Electronic Supplementary Material (ESI) for Analytical Methods
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Protein binders identification in the works of art using ion – pairing free reversed - phase liquid chromatography coupled with tandem mass spectrometry

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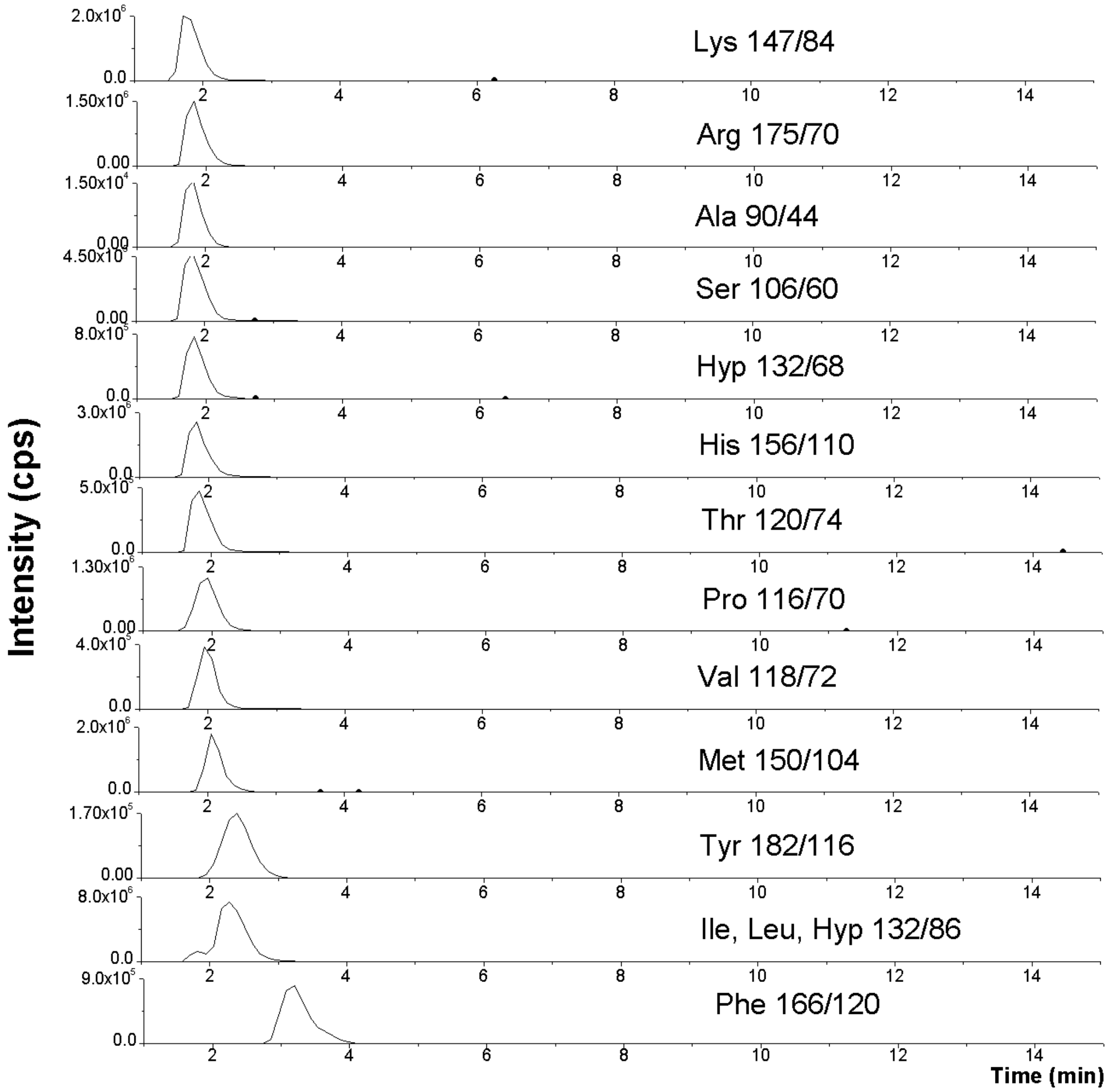

Fig. S1. Extracted ion currents (XIC) chromatograms of fourteen amino acids standard solution (6 µg/ml each), separated with Zorbax C18 column

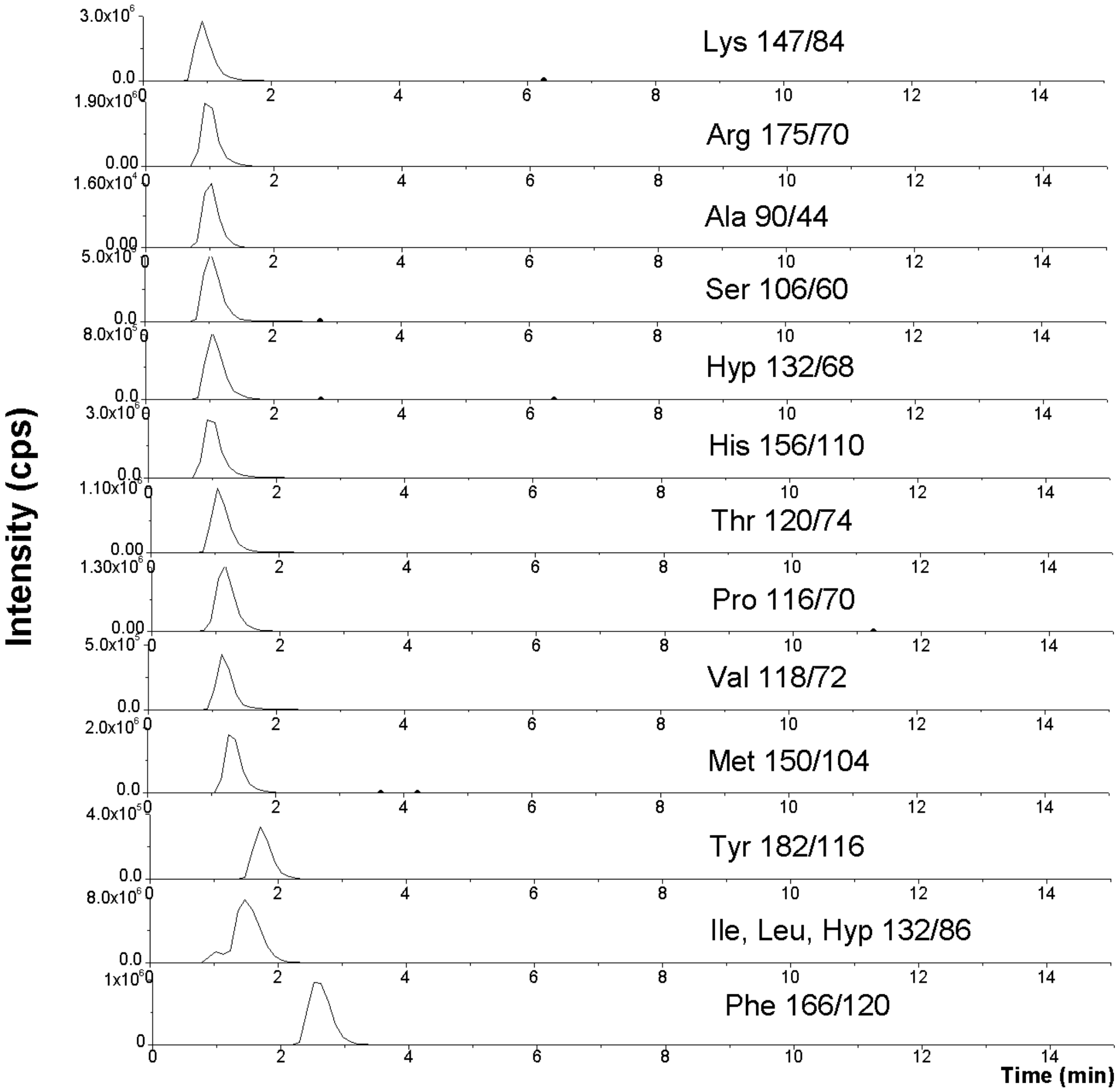

Fig. S2. Extracted ion currents (XIC) chromatograms of fourteen amino acids standard solution (6 µg/ml each), separated with Atlantis C18 column

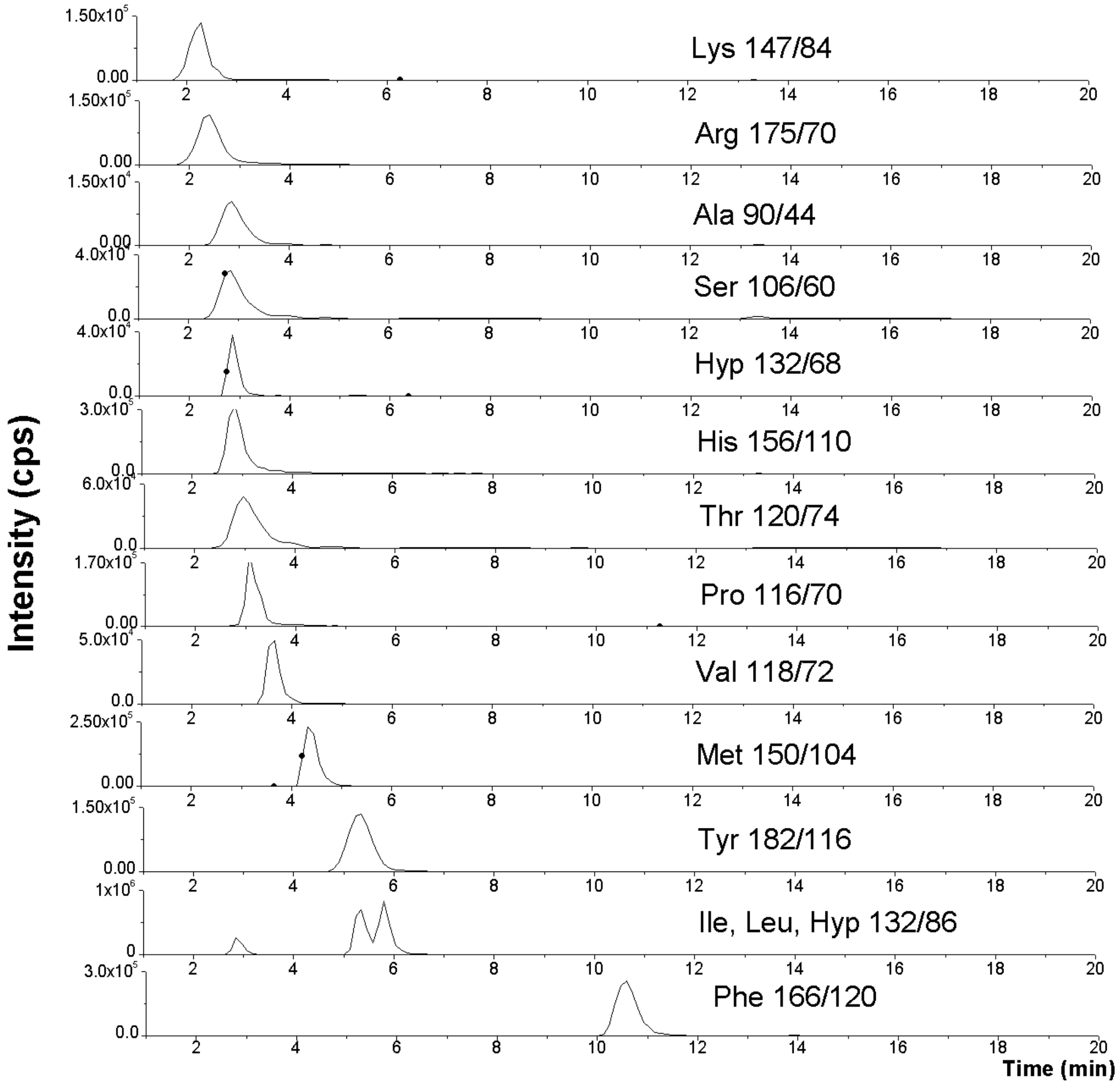

Fig. S3. Extracted ion currents (XIC) chromatograms of fourteen amino acids standard solution (6 µg/ml each), separated with Symmetry C18 column

Table S1. Relative amino acid concentrations determined for the reference materials, model paint samples and samples from the works of art.

Amino acid/sample name	Pro	Thr	Met	His	Arg	Ser	Tyr	Val	Lys	Phe	Ile	Leu	Hpr	Ala
Whole egg	0.0722	0.0172	0.0217	0.1227	0.0891	0.0109	0.0117	0.0124	0.0976	0.1422	0.1539	0.2465	n/p	0.0018
Egg yolk	0.0777	0.0153	0.0340	0.1313	0.0884	0.0091	0.0138	0.0124	0.1031	0.1528	0.1384	0.2219	n/p	0.0018
Egg white	0.0788	0.0152	0.0290	0.1431	0.0914	0.0090	0.0096	0.0120	0.0994	0.1570	0.1424	0.2113	n/p	0.0017
Casein	0.1605	0.0108	0.0219	0.1261	0.0538	0.0069	0.0234	0.0085	0.1199	0.1613	0.1114	0.1949	n/p	0.0006
Collagen	0.2960	0.0057	0.0109	0.0600	0.1685	0.0049	0.0034	0.0084	0.0597	0.0823	0.0748	0.1565	0.0657	0.0031
Fish glue	0.2948	0.0052	0.0084	0.0691	0.1888	0.0046	0.0027	0.0067	0.0919	0.0811	0.0557	0.1233	0.0649	0.0027
Rabbit glue	0.2848	0.0054	0.0054	0.0644	0.1964	0.0049	0.0028	0.0059	0.0916	0.0794	0.0655	0.1245	0.0663	0.0027
G1	0.2701	0.0032	0.0064	0.0561	0.1653	0.0034	0.0011	0.0032	0.0214	0.1193	0.0832	0.2254	0.0491	0.0012
G2	0.1632	0.0063	n/p	0.0281	0.0992	0.0044	0.0012	0.0072	0.0453	0.2151	0.1514	0.2782	0.0412	0.0021
G3	0.2942	0.0042	0.0033	0.0061	0.1913	0.0051	0.0012	0.0054	0.0733	0.1024	0.0921	0.1783	0.0453	0.0033
G4	0.2211	0.00312	0.0031	0.0233	0.2152	0.0031	0.0021	0.0052	0.1062	0.1514	0.0661	0.1703	0.0362	0.0021
G5	0.2071	0.0114	0.0095	0.0031	0.0732	0.0295	0.0213	0.0142	0.1114	0.1192	0.1531	0.2424	n/p	0.0021
G6	0.2052	0.0052	0.0061	0.0232	0.1854	0.0051	0.0061	0.0073	0.0681	0.140	0.105	0.210	n/p	0.0022
Ch1	0.0816	0.0101	0.0002	0.0883	0.0741	0.0067	0.00182	0.0085	0.0485	0.4022	0.1012	0.1747	n/p	0.0005
Ch2	0.0677	0.0139	0.0032	0.1432	0.0904	0.0041	0.0017	0.0054	0.1184	0.2621	0.1072	0.2233	n/p	0.0003
Ch3	0.0668	0.0156	n/p	0.1342	0.0906	0.0030	0.0007	0.0064	0.0584	0.327	0.134	0.232	n/p	0.0004
Ch4	0.0694	0.0135	0.0001	0.1825	0.1040	0.0052	0.0010	0.0073	0.0511	0.2936	0.1334	0.2432	n/p	0.0009
Ch5	0.0805	0.0168	0.0002	0.1064	0.1081	0.0032	0.0005	0.0077	0.0787	0.2252	0.1231	0.259	n/p	0.0008
Ch6	0.0446	0.0170	0.0027	0.3202	0.0399	0.0154	0.0142	0.0161	0.0947	0.1883	0.0845	0.1714	n/p	0.0011
Ch7	0.0863	0.0093	0.0001	0.0956	0.1352	0.0038	0.0009	0.0093	0.0370	0.1691	0.1514	0.1911	n/p	0.0006
Ch8	0.1113	0.0178	0.0022	0.0977	0.0635	0.0071	0.0078	0.0076	0.0414	0.2434	0.1223	0.2279	n/p	0.0005
Ch9	0.0870	0.0172	n/p	0.2382	0.1604	0.0053	0.0010	0.0051	0.0771	0.136	0.0920	0.1912	n/p	0.0004
Ch10	0.0586	0.0167	0.0002	0.155	0.0522	0.0049	0.0007	0.0091	0.0812	0.3697	0.1325	0.2451	n/p	0.0017

*n/p - no peak above detection limit; values corresponding to the half of the detection limit were used in the data matrix

** All uncertainties expressed as the two relative standard deviations (RSD) were in the range from 2 to 10%