGATGFPGAAGR	865-881	1459.692	1459.678	-10	0	2 Oxidation (P)
				GPPGPMGPPGLAGPPGESGR	994-1013	1832.860	1832.907	26	0	3 Oxidation (P)
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	23	3%	GIPGEFGLPGPAGAR	572-586	1427.728	1427.733	4	0	2 Oxidation (P)
				EGPVGLPGIDGRPGPIGPAGAR	463-484	2056.093	2056.169	37	0	Oxidation (P)

Sample B8 from the *Icon of St. Theodore Tyron*, church of Holy Virgin in Bariç

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	44	21%	GPAGPQGPR	1084 - 1092	836.437	836.482	54	0	
				GPAGPQGPR	1084 - 1092	852.432	852.477	52	0	Oxidation (P)
				GEGGPQGPR	352 - 360	854.412	854.478	78	0	
				GPAGPQGPR	1084 - 1092	868.427	868.498	82	0	2 Oxidation (P)
				GSEGPQGV	361 - 369	886.438	886.479	47	0	
				GVVGLPGQR	958 - 966	898.511	898.553	48	0	Oxidation (P)
				GERGFPGER	676 - 684	1020.486	1020.542	55	1	Oxidation (P)
				GAAGLPGPKGDR	733 - 744	1095.591	1095.615	23	1	
				GVQGGPAGPR	685 - 696	1105.575	1105.624	44	0	Oxidation (P)
				GDAGPKGADGAPGK	745 - 758	1261.566	1261.678	89	1	4 Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1427.703	1427.790	62	0	
				GEPGAGLPGPPGER	472 - 486	1435.681	1435.746	45	0	3 Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1459.692	1459.753	42	0	2 Oxidation (P)
				GETGPAGAPGPIGVGAR	1066 - 1083	1560.813	1560.862	31	0	
				GNSGEPGAPGSKGDTGAK	430 - 447	1586.741	1586.815	47	1	
				GPPGADGVAGPKGPAGER	493 - 510	1655.814	1655.864	31	1	Oxidation (P)
				DGEAGAQQPPGAPGAGER	612 - 630	1706.773	1706.850	45	0	Oxidation (P)
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1832.860	1832.952	50	0	3 Oxidation (P)
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1848.855	1848.933	43	0	4 Oxidation (P)
				GEPGPTGIQPPGAGEEGKR	448 - 468	2019.973	2020.070	48	1	2 Oxidation (P)
				GVQGGPAGPRGANGAPGNDGAK	685 - 708	2131.028	2131.201	81	1	2 Oxidation (P)
GETGPAGRPGEVPPGPPGAGEK	910 - 933	2216.058	2216.157	45	0	3 Oxidation (P)				
GFSGLQGGPPGPPGSPGEGQPSGASGPAGPR	1111 - 1140	2705.255	2705.376	45	0	3 Oxidation (P)				
GDAGAPGAPGSQGAPGLQGMPPGERGAAGLPGPK	709 - 741	2883.417	2883.536	41	1					

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	42	3%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.791	44	0	2 Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2131.201	41	0	3 Oxidation (P)
Collagen alpha-2(I) chain CO1A2_CANFA O46392	Canis familiaris	24	3%	GEPGAGSVGPGVAVGPR	979-996	1560.813	1560.862	31	0	
				GLPGVAGSVGEPGLGIAGPPGAR	883-906	2131.114	2131.201	41	0	3 Oxidation (P)
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	16	1%	GSAGPPGATGFPGAAGR	865-881	1459.692	1459.753	42	0	2 Oxidation (P)

Sample B15 from the *Icon of the Holy Virgin*, church of Holy Virgin in Barič

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	34	20%	GPAGPQQPR	1084 - 1092	836.437	836.436	-1	0	
				GFPGADGVAGPK	493 - 504	1088.537	1088.545	7	0	Oxidation (P)
				GNSGEPGAPGSK	430 - 441	1105.476	1105.476	0	0	3 Oxidation
				GSAGPPGATGFPGAAGR	865 - 881	1427.703	1427.696	-5	0	
				GEPGPAGLPGPPGER	472 - 486	1435.681	1435.672	-6	0	3 Oxidation (P)
				GETGPAGPAGPIGPVGAR	1066 - 1083	1560.813	1560.784	-18	0	
				GNSGEPGAPGSKGDTGAK	430 - 447	1586.741	1586.723	-11	1	
				GGPGRGFPAGDVAGPK	487 - 504	1615.782	1615.763	-12	1	2 Oxidation (P)
				GFPGERGVQPPGPAGPR	679 - 696	1796.867	1796.854	-8	1	4 Oxidation (P)
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1816.865	1816.841	-13	0	2 Oxidation (P)
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1832.860	1832.844	-9	0	3 Oxidation (P)
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1848.855	1848.841	-7	0	4 Oxidation (P)
				SGDRGETGPAGPAGPIGPVGAR	1062 - 1083	1975.994	1975.961	-17	1	
				GAPGADGPAGAPGTPGPQGIAGQR	934 - 957	2057.016	2057.015	0	0	
				GVQPPGPAGPRGANGAPNDGAK	685 - 708	2131.028	2131.074	22	1	2 Oxidation (P)
				GETGPAGRPGEVGPPGPPGAGEK	910 - 933	2216.058	2216.029	-13	0	3 Oxidation (P)
				GDRGETGPAGPPGAPGAPGVPVPAGK	1033 - 1061	2481.212	2481.154	-23	1	2 Oxidation (P)
				GFSGLQGPPGPPGSPGEGQGPSGASGPAGPR	1111 - 1140	2689.260	2689.183	-29	0	2 Oxidation (P)
				GFSGLQGPPGPPGSPGEGQGPSGASGPAGPR	1111 - 1140	2705.255	2705.189	-24	0	3 Oxidation (P)
				GLTGPIGPPGPAGAPGDKGEAGPSGPAGPTGAR	763 - 795	2853.413	2853.353	-21	1	2 Oxidation (P)
GPPGPMGPPGLAGPPGESGREGAPGAEGSPGR	994 - 1025	2882.349	2882.342	-2	1	2 Oxidation (P)				

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	25	3%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.696	-23	0	2 Oxidation (P)
				GPPGESGAAGPTGPIGSRGSPGPPGPDGNK	590 - 619	2705.240	2705.189	-19	1	5 Oxidation
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	24	1%	GEPGPAGLPGPPGER	472 - 486	1435.681	1435.672	-6	0	3 Oxidation (P)

Sample B16 from the *Icon of St. John*, church of Holy Virgin in Barič

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	70	17%	GPAGPQGPR	1084 - 1092	836.437	836.430	-9	0	
				GPAGPQGPR	1084 - 1092	852.432	852.422	-12	0	Oxidation (P)
				GPAGPQGPR	1084 - 1092	868.427	868.449	25	0	2 Oxidation (P)
				GVQGPPEGAPGR	685 - 696	1105.575	1105.541	-31	0	Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1427.703	1427.689	-10	0	
				GEPGPAGLPGPPGER	472 - 486	1435.681	1435.630	-36	0	3 Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1459.692	1459.650	-29	0	2 Oxidation (P)
				STGISVPGPMGPPSGPR	171 - 186	1560.732	1560.762	19	0	4 Oxidation (P)
				DGLNGLPGPIGPPGPR	1152 - 1167	1561.797	1561.761	-23	0	3 Oxidation (P)
				GNSGEPGAPGSKGDTGAK	430 - 447	1586.741	1586.709	-20	1	
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1832.860	1832.800	-33	0	3 Oxidation (P)
				GPPGPMGPPGLAGPPGESGR	994 - 1013	1848.855	1848.800	-30	0	4 Oxidation (P)
				SGDRGETGPAGPAGPIPVGAR	1062 - 1083	1975.994	1975.935	-30	1	
				GEPGPTGIQGPPEAGGEEGKR	448 - 468	2019.973	2019.912	-30	1	2 Oxidation (P)
				TGPPGPAGQDGRPGPPGPPGAR	552 - 573	2056.980	2056.957	-11	0	4 Oxidation (P)
				GVQGPPEGAPRGRGANGAPNDGAK	685 - 708	2131.028	2131.045	8	1	2 Oxidation (P)
				GETGPAGRPEVGPPEPPGAGEK	910 - 933	2216.058	2215.987	-32	0	3 Oxidation (P)
GFSGLQGPPEGPPGSPGEGQPSGASGPAGPR	1111 - 1140	2705.255	2705.134	-45	0	3 Oxidation (P)				

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) CO1A1_BOVIN P02453	Bos taurus	69	4%	GVQGPPEGAPGR	685 - 696	1105.575	1105.541	-31	0	Oxidation (P)
				GEPGPAGLPGPPGER	472 - 486	1435.681	1435.630	-36	0	3 Oxidation (P)
				DGLNGLPGPIGPPGPR	1152 - 1167	1561.797	1561.761	-23	0	3 Oxidation (P)
				TGPPGPAGQDGRPGPPGPPGAR	552 - 573	2056.980	2056.957	-11	0	4 Oxidation (P)
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	20	2%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.689	-27	0	2 Oxidation (P)
				GLPGVAGSVGEPGLGIAGPPGAR	881 - 904	2131.114	2131.045	-32	0	3 Oxidation (P)

Sample B17 from the *Icon of Three Serbian Saints – St. Arsenije, St. Archbishop Sava and St. Simon*, church of Holy Virgin in Barič

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	15	1%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.565	-114	0	2 Oxidation (P)

Sample from the iconostasis of the church Annunciation of The Holy Mother of God in Idvor

Sample II from the iconostasis of the church Annunciation of The Holy Mother of God in Idvor

Proteins identified by PMF analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	54	7%	GPAGPQGPR	1084 - 1092	836.437	836.433	-5	0	
				GPAGPQGPR	1084 - 1092	852.432	852.422	-12	0	Oxidation (P)
				GPAGPQGPR	1084 - 1092	868.427	868.449	25	0	2 Oxidation (P)
				GVVGLPGQR	958 - 966	898.511	898.505	-6	0	Oxidation (P)
				GVQGPPGPAGPR	685 - 696	1105.575	1105.572	-3	0	Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1427.703	1427.707	3	0	
				GEPGPAGLPGPPGER	472 - 486	1435.681	1435.682	0	0	3 Oxidation (P)
				GSAGPPGATGFPGAAGR	865 - 881	1459.692	1459.690	-1	0	2 Oxidation (P)
				GETGPAGPAGPIGPVGAR	1066 - 1083	1560.813	1560.812	-1	0	
				GNSGEPGAPGSKGDTGAK	430 - 447	1586.741	1586.662	-50	1	

Proteins identified by MS/MS analysis, corresponding m/z values and peptide sequences

Proteins identified	Taxonomy	Score	Sequence coverage	Identified peptides	Range	Calc. MH+	Meas. m/z	Dev. (ppm)	Miss	Modifications
Collagen alpha-2(I) chain CO1A2_BOVIN P02465	Bos taurus	23	1%	GIPGEFGLPGPAGAR	572 - 586	1427.728	1427.707	-15	0	2 Oxidation (P)
Collagen alpha-1(I) chain CO1A1_BOVIN P02453	Bos taurus	12	1%	GEPGPAGLPGPPGER	472 - 486	1435.681	1435.682	0	0	3 Oxidation (P)