

1 Table S1

2 Total peptides

No.	Sequence	Mass	<i>P</i> -Value	GRAVY	Fold Change	Protein origin
1	AAEEPQQKQEPLG	1552.63	0.940237217	-1.76	0.935212323	Otub1
2	AAEVDLPTTEELQGLVPR	1837.02	0.355710948	-0.17	1.96930503	F13a1
3	AALPADPPASVVVGPVVVPR	1911.24	0.945250123	0.95	0.96102063	Ahsg
4	AAPRPPPAISVSVS	1348.54	0.225964922	0.36	2.047731285	Zyx
5	AAPRPPPAISVSVSAPAF	1734.98	0.829148994	0.54	1.169803418	Zyx
6	AATELRGVV	915.04	0.024155158	0.74	1.414682434	Osbp
7	AAVPELLEQQEEDRSKL	1955.11	0.259152226	-0.95	2.069120145	Snx5
8	ADDDYDEPTDSL	1470.35	0.873845078	-1.79	1.091976679	Fgb
9	ADDDYDEPTDSLDA	1541.42	0.511804292	-1.54	0.694261485	Fgb
10	ADDDYDEPTDSLDA	1697.61	0.191401205	-1.73	1.828589326	Fgb
11	ADEAGSEAHREGET	1458.39	0.116036429	-1.58	1.775813813	Fga
12	ADEAGSEAHREGETRNT	1829.78	0.038844255	-1.81	0.273751904	Fga
13	ADEAGSEAHREGETRNTKRG	2171.19	0.422649731	-1.98	0.264793532	Fga
14	ADLPSLAADFVESK	1462.59	0.422649731	0.17	0.40497331	ALB
15	ADMQNLVERL	1188.35	0.101519561	-0.3	2.293802179	Cap1
16	ADMQNLVERLE	1317.46	0.055934498	-0.59	2.545790502	Cap1
17	ADPPASVVVGPVVVPR	1558.81	0.509041627	0.83	0.477854154	Ahsg
18	AEAVKPR	769.89	0.207009951	-0.81	0.292378001	Epg5
19	AEEGIAAGGVMDVN	1332.43	0.640960794	0.36	1.214961376	Rps12
20	AEEVEEERL	1103.13	0.422649731	-1.36	2.269826085	SRPP
21	AEEVEEERLK	1231.3	0.273441597	-1.61	2.290159494	SRPP
22	AEEVEEERLKY	1394.47	0.540984966	-1.58	1.84317279	SRPP
23	AEEVEEERLKYLD	1622.72	0.422649731	-1.32	1.760902892	SRPP
24	AELDPPFGAPAGAPGGP	1423.52	0.422649731	-0.08	1.78757845	Clta
25	AEQEPTAEQLAQIA	1498.58	0.630881512	-0.56	1.296045477	Arhgdia
26	AESSAATQSPS	1035.01	0.667600759	-0.65	1.445375195	Rtn3

27	AESSAATQSPSVS	1221.22	0.845592399	-0.28	0.900554478	Rtn3
28	AETEERSLDNF	1310.31	0.692316781	-1.37	0.785865912	Cdv3
29	AEVDLPTEELQGLVPR	1765.95	0.240473406	-0.29	2.970645716	F13a1
30	AFLEVNEEGSEAAASTAVVIAGR	2291.46	0.509417391	0.41	0.592615431	SERPINC1
31	AGSVADSDAVVKL	1231.34	0.422649731	0.68	0.596073878	LgalsI
32	AGSVADSDAVVKLDDGHLN	1882.97	0.372875734	-0.07	0.732965378	LgalsI
33	AGYKGRVT	850.96	0.130305588	-0.65	2.331397116	F2
34	AHREGETRNT	1170.19	0.422649731	-2.27	0.026234178	Fga
35	AIAANEADAVTL DAGLVYDAY	2126.26	0.362965862	0.57	0.424688401	TF
36	AIAANEADAVTL DAGLVYDAYLA PN	2521.71	0.408322398	0.5	0.344893828	TF
37	AIQVYYNPDQPPKP	1629.8	0.38823697	-1.17	2.676854924	Fgg
38	AIQVYYNPDQPPKPGM	1818.05	0.200661809	-0.93	2.403714448	Fgg
39	AIQVYYNPDQPPKPGMIDSATQ	2433.68	0.026910242	-0.78	4.522386976	Fgg
40	ALAVAASGPGSS	987.06	0.815294761	0.87	1.123341157	Pzp
41	ALAVAASGPGSSF	1134.23	0.069637291	1.02	13.63010667	Pzp
42	ALAVAASGPGSSFR	1290.42	0.135911074	0.62	5.97069204	Pzp
43	ALGLDEGEPAGSWDLTVEG	1915.99	0.290290242	-0.21	1.824677153	Cpn2
44	ALGLDEGEPAGSWDLTVEGR	2072.18	0.609421933	-0.42	1.636665009	Cpn2
45	ALPADPPASVVVGPVVVPR	1840.16	0.869177917	0.91	1.113339709	Ahsg
46	ANALAHKYH	1024.13	0.422649731	-0.66	0.574305412	HBB
47	ANELKATIDQNLEDL	1686.8	0.671117883	-0.64	0.74343981	Apoa4
48	APELLFAK	1035.23	0.365686132	0.87	0.561548673	ALB
49	AQQAADKYLYVD	1384.48	0.545070419	-0.59	1.421828303	Myh9
50	AQQAADKYLYVDKNF	1773.93	0.171631484	-0.78	3.04540419	Myh9
51	ASAGLLGAHAAAITAYALTLTK	2085.39	0.422649731	1	0.58140637	C4b
52	ASGVAVSDGVIK	1102.23	0.422649731	0.91	0.595134781	Cfl1
53	ASVSTVLTSKYR	1311.48	0.422649731	0.04	0.185136237	Hba
54	ASVVVGPVVVPR	1178.42	0.371969063	1.51	1.483757519	Ahsg

55	ATDELASKL	947.03	0.336906938	-0.13	1.820016853	Efh2
56	ATDELASKLS	1034.11	0.992044694	-0.2	0.995029467	Efh2
57	AVAASGPGSSFR	1106.18	0.403437926	0.26	0.86980259	Pzp
58	AVFVDLEPTVIDEV	1545.72	0.97992784	0.96	0.978262029	Tuba1b
59	AVMDDFAAFVEK	1342.51	0.29966917	0.58	0.32120133	ALB
60	AVPPNNSNAAEVDLPTEELQGLVP R	2630.84	0.335473997	-0.46	3.14326596	F13a1
61	DDDIAALVVDNG	1216.24	0.783989624	0.2	1.149938375	Actb
62	DDDYDEPTDSLDA	1470.35	0.991122042	-1.79	0.991761019	Fgb
63	DDPNLPR	939.96	0.376137356	-2.24	0.226643315	ALB
64	DDPSVPLQPVTPLQ	1505.66	0.906941897	-0.42	1.081235703	C4b
65	DDPSVPLQPVTPLQL	1618.82	0.807019459	-0.14	1.181866129	C4b
66	DDPSVPLQPVTPLQLFEG	1952.15	0.094302948	-0.18	3.138226542	C4b
67	DDPSVPLQPVTPLQLFEGR	2108.34	0.425773007	-0.41	1.782930855	C4b
68	DDPSVPLQPVTPLQLFEGRRS	2351.6	0.379295486	-0.62	0.251433069	C4b
69	DEAGSEAHREGET	1387.31	0.610641045	-1.84	1.350106038	Fga
70	DEAGSEAHREGETR	1543.5	0.422649731	-2.03	0.135425085	Fga
71	DEAGSEAHREGETRNT	1758.7	0.780823838	-2.04	0.661172574	Fga
72	DEAGSEAHREGETRNTK	1886.87	0.422649731	-2.15	0.108869544	Fga
73	DEAGSEAHREGETRNTKRG	2100.11	0.188791949	-2.18	0.006281138	Fga
74	DEFKPLVEEPQNLIK	1799.02	0.422649731	-0.86	0.629025299	ALB
75	DGAGDVAFVK	978.05	0.273383846	0.31	0.355460732	TF
76	DIFTGLIGPMK	1191.43	0.527238921	0.64	0.631441624	Cp
77	DKGEFLSEGGV	1194.24	0.545394898	-0.5	1.19616987	Fga
78	DKGEFLSEGGVR	1350.43	0.667494794	-0.81	1.260211513	Fga
79	DLEDELEPDPR	1327.34	0.2969219	-1.92	0.519759658	Proc
80	DLPSLAADFVESK	1391.51	0.422649731	0.05	0.410861998	ALB
81	DLPTEELQGLVPR	1466.63	0.122934384	-0.55	3.823181851	F13a1
82	DLSGTLESIPDK	1274.37	0.923700485	-0.55	1.048463537	Apoc1

83	DNQDFGDHATL	1232.2	0.565203434	-1.22	0.695375754	Serpinf2
84	DPGLRGNIL	954.08	0.184182753	-0.2	3.848445771	Gnptg
85	DPNYRPPGLPA	1359.48	0.422649731	-1.28	0.591301338	Saa2
86	DPPASVVVGPVVVP	1331.55	0.164796665	1.14	1.880295473	Ahsg
87	DPPASVVVGPVVVPR	1487.73	0.102193061	0.76	1.577534723	Ahsg
88	DSELQLSTGNGLFVNND	1822.87	0.238062019	-0.57	2.815604824	Serpina1a
89	DTDLEDELEPDPR	1543.53	0.470340333	-1.95	1.246901766	Proc
90	DTEDKGEFLSEGGGV	1539.54	0.639196333	-0.91	0.847699863	Fga
91	DTEDKGEFLSEGGGVR	1695.73	0.128489242	-1.14	4.256572662	Fga
92	DTTEKELLSYIDG	1598.65	0.241424447	-0.94	1.698989425	F2
93	DVFLGMFLYEYAR	1623.86	0.302372787	0.51	0.18647653	ALB
94	DVQETDTSQK	1150.14	0.356295455	-1.94	1.267088215	Serpina1a
95	DYDEPTDSLDA	1240.17	0.695344122	-1.48	0.68803529	Fgb
96	DYDEPTDSLDA	1396.36	0.218449713	-1.73	2.687008485	Fgb
97	DYSVLLLR	1077.27	0.23207397	1.08	0.405502888	ALB
98	EAGSEAHREGETRNT	1643.62	0.422649731	-1.94	0.330234262	Fga
99	EDELEPDPR	1099.1	0.793307694	-2.38	0.757153119	Proc
100	EDKGEFLSEGGGV	1323.35	0.542670982	-0.73	0.920212363	Fga
101	EDKGEFLSEGGGVR	1479.54	0.742473705	-1	1.133395409	Fga
102	EDPQTFYYAVAVVK	1629.8	0.417459447	-0.02	0.489986983	TF
103	EDVQETDTSQK	1279.25	0.67106891	-2.08	0.850960427	Serpina1a
104	EDVQETDTSQKDQ	1522.47	0.422649731	-2.3	0.630443929	Serpina1a
105	EDVQETDTSQKDQSPA	1777.74	0.422649731	-1.91	0.541486648	Serpina1a
106	EDYPQFSSPK	1197.24	0.481644722	-1.77	3.288475422	Serpinf2
107	EEDYPQFSSPK	1326.36	0.464828935	-1.93	0.626132618	Serpinf2
108	EEPPSLRPAPPPISGGGY	1820.98	0.584100317	-0.84	0.519082584	Fgb
109	EEQLQIRAE	1243.32	0.422649731	-1.54	1.90724169	KRT10
110	EETKQNEAFSLTAKG	1652.75	0.200950935	-1.18	0.182416479	C3
111	EETKQNEAFSLTAKGKG	1837.97	0.198819379	-1.29	0.296473069	C3

112	EEVEGSLLLGSVQGYMEQAS	2126.28	0.422649731	-0.12	1.89274924	Apoc3
113	EEVGADLEQVEVLQ	1557.64	0.7933279	-0.21	1.173299349	Sptan1
114	EFNAETFTFH	1242.29	0.422649731	-0.49	0.609098328	ALB
115	EGYYGYTGAFR	1283.34	0.422649731	-0.84	0.661516528	TF
116	ELQLSTGNGLFVNND	1620.71	0.374501337	-0.33	1.485880601	Serpina1a
117	EQLQDMGLVDFLSPEK	1849.06	0.422649731	-0.46	0.531756015	SERPINC1
118	ETKQNEAFSLTAKGKG	1708.86	0.183573345	-1.16	0.203211738	C3
119	ETKQNEAFSLTAKGKGR	1865.04	0.184352071	-1.35	0.506429026	C3
120	EVDLPTEELQGLVPR	1694.87	0.266779804	-0.43	3.359786269	F13a1
121	EVPLNTIIFMGR	1389.66	0.234334859	0.63	0.421142647	SERPINC1
122	EVQGFESATFLGYFK	1722.88	0.285967247	0.01	0.225172966	GSN
123	FGLEGDEESTMLEDSVSPK	2070.17	0.205229025	-0.73	0.402520075	Tln1
124	FKDLGEENFK	1226.33	0.381197225	-1.28	0.079522856	ALB
125	FQNALLVR	960.13	0.18950044	0.61	0.079029821	ALB
126	FQSGQVLSALPR	1302.47	0.265501667	0.11	2.168582838	Cpb2
127	FSALEVDETYVPK	1497.63	0.36977908	-0.15	0.228347494	ALB
128	FSSLMNLEEKPAAPAA	1604.81	0.344516593	-0.1	1.689051465	Apoa2
129	FVGGAENTAHPR	1255.33	0.201177857	-0.6	0.339567165	Igfbp5
130	FYAPELFFAK	1345.58	0.27082555	0.85	0.188910505	ALB
131	GDFATRGPGSKAENPTNPGP	1970.05	0.207890405	-1.31	0.145212307	Fga
132	GDSRGDFA	823.8	0.791784695	-1.06	1.206386065	Fga
133	GEDAAQAEKFQ	1193.21	0.880067318	-1.24	1.104565463	Cavin2
134	GEDAAQAEKFQHPN	1541.57	0.185333553	-1.56	0.219101373	Cavin2
135	GEDAAQAEKFQHPNT	1642.67	0.0585397	-1.51	0.519489356	Cavin2
136	GEDAAQAEKFQHPNTD	1757.76	0.211900123	-1.63	0.515929665	Cavin2
137	GEDAAQAEKFQHPNTDML	2002.11	0.422649731	-1.13	0.625868424	Cavin2
138	GEFLSEGGGV	950.98	0.996201104	0.14	1.00295768	Fga
139	GETSSRVLLAGAPQTSQ	1701.82	0.422649731	-0.34	0.654626016	Lox11
140	GFEPTLEALFGK	1308.47	0.184834043	0.08	0.362862556	Apob

141	GFRELACDDPEAEQVA	1749.84	0.665954947	-0.55	0.646470994	Ahsg
142	GGGGGGGLGSGGSIR	1145.18	0.422649731	-0.12	5.758714794	KRT9
143	GGGGGGGLGSGGSIRSS	1319.33	0.422649731	-0.2	2.852356546	KRT9
144	GGGGGGLGSGGSIR	988.99	0.422649731	0.19	1.956143231	KRT9
145	GGPGPLTLKEVEELE	1567.73	0.460675245	-0.49	0.577602138	Zyx
146	GGVAPQALAVAASGPGSSF	1643.79	0.089081678	0.7	2.385792563	Pzp
147	GLPAGALPLAGPPR	1286.52	0.595708612	0.34	1.324714	Ltbp1
148	GLSDHRTYH	1085.12	0.1918013	-1.53	0.111268761	Ahsg
149	GPEGPPGEPGPPGPP	1338.41	0.122534283	-1.45	0.494855275	Col5a2
150	GPGSKAENPTNPGP	1322.37	0.154330199	-1.55	1.70021425	Fga
151	GSEMVVAGKLQDQGPVLL	1956.21	0.422649731	0.14	1.603296551	Itih4
152	GSEMVVAGKLQDQGPVLLA	2027.29	0.504067074	0.23	1.356348966	Itih4
153	GSGGGSSGGSIGGR	1092.07	0.751891753	-0.46	0.813929235	KRT1
154	GSGGGSYGSGGGGGHGSY	1514.42	0.763766776	-0.73	1.256716999	KRT1
155	GSKAENPTNPGP	1168.21	0.003380179	-1.64	40.51339691	Fga
156	GVAPQALAVAASGPGSSF	1586.73	0.116765996	0.76	1.895538433	Pzp
157	HPDYSVLLLLR	1311.52	0.286021356	0.45	0.184727908	ALB
158	HPYFYAPELLFFAK	1743	0.392485783	0.23	0.317082859	ALB
159	HQADSPRV	908.95	0.422649731	-1.39	5.143249316	Flg
160	HQTVPQNTGGK	1166.24	0.422649731	-1.56	0.318818089	TF
161	HREGETRNT	1099.11	0.194784601	-2.72	5.713263052	Fga
162	HSTIFENLANK	1273.39	0.422649731	-0.56	0.335780833	TF
163	IAEVENDEMPADLPSLAADFVESK	2590.79	0.422649731	-0.18	0.719426259	ALB
164	ILTEQNQDQPEDDFI	1804.85	0.871895928	-1.21	1.164606844	Srgn
165	ILTEQNQDQPEDDFII	1918.01	0.486280714	-0.86	0.460565663	Srgn
166	IMNGEADAMSLDGGFVYIAGK	2159.43	0.307718127	0.35	0.029260435	TF
167	IPMQACQQKDVFASYLNSNIQSPS M	2801.16	0.422649731	-0.26	57.6418586	Zcche8
168	ISHELESSSEVN	1417.42	0.173589012	-0.67	1.71955747	Spp1

169	KEEPPSLRPAPPISGGGY	1949.16	0.331758492	-1	0.097699185	Fgb
170	KGEFLSEGGG	980.02	0.721346064	-0.67	0.727221231	Fga
171	KGEFLSEGGGV	1079.15	0.939865177	-0.23	1.021644494	Fga
172	KMADEAGSEAH	1145.19	0.993731657	-1.05	0.993777088	Fga
173	KNPLPSKETIEQEKQAGES	2113.27	0.196250812	-1.68	0.054909855	Tmsb4x
174	KTETQEKNPLPSKETIEQEKQAGE S	2830	0.186456252	-1.91	0.061744593	Tmsb4x
175	KVKDENNVVAQPQ	1468.6	0.527182098	-1.23	0.856056253	Azgp1
176	KVPQVSTPTLVEVSR	1639.88	0.323490036	-0.07	0.191721759	ALB
177	LAETEGRYCVQ	1268.39	0.422649731	-0.46	1.513650995	KRT10
178	LALDIEIATYR	1277.46	0.606570923	0.61	0.597754954	KRT1
179	LASVSTVLTSKYR	1424.63	0.422649731	0.33	0.576678802	Hba
180	LDELRDEGK	1074.14	0.265665868	-1.69	0.132410671	ALB
181	LDFTGNLIEDIEDGTFK	2014.13	0.422649731	-0.32	0.59882478	Ogn
182	LDNQDFGDHATL	1345.36	0.864789029	-0.8	1.079747202	Serpinf2
183	LEDELEPDPR	1212.25	0.828323542	-1.76	1.144116937	Proc
184	LEGDDDSRMEEVD	1610.6	0.422649731	-1.5	0.313802554	Hsp90aa1
185	LGMFLYEYAR	1262.47	0.422649731	0.31	0.558718149	ALB
186	LGPLVEQGRQ	1096.23	0.903545848	-0.56	0.919645106	Apoe
187	LHLPADDVVSIIIEVEE	1907.07	0.422649731	0.26	0.473298344	Vgf
188	LLVVPWTQR	1274.5	0.422649731	0.35	0.094702176	HBB
189	LVAASQAALGL	1013.18	0.502379513	1.65	0.252139902	ALB
190	LVNEVTEFAK	1149.29	0.286744671	0.17	0.129586464	ALB
191	MADEAGSEAHREGET	1589.59	0.771087323	-1.35	1.08633369	Fga
192	MADEAGSEAHREGETRNT	1960.98	0.00276285	-1.61	0.444628415	Fga
193	MDHYDSQQTND	1353.32	0.338030355	-2.28	0.596299655	Actn1
194	MDNLSPEEVQL	1274.39	0.213882684	-0.56	1.715716165	Snap23
195	MDNLSPEEVQLRA	1501.65	0.593591746	-0.68	1.306352645	Snap23
196	MDSASQDINLN	1207.26	0.422649731	-0.65	1.498064696	Tpd5212

197	MEDIDQSSLVS	1223.3	0.242273294	-0.18	0.725697089	Rtn4
198	MEDIDQSSLVSSS	1397.45	0.422649731	-0.28	0.556115067	Rtn4
199	MEDIDQSSLVSSSA	1468.53	0.752757875	-0.13	1.146053755	Rtn4
200	MEDSPTMVKV	1136.33	0.994298834	-0.18	1.006315891	Slc14a1
201	MEDSPTMVKVDR	1407.6	0.530251441	-0.82	0.687661492	Slc14a1
202	MEDVTLHIVE	1185.34	0.673010399	0.42	1.185998228	Cavin1
203	MEDVTLHIVERPY	1601.81	0.210762016	-0.25	2.393025447	Cavin1
204	MEEDYPQFSSPK	1457.55	0.658275885	-1.61	0.785964319	Serpinf2
205	MEIPVPVQPS	1096.29	0.440013711	0.22	0.544413156	Hspb6
206	MESVAAESSPALE	1320.41	0.465724726	0.06	1.238354064	Prkag1
207	MGGVAPQALAVAASGPGSSF	1774.98	0.422649731	0.76	1.584246237	Pzp
208	MQDEDDGYITL	1184.27	0.643667006	-0.62	1.391227948	Clec1b
209	MQDEDDGYITLN	1298.37	0.311177407	-0.88	0.831035462	Clec1b
210	MQSQESGVHY	1165.23	0.930527473	-1.09	0.965556067	Smim1
211	MYLGYEYVTAIR	1478.7	0.369516976	0.27	0.204866577	TF
212	NAAEVDLPTEELQGLVP	1794.94	0.422649731	-0.11	1.885525622	F13a1
213	NAAEVDLPTEELQGLVPR	1951.13	0.236690556	-0.36	3.31122877	F13a1
214	NALAVERTASVQ	1258.37	0.541780014	0.09	1.373000065	Cxcl5
215	NDNDNIFLSPLSISTAFAMTK	2299.54	0.422649731	0.04	0.711418636	SERPINC1
216	NELKATIDQNLEDL	1615.73	0.422649731	-0.81	0.647562143	Apoa4
217	NHAASRVAPDVTGSEVPGP	1958.08	0.518912923	-0.49	0.636126912	Creb3l3
218	NPDQPPKPGM	1080.21	0.691009842	-1.93	1.339692817	Fgg
219	NPLPSKETIEQEKQAGES	1985.1	0.187387133	-1.56	0.231015876	Tmsb4x
220	NQDQPEDDFII	1333.35	0.463626897	-1.3	1.604128055	Srgn
221	PADLPSLAADFVESK	1559.71	0.422649731	0.05	0.468675774	ALB
222	PDPAKSAPAPK	1078.21	0.422649731	-1.19	0.263163323	Hist2h2bb
223	PEDQPTPAIES	1183.21	0.192929918	-1.27	0.485693468	Apoc3
224	PELLFFAK	964.15	0.403612429	0.75	0.479090431	ALB
225	PEPAKSAPAPK	1092.24	0.443162302	-1.19	0.625682234	H2bc7

226	PEPAKSAPAPKKGS	1364.54	0.422649731	-1.3	0.595685853	H2bc7
227	PEPSKSAPAPK	1108.24	0.226274418	-1.43	0.361918032	H2bc3
228	PEPTKSAPAPK	1122.27	0.497972325	-1.42	0.48335109	H2bc14
229	PIITPVAQENQ	1209.34	0.24381187	-0.26	0.383720774	ApoE
230	PNIVPDGDFSSLV	1359.47	0.422649731	0.29	1.897808733	C4b
231	PPASVVVGPVVVPR	1372.65	0.422649731	1.06	1.837326121	Ahsg
232	PSLAADFVESK	1163.27	0.422649731	0.03	0.60372837	ALB
233	PYFYAPELFFAK	1605.86	0.422649731	0.49	0.494243347	ALB
234	QAQEQVQPKPLES	1481.6	0.687520931	-1.47	0.753637287	Apoa4
235	QNEAFSLTAK	1108.2	0.252487214	-0.57	1.714241696	C3
236	QSGQVLSALPR	1155.3	0.834173008	-0.14	0.877041654	Cpb2
237	QTALVELVK	1000.08	0.225037737	0.69	0.168317656	ALB
238	QVYYNPDQPPKP	1445.57	0.422649731	-1.89	1.700131291	Fgg
239	RGEAAEGPAAAA	1070.11	0.422649731	-0.26	1.495529841	Gdf11
240	RHPDYSVLLLLR	1467.71	0.249112736	0.03	0.184688925	ALB
241	RHPYFYAPELFFAK	1899.19	0.878085864	-0.09	0.931047464	ALB
242	RLLWENG	1001.09	0.924858119	-1.09	1.091154967	C3
243	RLLWENGLL	1227.41	0.007002316	-0.11	9.890498207	C3
244	RVNSGFE	807.85	0.017346253	-0.81	4.659368181	Spp2
245	SAEREAEEAATVA	1275.31	0.573153332	-0.12	0.754648002	Vat1
246	SASDLTWDNLK	1249.32	0.422649731	-0.75	0.472776303	TF
247	SCRQFSSS	900.95	0.334426898	-0.74	5.29055752	KRT9
248	SDAAVDTSSSEITTKDL	1652.7	0.422649731	-0.39	0.68483677	Ptma
249	SDEFSLADALPEQS	1508.53	0.186914953	-0.54	0.409753008	Mapk1ip11
250	SDSGALGQHV	969.99	0.422649731	-0.28	0.433065229	Septin2
251	SDTPASTFGG	938.93	0.588827821	-0.43	1.7164544	F13a1
252	SDTPASTFGGR	1095.11	0.367050287	-0.8	2.486101382	F13a1
253	SEAAPAAPAAAPPAEKAPA	1687.84	0.032944283	-0.09	0.318576992	H1-2
254	SEETKQNEAF	1182.19	0.53588239	-1.83	1.372203793	C3

255	SEETKQNEAFS	1269.26	0.343368483	-1.74	1.370847272	C3
256	SEETKQNEAFSL	1382.42	0.92743643	-1.28	1.10979013	C3
257	SEETKQNEAFSLTA	1554.6	0.219941406	-1.01	0.540687735	C3
258	SEETKQNEAFSLTAK	1682.77	0.65153056	-1.21	0.754251395	C3
259	SEETKQNEAFSLTAKG	1739.82	0.064677788	-1.16	0.196904528	C3
260	SEETKQNEAFSLTAKGK	1867.99	0.268960374	-1.32	0.26939191	C3
261	SEETKQNEAFSLTAKGKG	1925.05	0.135954296	-1.27	0.206595541	C3
262	SEETKQNEAFSLTAKGKGR	2081.23	0.19710834	-1.44	0.07215006	C3
263	SEFGDSSSPATR	1240.22	0.433113801	-1.07	1.51845544	Fga
264	SELEQLRQAEQL	1572.66	0.422649731	-1.28	1.700125176	Gnb4
265	SELQLSTGNGLFVNND	1707.78	0.659910146	-0.36	1.25467273	Serpina1a
266	SETAPAAPAAPAPAEKTPV	1775.94	0.34385387	-0.23	1.718525067	H1-4
267	SGGGGGGGLGSGGSIR	1232.25	0.539697736	-0.16	2.048706221	KRT9
268	SGQVLSALPR	1027.17	0.509363698	0.2	2.346007837	Cpb2
269	SGTLESIPDK	1046.12	0.619383981	-0.69	1.226999405	Apoc1
270	SHELESSSEVN	1304.26	0.38222984	-1.1	0.565624303	Spp1
271	SKAENPTNPGP	1111.16	0.957576552	-1.75	1.037547201	Fga
272	SKETIEQEQAGES	1563.61	0.190543936	-1.8	0.072571265	Tmsb4x
273	SLHTLFGDK	1017.13	0.339390181	-0.23	0.076154927	ALB
274	SLKDTTEKE	1050.11	0.422649731	-1.86	2.625563305	F2
275	SLKDTTEKELLDYIDG	1927.05	0.422649731	-0.83	0.496477565	F2
276	SLMNLEEKPAAPAA	1370.56	0.890133004	-0.27	1.07572275	Apoa2
277	SNAAEVDLPTEELQGLVPR	2038.2	0.185040253	-0.38	2.588454772	F13a1
278	SPVPDLVPGSF	1114.24	0.001830638	0.43	4.668724069	Fga
279	SQIPRLGDAVRA	1282.44	0.18520811	-0.23	0.061783237	Itih4
280	SQIPRLGDAVRAS	1369.52	0.341856591	-0.27	0.412737868	Itih4
281	SRSGGGGGGGLGSGGS	1206.17	0.422649731	-0.49	2.845445088	KRT9
282	SRSGGGGGGGLGSGGSI	1319.33	0.422649731	-0.2	1.802336798	KRT9
283	SRSGGGGGGGLGSGGSIR	1475.52	0.903452562	-0.44	1.109417236	KRT9

284	SRSGGGGGGGLGSGGSIRSS	1649.67	0.422649731	-0.48	2.634227849	KRT9
285	SRSGGGGGGGLGSGGSIRSSY	1812.84	0.422649731	-0.51	0.330576903	KRT9
286	SSGSVGESSKGP	1165.16	0.422649731	-0.83	3.381062503	KRT10
287	SSLMNLEEKAPAA	1457.64	0.849889372	-0.31	1.107613402	Apoa2
288	SSTQFNKGPS	1052.09	0.957012075	-1.32	1.027120217	Cnn2
289	STVKKQVTKTY	1282.48	0.04973525	-1	7.737387559	Fga
290	STVLTSKYR	1054.19	0.422649731	-0.52	0.239018911	Hba
291	SVASTVWTTDTEDKGEFLSEGGG V	2472.55	0.422649731	-0.34	0.076267388	Fga
292	SVESASGETLH	1116.13	0.032083275	-0.35	0.201934053	Ahsg
293	SVTVQETKE	1020.08	0.205875249	-0.91	0.82379915	Knq1
294	SVTVQETKEG	1077.14	0.057448683	-0.86	2.306085812	Knq1
295	SVTVQETKEGR	1233.32	0.055779337	-1.19	0.311891634	Knq1
296	SVVVGPPVVPR	1107.34	0.912909682	1.48	1.038771627	Ahsg
297	TAGWNIPMGLLYNK	1577.84	0.284450813	-0.03	0.12195738	TF
298	TDAEFHTFF	1114.16	0.443616912	-0.16	1.898197956	F2
299	TDAEFHTFFNE	1357.37	0.796233968	-0.76	0.85660733	F2
300	TDLEDELEPDPR	1428.44	0.329506979	-1.82	1.929784943	Proc
301	TDTEDKGEF	1041.02	0.305410364	-1.88	1.286431076	Fga
302	TDTEDKGEFL	1154.17	0.862446723	-1.31	0.865026988	Fga
303	TDTEDKGEFLSE	1370.36	0.14256587	-1.45	2.71091579	Fga
304	TDTEDKGEFLSEGG	1484.46	0.158405743	-1.3	1.713304498	Fga
305	TDTEDKGEFLSEGGG	1541.51	0.688489064	-1.24	0.766749537	Fga
306	TDTEDKGEFLSEGGGV	1640.65	0.689510891	-0.9	0.925486736	Fga
307	TDTEDKGEFLSEGGGVR	1796.83	0.040558755	-1.11	2.013953418	Fga
308	TDTEDKGEFLSEGGGVRGP	1951	0.422649731	-1.1	0.617601607	Fga
309	TDVETTYADFIASGR	1645.71	0.597297206	-0.3	0.532322037	Pkia
310	TEDKGEF	824.83	0.422649731	-1.81	58.64255869	Fga
311	TEDKGEFLSEGGGV	1424.46	0.471786062	-0.73	1.20861703	Fga

312	TEDKGEFLSEGGGVR	1580.64	0.787811359	-0.98	0.9169258	Fga
313	TEEKDPKKL	1087.22	0.422649731	-2.3	0.360388951	Fyb1
314	TEELQGLVPR	1141.27	0.777290611	-0.59	0.872845577	F13a1
315	TEGAELVDSVLDVV	1445.56	0.422649731	0.74	1.639686331	Tubb4b
316	TEKDAQPLEEADDDLSKLN	2374.41	0.343426457	-1.64	0.537648592	Arhgdib
317	TEKDAQPLEEADDDLSKLN	2537.58	0.422649731	-1.62	0.722265704	Arhgdib
318	TEQNQDQPEDDFII	1691.69	0.422649731	-1.57	0.655893816	Srgn
319	TETQKNPLPSKETIEQEQAGES	2701.83	0.26416482	-1.83	0.219019482	Tmsb4x
320	TIEQEQAGES	1219.25	0.185857233	-1.55	0.287519914	Tmsb4x
321	TKQNEAFSLTAKGKG	1579.74	0.422649731	-1	0.227425051	C3
322	TLEIPGSSDPNIVP	1438.57	0.325412189	-0.07	2.746129523	C4b
323	TLEIPGSSDPNIVPDGDFSS	2047.12	0.059065803	-0.36	3.263580916	C4b
324	TLEIPGSSDPNIVPDGDFSSLV	2259.41	0.312866335	0.04	4.823202711	C4b
325	TLEIPGSSDPNIVPDGDFSSLVR	2415.59	0.422649731	-0.16	6.246500863	C4b
326	TLPGSGATVAGTLLR	1413.61	0.549997134	0.6	1.407986967	F5
327	TNAENEFVTIK	1265.36	0.422649731	-0.55	2.791067707	KRT1
328	TNIEDPSSHVPEFSSSS	1819.82	0.422649731	-0.85	1.567068805	Fga
329	TQEKPLPSKETIEQEQAGES	2471.61	0.422649731	-1.8	0.270183037	Tmsb4x
330	TSRKKDPATK	1131.28	0.422649731	-2.17	0.214761104	Cpn1
331	TTDAEFHTFFNE	1458.47	0.514149425	-0.76	1.385609529	F2
332	TTDTEDKGEFLSEGGGV	1741.75	0.422649731	-0.89	0.357446314	Fga
333	TTFRLLWENG	1236.37	0.422649731	-0.38	0.374336157	C3
334	TVKKQVTKTY	1195.4	0.896425775	-1.02	1.130563476	Fga
335	TVWTTDTEDKGEFLSEGGGV	2128.19	0.451440068	-0.63	0.602179496	Fga
336	TYETTLEK	984.05	0.26588573	-1.31	0.100069995	ALB
337	VANALAHKYH	1123.26	0.422649731	-0.17	0.197951453	HBB
338	VAPEEHPVLLTEAPLNPK	1954.22	0.20122056	-0.27	0.448840249	Actb
339	VDLEPTVIDEI	1242.36	0.422649731	0.45	0.577100457	Tuba4a
340	VDPTEELQGLVPR	1565.76	0.19130806	-0.21	2.941798574	F13a1

341	VDVPAADLSDQVPDTSSET	1973.98	0.123708193	-0.56	0.462616852	C3
342	VDVPAADLSDQVPDTSSETR	213.17	0.422649731	-0.76	0.703881839	C3
343	VDVPAADLSDQVPDTSSETRILQ G	2654.82	0.422649731	-0.25	2.048248015	C3
344	VFDEFKPLVEEPQNLIK	2045.32	0.330187472	-0.35	0.147354863	ALB
345	VGGAENTAHR	1108.16	0.422649731	-0.91	0.379510436	Igfbp5
346	VGPAGKNGDRGET	1257.3	0.545056596	-1.29	0.389358414	Coll1a1
347	VGPVVVPR	822	0.014810775	1.09	4.910499179	Ahsg
348	VHLTPEEK	952.06	0.422649731	-1.05	0.545750266	HBB
349	VKDENVVAQPQ	1340.43	0.422649731	-1.01	2.53908682	Azgp1
350	VLGAFSDGLAHLNLK	1669.87	0.186071302	0.41	0.561445104	HBB
351	VLSGEDK	746.8	0.424586775	-0.59	2.195597481	Hba
352	VPDLVPGSF	930.05	0.001438672	0.79	7.494879697	Fga
353	VPPNNSNAAEVDLPTTELQGLVPR	2559.77	0.346564252	-0.55	1.55204139	F13a1
354	VPQVSTPTLVEVSR	1511.71	0.812080927	0.21	0.809964662	ALB
355	VQETDTSQKDQSPA	1533.54	0.422649731	-1.68	0.517400779	Serpina1a
356	VSTVLTSKYR	1153.32	0.422649731	-0.05	0.667247686	Hba
357	VVGPVVVPR	921.13	0.436584258	1.43	0.799122615	Ahsg
358	VVVGPVVVPR	1020.26	0.804315768	1.71	0.932557842	Ahsg
359	VYLIQGTQVYVFLTK	1772.08	0.308929225	0.81	0.207566698	Hpx
360	VYYNPDQPPKPGMIDSATQ	2121.31	0.135116704	-1.05	5.172399311	Fgg
361	YAPELLFFAK	1198.4	0.216442611	0.65	0.359850964	ALB
362	YDEPTDSLDA	1125.09	0.957187222	-1.28	0.959646439	Fgb
363	YDEPTSLDAR	1281.27	0.361762458	-1.57	1.80500521	Fgb
364	YEDEINKR	1066.12	0.422649731	-2.4	5.755999641	KRT1
365	YEDIAQKS	953	0.233333821	-1.28	5.563039383	KRT1
366	YFYAPELLFFAK	1508.75	0.422649731	0.67	0.388296074	ALB
367	YGFRDPGPQL	1149.25	0.718012699	-1.02	0.662636281	Chga
368	YNPDQPPKPGMIDSATQ	1859.01	0.242651873	-1.34	4.259158224	Fgg

369	YWGVASFLQK	1198.36	0.230621616	0.18	0.389544582	RBP4
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3 Table S2

4 Significantly differentiated peptide

No.	Sequence	P-value	Fold-change	Protein origin	Score
6	AATELRGVV	0.024155158	1.414682434	Osbp	0.123344
12	ADEAGSEAHREGET RNT	0.038844255	0.273751904	Fga	0.118488
39	AIQVYYNPDQPPKP GMIDSATQ	0.026910242	4.522386976	Fgg	0.12735
155	GSKAENPTNPGP	0.003380179	40.51339691	Fga	0.411249
192	MADEAGSEAHREG ETRNT	0.00276285	0.444628415	Fga	0.0940532
243	RLLWENGNLL	0.007002316	9.890498207	C3	0.547936
244	RVNSGFE	0.017346253	4.659368181	Spp2	0.231696
253	SEAAPAAPAAAPPA EKAPA	0.032944283	0.318576992	H1-2	0.451463
278	SPVPDLVPGSF	0.001830638	4.668724069	Fga	0.776414
289	STVKKQVTKTY	0.04973525	7.737387559	Fga	0.0376532
292	SVESASGETLH	0.032083275	0.201934053	Ahsg	0.106249
307	TDTEDKGEFLSEGG GVR	0.040558755	2.013953418	Fga	0.210199
347	VGPVVVPR	0.014810775	4.910499179	Ahsg	0.273041
352	VPDLVPGSF	0.001438672	7.494879697	Fga	0.635403

5 Table S3

6 Physicochemical properties of peptides

No.	Sequence	Score	GRAVY	IP	Extinction coefficient
155	GSKAENPTNPGP	0.411249	-1.64	7.0	0 M ⁻¹ cm ⁻¹
243	RLLWENGNLL	0.547936	-0.11	7.0	5690 M ⁻¹ cm ⁻¹
278	SPVPDLVPGSF	0.776414	0.43	3.12	0 M ⁻¹ cm ⁻¹

352	VPDLVPGSF	0.635403	0.79	3.12	0 M ⁻¹ cm ⁻¹
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