A	B	C	D	E	F	G	H	I	J	K	L	M
	33N vs. 33D		33N vs. 44D		33D vs. 44D							
Spot No.	ANOVA	Avg Ratio	ANOVA	Avg Ratio	ANOVA	Avg Ratio	Protein Name (from Uniprot)	Accession Number	Molecular weight	Peptide count	MS & MS/MS score	Peptide sequence (ion score)
551	0.04	-1.46										
964	0.0054	1.45										
1133	0.015	1.66										
1138	0.032	1.71										
1202	0.015	-1.37										
1251	0.0093	1.44										
1270	0.015	-1.32										
1320	0.018	-1.29										
1326	0.014	-1.6										
1368	0.012	-1.45										
1447	0.0059	-1.67										
1449	0.015	-1.64										
1530	0.031	1.87										
1949	0.022	1.64										
1956	0.036	2.93										
430			0.0014	-1.56								
439			0.015	1.47								
477			0.0048	-1.29								
548			0.02	1.39								
881			0.035	1.41								
1005			0.013	1.74								
1168			0.046	1.15								
1247			0.016	-1.34								
1299			0.023	-1.5								
1308			0.024	-1.5								
1331			0.037	-1.54								
1341			0.045	-1.49								
1358			0.031	-4.53								
1431			0.0054	-1.66								
1484			0.015	-1.44								
1501			0.023	1.77								
1532			0.0051	2.07								
1552			0.019	1.85								
1557			0.02	1.57								
1559			0.02	1.44								
1571			0.0052	-1.26								
1611			0.045	-1.32								
1827			0.0017	2.35								
1846			0.032	1.56								
1864			0.014	1.75								
1878			0.0044	1.7								
1881			0.00093	2.05								
1896			0.01	1.88								
1897			0.0084	1.74								
1901			0.0038	1.79								
1904			0.0053	1.83								
1909			0.017	-2.88								
1924			0.00058	1.72								
1926			0.028	1.52								
1932			0.014	1.54								
1937			0.0098	1.54								
2027			0.012	-1.36								
151					0.031	1.32						
349					0.014	-1.18						
698					0.026	-1.23						
866					0.0087	1.62						
898					0.0012	1.42						
911					0.027	1.77						
955					0.0076	1.34						
976					0.026	1.3						
1013					0.018	1.54						
1028					0.015	1.3						
1097					0.0071	1.24						
1167					0.0073	-1.34						
1184					0.03	1.6						
1360					0.0035	-1.18						
1580					0.021	1.27						
1590					0.027	1.3						
1634					0.01	1.64						
1666					0.021	1.74						
1689					0.02	1.92						
1746					0.029	1.51						
2053					0.0021	-1.84						
a	b	c	d	e	f	g						
204	0.012	1.57	0.0007	1.74			Serum Albumin, chain A	P02768	65694.5	19	289	187
429	0.0049	-1.29	0.0014	-1.37								
513	0.0072	-1.55	0.00056	-1.61								
526	0.00088	-1.66	0.0093	-1.47								
541	0.0073	-1.53	0.012	-1.5			Transferrin variant	Q53H26	77029.6	15	270	203
561	0.0077	2.75	0.0071	2.4								
575	0.0072	-1.22	0.0062	-1.18			alpha 1-B glycoprotein	P04217	51908.4	12	507	441
579	0.015	-1.31	0.0054	-1.31			alpha 1-B glycoprotein	P04217	51908.4	11	465	408
614	0.036	1.7	0.0037	1.64			Transferrin variant	Q53H26	77029.6	27	701	509
848	0.02	1.29	0.014	1.6								
990	0.00066	1.67	0.041	1.6			Apolipoprotein H (beta-2-glycoprotein 1)	P02749	38272.7	11	175	114
1000	0.042	1.29	0.0073	1.73			Tubulin beta - 2A chain	Q13885	49884	14	179	83
1008	0.00063	2.94	0.018	2.62			Keratin type II, cytoskeletal 1	P04264	65846.9	19	286	166
1017	0.016	1.86	0.0087	2.26			Alpha-1-antitrypsin (Serpin A1)	P01009	46707	23	750	532
1096	0.0042	1.51	0.018	1.47								
1110	0.021	1.18	0.033	1.19								
1118	0.0025	1.54	0.0002	1.99			Pigment epithelium-derived factor (Serpin F1)	P02768	46372.4	11	205	140
1125	0.00074	2.45	0.0017	2.26			Pigment epithelium-derived factor (Serpin F1)	P02768	46372.4	15	436	326
1126	0.0025	2.03	0.0027	1.91			Pigment epithelium-derived factor (Serpin F1)	P02768	46372.4	14	222	99
1141	0.0002	2.07	0.038	1.97			Pigment epithelium-derived factor (Serpin F1)	P02768	46372.4	14	409	298
1148	0.0004	2.36	0.022	2.59								
1172	0.0084	1.52	0.00097	1.53								
1188	0.032	1.26	0.004	1.23			Serum Albumin, Chain A	P02768	47329.7	11	210	112
1268	0.0062	-1.38	0.0069	-1.55			Glutamine synthetase	P15104	42037.3	15	307	147
1278	0.0046	-1.46	0.037	-1.4			Creatine kinase B-type	P12277	42591.3	18	414	266
1313	0.000041	-1.88	0.0081	-1.51								
1324	0.01	-1.49	0.023	-1.53			Fructose-bisphosphate aldolase A	P04075	39307.3	9	158	78
1332	0.042	-1.28	0.011	-1.49			Aspartate aminotransferase, cytoplasmic	P17174	46106.5	14	233	96
1359	0.031	-6.93	0.038	-6.5								
1363	0.0046	-1.27	0.00067	-1.41			Aspartate aminotransferase, cytoplasmic	P17174	46106.5	9	99	45
1397	0.021	-1.48	0.0022	-1.55			Aging-associated gene 9 protein	Q2TSD0	36026.4	5	213	183
1451	0.0015	-2.05	0.0023	-1.75			Glyceraldehyde-3-phosphate dehydrogenase	P04406	36030.4	4	150	113
1454	0.029	-1.45	0.028	-1.42								
1456	1.9E-06	-1.92	0.00025	-1.67			Glyceraldehyde-3-phosphate dehydrogenase	P04406	36030.4	12	371	291
1469	0.0031	-1.58	0.0058	-1.52			Glyceraldehyde-3-phosphate dehydrogenase	P04406	36030.4	10	318	223
1470	0.0061	-1.8	0.0026	-1.72								
1472	0.003	2.01	0.00027	2.01			Clusterin, ApoJ	P10909	48772.1	15	140	61
1493	0.012	1.98	0.0048	1.85								
1500	0.006	2.45	0.00081	2.24								
1516	0.0065	1.52	0.0015	1.9								
1521	0.012	2.14	0.00043	3.34			Apolipoprotein E4	P02649	36184.9	11	95	46
1523	0.00084	1.78	2.3E-06	2.17			Clusterin, ApoJ	P10909	16266.8	4	97	52
1527	0.0022	2.02	0.00008	2.42			Apolipoprotein E4	P02649	36184.9	19	485	356
1535	0.0044	1.85	0.00012	1.94			Complement component 4A	Q5JNX2	29598.7	9	216	170
1545	0.038	1.61	0.039	1.72								
1554	0.015	2.05	0.0023	2.58			Transthyretin	P02766	12470.3	6	189	119
1581	0.0058	1.81	0.021	1.78								
1779	0.029	-1.98	0.015	-2.14			Ig Kappa chain C region; IGKC	P01834	65694.5	17	108	36
1845	0.045	1.45	0.0051	1.51			Prostaglandin-H2- D-isomerase; cerebrin 28	P41222	21015.3	5	130	98
1860	0.027	1.8	0.0025	1.92								
1900	0.022	1.36	0.00005	1.48								
1912	0.025	-1.78	0.016	-1.84			Apolipoprotein A-1	P02647	28061.5	23	380	144
1921	0.0074	1.62	0.00057	1.82								
1980	0.012	2.14	0.019	2.1								
1982	0.011	1.66	0.0022	1.62			Superoxide dismutase (Mn), mitochondrial	P04179	24706.6	4	98	49
1987	0.0083	1.79	0.005	1.72								
2067	0.00043	-1.95	8.9E-06	-2.09			Apolipoprotein A-1	P02647	28061.5	21	721	504
2068	0.0031	-2.25	0.00071	-2.24			Apolipoprotein A-1	P02647	28061.5	23	624	377
1315	0.0011	-1.64			0.033	1.39						
1573	0.011	1.53			0.018	-1.38						
592			0.0048	1.75	0.017	1.63						
596			0.00024	2.11	0.0038	1.69						
599			5.8E-06	2.14	0.000055	1.58						
1043			0.018	1.89	0.048	1.62						
1050			0.0063	2.06	0.014	1.83						
1114			0.0039	1.56	0.00086	1.24						
1403			0.021	-1.3	0.019	-1.15						
1549			9.5E-06	1.91	0.007	1.43						
1585			0.00054	1.65	0.0079	1.4						
1255	0.000067	-3.54	0.0057	-2.12	0.00056	1.67						
1546	0.00022	1.76	2.4E-06	4.26	0.00032	2.43						

H: Protein named as sugegsted by Uniprot; http://www.uniprot.org/
I: Protein accession # from Uniprot; http://www.uniprot.org/
J: Molecular weight from Uniprot
K: Peptide count: Number of peptides that matched the theoretical digest of the primary protein identified.
L: MS & MS/MS score: score of the quality of the peptide mass fingerprint and the quality of the MS/MS peptide fragmnet. L>=95 is considered significant.
M: Peptide sequence ion score: score of the quality of the MS/MS peptide fragment. Scores of 20 or greater are considered significant.