

Supplementary Table I. Correctly identified peptide sequences

Protein	Sequence	Mass	RC	APMA-score	D-score
CADC_HUMAN	RQKKKHTLMTSKEDIR	1000.79	19	0.992021169	0.01
THRB_HUMAN	SPQELLCGASLISDR	1016.71	23.8	0.958024835	0.01
THRB_HUMAN	SPQELLCGASLISDR	1020.79	21.8	0.985493593	0.01
A2HS_HUMAN	EHAVEGDCDFQLLK	1023.85	22.05	0.317300419	0.01
A2HS_HUMAN	EHAVEGDCDFQLLK	1028.1	19.15	0.933585514	0.01
THRB_HUMAN	SDYIHPVCLPDRETAASLLQAGYK	1033.72	24	0.992021169	0.01
THRB_HUMAN	RGDACEGDSGGPFVMK	1035.23	13.4	0.992021169	0.01
THRB_HUMAN	RGDACEGDSGGPFVMK	1038.91	13.3	0.992021169	0.01
FETA_HUMAN	HEMTPVNPVGVCCTSSYANR	1046.21	20.5	0.992021169	0.01
LAC_HUMAN	SYSCQVTHEGSTVEK	1049.44	17.1	0.992021169	0.01
VGLL_HSV7J	YNEVLPRSEFSNLLIR	1049.51	27.3	0.992021169	0.01
THRB_HUMAN	TTHGLPCLAWASAQAK	1050.35	24.8	0.992021169	0.01
FETA_HUMAN	HEMTPVNPVGVCCTSSYANR	1051.41	18.3	0.992021169	0.01
LAC_HUMAN	SYSCQVTHEGSTVEK	1053.35	16.75	0.841478237	0.01
AJ276395	YSFCTDHTVLVQTR	1056.92	20.68	0.938683832	0.01
AJ276395	YSFCTDHTVLVQTR	1061.51	21.16	0.989638001	0.01
THRB_HUMAN	RQECVIPVCGQDQVTVMTPR	1068.78	21.53	0.886401326	0.01
THRB_HUMAN	RQECVIPVCGQDQVTVMTPR	1074.09	19.33	0.970455038	0.01
THRB_HUMAN	RQECVIPVCGQDQVTVMTPR	1079.67	21.65	0.950163925	0.01
THRB_HUMAN	KSPQELLCGASLISDR	1080.93	20.36	0.987725156	0.01
THRB_HUMAN	KSPQELLCGASLISDR	1084.56	19.43	0.980054669	0.01
FETA_HUMAN	CFQTENPLECQDKGEEELQK	1085.41	22.3	0.992021169	0.01
FETA_HUMAN	CFQTENPLECQDKGEEELQK	1090.77	21.3	0.927563755	0.01
FETA_HUMAN	IMSYICSQQDTLSNK	1091.2	18.6	0.992021169	0.01
FIBB_HUMAN	NYCGLPGEYWLGNK	1091.29	24.8	0.992021169	0.01
THRB_HUMAN	NPDGDEEGVWCYVAGK	1095.85	21.85	0.977206062	0.01
K2C1_HUMAN	GSYSGSGSSYGSGGGSYSGGGGGGHGSYSGSSSGGYR	1105.15	14.5	0.992021169	0.01
THRB_HUMAN	WYQMGIVSWGEGCDR	1115.79	40.07	0.985224986	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGK	1116.44	19.7	0.920343147	0.01
FINC_HUMAN	GNLLQCICTGNGR	1117.62	24.6	0.992021169	0.01
THRB_HUMAN	WYQMGIVSWGEGCDR	1119.93	28.37	0.969319243	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGK	1120.38	19.57	0.802584429	0.01
FINC_HUMAN	GNLLQCICTGNGR	1121.88	24	0.992021169	0.01
THRB_HUMAN	WYQMGIVSWGEGCDR	1123.42	21.8	0.992021169	0.01
CAN1_HUMAN	LDETDDPDDYGDRESGCSFVLALMQK	1124.74	25.9	0.992021169	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGK	1128.34	19	0.992021169	0.01
THRB_HUMAN	WYQMGIVSWGEGCDR	1128.55	21.7	0.992021169	0.01
KAC_HUMAN	VYACEVTHQGLSSPVTK	1131.46	19.6	0.992021169	0.01
FINC_HUMAN	AAHEEICTTNEGVMYR	1133.57	19.8	0.992021169	0.01

THRB_HUMAN	TFGSGEADCGLRPLFEK	1135.53	20.72	0.911526929	0.01
KAC_HUMAN	VYACEVTHQGLSSPVTK	1135.64	19.6	0.992021169	0.01
FINC_HUMAN	FGFCPMAAHEEICTTNEGVMYR	1137.73	26.4	0.992021169	0.01
FINC_HUMAN	AAHEEICTTNEGVMYR	1138	18.3	0.975825022	0.01
THRB_HUMAN	TFGSGEADCGLRPLFEK	1140.04	21.55	0.98977084	0.01
THRB_HUMAN	PVAFSDYIHPVCLPDR	1141.17	23.8	0.992021169	0.01
FINC_HUMAN	AAHEEICTTNEGVMYR	1142.03	18.6	0.992021169	0.01
THRB_HUMAN	CLPDRETAASLLQAGYK	1143.78	14.5	0.992021169	0.01
FINC_HUMAN	AAHEEICTTNEGVMYR	1145.84	15.5	0.992021169	0.01
FINC_HUMAN	CDPHEATCYDDGK	1169.86	17.75	0.927563755	0.01
EGF_HUMAN	YACNCVVG YIGER	1175.13	15.5	0.992021169	0.01
THRB_HUMAN	HQDFNSAVQLVENFCR	1175.79	24.38	0.982655793	0.01
BC006011	ALCELESGIPAAESQIVYAERPLTDNHR	1176.37	24.97	0.975069796	0.01
BC006011	ALCELESGIPAAESQIVYAERPLTDNHR	1178.78	24.27	0.938683832	0.01
THRB_HUMAN	HQDFNSAVQLVENFCR	1180.13	24.66	0.988601868	0.01
THRB_HUMAN	LAVTTHGLPCLAWASQAQAK	1191.77	22.58	0.986920318	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGKR	1194.62	19.2	0.981867553	0.01
THRB_HUMAN	RITDNMFCAGYKPDEGK	1195.13	21	0.992021169	0.01
THRB_HUMAN	LAVTTHGLPCLAWASQAQAK	1195.33	22.43	0.972491784	0.01
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1197.46	26.3	0.900522079	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGKR	1198.47	18.75	0.802584429	0.01
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1199.55	26.8	0.992021169	0.01
THRB_HUMAN	KPVAFSDYIHPVCLPDR	1200.92	22.4	0.984355976	0.01
CANS_HUMAN	PGAFAEAGFHLNEHLYNMIIR	1201.43	30.03	0.987533377	0.01
THRB_HUMAN	KPVAFSDYIHPVCLPDR	1204.7	22.6	0.966763935	0.01
FINC_HUMAN	LLCQCLGFGSGHFR	1212.01	23.65	0.738878819	0.01
THRB_HUMAN	KPVAFSDYIHPVCLPDRETAASLLQAGYK	1212.07	25.63	0.927563755	0.01
THRB_HUMAN	KPVAFSDYIHPVCLPDRETAASLLQAGYK	1214.77	24.8	0.980541042	0.01
FINC_HUMAN	LLCQCLGFGSGHFR	1216.56	23.55	0.960121799	0.01
FINC_HUMAN	LLCQCLGFGSGHFR	1220.18	24.2	0.971509758	0.01
FINC_HUMAN	GFNCESKPEAEETCFDKYTGNTRYR	1226.27	20.1	0.992021169	0.01
THRB_HUMAN	SEGSSVNLSPPLEQCVDPDR	1229.34	19.08	0.984355976	0.01
FINC_HUMAN	GFNCESKPEAEETCFDKYTGNTRYR	1230.9	21	0.900522079	0.01
THRB_HUMAN	SEGSSVNLSPPLEQCVDPDR	1233.1	18.16	0.973408379	0.01
CANS_HUMAN	SGTICSELPGAFAEAGFHLNEHLYNMIIR	1243.91	29.5	0.867630377	0.01
CANS_HUMAN	LPGAFAEAGFHLNEHLYNMIIR	1257.31	30	0.867630377	0.01
IBP1_HUMAN	LALCPPVSASCSEVTR	1259.58	22	0.992021169	0.01
IBP1_HUMAN	LALCPPVSASCSEVTR	1263.58	22.1	0.992021169	0.01
THRB_HUMAN	WYQMGIVSWGEGCDRDGK	1269.8	23.2	0.986002536	0.01
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	1271.16	18.98	0.969319243	0.01
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	1275.06	18.23	0.963744469	0.01
FINC_HUMAN	QDGLWCSTTSNYEQDQK	1291.86	17.1	0.992021169	0.01

THRB_HUMAN	LKKPVAFSDYIHPVCLPDRETAASLLQAGYK	1295.33	16	0.992021169	0.01
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	1309.91	23.08	0.975825022	0.01
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	1313.9	22.45	0.971509758	0.01
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1321.84	21.33	0.988091541	0.01
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1325.91	21.1	0.988762395	0.01
CANS_HUMAN	YSDESGNMDFDNFISCLVR	1328.3	29.7	0.985752608	0.01
CANS_HUMAN	YSDESGNMDFDNFISCLVR	1332.57	29.27	0.977206062	0.01
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1371.05	22	0.946846285	0.01
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1375.23	21.5	0.992021169	0.01
FINC_HUMAN	GFNCESKPEAEETCFDK	1410.06	21.1	0.992021169	0.01
FINC_HUMAN	GFNCESKPEAEETCFDK	1418.46	19.1	0.992021169	0.01
FETA_HUMAN	GQCI IHAENDEKPEGLSPNLNR	1443.02	20.5	0.992021169	0.01
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1492.41	22.27	0.969319243	0.01
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1496.99	21.8	0.992021169	0.01
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1500.66	19.77	0.982270429	0.01
THRB_HUMAN	QECSIPVCGQDQVTVMTPR	1524.17	21.8	0.992021169	0.01
THRB_HUMAN	RQECIPVCGQDQVTVMTPR	1602.61	20.8	0.992021169	0.01
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1799.37	26.8	0.992021169	0.01
CAN1_HUMAN	DLGPNSSK	409.45	6.6	0.992021169	0.01
IBP1_HUMAN	IPGSPEIR	434.93	10.75	0.927563755	0.01
PDX2_HUMAN	TDEGIAYR	462.75	11.4	0.992021169	0.01
CAN1_HUMAN	MAIESAGFK	485.4	13.2	0.992021169	0.01
THRB_HUMAN	SLEDKTER	489.42	8.9	0.802584429	0.01
CAN1_HUMAN	GHAYSVTGAK	496.03	13.6	0.992021169	0.01
CAN1_HUMAN	SEQFINLR	504.12	14.5	0.738878819	0.01
YA13_HUMAN	WYTERLR	512.2	12.6	0.992021169	0.01
CAN1_HUMAN	DFFLANASR	521.19	16.4	0.974265871	0.01
	LSSPATLNSR	523.93	12.1	0.992021169	0.01
U43756	FQGRVTVTR	532.48	14.4	0.992021169	0.01
K2C1_HUMAN	GSGGGSSGGSIGGR	547.17	6.4	0.992021169	0.01
FINC_HUMAN	STTPDITGYR	555.95	14.1	0.992021169	0.01
BC006011	VLVEQQQDR	557.76	10.1	0.992021169	0.01
AC004877	AHLTRHLRTHGTGER	562.48	5	0.992021169	0.01
IBP1_HUMAN	AQETSGEEISK	589.76	7.9	0.992021169	0.01
PDX2_HUMAN	RLSEDYGVLK	590.53	17.7	0.900522079	0.01
A1AT_HUMAN	TDTSHHDQDHPTFNK	594.25	16.2	0.978437859	0.01
THRB_HUMAN	ELLESYIDGR	597.96	15.57	0.938683832	0.01
CAN1_HUMAN	IRLDETDDPDDYGDR	599.13	17.7	0.992021169	0.01
CAN1_HUMAN	RDFFLANASR	599.16	20.15	0.900522079	0.01
THRB_HUMAN	ETAASLLQAGYK	626.54	14.45	0.867630377	0.01
FINC_HUMAN	GEWTCIAYSQLR	626.69	23.6	0.992021169	0.01
CAN1_HUMAN	YLGQDYEQLR	643.09	13.8	0.867630377	0.01

FINC_HUMAN	PGCYDNGK	648.87	15.6	0.970455038	0.01
FINC_HUMAN	CNDQDTR	651.55	11.7	0.802584429	0.01
FINC_HUMAN	PGCYDNGK	652.52	14.05	0.920343147	0.01
CAN1_HUMAN	RGSTAGGCR	654.27	11.95	0.317300419	0.01
CAN1_HUMAN	RGSTAGGCR	658.16	10.4	0.992021169	0.01
FINC_HUMAN	WCGTTQNYDADQK	658.39	17	0.900522079	0.01
THRB_HUMAN	ENLDRDIALMK	659.51	18.75	0.965319781	0.01
FINC_HUMAN	WCGTTQNYDADQK	660.95	18	0.992021169	0.01
THRB_HUMAN	ENLDRDIALMK	667.7	19.1	0.992021169	0.01
MPP3_HUMAN	SLSYLMKIHEK	675.07	16	0.992021169	0.01
THRB_HUMAN	SPQELLCGASLISDR	677.97	24	0.992021169	0.01
THRB_HUMAN	YTACETAR	679.28	15.5	0.900522079	0.01
CANS_HUMAN	SMVAVMDSDTTGK	679.41	7.1	0.992021169	0.01
THRB_HUMAN	SPQELLCGASLISDR	680.63	23.9	0.992021169	0.01
CANS_HUMAN	SMVAVMDSDTTGK	687.49	7.2	0.802584429	0.01
FIBB_HUMAN	CHAANPNGR	691.71	14.2	0.900522079	0.01
FIBB_HUMAN	CHAANPNGR	696.03	14.4	0.972491784	0.01
LAC_HUMAN	SYSCQVTHEGSTVEK	700.21	16.8	0.971509758	0.01
LAC_HUMAN	SYSCQVTHEGSTVEK	703.03	16.7	0.965319781	0.01
FETA_HUMAN	HNCFLAHK	706.78	17.05	0.317300419	0.01
AJ276395	YSFCTDHTVLVQTR	707.91	21.35	0.963744469	0.01
FETA_HUMAN	HNCFLAHK	710.84	16.85	0.911526929	0.01
THRB_HUMAN	KSPQELLCGASLISDR	720.83	20.6	0.992021169	0.01
THRB_HUMAN	KSPQELLCGASLISDR	723.51	21.55	0.867630377	0.01
NRP1_HUMAN	GIIIQGKGHRENK	726.18	13.43	0.886401326	0.01
FIBB_HUMAN	NYCGLPGEYWLGNK	727.37	24.8	0.992021169	0.01
FINC_HUMAN	CHEGGQSYK	730.16	12.8	0.867630377	0.01
CAN1_HUMAN	CLQSGTLFR	734.86	15.9	0.984656785	0.01
CAN1_HUMAN	CLQSGTLFR	738.38	15.7	0.992021169	0.01
	LGEHNIDVLEGNEQFINAAK	738.43	24.1	0.992021169	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGK	744.97	18.23	0.955695216	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGK	747.67	15.95	0.96201929	0.01
FINC_HUMAN	AAHEEICTTNEGVMYR	756.42	18.2	0.927563755	0.01
THRB_HUMAN	TFGSGEADCGLRPLFEK	757.66	21.1	0.992021169	0.01
KAC_HUMAN	VYACEVTHQGLSSPVTK	757.81	19	0.992021169	0.01
FINC_HUMAN	AAHEEICTTNEGVMYR	759.18	18.1	0.938683832	0.01
FINC_HUMAN	AAHEEICTTNEGVMYR	761.61	18.6	0.992021169	0.01
BC021172	HQCSIDLKK	762.23	14.9	0.992021169	0.01
CAN1_HUMAN	LDETDDPDDYGDR	763.67	11.6	0.992021169	0.01
CANS_HUMAN	TDGFGIDTCR	764.83	13.7	0.992021169	0.01
IBP1_HUMAN	ALPGEQQPLHALTR	766.2	19.27	0.966763935	0.01
THRB_HUMAN	SGIECQLWR	768.01	16.9	0.973408379	0.01

CANS_HUMAN	TDGFGIDTCR	768.33	19.4	0.992021169	0.01
FINC_HUMAN	CDPHEATCYDDGK	780.51	17.7	0.900522079	0.01
THRB_HUMAN	TATSEYQTFNPR	781.86	17.8	0.965319781	0.01
THRB_HUMAN	HQDFNSAVQLVENFCR	784.45	24.02	0.972491784	0.01
CAN1_HUMAN	TKGFSLESCR	785.65	13.3	0.992021169	0.01
FINC_HUMAN	CDPHEATCYDDGK	785.79	17.6	0.920343147	0.01
THRB_HUMAN	HQDFNSAVQLVENFCR	787.14	24.93	0.969319243	0.01
CAN1_HUMAN	TKGFSLESCR	789.99	13.2	0.992021169	0.01
THRB_HUMAN	RITDNMFCAGYKPDEGK	796.86	20.4	0.992021169	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGKR	796.91	17.75	0.317300419	0.01
THRB_HUMAN	LAVTTTHGLPCLAWASQAK	797.21	23.48	0.946846285	0.01
FINC_HUMAN	RPGGEPSPEGTTGQSYNQYSQR	799.47	13.9	0.992021169	0.01
THRB_HUMAN	RITDNMFCAGYKPDEGK	799.59	20.65	0.617069415	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGKR	799.84	16.83	0.979005151	0.01
FIBG_HUMAN	CHAGHLNGVYYQGGTYSK	800.3	19.95	0.96201929	0.01
THRB_HUMAN	KPVAFSDYIHPVCLPDR	801.2	20.92	0.968092654	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGKR	802.23	14.35	0.927563755	0.01
FIBG_HUMAN	CHAGHLNGVYYQGGTYSK	802.81	19.7	0.867630377	0.01
THRB_HUMAN	KPVAFSDYIHPVCLPDR	803.65	20.25	0.963744469	0.01
FINC_HUMAN	TFYSCTTEGR	804.39	18.77	0.979543361	0.01
THRB_HUMAN	ITDNMFCAGYKPDEGKR	804.87	14.25	0.738878819	0.01
FINC_HUMAN	TFYSCTTEGR	808.15	18.33	0.972491784	0.01
FINC_HUMAN	LLCQCLGFGSGHFR	808.81	22.9	0.992021169	0.01
FINC_HUMAN	LLCQCLGFGSGHFR	811.31	24.27	0.927563755	0.01
THRB_HUMAN	SEGSSVNLSPPLEQCVDPDR	820.31	17.9	0.983717531	0.01
THRB_HUMAN	SEGSSVNLSPPLEQCVDPDR	822.61	19.45	0.950163925	0.01
THRB_HUMAN	VEEETGDGLDEDSR	833.64	11.8	0.992021169	0.01
FETA_HUMAN	LVLDDVAHVHEHCCR	839.57	19.4	0.992021169	0.01
FINC_HUMAN	PHEATCYDDGK	839.68	16.1	0.992021169	0.01
FINC_HUMAN	WCHDNGVNYK	839.89	16.73	0.976535843	0.01
FINC_HUMAN	PHEATCYDDGK	843.82	15.65	0.886401326	0.01
FINC_HUMAN	WCHDNGVNYK	843.97	16.65	0.984656785	0.01
KAC_HUMAN	HKVYACEVTHQGLSSPVTK	846.15	19.7	0.992021169	0.01
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	847.91	18	0.965319781	0.01
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	850.74	16.6	0.992021169	0.01
FINC_HUMAN	GEWTCKPIAEK	852.72	18.27	0.802584429	0.01
FINC_HUMAN	GEWTCKPIAEK	856.81	18.4	0.992021169	0.01
FINC_HUMAN	QDGLWCSTTSNYEQDQK	861.7	19.17	0.886401326	0.01
FINC_HUMAN	QDGLWCSTTSNYEQDQK	864.31	18.7	0.938683832	0.01
FETA_HUMAN	GDVLDCLQDGEK	872.48	19	0.992021169	0.01
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	873.74	24.77	0.969319243	0.01
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	876.43	25.13	0.968092654	0.01

THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	881.52	20.1	0.992021169	0.01
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	884.08	17.4	0.968092654	0.01
CANS_HUMAN	YSDESGNMDFDNFISCLVR	886.15	29.55	0.969319243	0.01
CAN1_HUMAN	LEICNLTPDALK	887.33	21.2	0.975069796	0.01
CANS_HUMAN	YSDESGNMDFDNFISCLVR	888.93	29.27	0.984656785	0.01
ALBU_HUMAN	SLHTLFGDKLCT	889.83	23.7	0.982655793	0.01
CAN1_HUMAN	LEICNLTPDALK	891.21	21.62	0.970455038	0.01
CAN1_HUMAN	IRLDETDDPDDYGDR	899.33	18.1	0.992021169	0.01
THRB_HUMAN	LAACLEGNCAEGLGTNYR	920.16	21.4	0.992021169	0.01
CAN1_HUMAN	ESGCSFVLALMQK	932.98	25.2	0.992021169	0.01
FINC_HUMAN	GEWTCIAYSQLR	935.76	20.9	0.992021169	0.01
FINC_HUMAN	GEWTCIAYSQLR	939.64	22.86	0.986702343	0.01
FINC_HUMAN	GFNCESKPEAEETCFDK	940.64	20.97	0.955695216	0.01
FETA_HUMAN	LLACGEGAADIIIGHLCIR	942.85	29.6	0.992021169	0.01
FINC_HUMAN	GFNCESKPEAEETCFDK	945.98	21.5	0.992021169	0.01
FETA_HUMAN	LLACGEGAADIIIGHLCIR	947.18	28	0.992021169	0.01
THRB_HUMAN	GDACEGDSGGPFVMK	957.11	13.8	0.992021169	0.01
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	959.95	19.3	0.802584429	0.01
THRB_HUMAN	GDACEGDSGGPFVMK	960.88	13.8	0.992021169	0.01
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	962.69	19.47	0.968092654	0.01
THRB_HUMAN	GDACEGDSGGPFVMK	964.99	18	0.992021169	0.01
FETA_HUMAN	DLCQAQGVALQTMK	975.43	18.5	0.992021169	0.01
FETA_HUMAN	DLCQAQGVALQTMK	978.9	18.5	0.992021169	0.01
FINC_HUMAN	WCGTTQNYDADQK	987.02	17.65	0.987725156	0.01
FETA_HUMAN	ESSLLNQHACAVMK	987.25	17.5	0.992021169	0.01
FINC_HUMAN	WCGTTQNYDADQK	990.9	17.55	0.968092654	0.01
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	995.39	22.1	0.970455038	0.01
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	998.01	21.9	0.927563755	0.01
				0.949357173	0.01
CADC_HUMAN	RQKKKHTLMTSKEDIR	1000.79	19	0.920343147	0.1
THRB_HUMAN	SPQELLCGASLISDR	1016.71	23.8	0.59866288	0.1
THRB_HUMAN	SPQELLCGASLISDR	1020.79	21.8	0.855723281	0.1
A2HS_HUMAN	EHAVEGDCDFQLLK	1028.1	19.15	0.404647962	0.1
THRB_HUMAN	SDYIHPVCLPDRETAASLLQAGYK	1033.72	24	0.920343147	0.1
THRB_HUMAN	RGDACEGDSGGPFVMK	1035.23	13.4	0.920343147	0.1
THRB_HUMAN	RGDACEGDSGGPFVMK	1038.91	13.3	0.920343147	0.1
FETA_HUMAN	HEMTPVNPVGVCCTSSYANR	1046.21	20.5	0.920343147	0.1
LAC_HUMAN	SYSCQVTHEGSTVEK	1049.44	17.1	0.920343147	0.1
VGLL_HSV7J	YNEVLPRSEFSNLLIR	1049.51	27.3	0.920343147	0.1
THRB_HUMAN	TTHGLPCLAWASAQAK	1050.35	24.8	0.920343147	0.1
FETA_HUMAN	HEMTPVNPVGVCCTSSYANR	1051.41	18.3	0.920343147	0.1

LAC_HUMAN	SYSCQVTHEGSTVEK	1053.35	16.75	0.04550454	0.1
AJ276395	YSFCTDHTVLVQTR	1056.92	20.68	0.441748075	0.1
AJ276395	YSFCTDHTVLVQTR	1061.51	21.16	0.896667649	0.1
THRB_HUMAN	RQEC SIPVCGQDQVTVMTPR	1068.78	21.53	0.153114961	0.1
THRB_HUMAN	RQEC SIPVCGQDQVTVMTPR	1074.09	19.33	0.711102275	0.1
THRB_HUMAN	RQEC SIPVCGQDQVTVMTPR	1079.67	21.65	0.531964138	0.1
THRB_HUMAN	KSPQELLCGASLISDR	1080.93	20.36	0.877729233	0.1
THRB_HUMAN	KSPQELLCGASLISDR	1084.56	19.43	0.802584429	0.1
FETA_HUMAN	CFQTENPLECQDKGEEELQK	1085.41	22.3	0.920343147	0.1
FETA_HUMAN	CFQTENPLECQDKGEEELQK	1090.77	21.3	0.363292731	0.1
FETA_HUMAN	IMSYICSQQDTLSNK	1091.2	18.6	0.920343147	0.1
FIBB_HUMAN	NYCGLPGEYWLGN DK	1091.29	24.8	0.920343147	0.1
THRB_HUMAN	NPDGDEEGVWCYVAGK	1095.85	21.85	0.775093636	0.1
K2C1_HUMAN	GSYSGSGSSYSGSGSGSGGGGGHGSYSGSGSSSGGYR	1105.15	14.5	0.920343147	0.1
THRB_HUMAN	WYQMGIVSWGEGCDR	1115.79	40.07	0.853081616	0.1
THRB_HUMAN	ITDNMFCAGYKPDEGK	1116.44	19.7	0.317300419	0.1
FINC_HUMAN	GNLLQCICTGNR	1117.62	24.6	0.920343147	0.1
THRB_HUMAN	WYQMGIVSWGEGCDR	1119.93	28.37	0.700517965	0.1
THRB_HUMAN	ITDNMFCAGYKPDEGK	1120.38	19.57	0.014244522	0.1
FINC_HUMAN	GNLLQCICTGNR	1121.88	24	0.920343147	0.1
THRB_HUMAN	WYQMGIVSWGEGCDR	1123.42	21.8	0.920343147	0.1
CAN1_HUMAN	LDETDDPDDYGDRESGCSFVLALMQK	1124.74	25.9	0.920343147	0.1
THRB_HUMAN	ITDNMFCAGYKPDEGK	1128.34	19	0.920343147	0.1
THRB_HUMAN	WYQMGIVSWGEGCDR	1128.55	21.7	0.920343147	0.1
KAC_HUMAN	VYACEVTHQGLSSPVTK	1131.46	19.6	0.920343147	0.1
FINC_HUMAN	AAHEEICTTNEGVMYR	1133.57	19.8	0.920343147	0.1
THRB_HUMAN	TFGSGEADCGLRPLFEK	1135.53	20.72	0.266509688	0.1
KAC_HUMAN	VYACEVTHQGLSSPVTK	1135.64	19.6	0.920343147	0.1
FINC_HUMAN	FGFCPMAAHEEICTTNEGVMYR	1137.73	26.4	0.920343147	0.1
FINC_HUMAN	AAHEEICTTNEGVMYR	1138	18.3	0.761863246	0.1
THRB_HUMAN	TFGSGEADCGLRPLFEK	1140.04	21.55	0.897985133	0.1
THRB_HUMAN	PVAFSDYIHPVCLPDR	1141.17	23.8	0.920343147	0.1
FINC_HUMAN	AAHEEICTTNEGVMYR	1142.03	18.6	0.920343147	0.1
THRB_HUMAN	CLPDRETAASLLQAGYK	1143.78	14.5	0.920343147	0.1
FINC_HUMAN	AAHEEICTTNEGVMYR	1145.84	15.5	0.920343147	0.1
FINC_HUMAN	CDPHEATCYDDGK	1169.86	17.75	0.363292731	0.1
EGF_HUMAN	YACNCVVG YIGER	1175.13	15.5	0.920343147	0.1
THRB_HUMAN	HQDFNSAVQLVENFCR	1175.79	24.38	0.827900862	0.1
BC006011	ALCELESGIPAAESQIVYAERPLTDNHR	1176.37	24.97	0.754656935	0.1
BC006011	ALCELESGIPAAESQIVYAERPLTDNHR	1178.78	24.27	0.441748075	0.1
THRB_HUMAN	HQDFNSAVQLVENFCR	1180.13	24.66	0.886401326	0.1
THRB_HUMAN	LAVTTHGLPCLAWASAQAK	1191.77	22.58	0.86978084	0.1

THRB_HUMAN	ITDNMFCAGYKPDEGKR	1194.62	19.2	0.82020902	0.1
THRB_HUMAN	RITDNMFCAGYKPDEGK	1195.13	21	0.920343147	0.1
THRB_HUMAN	LAVTTTHGLPCLAWASQAQAK	1195.33	22.43	0.730220003	0.1
FETA_HUMAN	RPCFSSLVDETYVPPAFSDDKFIFHK	1197.46	26.3	0.211287898	0.1
THRB_HUMAN	ITDNMFCAGYKPDEGKR	1198.47	18.75	0.014244522	0.1
FETA_HUMAN	RPCFSSLVDETYVPPAFSDDKFIFHK	1199.55	26.8	0.920343147	0.1
THRB_HUMAN	KPVAFSDYIHPVCLPDR	1200.92	22.4	0.844546479	0.1
CANS_HUMAN	PGAFAEAGFHLNEHLYNMIIR	1201.43	30.03	0.87583413	0.1
THRB_HUMAN	KPVAFSDYIHPVCLPDR	1204.7	22.6	0.676917461	0.1
FINC_HUMAN	LLCQCLGFGSGHFR	1212.01	23.65	0.664368423	0.1
THRB_HUMAN	KPVAFSDYIHPVCLPDRETAASLLQAGYK	1212.07	25.63	0.363292731	0.1
THRB_HUMAN	KPVAFSDYIHPVCLPDRETAASLLQAGYK	1214.77	24.8	0.80730353	0.1
FINC_HUMAN	LLCQCLGFGSGHFR	1216.56	23.55	0.617069415	0.1
FINC_HUMAN	LLCQCLGFGSGHFR	1220.18	24.2	0.720980736	0.1
FINC_HUMAN	GFNCESKPEAEETCFDKYTGNTRYR	1226.27	20.1	0.920343147	0.1
THRB_HUMAN	SEGSSVNLSPPLEQCVPDR	1229.34	19.08	0.844546479	0.1
FINC_HUMAN	GFNCESKPEAEETCFDKYTGNTRYR	1230.9	21	0.211287898	0.1
THRB_HUMAN	SEGSSVNLSPPLEQCVPDR	1233.1	18.16	0.738878819	0.1
CANS_HUMAN	SGTICSELPGAFAEAGFHLNEHLYNMIIR	1243.91	29.5	0.09556777	0.1
CANS_HUMAN	LPGAFAEAGFHLNEHLYNMIIR	1257.31	30	0.09556777	0.1
IBP1_HUMAN	LALCPPVSASCSEVTR	1259.58	22	0.920343147	0.1
IBP1_HUMAN	LALCPPVSASCSEVTR	1263.58	22.1	0.920343147	0.1
THRB_HUMAN	WYQMGIVSWGEGCDRDGK	1269.8	23.2	0.860732955	0.1
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	1271.16	18.98	0.700517965	0.1
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	1275.06	18.23	0.6494311	0.1
FINC_HUMAN	QDGHLWCSTTSNYEQDQK	1291.86	17.1	0.920343147	0.1
THRB_HUMAN	LKKPVAFSDYIHPVCLPDRETAASLLQAGYK	1295.33	16	0.920343147	0.1
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	1309.91	23.08	0.761863246	0.1
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	1313.9	22.45	0.720980736	0.1
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1321.84	21.33	0.881351668	0.1
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1325.91	21.1	0.88799068	0.1
CANS_HUMAN	YSDESGNMDFDNFISCLVR	1328.3	29.7	0.858272134	0.1
CANS_HUMAN	YSDESGNMDFDNFISCLVR	1332.57	29.27	0.775093636	0.1
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1371.05	22	0.504977757	0.1
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1375.23	21.5	0.920343147	0.1
FINC_HUMAN	GFNCESKPEAEETCFDK	1410.06	21.1	0.920343147	0.1
FINC_HUMAN	GFNCESKPEAEETCFDK	1418.46	19.1	0.920343147	0.1
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	1443.02	20.5	0.920343147	0.1
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1492.41	22.27	0.700517965	0.1
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1496.99	21.8	0.920343147	0.1
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1500.66	19.77	0.824138295	0.1
THRB_HUMAN	QEC SIPVC GQDQVTVAMTPR	1524.17	21.8	0.920343147	0.1

THRB_HUMAN	RQECSPVCGQDQVTVMTPR	1602.61	20.8	0.920343147	0.1
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1799.37	26.8	0.920343147	0.1
CAN1_HUMAN	DLGPNSSK	409.45	6.6	0.920343147	0.1
IBP1_HUMAN	IPGSPEIR	434.93	10.75	0.363292731	0.1
PDX2_HUMAN	TDEGIAYR	462.75	11.4	0.920343147	0.1
CAN1_HUMAN	MAIESAGFK	485.4	13.2	0.920343147	0.1
THRB_HUMAN	SLEDKTER	489.42	8.9	0.014244522	0.1
CAN1_HUMAN	GHAYSVTGAK	496.03	13.6	0.920343147	0.1
CAN1_HUMAN	SEQFINLR	504.12	14.5	0.664368423	0.1
YA13_HUMAN	WYTERLR	512.2	12.6	0.920343147	0.1
CAN1_HUMAN	DFFLANASR	521.19	16.4	0.747009112	0.1
	LSSPATLNSR	523.93	12.1	0.920343147	0.1
U43756	FQGRVTVTR	532.48	14.4	0.920343147	0.1
K2C1_HUMAN	GSGGGSSGGSIGGR	547.17	6.4	0.920343147	0.1
FINC_HUMAN	STTPDITGYR	555.95	14.1	0.920343147	0.1
BC006011	VLVEQQQDR	557.76	10.1	0.920343147	0.1
AC004877	AHLTRHLRTHGTGER	562.48	5	0.920343147	0.1
IBP1_HUMAN	AQETSSEEISK	589.76	7.9	0.920343147	0.1
PDX2_HUMAN	RLSEDYGVLK	590.53	17.7	0.211287898	0.1
A1AT_HUMAN	TDTSHHDQDHPTFNK	594.25	16.2	0.786949185	0.1
THRB_HUMAN	ELLESYIDGR	597.96	15.57	0.441748075	0.1
CAN1_HUMAN	IRLDETDDPDDYGDR	599.13	17.7	0.920343147	0.1
CAN1_HUMAN	RDFFLANASR	599.16	20.15	0.211287898	0.1
THRB_HUMAN	ETAASLLQAGYK	626.54	14.45	0.09556777	0.1
FINC_HUMAN	GEWTCIAYSQLR	626.69	23.6	0.920343147	0.1
CAN1_HUMAN	YLGQDYEQLR	643.09	13.8	0.09556777	0.1
FINC_HUMAN	PGCYDNGK	648.87	15.6	0.711102275	0.1
FINC_HUMAN	CNDQDTR	651.55	11.7	0.014244522	0.1
FINC_HUMAN	PGCYDNGK	652.52	14.05	0.317300419	0.1
CAN1_HUMAN	RGSTAGGCR	658.16	10.4	0.920343147	0.1
FINC_HUMAN	WCGTTQNYDADQK	658.39	17	0.211287898	0.1
THRB_HUMAN	ENLDRDIALMK	659.51	18.75	0.663715257	0.1
FINC_HUMAN	WCGTTQNYDADQK	660.95	18	0.920343147	0.1
THRB_HUMAN	ENLDRDIALMK	667.7	19.1	0.920343147	0.1
MPP3_HUMAN	SLSYLMKIHEK	675.07	16	0.920343147	0.1
THRB_HUMAN	SPQELLCGASLISDR	677.97	24	0.920343147	0.1
THRB_HUMAN	YTACETAR	679.28	15.5	0.211287898	0.1
CANS_HUMAN	SMVAVMDSDTTGK	679.41	7.1	0.920343147	0.1
THRB_HUMAN	SPQELLCGASLISDR	680.63	23.9	0.920343147	0.1
CANS_HUMAN	SMVAVMDSDTTGK	687.49	7.2	0.014244522	0.1
FIBB_HUMAN	CHAANPNGR	691.71	14.2	0.211287898	0.1
FIBB_HUMAN	CHAANPNGR	696.03	14.4	0.730220003	0.1

LAC_HUMAN	SYSCQVTHEGSTVEK	700.21	16.8	0.720980736	0.1
LAC_HUMAN	SYSCQVTHEGSTVEK	703.03	16.7	0.663715257	0.1
AJ276395	YSFCTDHTVLVQTR	707.91	21.35	0.6494311	0.1
FETA_HUMAN	HNCFLAHK	710.84	16.85	0.266509688	0.1
THRB_HUMAN	KSPQELLCGASLISDR	720.83	20.6	0.920343147	0.1
THRB_HUMAN	KSPQELLCGASLISDR	723.51	21.55	0.09556777	0.1
NRP1_HUMAN	GIIIQGGKHRENK	726.18	13.43	0.153114961	0.1
FIBB_HUMAN	NYCGLPGEYWLGNK	727.37	24.8	0.920343147	0.1
FINC_HUMAN	CHEGGQSYK	730.16	12.8	0.09556777	0.1
CAN1_HUMAN	CLQSGTLFR	734.86	15.9	0.847498938	0.1
CAN1_HUMAN	CLQSGTLFR	738.38	15.7	0.920343147	0.1
	LGEHNIDVLEGNEQFINAAK	738.43	24.1	0.920343147	0.1
THRB_HUMAN	ITDNMFCAGYKPDEGK	744.97	18.23	0.578508489	0.1
THRB_HUMAN	ITDNMFCAGYKPDEGK	747.67	15.95	0.633933271	0.1
FINC_HUMAN	AAHEEICTTNEGVMYR	756.42	18.2	0.363292731	0.1
THRB_HUMAN	TFGSGEADCGLRPLFEK	757.66	21.1	0.920343147	0.1
KAC_HUMAN	VYACEVTHQGLSSPVTK	757.81	19	0.920343147	0.1
FINC_HUMAN	AAHEEICTTNEGVMYR	759.18	18.1	0.441748075	0.1
FINC_HUMAN	AAHEEICTTNEGVMYR	761.61	18.6	0.920343147	0.1
BC021172	HQCSIDLKK	762.23	14.9	0.920343147	0.1
CAN1_HUMAN	LDETDDPDDYGDR	763.67	11.6	0.920343147	0.1
CANS_HUMAN	TDGFGIDTCR	764.83	13.7	0.920343147	0.1
IBP1_HUMAN	ALPGEQQPLHALTR	766.2	19.27	0.676917461	0.1
THRB_HUMAN	SGIECQLWR	768.01	16.9	0.738878819	0.1
CANS_HUMAN	TDGFGIDTCR	768.33	19.4	0.920343147	0.1
FINC_HUMAN	CDPHEATCYDDGK	780.51	17.7	0.211287898	0.1
THRB_HUMAN	TATSEYQTFFNPR	781.86	17.8	0.663715257	0.1
THRB_HUMAN	HQDFNSAVQLVENFCR	784.45	24.02	0.730220003	0.1
CAN1_HUMAN	TKGFSLESCR	785.65	13.3	0.920343147	0.1
FINC_HUMAN	CDPHEATCYDDGK	785.79	17.6	0.317300419	0.1
THRB_HUMAN	HQDFNSAVQLVENFCR	787.14	24.93	0.700517965	0.1
CAN1_HUMAN	TKGFSLESCR	789.99	13.2	0.920343147	0.1
THRB_HUMAN	RITDNMFCAGYKPDEGK	796.86	20.4	0.920343147	0.1
THRB_HUMAN	LAVTTHGLPCLAWASAQAK	797.21	23.48	0.504977757	0.1
FINC_HUMAN	RPGGEPSPEGTTGQSYNQYSQR	799.47	13.9	0.920343147	0.1
THRB_HUMAN	ITDNMFCAGYKPDEGKR	799.84	16.83	0.792425812	0.1
FIBG_HUMAN	CHAGHLNGVYYQGGTYSK	800.3	19.95	0.633933271	0.1
THRB_HUMAN	KPVAFSDYIHPVCLPDR	801.2	20.92	0.68915192	0.1
THRB_HUMAN	ITDNMFCAGYKPDEGKR	802.23	14.35	0.363292731	0.1
THRB_HUMAN	KPVAFSDYIHPVCLPDR	803.65	20.25	0.6494311	0.1
FINC_HUMAN	TFYSCTTEGR	804.39	18.77	0.797631076	0.1
THRB_HUMAN	ITDNMFCAGYKPDEGKR	804.87	14.25	0.664368423	0.1

FINC_HUMAN	TFYSCCTTEGR	808.15	18.33	0.730220003	0.1
FINC_HUMAN	LLCQCLGFGSGHFR	808.81	22.9	0.920343147	0.1
FINC_HUMAN	LLCQCLGFGSGHFR	811.31	24.27	0.363292731	0.1
THRB_HUMAN	SEGSSVNLSPPLEQCVPR	820.31	17.9	0.838287316	0.1
THRB_HUMAN	SEGSSVNLSPPLEQCVPR	822.61	19.45	0.531964138	0.1
THRB_HUMAN	VEEETGDGLDESDR	833.64	11.8	0.920343147	0.1
FETA_HUMAN	LVLDVAHVHEHCCR	839.57	19.4	0.920343147	0.1
FINC_HUMAN	PHEATCYDDGK	839.68	16.1	0.920343147	0.1
FINC_HUMAN	WCHDNGVNYK	839.89	16.73	0.768664585	0.1
FINC_HUMAN	WCHDNGVNYK	843.97	16.65	0.847498938	0.1
KAC_HUMAN	HKVYACEVTHQGLSSPVTK	846.15	19.7	0.920343147	0.1
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	847.91	18	0.663715257	0.1
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	850.74	16.6	0.920343147	0.1
FINC_HUMAN	GEWTCKPIAEK	852.72	18.27	0.014244522	0.1
FINC_HUMAN	GEWTCKPIAEK	856.81	18.4	0.920343147	0.1
FINC_HUMAN	QDGHLWCSTTSNYEQDQK	861.7	19.17	0.153114961	0.1
FINC_HUMAN	QDGHLWCSTTSNYEQDQK	864.31	18.7	0.441748075	0.1
FETA_HUMAN	GDVLDCLQDGEK	872.48	19	0.920343147	0.1
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	873.74	24.77	0.700517965	0.1
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	876.43	25.13	0.68915192	0.1
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	881.52	20.1	0.920343147	0.1
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	884.08	17.4	0.68915192	0.1
CANS_HUMAN	YSDESGNMDFDNFISCLVR	886.15	29.55	0.700517965	0.1
CAN1_HUMAN	LEICNLTPDALK	887.33	21.2	0.754656935	0.1
CANS_HUMAN	YSDESGNMDFDNFISCLVR	888.93	29.27	0.847498938	0.1
ALBU_HUMAN	SLHTLFGDKLCT	889.83	23.7	0.827900862	0.1
CAN1_HUMAN	LEICNLTPDALK	891.21	21.62	0.711102275	0.1
CAN1_HUMAN	IRLDETDDPDDYGDR	899.33	18.1	0.920343147	0.1
THRB_HUMAN	LAACLEGNCAEGLGTNYR	920.16	21.4	0.920343147	0.1
CAN1_HUMAN	ESGCSFVLALMQK	932.98	25.2	0.920343147	0.1
FINC_HUMAN	GEWTCIAYSQLR	935.76	20.9	0.920343147	0.1
FINC_HUMAN	GEWTCIAYSQLR	939.64	22.86	0.867630377	0.1
FINC_HUMAN	GFNCESKPEAEETCFDK	940.64	20.97	0.578508489	0.1
FETA_HUMAN	LLACGEGAADIIIGHLCIR	942.85	29.6	0.920343147	0.1
FINC_HUMAN	GFNCESKPEAEETCFDK	945.98	21.5	0.920343147	0.1
FETA_HUMAN	LLACGEGAADIIIGHLCIR	947.18	28	0.920343147	0.1
THRB_HUMAN	GDACEGDSGGPFVMK	957.11	13.8	0.920343147	0.1
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	959.95	19.3	0.014244522	0.1
THRB_HUMAN	GDACEGDSGGPFVMK	960.88	13.8	0.920343147	0.1
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	962.69	19.47	0.68915192	0.1
THRB_HUMAN	GDACEGDSGGPFVMK	964.99	18	0.920343147	0.1
FETA_HUMAN	DLCQAQGVALQTMK	975.43	18.5	0.920343147	0.1

FETA_HUMAN	DLCQAQGVALQTMK	978.9	18.5	0.920343147	0.1
FINC_HUMAN	WCGTTQNYDADQK	987.02	17.65	0.877729233	0.1
FETA_HUMAN	ESSLLNQHACAVMK	987.25	17.5	0.920343147	0.1
FINC_HUMAN	WCGTTQNYDADQK	990.9	17.55	0.68915192	0.1
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	995.39	22.1	0.711102275	0.1
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	998.01	21.9	0.363292731	0.1
				0.720393692	
THRB_HUMAN	RGDACEGDSGGPFVMK	1038.91	13.3	0.841478237	0.2
FETA_HUMAN	HEMTPVNPVGQCCTSSYANR	1051.41	18.3	0.841478237	0.2
AJ276395	YSFCTDHTVLVQTR	1056.92	20.68	0.123922949	0.2
THRB_HUMAN	RQEC SIPVCGQDQVTVAMTPR	1079.67	21.65	0.211287898	0.2
FETA_HUMAN	CFQTENPLECQDKGEEELQK	1085.41	22.3	0.841478237	0.2
K2C1_HUMAN	GSYGSGGSSYSGSGGSGSGGGGGHGSYSGSGSSSGGYR	1105.15	14.5	0.841478237	0.2
FINC_HUMAN	GNLLQCICTGNGR	1121.88	24	0.841478237	0.2
THRB_HUMAN	WYQMGIVSWGEGCDR	1123.42	21.8	0.841478237	0.2
KAC_HUMAN	VYACEVTHQGLSSPVTK	1135.64	19.6	0.841478237	0.2
THRB_HUMAN	PVAFSDYIHPVCLPDR	1141.17	23.8	0.841478237	0.2
EGF_HUMAN	YACNCVVG YIGER	1175.13	15.5	0.841478237	0.2
THRB_HUMAN	HQDFNSAVQLVENFCR	1180.13	24.66	0.775093636	0.2
THRB_HUMAN	RITDNMFCAGYKPDEGK	1195.13	21	0.841478237	0.2
THRB_HUMAN	KPVAFSDYIHPVCLPDR	1200.92	22.4	0.694937804	0.2
FINC_HUMAN	GFNCESKPEAEETCFDKYTGNTYR	1230.9	21	0.014244522	0.2
CANS_HUMAN	SGTICSSSELPGAFAEAGFHLNEHLYNMIIR	1243.91	29.5	0.664368423	0.2
THRB_HUMAN	NPDSSTTG PWCYTTDPTVR	1271.16	18.98	0.441748075	0.2
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	1309.91	23.08	0.544467774	0.2
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	1313.9	22.45	0.475042763	0.2
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1325.91	21.1	0.778177834	0.2
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1492.41	22.27	0.441748075	0.2
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1500.66	19.77	0.65671621	0.2
THRB_HUMAN	QEC SIPVCGQDQVTVAMTPR	1524.17	21.8	0.841478237	0.2
THRB_HUMAN	SPQELLCGASLISDR	1016.71	23.8	0.292499424	0.2
YA13_HUMAN	WYTERLR	512.2	12.6	0.841478237	0.2
CAN1_HUMAN	DFFLANASR	521.19	16.4	0.518815555	0.2
U43756	FQGRVTVTR	532.48	14.4	0.841478237	0.2
FINC_HUMAN	STTPDITGYR	555.95	14.1	0.841478237	0.2
AC004877	AHLTRHLRTHGTGER	562.48	5	0.841478237	0.2
THRB_HUMAN	ELLESYIDGR	597.96	15.57	0.123922949	0.2
FINC_HUMAN	GEWTCIAYSQLR	626.69	23.6	0.841478237	0.2
CAN1_HUMAN	YLGQDYEQLR	643.09	13.8	0.664368423	0.2
FINC_HUMAN	WCGTTQNYDADQK	660.95	18	0.841478237	0.2
THRB_HUMAN	ENLDRDIALMK	667.7	19.1	0.841478237	0.2

MPP3_HUMAN	SLSYLMKIHEK	675.07	16	0.841478237	0.2
THRB_HUMAN	SPQELLCGASLISDR	677.97	24	0.841478237	0.2
FIBB_HUMAN	CHAANPNGR	691.71	14.2	0.014244522	0.2
LAC_HUMAN	SYSCQVTHEGSTVEK	700.21	16.8	0.475042763	0.2
FETA_HUMAN	HNCFLAHK	710.84	16.85	0.026416192	0.2
THRB_HUMAN	KSPQELLCGASLISDR	720.83	20.6	0.841478237	0.2
CAN1_HUMAN	CLQSGTLFR	734.86	15.9	0.700517965	0.2
THRB_HUMAN	ITDNMFCAGYKPDEGK	744.97	18.23	0.266509688	0.2
FINC_HUMAN	AAHEEICTTNEGVMYR	761.61	18.6	0.841478237	0.2
BC021172	HQCSIDLK	762.23	14.9	0.841478237	0.2
CANS_HUMAN	TDGFGIDTCR	764.83	13.7	0.841478237	0.2
IBP1_HUMAN	ALPGEQQPLHALTR	766.2	19.27	0.404647962	0.2
CANS_HUMAN	TDGFGIDTCR	768.33	19.4	0.841478237	0.2
THRB_HUMAN	TATSEYQTFNPR	781.86	17.8	0.384528956	0.2
THRB_HUMAN	HQDFNSAVQLVENFCR	784.45	24.02	0.490403529	0.2
THRB_HUMAN	RITDNMFCAGYKPDEGK	796.86	20.4	0.841478237	0.2
THRB_HUMAN	LAVTTHGLPCLAWASAQAK	797.21	23.48	0.182410368	0.2
FINC_HUMAN	RPGGEPSPEGTTGQSYNQYSQR	799.47	13.9	0.841478237	0.2
THRB_HUMAN	ITDNMFCAGYKPDEGKR	799.84	16.83	0.59866288	0.2
THRB_HUMAN	KPVAFSDYIHPVCLPDR	801.2	20.92	0.423702278	0.2
THRB_HUMAN	ITDNMFCAGYKPDEGKR	802.23	14.35	0.069025152	0.2
THRB_HUMAN	SEGSSVNLSPPLEQCVPR	822.61	19.45	0.211287898	0.2
FETA_HUMAN	LVLDAHVHEHCCR	839.57	19.4	0.841478237	0.2
FINC_HUMAN	WCHDNGVNYK	843.97	16.65	0.700517965	0.2
FINC_HUMAN	QDGHLWCSTTSNYEQDQK	861.7	19.17	0.032787118	0.2
FETA_HUMAN	GDVLDCLQDGEK	872.48	19	0.841478237	0.2
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	884.08	17.4	0.423702278	0.2
CAN1_HUMAN	LEICNLTPDALK	887.33	21.2	0.531964138	0.2
ALBU_HUMAN	SLHTLFGDKLCT	889.83	23.7	0.663715257	0.2
CAN1_HUMAN	LEICNLTPDALK	891.21	21.62	0.458842652	0.2
CAN1_HUMAN	IRLDETDDPDDYGDR	899.33	18.1	0.841478237	0.2
CAN1_HUMAN	ESGCSFVLALMQK	932.98	25.2	0.841478237	0.2
FETA_HUMAN	LLACGEGAADIIGHLCIR	942.85	29.6	0.841478237	0.2
FINC_HUMAN	GFNCEKPEAEETCFDK	945.98	21.5	0.841478237	0.2
THRB_HUMAN	GDACEGDSGGPFVMK	957.11	13.8	0.841478237	0.2
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	962.69	19.47	0.423702278	0.2
CAN1_HUMAN	DLGPNSSK	409.45	6.6	0.841478237	0.2
IBP1_HUMAN	IPGSPEIR	434.93	10.75	0.069025152	0.2
PDX2_HUMAN	TDEGIAYR	462.75	11.4	0.841478237	0.2
CADC_HUMAN	RQKKKHTLMTSKEDIR	1000.79	19	0.841478237	0.2
THRB_HUMAN	SPQELLCGASLISDR	1020.79	21.8	0.716125371	0.2
A2HS_HUMAN	EHAVEGDCDFQLLK	1028.1	19.15	0.09556777	0.2

THRB_HUMAN	SDYIHPVCLPDRETAASLLQAGYK	1033.72	24	0.841478237	0.2
THRB_HUMAN	RGDACEGDSGGPFVMK	1035.23	13.4	0.841478237	0.2
FETA_HUMAN	HEMTPVNPVGVCCTSSYANR	1046.21	20.5	0.841478237	0.2
LAC_HUMAN	SYSCQVTHEGSTVEK	1049.44	17.1	0.841478237	0.2
VGLL_HSV7J	YNEVLPRSEFSNLLIR	1049.51	27.3	0.841478237	0.2
THRB_HUMAN	TTHGLPCLAWASAQAK	1050.35	24.8	0.841478237	0.2
AJ276395	YSFCTDHTVLVQTR	1061.51	21.16	0.795061104	0.2
THRB_HUMAN	RQECIPVCGQDQVTVMTPR	1068.78	21.53	0.032787118	0.2
THRB_HUMAN	RQECIPVCGQDQVTVMTPR	1074.09	19.33	0.458842652	0.2
THRB_HUMAN	KSPQELLCGASLISDR	1080.93	20.36	0.758312899	0.2
THRB_HUMAN	KSPQELLCGASLISDR	1084.56	19.43	0.617069415	0.2
FETA_HUMAN	CFQTENPLECQDKGEEELQK	1090.77	21.3	0.069025152	0.2
FETA_HUMAN	IMSYICSQQDTLSNK	1091.2	18.6	0.841478237	0.2
FIBB_HUMAN	NYCGLPGEYWLGN DK	1091.29	24.8	0.841478237	0.2
THRB_HUMAN	NPDGDEEGVWCYVAGK	1095.85	21.85	0.567702774	0.2
THRB_HUMAN	WYQMGIVSWGEGCDR	1115.79	40.07	0.711102275	0.2
FINC_HUMAN	GNLLQCICTGNR	1117.62	24.6	0.841478237	0.2
THRB_HUMAN	WYQMGIVSWGEGCDR	1119.93	28.37	0.441748075	0.2
CAN1_HUMAN	LDETDDPDDYGDRESGCSFVLALMQK	1124.74	25.9	0.841478237	0.2
THRB_HUMAN	ITDNMFCAGYKPDEGK	1128.34	19	0.841478237	0.2
THRB_HUMAN	WYQMGIVSWGEGCDR	1128.55	21.7	0.841478237	0.2
KAC_HUMAN	VYACEVTHQGLSSPVTK	1131.46	19.6	0.841478237	0.2
FINC_HUMAN	AAHEEICTTNEGVMYR	1133.57	19.8	0.841478237	0.2
FINC_HUMAN	FGFCPMAAHEEICTTNEGVMYR	1137.73	26.4	0.841478237	0.2
FINC_HUMAN	AAHEEICTTNEGVMYR	1138	18.3	0.544467774	0.2
THRB_HUMAN	TFGSGEADCGLRPLFEK	1140.04	21.55	0.797631076	0.2
FINC_HUMAN	AAHEEICTTNEGVMYR	1142.03	18.6	0.841478237	0.2
THRB_HUMAN	CLPDRETAASLLQAGYK	1143.78	14.5	0.841478237	0.2
FINC_HUMAN	AAHEEICTTNEGVMYR	1145.84	15.5	0.841478237	0.2
FINC_HUMAN	CDPHEATCYDDGK	1169.86	17.75	0.069025152	0.2
THRB_HUMAN	HQDFNSAVQLVENFCR	1175.79	24.38	0.663715257	0.2
BC006011	ALCELESGIPAAESQIVYAERPLTDNHR	1176.37	24.97	0.531964138	0.2
BC006011	ALCELESGIPAAESQIVYAERPLTDNHR	1178.78	24.27	0.123922949	0.2
THRB_HUMAN	LAVTTHGLPCLAWASAQAK	1191.77	22.58	0.743007025	0.2
THRB_HUMAN	ITDNMFCAGYKPDEGKR	1194.62	19.2	0.6494311	0.2
THRB_HUMAN	LAVTTHGLPCLAWASAQAK	1195.33	22.43	0.490403529	0.2
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1197.46	26.3	0.014244522	0.2
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1199.55	26.8	0.841478237	0.2
CANS_HUMAN	PGAFEAGFHLNEHLYNMIIR	1201.43	30.03	0.754656935	0.2
THRB_HUMAN	KPVAFSDYIHPVCLPDR	1204.7	22.6	0.404647962	0.2
THRB_HUMAN	KPVAFSDYIHPVCLPDRETAASLLQAGYK	1212.07	25.63	0.069025152	0.2
THRB_HUMAN	KPVAFSDYIHPVCLPDRETAASLLQAGYK	1214.77	24.8	0.625682521	0.2

FINC_HUMAN	LLCQCLGFGSGHFR	1216.56	23.55	0.317300419	0.2
FINC_HUMAN	LLCQCLGFGSGHFR	1220.18	24.2	0.475042763	0.2
FINC_HUMAN	GFNCESKPEAEETCFDKYTGTNTYR	1226.27	20.1	0.841478237	0.2
THRB_HUMAN	SEGSSVNLSPPLEQCVDPDR	1229.34	19.08	0.694937804	0.2
THRB_HUMAN	SEGSSVNLSPPLEQCVDPDR	1233.1	18.16	0.504977757	0.2
CANS_HUMAN	LPGAFEAGFHLNEHLYNMIIR	1257.31	30	0.664368423	0.2
IBP1_HUMAN	LALCPPVSASCSEVTR	1259.58	22	0.841478237	0.2
IBP1_HUMAN	LALCPPVSASCSEVTR	1263.58	22.1	0.841478237	0.2
THRB_HUMAN	WYQMGIVSWGEGCDRDGK	1269.8	23.2	0.725676425	0.2
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	1275.06	18.23	0.363292731	0.2
FINC_HUMAN	QDGLWCSTTSNYEQDQK	1291.86	17.1	0.841478237	0.2
THRB_HUMAN	LKKPVAFSDYIHPVCLPDRETAASLLQAGYK	1295.33	16	0.841478237	0.2
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1321.84	21.33	0.76531241	0.2
CANS_HUMAN	YSDESGNMDFDNFISCLVR	1328.3	29.7	0.720980736	0.2
CANS_HUMAN	YSDESGNMDFDNFISCLVR	1332.57	29.27	0.567702774	0.2
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1371.05	22	0.182410368	0.2
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1375.23	21.5	0.841478237	0.2
FINC_HUMAN	GFNCESKPEAEETCFDK	1410.06	21.1	0.841478237	0.2
FINC_HUMAN	GFNCESKPEAEETCFDK	1418.46	19.1	0.841478237	0.2
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	1443.02	20.5	0.841478237	0.2
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1496.99	21.8	0.841478237	0.2
THRB_HUMAN	RQECVIPVCGQDQVTVAMTPR	1602.61	20.8	0.841478237	0.2
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1799.37	26.8	0.841478237	0.2
CAN1_HUMAN	MAIESAGFK	485.4	13.2	0.841478237	0.2
CAN1_HUMAN	GHAYSVTGAK	496.03	13.6	0.841478237	0.2
	LSSPATLNSR	523.93	12.1	0.841478237	0.2
K2C1_HUMAN	GSGGGSSGGSIGGR	547.17	6.4	0.841478237	0.2
BC006011	VLVEQQQDR	557.76	10.1	0.841478237	0.2
IBP1_HUMAN	AQETSGEEISK	589.76	7.9	0.841478237	0.2
PDX2_HUMAN	RLSEDYGVLK	590.53	17.7	0.014244522	0.2
A1AT_HUMAN	TDTSHHDQDHPTFNK	594.25	16.2	0.588818231	0.2
CAN1_HUMAN	IRLDETDDPDDYGDR	599.13	17.7	0.841478237	0.2
CAN1_HUMAN	RDFFLANASR	599.16	20.15	0.014244522	0.2
THRB_HUMAN	ETAASLLQAGYK	626.54	14.45	0.664368423	0.2
FINC_HUMAN	PGCYDNGK	648.87	15.6	0.458842652	0.2
FINC_HUMAN	PGCYDNGK	652.52	14.05	0.04550454	0.2
CAN1_HUMAN	RGSTAGGCR	658.16	10.4	0.841478237	0.2
FINC_HUMAN	WCGTTQNYDADQK	658.39	17	0.014244522	0.2
THRB_HUMAN	ENLDRDIALMK	659.51	18.75	0.384528956	0.2
THRB_HUMAN	YTACETAR	679.28	15.5	0.014244522	0.2
CANS_HUMAN	SMVAVMDSDTTGK	679.41	7.1	0.841478237	0.2
THRB_HUMAN	SPQELLCGASLISDR	680.63	23.9	0.841478237	0.2

FIBB_HUMAN	CHAANPNGR	696.03	14.4	0.490403529	0.2
LAC_HUMAN	SYSCQVTHEGSTVEK	703.03	16.7	0.384528956	0.2
AJ276395	YSFCTDHTVLVQTR	707.91	21.35	0.363292731	0.2
THRB_HUMAN	KSPQELLCGASLISDR	723.51	21.55	0.664368423	0.2
NRP1_HUMAN	GIIIQGGKHRENK	726.18	13.43	0.032787118	0.2
FIBB_HUMAN	NYCGLPGEYWLGNCK	727.37	24.8	0.841478237	0.2
FINC_HUMAN	CHEGGQSYK	730.16	12.8	0.664368423	0.2
CAN1_HUMAN	CLQSGTLFR	738.38	15.7	0.841478237	0.2
	LGEHNIDVLEGNEQFINAAK	738.43	24.1	0.841478237	0.2
THRB_HUMAN	ITDNMFCAGYKPDEGK	747.67	15.95	0.340894075	0.2
FINC_HUMAN	AAHEEICTTNEGVMYR	756.42	18.2	0.069025152	0.2
THRB_HUMAN	TFGSGEADCGLRPLFEK	757.66	21.1	0.841478237	0.2
KAC_HUMAN	VYACEVTHQGLSSPVTK	757.81	19	0.841478237	0.2
FINC_HUMAN	AAHEEICTTNEGVMYR	759.18	18.1	0.123922949	0.2
CAN1_HUMAN	LDETDDPDDYGDR	763.67	11.6	0.841478237	0.2
THRB_HUMAN	SGIECQLWR	768.01	16.9	0.504977757	0.2
FINC_HUMAN	CDPHEATCYDDGK	780.51	17.7	0.014244522	0.2
CAN1_HUMAN	TKGFSLESCR	785.65	13.3	0.841478237	0.2
FINC_HUMAN	CDPHEATCYDDGK	785.79	17.6	0.04550454	0.2
THRB_HUMAN	HQDFNSAVQLVENFCR	787.14	24.93	0.441748075	0.2
CAN1_HUMAN	TKGFSLESCR	789.99	13.2	0.841478237	0.2
FIBG_HUMAN	CHAGHLNGVYYQGGTYSK	800.3	19.95	0.340894075	0.2
FIBG_HUMAN	CHAGHLNGVYYQGGTYSK	802.81	19.7	0.664368423	0.2
THRB_HUMAN	KPVAFSDYIHPVCLPDR	803.65	20.25	0.363292731	0.2
FINC_HUMAN	TFYSCTTEGR	804.39	18.77	0.608071084	0.2
FINC_HUMAN	TFYSCTTEGR	808.15	18.33	0.490403529	0.2
FINC_HUMAN	LLCQCLGFGSGHFR	808.81	22.9	0.841478237	0.2
FINC_HUMAN	LLCQCLGFGSGHFR	811.31	24.27	0.069025152	0.2
THRB_HUMAN	SEGSSVNLSPPLEQCVPR	820.31	17.9	0.68314913	0.2
THRB_HUMAN	VEEETGDGLDEDSR	833.64	11.8	0.841478237	0.2
FINC_HUMAN	PHEATCYDDGK	839.68	16.1	0.841478237	0.2
FINC_HUMAN	WCHDNGVNYK	839.89	16.73	0.556367811	0.2
KAC_HUMAN	HKVYACEVTHQGLSSPVTK	846.15	19.7	0.841478237	0.2
THRB_HUMAN	NPDSSTTGWCYTTPDPTVR	847.91	18	0.384528956	0.2
THRB_HUMAN	NPDSSTTGWCYTTPDPTVR	850.74	16.6	0.841478237	0.2
FINC_HUMAN	GEWTCKPIAEK	856.81	18.4	0.841478237	0.2
FINC_HUMAN	QDGLWCSTTSNYEQDQK	864.31	18.7	0.123922949	0.2
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	873.74	24.77	0.441748075	0.2
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	876.43	25.13	0.423702278	0.2
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	881.52	20.1	0.841478237	0.2
CANS_HUMAN	YSDESGNMDFDNFISCLVR	886.15	29.55	0.441748075	0.2
CANS_HUMAN	YSDESGNMDFDNFISCLVR	888.93	29.27	0.700517965	0.2

THRB_HUMAN	LAACLEGNCAEGLGTNYR	920.16	21.4	0.841478237	0.2
FINC_HUMAN	GEWTCAIYSQLR	935.76	20.9	0.841478237	0.2
FINC_HUMAN	GEWTCAIYSQLR	939.64	22.86	0.738878819	0.2
FINC_HUMAN	GFNCESKPEAEETCFDK	940.64	20.97	0.266509688	0.2
FETA_HUMAN	LLACGEGAADIIIGHLCIR	947.18	28	0.841478237	0.2
THRB_HUMAN	GDACEGDSGGPFVMK	960.88	13.8	0.841478237	0.2
THRB_HUMAN	GDACEGDSGGPFVMK	964.99	18	0.841478237	0.2
FETA_HUMAN	DLCQAQGVALQTMK	975.43	18.5	0.841478237	0.2
FETA_HUMAN	DLCQAQGVALQTMK	978.9	18.5	0.841478237	0.2
FETA_HUMAN	ESSLLNQHACAVMK	987.25	17.5	0.841478237	0.2
FINC_HUMAN	WCGTTQNYDADQK	990.9	17.55	0.423702278	0.2
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	995.39	22.1	0.458842652	0.2
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	998.01	21.9	0.069025152	0.2
				0.615243253	
CADC_HUMAN	RQKKKHTLMTSKEDIR	1000.79	19	0.617069415	0.5
THRB_HUMAN	SPQELLCGASLISDR	1016.71	23.8	0.01376559	0.5
THRB_HUMAN	SPQELLCGASLISDR	1020.79	21.8	0.363292731	0.5
THRB_HUMAN	SDYIHPVCLPDRETAASLLQAGYK	1033.72	24	0.617069415	0.5
THRB_HUMAN	RGDACEGDSGGPFVMK	1035.23	13.4	0.617069415	0.5
THRB_HUMAN	RGDACEGDSGGPFVMK	1038.91	13.3	0.617069415	0.5
FETA_HUMAN	HEMTPVNPVGVCCTSSYANR	1046.21	20.5	0.617069415	0.5
LAC_HUMAN	SYSCQVTHEGSTVEK	1049.44	17.1	0.617069415	0.5
VGLL_HSV7J	YNEVLPRSEFSNLLIR	1049.51	27.3	0.617069415	0.5
THRB_HUMAN	TTHGLPCLAWASAQAK	1050.35	24.8	0.617069415	0.5
FETA_HUMAN	HEMTPVNPVGVCCTSSYANR	1051.41	18.3	0.617069415	0.5
AJ276395	YSFCTDHTVLVQTR	1061.51	21.16	0.516104601	0.5
THRB_HUMAN	RQECIPVCGQDQVTVAMTPR	1074.09	19.33	0.06403701	0.5
THRB_HUMAN	RQECIPVCGQDQVTVAMTPR	1079.67	21.65	0.179912116	0.5
THRB_HUMAN	KSPQELLCGASLISDR	1080.93	20.36	0.441748075	0.5
THRB_HUMAN	KSPQELLCGASLISDR	1084.56	19.43	0.211287898	0.5
FETA_HUMAN	CFQTENPLECQDKGEEELQK	1085.41	22.3	0.617069415	0.5
FETA_HUMAN	IMSYICSQQDTLSNK	1091.2	18.6	0.617069415	0.5
FIBB_HUMAN	NYCGLPGEYWLGN DK	1091.29	24.8	0.617069415	0.5
THRB_HUMAN	NPDGDEEGVWCYVAGK	1095.85	21.85	0.153114961	0.5
K2C1_HUMAN	GSYSGSGSSYSGSGSGSGGGGGHGSYSGSGSSSGGYR	1105.15	14.5	0.617069415	0.5
THRB_HUMAN	WYQMGIVSWGEGCDR	1115.79	40.07	0.354474936	0.5
FINC_HUMAN	GNLLQCICTGNGR	1117.62	24.6	0.617069415	0.5
THRB_HUMAN	WYQMGIVSWGEGCDR	1119.93	28.37	0.054464583	0.5
FINC_HUMAN	GNLLQCICTGNGR	1121.88	24	0.617069415	0.5
THRB_HUMAN	WYQMGIVSWGEGCDR	1123.42	21.8	0.617069415	0.5
CAN1_HUMAN	LDETDPPDDYGDRESGCSFVLALMQK	1124.74	25.9	0.617069415	0.5

THRB_HUMAN	ITDNMFCAGYKPDEGK	1128.34	19	0.617069415	0.5
THRB_HUMAN	WYQMGIVSWGEGCDR	1128.55	21.7	0.617069415	0.5
KAC_HUMAN	VYACEVTHQGLSSPVTK	1131.46	19.6	0.617069415	0.5
FINC_HUMAN	AAHEEICTTNEGVMYR	1133.57	19.8	0.617069415	0.5
KAC_HUMAN	VYACEVTHQGLSSPVTK	1135.64	19.6	0.617069415	0.5
FINC_HUMAN	FGFCPMAAHEEICTTNEGVMYR	1137.73	26.4	0.617069415	0.5
FINC_HUMAN	AAHEEICTTNEGVMYR	1138	18.3	0.129721245	0.5
THRB_HUMAN	TFGSGEADCGLRPLFEK	1140.04	21.55	0.521498949	0.5
THRB_HUMAN	PVAFSDYIHPVCLPDR	1141.17	23.8	0.617069415	0.5
FINC_HUMAN	AAHEEICTTNEGVMYR	1142.03	18.6	0.617069415	0.5
THRB_HUMAN	CLPDRETAASLLQAGYK	1143.78	14.5	0.617069415	0.5
FINC_HUMAN	AAHEEICTTNEGVMYR	1145.84	15.5	0.617069415	0.5
EGF_HUMAN	YACNCVVG YIGER	1175.13	15.5	0.617069415	0.5
THRB_HUMAN	HQDFNSAVQLVENFCR	1175.79	24.38	0.277045343	0.5
BC006011	ALCELESGIPAAESQIVYAERPLTDNHR	1176.37	24.97	0.118157335	0.5
THRB_HUMAN	HQDFNSAVQLVENFCR	1180.13	24.66	0.475042763	0.5
THRB_HUMAN	LAVTTHGLPCLAWASAQAK	1191.77	22.58	0.412394356	0.5
THRB_HUMAN	ITDNMFCAGYKPDEGKR	1194.62	19.2	0.255793413	0.5
THRB_HUMAN	RITDNMFCAGYKPDEGK	1195.13	21	0.617069415	0.5
THRB_HUMAN	LAVTTHGLPCLAWASAQAK	1195.33	22.43	0.084670279	0.5
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1199.55	26.8	0.617069415	0.5
THRB_HUMAN	KPVAFSDYIHPVCLPDR	1200.92	22.4	0.326882632	0.5
CANS_HUMAN	PGAFAEAGFHLNEHLYNMIIR	1201.43	30.03	0.434647114	0.5
THRB_HUMAN	KPVAFSDYIHPVCLPDR	1204.7	22.6	0.037249387	0.5
THRB_HUMAN	KPVAFSDYIHPVCLPDRETAASLLQAGYK	1214.77	24.8	0.222638367	0.5
FINC_HUMAN	LLCQCLGFGSGHFR	1216.56	23.55	0.014244522	0.5
FINC_HUMAN	LLCQCLGFGSGHFR	1220.18	24.2	0.074133616	0.5
FINC_HUMAN	GFNCESKPEAEETCFDKYTGNTRYR	1226.27	20.1	0.617069415	0.5
THRB_HUMAN	SEGSSVNLSPPLEQCVPCR	1229.34	19.08	0.326882632	0.5
THRB_HUMAN	SEGSSVNLSPPLEQCVPCR	1233.1	18.16	0.09556777	0.5
IBP1_HUMAN	LALCPPVSASCSEVTR	1259.58	22	0.617069415	0.5
IBP1_HUMAN	LALCPPVSASCSEVTR	1263.58	22.1	0.617069415	0.5
THRB_HUMAN	WYQMGIVSWGEGCDRDKG	1269.8	23.2	0.380372669	0.5
THRB_HUMAN	NPDSSTTGWCYTTDPTVR	1271.16	18.98	0.054464583	0.5
THRB_HUMAN	NPDSSTTGWCYTTDPTVR	1275.06	18.23	0.02328627	0.5
FINC_HUMAN	QDGLWCSTTSNYEQDQK	1291.86	17.1	0.617069415	0.5
THRB_HUMAN	LKKPVAFSDYIHPVCLPDRETAASLLQAGYK	1295.33	16	0.617069415	0.5
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	1309.91	23.08	0.129721245	0.5
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	1313.9	22.45	0.074133616	0.5
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1321.84	21.33	0.455497092	0.5
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1325.91	21.1	0.481284777	0.5
CANS_HUMAN	YSDESGNMDFDNFISCLVR	1328.3	29.7	0.371924398	0.5

CANS_HUMAN	YSDESGNMDFDNFISCLVR	1332.57	29.27	0.153114961	0.5
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1371.05	22	0.664368423	0.5
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1375.23	21.5	0.617069415	0.5
FINC_HUMAN	GFNCESKPEAEETCFDK	1410.06	21.1	0.617069415	0.5
FINC_HUMAN	GFNCESKPEAEETCFDK	1418.46	19.1	0.617069415	0.5
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	1443.02	20.5	0.617069415	0.5
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1492.41	22.27	0.054464583	0.5
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1496.99	21.8	0.617069415	0.5
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1500.66	19.77	0.266509688	0.5
THRB_HUMAN	QECSIPVCGQDQVTVAMTPR	1524.17	21.8	0.617069415	0.5
THRB_HUMAN	RQECSIPVCGQDQVTVAMTPR	1602.61	20.8	0.617069415	0.5
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1799.37	26.8	0.617069415	0.5
CAN1_HUMAN	DLGPNSSK	409.45	6.6	0.617069415	0.5
PDX2_HUMAN	TDEGIAYR	462.75	11.4	0.617069415	0.5
CAN1_HUMAN	MAIESAGFK	485.4	13.2	0.617069415	0.5
CAN1_HUMAN	GHAYSVTGAK	496.03	13.6	0.617069415	0.5
YA13_HUMAN	WYTERLR	512.2	12.6	0.617069415	0.5
CAN1_HUMAN	DFFLANASR	521.19	16.4	0.106752558	0.5
	LSSPATLNSR	523.93	12.1	0.617069415	0.5
U43756	FQGRVTVTR	532.48	14.4	0.617069415	0.5
K2C1_HUMAN	GSGGGSSGGSIGGR	547.17	6.4	0.617069415	0.5
FINC_HUMAN	STTPDITGYR	555.95	14.1	0.617069415	0.5
BC006011	VLVEQQQDR	557.76	10.1	0.617069415	0.5
AC004877	AHLTRHLRTHTGER	562.48	5	0.617069415	0.5
IBP1_HUMAN	AQETSGEEISK	589.76	7.9	0.617069415	0.5
A1AT_HUMAN	TDTSHHDQDHPTFNK	594.25	16.2	0.176570753	0.5
CAN1_HUMAN	IRLDETDDPDDYGDR	599.13	17.7	0.617069415	0.5
FINC_HUMAN	GEWTCIAYSQLR	626.69	23.6	0.617069415	0.5
FINC_HUMAN	PGCYDNGK	648.87	15.6	0.06403701	0.5
CAN1_HUMAN	RGSTAGGCR	658.16	10.4	0.617069415	0.5
FINC_HUMAN	WCGTTQNYDADQK	660.95	18	0.617069415	0.5
THRB_HUMAN	ENLDRDIALMK	667.7	19.1	0.617069415	0.5
MPP3_HUMAN	SLSYLMKIHEK	675.07	16	0.617069415	0.5
THRB_HUMAN	SPQELLCGASLISDR	677.97	24	0.617069415	0.5
CANS_HUMAN	SMVAVMDSDTTGK	679.41	7.1	0.617069415	0.5
THRB_HUMAN	SPQELLCGASLISDR	680.63	23.9	0.617069415	0.5
FIBB_HUMAN	CHAANPNGR	696.03	14.4	0.084670279	0.5
LAC_HUMAN	SYSCQVTHEGSTVEK	700.21	16.8	0.074133616	0.5
LAC_HUMAN	SYSCQVTHEGSTVEK	703.03	16.7	0.029800398	0.5
AJ276395	YSFCTDHTVLVQTR	707.91	21.35	0.02328627	0.5
THRB_HUMAN	KSPQELLCGASLISDR	720.83	20.6	0.617069415	0.5
FIBB_HUMAN	NYCGLPGEYWLGNK	727.37	24.8	0.617069415	0.5

CAN1_HUMAN	CLQSGTLFR	734.86	15.9	0.336271688	0.5
CAN1_HUMAN	CLQSGTLFR	738.38	15.7	0.617069415	0.5
	LGEHNIDVLEGNEQFINAAK	738.43	24.1	0.617069415	0.5
THRB_HUMAN	ITDNMFCAGYKPDEGK	744.97	18.23	0.021475698	0.5
THRB_HUMAN	ITDNMFCAGYKPDEGK	747.67	15.95	0.017927047	0.5
THRB_HUMAN	TFGSGEADCGLRPLFEK	757.66	21.1	0.617069415	0.5
KAC_HUMAN	VYACEVTHQGLSSPVTK	757.81	19	0.617069415	0.5
FINC_HUMAN	AAHEEICTTNEGVMYR	761.61	18.6	0.617069415	0.5
BC021172	HQCSIDLKK	762.23	14.9	0.617069415	0.5
CAN1_HUMAN	LDETDDPDDYGDR	763.67	11.6	0.617069415	0.5
CANS_HUMAN	TDGFGIDTCR	764.83	13.7	0.617069415	0.5
IBP1_HUMAN	ALPGEQQPLHALTR	766.2	19.27	0.037249387	0.5
THRB_HUMAN	SGIECQLWR	768.01	16.9	0.09556777	0.5
CANS_HUMAN	TDGFGIDTCR	768.33	19.4	0.617069415	0.5
THRB_HUMAN	TATSEYQTFFNPR	781.86	17.8	0.029800398	0.5
THRB_HUMAN	HQDFNSAVQLVENFCR	784.45	24.02	0.084670279	0.5
CAN1_HUMAN	TKGFSLESCR	785.65	13.3	0.617069415	0.5
THRB_HUMAN	HQDFNSAVQLVENFCR	787.14	24.93	0.054464583	0.5
CAN1_HUMAN	TKGFSLESCR	789.99	13.2	0.617069415	0.5
THRB_HUMAN	RITDNMFCAGYKPDEGK	796.86	20.4	0.617069415	0.5
THRB_HUMAN	LAVTTHGLPCLAWASQAQK	797.21	23.48	0.664368423	0.5
FINC_HUMAN	RPGGEPSPEGTTGQSYNQYSQR	799.47	13.9	0.617069415	0.5
THRB_HUMAN	ITDNMFCAGYKPDEGKR	799.84	16.83	0.188232726	0.5
THRB_HUMAN	KPVAFSDYIHPVCLPDR	801.2	20.92	0.04550454	0.5
FINC_HUMAN	TFYSCTTEGR	804.39	18.77	0.199812839	0.5
FINC_HUMAN	TFYSCTTEGR	808.15	18.33	0.084670279	0.5
FINC_HUMAN	LLCQCLGFGSGHFR	808.81	22.9	0.617069415	0.5
THRB_HUMAN	SEGSSVNLSPPLEQCVDPDR	820.31	17.9	0.307524691	0.5
THRB_HUMAN	SEGSSVNLSPPLEQCVDPDR	822.61	19.45	0.179912116	0.5
THRB_HUMAN	VEEETGDGLDEDSR	833.64	11.8	0.617069415	0.5
FETA_HUMAN	LVLDVAHVHEHCCR	839.57	19.4	0.617069415	0.5
FINC_HUMAN	PHEATCYDDGK	839.68	16.1	0.617069415	0.5
FINC_HUMAN	WCHDNGVNYK	843.97	16.65	0.336271688	0.5
KAC_HUMAN	HKVYACEVTHQGLSSPVTK	846.15	19.7	0.617069415	0.5
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	847.91	18	0.029800398	0.5
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	850.74	16.6	0.617069415	0.5
FINC_HUMAN	GEWTCKPIAEK	856.81	18.4	0.617069415	0.5
FETA_HUMAN	GDVLDCLQDGEK	872.48	19	0.617069415	0.5
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	873.74	24.77	0.054464583	0.5
THRB_HUMAN	GQPSVLQVVNLPIVERPVCK	876.43	25.13	0.04550454	0.5
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	881.52	20.1	0.617069415	0.5
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	884.08	17.4	0.04550454	0.5

CANS_HUMAN	YSDESGNMDFDNFISCLVR	886.15	29.55	0.054464583	0.5
CAN1_HUMAN	LEICNLTPDALK	887.33	21.2	0.118157335	0.5
CANS_HUMAN	YSDESGNMDFDNFISCLVR	888.93	29.27	0.336271688	0.5
ALBU_HUMAN	SLHTLFGDKLCT	889.83	23.7	0.277045343	0.5
CAN1_HUMAN	LEICNLTPDALK	891.21	21.62	0.06403701	0.5
CAN1_HUMAN	IRLDETDDPDDYGDR	899.33	18.1	0.617069415	0.5
THRB_HUMAN	LAACLEGNCAEGLGTNYR	920.16	21.4	0.617069415	0.5
CAN1_HUMAN	ESGCSFVLALMQK	932.98	25.2	0.617069415	0.5
FINC_HUMAN	GEWTCIAYSQLR	935.76	20.9	0.617069415	0.5
FINC_HUMAN	GEWTCIAYSQLR	939.64	22.86	0.404647962	0.5
FINC_HUMAN	GFNCESKPEAEETCFDK	940.64	20.97	0.021475698	0.5
FETA_HUMAN	LLACGEGAADIIIGHLCIR	942.85	29.6	0.617069415	0.5
FINC_HUMAN	GFNCESKPEAEETCFDK	945.98	21.5	0.617069415	0.5
FETA_HUMAN	LLACGEGAADIIIGHLCIR	947.18	28	0.617069415	0.5
THRB_HUMAN	GDACEGDSGGPFVMK	957.11	13.8	0.617069415	0.5
THRB_HUMAN	GDACEGDSGGPFVMK	960.88	13.8	0.617069415	0.5
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	962.69	19.47	0.04550454	0.5
THRB_HUMAN	GDACEGDSGGPFVMK	964.99	18	0.617069415	0.5
FETA_HUMAN	DLCQAQGVALQTMK	975.43	18.5	0.617069415	0.5
FETA_HUMAN	DLCQAQGVALQTMK	978.9	18.5	0.617069415	0.5
FETA_HUMAN	ESSLLNQHACAVMK	987.25	17.5	0.617069415	0.5
FINC_HUMAN	WCGTTQNYDADQK	990.9	17.55	0.04550454	0.5
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	995.39	22.1	0.06403701	0.5
				0.434325683	
CADC_HUMAN	RQKKKHTLMTSKEDIR	1000.79	19	0.317300419	1
THRB_HUMAN	SPQELLCGASLISDR	1020.79	21.8	0.069025152	1
THRB_HUMAN	SDYIHPVCLPDRETAASLLQAGYK	1033.72	24	0.317300419	1
THRB_HUMAN	RGDACEGDSGGPFVMK	1035.23	13.4	0.317300419	1
THRB_HUMAN	RGDACEGDSGGPFVMK	1038.91	13.3	0.317300419	1
FETA_HUMAN	HEMTPVNPVGVCCTSSYANR	1046.21	20.5	0.317300419	1
LAC_HUMAN	SYSCQVTHEGSTVEK	1049.44	17.1	0.317300419	1
VGLL_HSV7J	YNEVLPRSEFSNLLIR	1049.51	27.3	0.317300419	1
THRB_HUMAN	TTHGLPCLAWASAQAK	1050.35	24.8	0.317300419	1
FETA_HUMAN	HEMTPVNPVGVCCTSSYANR	1051.41	18.3	0.317300419	1
AJ276395	YSFCTDHTVLVQTR	1061.51	21.16	0.194034556	1
THRB_HUMAN	RQEC SIPVCGQDQVTVAMTPR	1074.36	19.7	0.021475698	1
THRB_HUMAN	KSPQELLCGASLISDR	1080.93	20.36	0.123922949	1
FETA_HUMAN	CFQTENPLECQDKGEEELQK	1085.41	22.3	0.317300419	1
FETA_HUMAN	IMSYICSQQDTLSNK	1091.2	18.6	0.317300419	1
FIBB_HUMAN	NYCGLPGEYWLGN DK	1091.29	24.8	0.317300419	1
THRB_HUMAN	NPDGDEEGVWCYVAGK	1095.85	21.85	0.032787118	1

K2C1_HUMAN	GSYSGSGSSSYSGSGGSGSGGGGGHGSYSGSGSSSGGYR	1105.15	14.5	0.317300419	1
FINC_HUMAN	GNLLQCICTGNR	1117.62	24.6	0.317300419	1
FINC_HUMAN	GNLLQCICTGNR	1121.88	24	0.317300419	1
THRB_HUMAN	WYQMGIVSWGEGCDR	1123.42	21.8	0.317300419	1
CAN1_HUMAN	LDETDDPDDYGDRESGCSFVLALMQK	1124.74	25.9	0.317300419	1
THRB_HUMAN	ITDNMFCAGYKPDEGK	1128.34	19	0.317300419	1
THRB_HUMAN	WYQMGIVSWGEGCDR	1128.55	21.7	0.317300419	1
KAC_HUMAN	VYACEVTHQGLSSPVTK	1131.46	19.6	0.317300419	1
FINC_HUMAN	AAHEEICTTNEGVMYR	1133.57	19.8	0.317300419	1
KAC_HUMAN	VYACEVTHQGLSSPVTK	1135.64	19.6	0.317300419	1
FINC_HUMAN	FGFCPMAAHEEICTTNEGVMYR	1137.73	26.4	0.317300419	1
THRB_HUMAN	TFGSGEADCGLRPLFEK	1140.04	21.55	0.199812839	1
THRB_HUMAN	PVAFSDYIHPVCLPDR	1141.17	23.8	0.317300419	1
FINC_HUMAN	AAHEEICTTNEGVMYR	1142.03	18.6	0.317300419	1
THRB_HUMAN	CLPDRETAASLLQAGYK	1143.78	14.5	0.317300419	1
FINC_HUMAN	AAHEEICTTNEGVMYR	1145.84	15.5	0.317300419	1
EGF_HUMAN	YACNCVVG YIGER	1175.13	15.5	0.317300419	1
THRB_HUMAN	HQDFNSAVQLVENFCR	1180.13	24.66	0.153114961	1
THRB_HUMAN	LAVTTTHGLPCLAWASAQAK	1191.77	22.58	0.101128609	1
THRB_HUMAN	RITDNMFCAGYKPDEGK	1195.13	21	0.317300419	1
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1199.55	26.8	0.317300419	1
THRB_HUMAN	KPVAFSDYIHPVCLPDR	1200.92	22.4	0.049902351	1
CANS_HUMAN	PGAFAEAGFHLNEHLYNMIIR	1201.43	30.03	0.118157335	1
THRB_HUMAN	KPVAFSDYIHPVCLPDRETAASLLQAGYK	1214.77	24.8	0.015819081	1
FINC_HUMAN	GFNCESKPEAEETCFDKYTGNTRYR	1226.27	20.1	0.317300419	1
IBP1_HUMAN	LALCPPVSASCSEVTR	1259.58	22	0.317300419	1
IBP1_HUMAN	LALCPPVSASCSEVTR	1263.58	22.1	0.317300419	1
FINC_HUMAN	QDGLWCSTTSNYEQDQK	1291.86	17.1	0.317300419	1
THRB_HUMAN	LKKPVAFSDYIHPVCLPDRETAASLLQAGYK	1295.33	16	0.317300419	1
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1321.84	21.33	0.13554562	1
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1325.91	21.1	0.158985246	1
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1375.23	21.5	0.317300419	1
FINC_HUMAN	GFNCESKPEAEETCFDK	1410.06	21.1	0.317300419	1
FINC_HUMAN	GFNCESKPEAEETCFDK	1418.46	19.1	0.317300419	1
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	1443.02	20.5	0.317300419	1
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1496.99	21.8	0.317300419	1
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1500.66	19.77	0.026416192	1
THRB_HUMAN	QECSIPVCGQDQVTVAMTPR	1524.17	21.8	0.317300419	1
THRB_HUMAN	RQECSIPVCGQDQVTVAMTPR	1602.61	20.8	0.317300419	1
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1799.37	26.8	0.317300419	1
CAN1_HUMAN	DLGPNSSK	409.45	6.6	0.317300419	1
PDX2_HUMAN	TDEGIAYR	462.75	11.4	0.317300419	1

CAN1_HUMAN	MAIESAGFK	485.4	13.2	0.317300419	1
CAN1_HUMAN	GHAYSVTGAK	496.03	13.6	0.317300419	1
YA13_HUMAN	WYTERLR	512.2	12.6	0.317300419	1
CAN1_HUMAN	DFFLANASR	521.19	16.4	0.34158348	1
	LSSPATLNSR	523.93	12.1	0.317300419	1
U43756	FQGRVTVTR	532.48	14.4	0.317300419	1
K2C1_HUMAN	GSGGGSSGGSIGGR	547.17	6.4	0.317300419	1
FINC_HUMAN	STTPDITGYR	555.95	14.1	0.317300419	1
BC006011	VLVEQQQDR	557.76	10.1	0.317300419	1
AC004877	AHLTRHLRTHGTGER	562.48	5	0.317300419	1
IBP1_HUMAN	AQETSSEEISK	589.76	7.9	0.317300419	1
A1AT_HUMAN	TDTSHHDQDHPTFNK	594.25	16.2	0.015994347	1
CAN1_HUMAN	IRLDETDDPDDYGDR	599.13	17.7	0.317300419	1
FINC_HUMAN	GEWTCIAYSQLR	626.69	23.6	0.317300419	1
CAN1_HUMAN	RGSTAGGCR	658.16	10.4	0.317300419	1
FINC_HUMAN	WCGTTQNYDADQK	660.95	18	0.317300419	1
THRB_HUMAN	ENLDRDIALMK	667.7	19.1	0.317300419	1
MPP3_HUMAN	SLSYLMKIHEK	675.07	16	0.317300419	1
THRB_HUMAN	SPQELLCGASLISDR	677.97	24	0.317300419	1
CANS_HUMAN	SMVAVMDSDTTGK	679.41	7.1	0.317300419	1
THRB_HUMAN	SPQELLCGASLISDR	680.63	23.9	0.317300419	1
THRB_HUMAN	KSPQELLCGASLISDR	720.83	20.6	0.317300419	1
FIBB_HUMAN	NYCGLPGEYWLGNDK	727.37	24.8	0.317300419	1
CAN1_HUMAN	CLQSGTLFR	734.86	15.9	0.054464583	1
CAN1_HUMAN	CLQSGTLFR	738.38	15.7	0.317300419	1
	LGEHNIDVLEGNEQFINAAK	738.43	24.1	0.317300419	1
THRB_HUMAN	TFGSGEADCGLRPLFEK	757.66	21.1	0.317300419	1
KAC_HUMAN	VYACEVTHQGLSSPVTK	757.81	19	0.317300419	1
FINC_HUMAN	AAHEEICTTNEGVMYR	761.61	18.6	0.317300419	1
CAN1_HUMAN	LDETDDPDDYGDR	763.67	11.6	0.317300419	1
CANS_HUMAN	TDGFGIDTCR	764.83	13.7	0.317300419	1
CANS_HUMAN	TDGFGIDTCR	768.33	19.4	0.317300419	1
CAN1_HUMAN	TKGFSLESCR	785.65	13.3	0.317300419	1
CAN1_HUMAN	TKGFSLESCR	789.99	13.2	0.317300419	1
THRB_HUMAN	RITDNMFCAGYKPDEGK	796.86	20.4	0.317300419	1
FINC_HUMAN	RPGGEPSPEGTTGQSYNQYSQR	799.47	13.9	0.317300419	1
FINC_HUMAN	LLCQCLGFGSGHFR	808.81	22.9	0.317300419	1
THRB_HUMAN	SEGSSVNLSPPLEQCVPDR	820.31	17.9	0.041282837	1
THRB_HUMAN	VEEETGDGLDEDSR	833.64	11.8	0.317300419	1
FETA_HUMAN	LVLDVAHVHEHCCR	839.57	19.4	0.317300419	1
FINC_HUMAN	PHEATCYDDGK	839.68	16.1	0.317300419	1
FINC_HUMAN	WCHDNGVNYK	843.97	16.65	0.054464583	1

KAC_HUMAN	HKVYACEVTHQGLSSPVTK	846.15	19.7	0.317300419	1
THRB_HUMAN	NPDSSTTGWCYTDDPTVR	850.74	16.6	0.317300419	1
FINC_HUMAN	GEWTCKPIAEK	856.81	18.4	0.317300419	1
FETA_HUMAN	GDVLDCLQDGEK	872.48	19	0.317300419	1
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	881.52	20.1	0.317300419	1
CAN1_HUMAN	LEICNLTPDALK	887.33	21.2	0.179912116	1
CAN1_HUMAN	IRLDETDDPDDYGDR	899.33	18.1	0.317300419	1
THRB_HUMAN	LAACLEGNAEGLGTNYR	920.16	21.4	0.317300419	1
CAN1_HUMAN	ESGCSFVLALMQK	932.98	25.2	0.317300419	1
FINC_HUMAN	GEWTCTIAYSQLR	935.76	20.9	0.317300419	1
FETA_HUMAN	LLACGEGAADIIIGHLCIR	942.85	29.6	0.317300419	1
FINC_HUMAN	GFNCESKPEAEETCFDK	945.98	21.5	0.317300419	1
FETA_HUMAN	LLACGEGAADIIIGHLCIR	947.18	28	0.317300419	1
THRB_HUMAN	GDACEGDSGGPFVMK	957.11	13.8	0.317300419	1
THRB_HUMAN	GDACEGDSGGPFVMK	960.88	13.8	0.317300419	1
THRB_HUMAN	GDACEGDSGGPFVMK	964.99	18	0.317300419	1
FETA_HUMAN	DLCQAQGVALQTMK	975.43	18.5	0.317300419	1
FETA_HUMAN	DLCQAQGVALQTMK	978.9	18.5	0.317300419	1
FETA_HUMAN	ESSLLNQHACAVMK	987.25	17.5	0.317300419	1
				0.281815596	
CADC_HUMAN	RQKKKHTLMTSKEDIR	1000.79	19	0.04550454	2
THRB_HUMAN	SDYIHPVCLPDRETAASLLQAGYK	1033.72	24	0.04550454	2
THRB_HUMAN	RGDACEGDSGGPFVMK	1035.23	13.4	0.04550454	2
THRB_HUMAN	RGDACEGDSGGPFVMK	1038.91	13.3	0.04550454	2
VGLL_HSV7J	YNEVLPRSEFSNLLIR	1049.51	27.3	0.04550454	2
THRB_HUMAN	TTHGLPCLAWASQAK	1050.35	24.8	0.04550454	2
AJ276395	YSFCTDHTVLVQTR	1061.51	21.16	0.013415967	2
THRB_HUMAN	KSPQELLCGASLISDR	1080.93	20.36	0.131900915	2
FETA_HUMAN	CFQTENPLECQDKGEEELQK	1085.41	22.3	0.04550454	2
FETA_HUMAN	IMSYICSQQDTLSNK	1091.2	18.6	0.04550454	2
FIBB_HUMAN	NYCGLPGEYWLGNK	1091.29	24.8	0.04550454	2
K2C1_HUMAN	GSYSGSGSSYSGSGSGSGGGGGHGSYSGSGSSSGGYR	1105.15	14.5	0.04550454	2
FINC_HUMAN	GNLLQCICTGNGR	1121.88	24	0.04550454	2
THRB_HUMAN	WYQMGIVSWGEGCDR	1123.42	21.8	0.04550454	2
CAN1_HUMAN	LDETDDPDDYGDRSGCSFVLALMQK	1124.74	25.9	0.04550454	2
THRB_HUMAN	WYQMGIVSWGEGCDR	1128.55	21.7	0.04550454	2
FINC_HUMAN	FGFCPMAAHEEICTTNEGVMYR	1137.73	26.4	0.04550454	2
THRB_HUMAN	PVAFSDYIHPVCLPDR	1141.17	23.8	0.04550454	2
FINC_HUMAN	AAHEEICTTNEGVMYR	1142.03	18.6	0.04550454	2
FINC_HUMAN	AAHEEICTTNEGVMYR	1145.84	15.5	0.04550454	2
EGF_HUMAN	YACNCVVGYIGER	1175.13	15.5	0.04550454	2

THRB_HUMAN	HQDFNSAVQLVENFCR	1180.13	24.66	0.032787118	2
THRB_HUMAN	LAVTTHGLPCLAWASQAK	1191.77	22.58	0.474998187	2
THRB_HUMAN	RITDNMFCAGYKPDEGK	1195.13	21	0.04550454	2
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1199.55	26.8	0.04550454	2
CANS_HUMAN	PGAFAEAGFHLNEHLYNMIIR	1201.43	30.03	0.179912116	2
FINC_HUMAN	GFNCESKPEAEETCFDKYTGNTRYR	1226.27	20.1	0.04550454	2
IBP1_HUMAN	LALCPPVSASCSEVTR	1259.58	22	0.04550454	2
IBP1_HUMAN	LALCPPVSASCSEVTR	1263.58	22.1	0.04550454	2
FINC_HUMAN	QDGHLWCSTTSNYESQDQK	1291.86	17.1	0.04550454	2
THRB_HUMAN	LKKPVAFSDYIHPVCLPDRETAASLLQAGYK	1295.33	16	0.04550454	2
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1321.84	21.33	0.072720041	2
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	1325.91	21.1	0.026168277	2
THRB_HUMAN	LAACLEGNCAEGLGTNYR	1375.23	21.5	0.04550454	2
FINC_HUMAN	GFNCESKPEAEETCFDK	1410.06	21.1	0.04550454	2
FINC_HUMAN	GFNCESKPEAEETCFDK	1418.46	19.1	0.04550454	2
FETA_HUMAN	GQCIIHAENDEKPEGLSPNLNR	1443.02	20.5	0.04550454	2
THRB_HUMAN	DKLAACLEGNCAEGLGTNYR	1496.99	21.8	0.04550454	2
THRB_HUMAN	QECSIPVCGQDQVTVMTPR	1524.17	21.8	0.04550454	2
THRB_HUMAN	RQECSIPVCGQDQVTVMTPR	1602.61	20.8	0.04550454	2
FETA_HUMAN	RPCFSSLVVDETYVPPAFSDDKFIFHK	1799.37	26.8	0.04550454	2
CAN1_HUMAN	DLGPNSSK	409.45	6.6	0.04550454	2
PDX2_HUMAN	TDEGIAYR	462.75	11.4	0.04550454	2
CAN1_HUMAN	MAIESAGFK	485.4	13.2	0.04550454	2
CAN1_HUMAN	GHAYSVTGAK	496.03	13.6	0.04550454	2
YA13_HUMAN	WYTERLR	512.2	12.6	0.04550454	2
	LSSPATLNSR	523.93	12.1	0.04550454	2
U43756	FQGRVTVTR	532.48	14.4	0.04550454	2
K2C1_HUMAN	GSGGGSSGGSIGGR	547.17	6.4	0.04550454	2
FINC_HUMAN	STTPDITGYR	555.95	14.1	0.04550454	2
BC006011	VLVEQQQDR	557.76	10.1	0.04550454	2
AC004877	AHLTRHLRTHGTGER	562.48	5	0.04550454	2
IBP1_HUMAN	AQETSGEEISK	589.76	7.9	0.04550454	2
CAN1_HUMAN	IRLDETDDPDDYGDR	599.13	17.7	0.04550454	2
FINC_HUMAN	GEWTCIAYSQLR	626.69	23.6	0.04550454	2
CAN1_HUMAN	RGSTAGGCR	658.16	10.4	0.04550454	2
FINC_HUMAN	WCGTTQNYDADQK	660.95	18	0.04550454	2
THRB_HUMAN	ENLDRDIALMK	667.7	19.1	0.04550454	2
MPP3_HUMAN	SLSYLMKIHEK	675.07	16	0.04550454	2
THRB_HUMAN	SPQELLCGASLISDR	677.97	24	0.04550454	2
CANS_HUMAN	SMVAVMDSDTTGK	679.41	7.1	0.04550454	2
THRB_HUMAN	SPQELLCGASLISDR	680.63	23.9	0.04550454	2
THRB_HUMAN	KSPQELLCGASLISDR	720.83	20.6	0.04550454	2

FIBB_HUMAN	NYCGLPGEYWLGN DK	727.37	24.8	0.04550454	2
CAN1_HUMAN	CLQSGTLFR	738.38	15.7	0.04550454	2
	LGEHNIDVLEGN EQFINAAK	738.43	24.1	0.04550454	2
THRB_HUMAN	TFGSGEADCGLRPLFEK	757.66	21.1	0.04550454	2
FINC_HUMAN	AAHEEICTTNEGVMYR	761.61	18.6	0.04550454	2
CAN1_HUMAN	LDETDDPDDYGDR	763.67	11.6	0.04550454	2
CANS_HUMAN	TDGFGIDTCR	764.83	13.7	0.04550454	2
CANS_HUMAN	TDGFGIDTCR	768.33	19.4	0.04550454	2
CAN1_HUMAN	TKGFSLESCR	785.65	13.3	0.04550454	2
CAN1_HUMAN	TKGFSLESCR	789.99	13.2	0.04550454	2
THRB_HUMAN	RITDNMFCAGYKPDEGK	796.86	20.4	0.04550454	2
FINC_HUMAN	RPGGEPSPEGTTGQSYNQYSQR	799.47	13.9	0.04550454	2
FINC_HUMAN	LLCQCLGFGSGHFR	808.81	22.9	0.04550454	2
THRB_HUMAN	VEEETGDGLDEDSR	833.64	11.8	0.04550454	2
FETA_HUMAN	LVLDVAHVHEHCCR	839.57	19.4	0.04550454	2
FINC_HUMAN	PHEATCYDDGK	839.68	16.1	0.04550454	2
KAC_HUMAN	HKVYACEVTHQGLSSPVTK	846.15	19.7	0.04550454	2
FINC_HUMAN	GEWTCKPIAEK	856.81	18.4	0.04550454	2
FETA_HUMAN	GDVLDCLQDGEK	872.48	19	0.04550454	2
THRB_HUMAN	LKKPVAFSDYIHPVCLPDR	881.52	20.1	0.04550454	2
CAN1_HUMAN	IRLDETDDPDDYGDR	899.33	18.1	0.04550454	2
THRB_HUMAN	LAACLEGNCAEGLGTNYR	920.16	21.4	0.04550454	2
CAN1_HUMAN	ESGCSFVLALMQK	932.98	25.2	0.04550454	2
FINC_HUMAN	GEWTCIAYSQLR	935.76	20.9	0.04550454	2
FINC_HUMAN	GEWTCIAYSQLR	939.64	22.86	0.664368423	2
FETA_HUMAN	LLACGEGAADIIIGHLCIR	942.85	29.6	0.04550454	2
FINC_HUMAN	GFNCESKPEAEETCFDK	945.98	21.5	0.04550454	2
FETA_HUMAN	LLACGEGAADIIIGHLCIR	947.18	28	0.04550454	2
THRB_HUMAN	GDACEGDSGGPFVMK	957.11	13.8	0.04550454	2
THRB_HUMAN	GDACEGDSGGPFVMK	960.88	13.8	0.04550454	2
THRB_HUMAN	GDACEGDSGGPFVMK	964.99	18	0.04550454	2
FETA_HUMAN	DLCQAQGVALQTMK	975.43	18.5	0.04550454	2
FETA_HUMAN	DLCQAQGVALQTMK	978.9	18.5	0.04550454	2
FINC_HUMAN	WCGTTQNYDADQK	987.02	17.65	0.131900915	2
FETA_HUMAN	ESSLLNQHACAVMK	987.25	17.5	0.04550454	2
				0.058959959	

Table of correctly identified yeast peptide sequences

CTT1	FNCYVQMTPEQATK	1002.95	12.47	0.972491784	0.01
CDC60	FMSSMAYPYMNGVMHAGHCFTLSK	1005.4	11.6	0.992021169	0.01
GFA1	CGIFGYCNYLVER	1005.42	19.65	0.96201929	0.01

EFT2	CFGPDGNGPNLVIDQTK	1006.54	18.05	0.983717531	0.01
CTT1	FNCYVQTMTPAQATK	1007.4	11.18	0.980054669	0.01
KAP95	AESIDPQQHLPGVVQACLIQLDHPK	1007.95	22	0.992021169	0.01
KAP95	AESIDPQQHLPGVVQACLIQLDHPK	1010.9	21.15	0.968092654	0.01
NEW1	FNVALDCISDKENTVK	1012.46	16.17	0.953091973	0.01
NEW1	FNVALDCISDKENTVK	1016.85	15	0.992021169	0.01
CWC2	CEYLHHIPDEEDIGK	1017.78	11.85	0.963744469	0.01
YDL183C	AEQVDTQPLHVYPPGISSPDECLR	1018.03	17.2	0.992021169	0.01
PPH21	CGNQAAIMEVDENHNR	1019.38	14.6	0.992021169	0.01
NOT5	CGNDFVYNEDFEKL	1025.64	18.1	0.980541042	0.01
DED81	CSDDPRVTESVDVLMNVGEITGGSMR	1032	19.8	0.992021169	0.01
FBA1	AAAFGNCHGLYAGDIALRPEILAEHQK	1032.36	23.89	0.973408379	0.01
RPO21	CQTCQEGMNECPGHFGHIDLAK	1034.14	12.45	0.911526929	0.01
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1035.11	16.2	0.969319243	0.01
FBA1	AAAFGNCHGLYAGDIALRPEILAEHQK	1035.31	23.15	0.974265871	0.01
SUI2	ADVEVSCFSYEGIDAIK	1037.79	19.11	0.987533377	0.01
RPO21	CQTCQEGMNECPGHFGHIDLAK	1039.86	10.5	0.973408379	0.01
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1040.57	15.01	0.977839062	0.01
SUI2	ADVEVSCFSYEGIDAIK	1042.05	21.1	0.977206062	0.01
DED81	CSDDPRVTESVDVLMNVGEITGGSMR	1042.7	15.8	0.992021169	0.01
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1045.98	16.88	0.979005151	0.01
RPO21	CQTCQEGMNECPGHFGHIDLAK	1049.06	10.5	0.992021169	0.01
GUA1	CGIVHETKPIYGIQFHPEVTHSTQ GK	1049.32	21.44	0.966763935	0.01
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1051.81	17.63	0.977206062	0.01
YNR046W	ACDTSNDNFPLQYDGSK	1051.88	17.49	0.972491784	0.01
YNR046W	ACDTSNDNFPLQYDGSK	1056.46	18.52	0.980054669	0.01
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1061.15	10	0.992021169	0.01
ILS1	CGLEATDDVLVEYELVK	1063.2	22.1	0.98733551	0.01
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1063.59	10	0.992021169	0.01
NIT2	AVDTQCYVLMPGQVGMHDLSDPEWEK	1065.82	30.7	0.992021169	0.01
RPB4	ACDTADEAKTLIPSLNNK	1067	31.9	0.992021169	0.01
ILS1	CGLEATDDVLVEYELVK	1067.41	27.21	0.988601868	0.01
CDC19	AEVSDVGNAILDGADCVML	1069.38	26.1	0.992021169	0.01
YML096W	CGKPVIELLNVSFENPR	1072.05	19.4	0.992021169	0.01
CDC19	ACDDKIMYVDYKNITK	1074.28	14.03	0.970455038	0.01
EFT2	AEQLYEGPADDANCIAIK	1075.33	17.64	0.982655793	0.01
YML096W	CGKPVIELLNVSFENPR	1076.06	22	0.992021169	0.01
EFT2	AEQLYEGPADDANCIAIK	1079.74	17.61	0.984656785	0.01
CDC19	ACDDKIMYVDYKNITK	1082.65	13	0.980541042	0.01
UTP7	AELFLNETCHSATY LQNEQYFAVAQK	1083.44	20.4	0.984946245	0.01
APN1	CEQLGIGLYNLHPGSTLK	1086.15	17.1	0.992021169	0.01
UTP7	AELFLNETCHSATY LQNEQYFAVAQK	1086.25	17	0.992021169	0.01

CDC19	ACDDKIMYVDYKNITK	1086.96	15.45	0.938683832	0.01
POM152	ACAANVDQISFLEPINLK	1087.51	22.77	0.980054669	0.01
BIO2	ACTGGILGLGESEDDHIGFIYTLNMSPH	1091.17	16.3	0.992021169	0.01
POM152	ACAANVDQISFLEPINLK	1092.25	26.08	0.989900316	0.01
HIS7	ACEALGAGEILLNCIDK	1094.67	22.9	0.992021169	0.01
RPL34A	CGDCGSALQGISTLRPR	1094.98	17.28	0.955695216	0.01
YNL087W	AENFICEVNIPTIELVR	1095.33	37.87	0.983378362	0.01
YNL087W	AENFICEVNIPTIELVR	1099.24	41.63	0.984043137	0.01
YJL055W	FNLNWSDEGHAHEDCAK	1101.43	12.05	0.989501667	0.01
HIS7	ACEALGAGEILLNCIDK	1105.06	23.9	0.900522079	0.01
RPC40	CFPPGVIGIDEGSDEAYVK	1112.63	19.05	0.983024762	0.01
CDC43	FNGELCIPQEIFNDFSK	1115.61	26.4	0.992746497	0.01
RPC40	CFPPGVIGIDEGSDEAYVK	1117.17	19.72	0.983717531	0.01
SPT15	AAPSEKDTSATSGIVPTLQNIVATVTLGCR	1120.09	29.8	0.950163925	0.01
RRP12	AAIGCLESLLIAQDAQAWNNTYDLNVTPK	1121.5	28.03	0.841478237	0.01
SPT15	AAPSEKDTSATSGIVPTLQNIVATVTLGCR	1123.29	29	0.987725156	0.01
K1CJ_HUMAN	AETECQNTHEYQQLLDIK	1128.32	23.6	0.992021169	0.01
SPT4	ACMLCGIVQTTNEFNR	1128.74	18.55	0.977206062	0.01
YBR025C	CFDDAEIIHVEGDVDPVR	1129.18	19.34	0.984656785	0.01
YFL034W	ACLPGEDKEVESSNDFLGESHYKPPSTPK	1131.34	13.35	0.985752608	0.01
K1CJ_HUMAN	AETECQNTHEYQQLLDIK	1132.41	26.25	0.983717531	0.01
YBR025C	CFDDAEIIHVEGDVDPVR	1133.36	20.14	0.975825022	0.01
CCA1	FNEENCQDMDKINHVNINILNSHLK	1134.23	14.8	0.992021169	0.01
SPT4	ACMLCGIVQTTNEFNR	1136.15	13	0.992021169	0.01
ADE6	CGLSGFSVSDLLIPGNEQPWELNIGKPYH	1137.02	27.9	0.992021169	0.01
LYS4	CGLFNNDQVLNHAIEFTGDSLNALPIDHR	1152.55	27.2	0.992021169	0.01
GCV2	AVDVLKNPDVSGCLVQYPATDGSILPPDSMK	1156.81	20	0.992021169	0.01
RHO5	CGFMGYTECSAATQAGVR	1162.5	14.9	0.992021169	0.01
YCL019W	AVCDNTPSIDTDPPEYRSSDHATPNIMPK	1175.51	27.8	0.992021169	0.01
GPA2	FNVNLEPECELTQQDLR	1181.95	30	0.992021169	0.01
GPA2	FNVNLEPECELTQQDLR	1187.13	17.9	0.992021169	0.01
TIF4632	ACDEPHWSSMYAQLCGK	1191.06	15.2	0.979543361	0.01
TEF2	ATVIVLNHPGQISAGYSPVLDCHTAHIACR	1200.5	14.45	0.886401326	0.01
MYO3	FNSQFEPKAGNITNYLLEK	1208.52	19.95	0.98977084	0.01
FRS1	ATWVEVLPLTLCSDENFK	1215.52	23.2	0.992021169	0.01
YPR148C	AAVDCECEFQNLHNEK	1217.2	11.1	0.992021169	0.01
MYO5	FNNQFEPKAGNITNYLLEK	1222.19	20.85	0.985224986	0.01
MYO5	FNNQFEPKAGNITNYLLEK	1226.67	26.24	0.989638001	0.01
GCN20	AALCLNNPHILVLDEPSNHLDTTGLDALVEALK	1246.39	70	0.992021169	0.01
SUI2	ADVEVSCFSYEGIDAIDALK	1251.7	29.6	0.991858342	0.01
ADE4	CGILGIVLANQTTTPVAPELDCGICIFLQHR	1255.65	23	0.992021169	0.01
SUI2	ADVEVSCFSYEGIDAIDALK	1255.97	28.34	0.982655793	0.01

TCI1	ACELDPEGQVGGPDKFFTMGQIMGGQDGVSIITR	1262.34	24	0.992021169	0.01
TCI1	ACELDPEGQVGGPDKFFTMGQIMGGQDGVSIITR	1264.45	70	0.992021169	0.01
ADE4	CGILGIVLANQTTTPVAPELCDGCIFLQHR	1264.77	22.9	0.981004262	0.01
RAT1	AESECDLDAEIKDEIVADVNDRENSETTEVSR	1270.68	18.85	0.96201929	0.01
RAT1	AESECDLDAEIKDEIVADVNDRENSETTEVSR	1273.83	25.6	0.969319243	0.01
YHR029C	AFAPVINVYEDPVC GSGSVALAR	1282.96	18.1	0.992021169	0.01
YHR029C	AFAPVINVYEDPVC GSGSVALAR	1286.67	19.7	0.992021169	0.01
SLG1	ADSYNWQSSSHCNSECSAK	1288.77	21.1	0.992021169	0.01
DBP2	AEGFDKPTGIQCQGWP MALSGR	1289.65	16.8	0.987911124	0.01
DBP2	AEGFDKPTGIQCQGWP MALSGR	1293.65	17.5	0.992021169	0.01
DBP2	AEGFDKPTGIQCQGWP MALSGR	1296.95	13.85	0.950163925	0.01
NAM9	CQPDELISLATEMMNPNETTK	1297.44	26.9	0.992021169	0.01
RIM11	FNALQCLCSPYFDELKLDDGKINQITTDLK	1301.46	22.4	0.992021169	0.01
YLR004C	AANADSCSVSTSSINVDDADVALR	1305.21	26.4	0.992021169	0.01
TRM1	CFALYGGANMVSHESTHESALR	1317.18	13.8	0.992021169	0.01
RPL21A	CRQEFLE R	1317.2	19.8	0.992811842	0.01
ACS2	ACIIDPVTGVELEGNDVEGV LAVK	1334.58	23.15	0.946846285	0.01
GAR1	CGDGVQATSFK	1339.59	20.45	0.867630377	0.01
ACS2	ACIIDPVTGVELEGNDVEGV LAVK	1339.72	24.8	0.973408379	0.01
URA2	AAYALGGLGSGFANNEKELVDLCNVA FSSSPQVLVEK	1343.07	24.11	0.974265871	0.01
YEF3	AVDNIPVGPNFDDEEDEGEDLCNCEFS LAYGAK	1344.63	23.46	0.975825022	0.01
URA2	AAYALGGLGSGFANNEKELVDLCNVA FSSSPQVLVEK	1346	26.23	0.975069796	0.01
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1347.26	26.41	0.983717531	0.01
YEF3	AVDNIPVGPNFDDEEDEGEDLCNCEFS LAYGAK	1350.97	24.4	0.968092654	0.01
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1352.07	26.57	0.985224986	0.01
EFT2	AEQLYEGPADDANCIAIKNCD	1355.19	21.15	0.968092654	0.01
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1355.39	24.14	0.979543361	0.01
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1359.93	25.16	0.982655793	0.01
EFT2	AEQLYEGPADDANCIAIKNCD	1363.82	21.3	0.992021169	0.01
CCT6	AAAAQDEITGDGTTTVVCLVGELLR	1366.27	29.37	0.965319781	0.01
YBR096W	CGFHETVPLENLSQEYCSEI	1377.33	21.54	0.973408379	0.01
ADH1	AAHIPQGTDLAQVAPILCAGITVYK	1390.22	22.1	0.992021169	0.01
MVD1	ACVLVVSDIKK	1410.71	12.95	0.802584429	0.01
STE20	CSDGDPSTKYANLVKIGQGASGGVYT	1413.29	11.6	0.992021169	0.01
TUB1	AFHESNSVSEITNACFEPGNQMVK	1434.19	15.6	0.983378362	0.01
TUB1	AFHESNSVSEITNACFEPGNQMVK	1438.81	18.88	0.973408379	0.01
TUB1	AFHESNSVSEITNACFEPGNQMVK	1442.2	14.73	0.980054669	0.01
ARD2	CSECHQHNVFVYLPVDDLT K	1446.79	20.63	0.992021169	0.01
TUB1	AFHESNSVSEITNACFEPGNQMVK	1446.83	16.93	0.911526929	0.01
ARO1	AALYALHSLGCK	1482.7	14	0.992021169	0.01
MAL13	CQNALITLPISK	1529.28	22.3	0.992021169	0.01
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1552.22	16.6	0.992021169	0.01

YMR259C	AFCIRCQLEFPAILEELLSKSVK	1556.63	36.9	0.992021169	0.01
LPD1	AAQLGFNTACVEK	1578.7	16.8	0.992021169	0.01
LPD1	AAQLGFNTACVEK	1587.89	16.8	0.992021169	0.01
SPT15	AAPSEKDTSATSGIVPTLQNIVATVTLGCR	1684.49	29.2	0.992021169	0.01
CDC19	ACDDKIMYVDYK	1691.56	12.87	0.992177612	0.01
CDC19	ACDDKIMYVDYK	1700.06	14.68	0.990149678	0.01
CDC19	ACDDKIMYVDYK	1717.24	15.33	0.979005151	0.01
DED1	ACVVYGGSPIGNQLR	1769.91	15.35	0.983378362	0.01
GRX3	CGFSR	403.6	17.8	0.992021169	0.01
GCD10	CRPYQSIR	420.41	17.9	0.992021169	0.01
RPL21A	CRQEFLER	437.12	20	0.927563755	0.01
RPL21A	CRQEFLER	440.23	19.48	0.966763935	0.01
FAS1	CFGPIK	446.52	22.1	0.992021169	0.01
FAS1	CFGPIK	451.2	21.7	0.927563755	0.01
YJR124C	CFGPVR	458.22	21.05	0.943055829	0.01
MVD1	ACVLVVSDIKK	468.52	13.96	0.971509758	0.01
NGR1	CFGFVR	483.08	24.6	0.992021169	0.01
TEF2	CGGIDKR	493.23	16.2	0.970455038	0.01
ASN2	ADWGCAEDPSGR	498.75	17.3	0.992021169	0.01
SML1	CQQQQAPSTLR	499.73	16.3	0.992021169	0.01
YNL247W	CQPWNK	502.08	19	0.992021169	0.01
PDB1	CQMVFR	506.37	22.07	0.738878819	0.01
YNL247W	CQPWNK	506.66	19.1	0.992021169	0.01
PDB1	CQMVFR	511.19	20.72	0.984043137	0.01
BUD3	ACSITIPYFYK	515.11	18.55	0.991232085	0.01
FAS1	CFGPIKVELPTK	521.23	17.55	0.938683832	0.01
CCT3	ACTIMLR	522.53	21.06	0.96201929	0.01
ADE3	ACAQQFR	526.21	17.8	0.992021169	0.01
ADE3	ACAQQFR	530.77	17.7	0.986002536	0.01
MBR1	CQQTNLNPLCK	535.67	21.3	0.992021169	0.01
ASN2	CGIFAAFK	542.59	16.65	0.96201929	0.01
ASN2	CGIFAAFK	547.13	28.1	0.933585514	0.01
ASN1	CGIFAAFR	556.84	20.71	0.971509758	0.01
ASN1	CGIFAAFR	561.28	19.47	0.972491784	0.01
SPR3	CRNRDLPLLDNK	562.96	12.1	0.992021169	0.01
CDC19	ACDDKIMYVDYK	567.78	15.16	0.975069796	0.01
CDC19	ACDDKIMYVDYK	570.35	13.19	0.975825022	0.01
CDC19	ACDDKIMYVDYK	573.37	13.91	0.975825022	0.01
ARG3	FMHCLPR	574.74	19.1	0.989217945	0.01
LPD1	AAQLGFNTACVEKR	579.59	12.52	0.965319781	0.01
LPD1	AAQLGFNTACVEKR	582.63	12.43	0.978437859	0.01
GPX2	CGFTPQYK	586.2	20.61	0.900522079	0.01

DED1	ACVVYGGSPIGNQLR	588.02	13.1	0.992021169	0.01
GPX2	CGFTPQYK	590.74	21.62	0.966763935	0.01
SLA2	ACIVYTWDHQSSK	592.84	14	0.992021169	0.01
MES1	CGALLDPFELINPR	596.25	25.9	0.953091973	0.01
CDD1	ACELSYSPYSHFR	597.53	17.4	0.992021169	0.01
CDD1	ACELSYSPYSHFR	599.88	17.4	0.973408379	0.01
RRP5	ACQYMDSYTIHTK	600.3	17.63	0.946846285	0.01
RRP5	ACQYMDSYTIHTK	602.79	17.13	0.976535843	0.01
RRP5	ACQYMDSYTIHTK	605.69	16.13	0.983378362	0.01
YDR307W	CGLLGHDLR	606.22	15.6	0.992021169	0.01
EMP24	CFFEDLSK	609.05	18.96	0.975825022	0.01
PUS1	CGCPVER	610.1	18.35	0.981004262	0.01
RGA1	CGENIADLR	610.36	15.3	0.992021169	0.01
YDR307W	CGLLGHDLR	611.08	16.2	0.992021169	0.01
GIS2	CFNCNQTGHISR	612.64	14.99	0.955695216	0.01
EMP24	CFFEDLSK	613.28	19.05	0.971509758	0.01
POL5	ACEEDSANR	616.27	16.5	0.992021169	0.01
PUS1	CGCPVER	618.94	18.4	0.986702343	0.01
ODC1	AAVDHYTGVMDCCLK	620.89	14.6	0.992021169	0.01
GCD10	CRPYQSIR	625.82	18.27	0.911526929	0.01
YLR126C	CQNQGFYR	626.58	19.4	0.992021169	0.01
NCL1	FNLQNCMR	627.41	17.28	0.974265871	0.01
GCD10	CRPYQSIR	630.29	18.3	0.938683832	0.01
SLA2	ACSVEETAPK	631.61	17.9	0.992021169	0.01
NCL1	FNLQNCMR	632.11	12.6	0.989900316	0.01
DLD1	AVAQLNHCNSFQFAK	639.41	14.27	0.943055829	0.01
SEC14	AAGHLVETSCTIMDLK	639.92	14.38	0.96201929	0.01
SEC14	AAGHLVETSCTIMDLK	642.77	14.93	0.975825022	0.01
SEC14	AAGHLVETSCTIMDLK	645.21	15.25	0.96201929	0.01
RPL34A	CGDCGSALQGISTLR	646.39	14.63	0.976535843	0.01
YMR031C	CEQDITEAR	646.99	19	0.992021169	0.01
SEC14	AAGHLVETSCTIMDLK	648.26	16.51	0.969319243	0.01
SAM1	ACLAEDPHSK	649.4	17.7	0.992021169	0.01
RPL34A	CGDCGSALQGISTLR	652.15	14.53	0.965319781	0.01
RPL21A	CRQEFLER	654.77	19.53	0.975825022	0.01
RPL21A	CRQEFLER	659.37	19.52	0.978437859	0.01
PDR5	FPCAIEYVPR	659.92	16.58	0.983378362	0.01
PIM1	CQTQNPLILIDEIDK	660.57	18.9	0.992021169	0.01
IPI2	CGLSFFEGILSSIIEF	664.3	21.5	0.992021169	0.01
GAR1	CGDGVQATSFK	670.96	19.95	0.975069796	0.01
GAR1	CGDGVQATSFK	675.33	19.8	0.977839062	0.01
NEW1	FNVALDCISDKENTVK	675.59	14.3	0.946846285	0.01

YDL193W	CFGLFRYGQYQYNK	675.99	19	0.992021169	0.01
CWC2	CEYLHHIPDEEDIGK	676.51	15.97	0.965319781	0.01
HIF1	CQQTLDLSPK	685.76	14.65	0.991327384	0.01
DUS1	CQPYFRPVNGITGDKR	696.84	12.5	0.992021169	0.01
YJR149W	ACIAGAIASLPLSHLDFR	698.4	23.7	0.992021169	0.01
MVD1	ACVLVVSDIKK	701.89	17.16	0.978437859	0.01
SEN1	FNDIVCQWR	704.91	13	0.992021169	0.01
MVD1	ACVLVVSDIKK	706.46	16.36	0.983717531	0.01
YOR175C	CGLGYNGYDSK	707.57	13.6	0.992021169	0.01
FBA1	CQYAYLTGIR	708.44	18.74	0.973408379	0.01
SCC2	ACSSCLSHLHPYINK	710.21	10.5	0.992021169	0.01
MSB3	FNLNRLDQDEIDRCR	712.8	18.57	0.984656785	0.01
FBA1	CQYAYLTGIR	712.95	18.9	0.984946245	0.01
CDC19	ACDDKIMYVDYKNITK	716.92	13.75	0.953091973	0.01
EFT2	AEQLYEGPADDANCIAIK	717.37	16.22	0.972491784	0.01
CDC19	ACDDKIMYVDYKNITK	719.77	13.97	0.982270429	0.01
EFT2	AEQLYEGPADDANCIAIK	720.34	17.23	0.974265871	0.01
CDC19	ACDDKIMYVDYKNITK	722.47	13.06	0.965319781	0.01
GCD11	CQRP GCPGR	723.49	16.9	0.992021169	0.01
APN1	CEQLGIGLYNLHPGSTLK	724.74	20.63	0.968092654	0.01
MIS1	ATVTVCHSHTR	724.85	16.4	0.992021169	0.01
CDC19	ACDDKIMYVDYKNITK	725.42	13.09	0.946846285	0.01
ARO1	CSAEAEFQALR	726.64	13.32	0.911526929	0.01
APN1	CEQLGIGLYNLHPGSTLK	727.65	19.86	0.975825022	0.01
SHM2	CGAYLMVDMAH	728.13	11.5	0.992021169	0.01
HIS7	ACEALGAGEILLNCIDK	730.24	22.97	0.973408379	0.01
RPL34A	CGDCGSALQGISTLRPR	730.79	17.02	0.973408379	0.01
ARO1	CSAEAEFQALR	731.46	14.47	0.983024762	0.01
RPT5	ACAAQT NATFLK	734.02	16.72	0.984355976	0.01
ADE12	CQNLLGNGVVIHVPSFFK	734.51	23.4	0.992021169	0.01
YJL055W	FNLNWSDEGHAHEDCAK	734.63	21.34	0.977839062	0.01
ADE12	CQNLLGNGVVIHVPSFFK	737.24	24.9	0.841478237	0.01
ARO1	AALYALHSLGCK	738.05	16.96	0.980054669	0.01
RPT5	ACAAQT NATFLK	738.48	16.19	0.977839062	0.01
ARO4	AVDACQAAASHHFMGVTK	742.45	26	0.992021169	0.01
SML1	CQQQQAPSTLR	744.39	18.65	0.963744469	0.01
ASN2	ADWGCAEDPSGR	746.29	18.88	0.970455038	0.01
SEN1	ACLMNSATALLR	746.35	18.1	0.992021169	0.01
SML1	CQQQQAPSTLR	748.71	18.63	0.955695216	0.01
ASN2	ADWGCAEDPSGR	750.65	20.29	0.968092654	0.01
TFB3	FLVNPECYHR	753.51	16.8	0.992021169	0.01
YBR025C	CFDDAEIIHVEGDVDPVR	756.36	20.56	0.977206062	0.01

YDR193W	FNDSLMSFCVK	764.41	25.1	0.992021169	0.01
CTL1	FNEYMCSFLNASDLIRK	766.39	21	0.992021169	0.01
ACO1	ACQDATAQMAILQFMSAGLP	774.33	24.2	0.992021169	0.01
YLR427W	CGNFPPANLGSIK	777.12	30.7	0.992021169	0.01
FAS1	CFGPIKVELPTK	780.53	16.13	0.960121799	0.01
YCP4	ACLSYLAHHGIIIFLPLGYK	782.13	33.9	0.992021169	0.01
FAS1	CFGPIKVELPTK	785.17	17	0.978437859	0.01
YOR289W	CSCNILGNFK	786.02	14.8	0.992021169	0.01
LPD1	AAQLGFNTACVEK	790.51	16.66	0.977839062	0.01
LPD1	AAQLGFNTACVEK	794.95	17.05	0.975825022	0.01
PGU1	FMNNYCYNGHGISVGSVGGR	796.03	14.25	0.933585514	0.01
CBF1	AAILACAAEYIQK	797.03	18.06	0.958024835	0.01
TIF4632	ACDEPHWSSMYAQLCGK	800.04	14.26	0.978437859	0.01
CCA1	FNEENCQDMDK	800.53	19.9	0.992021169	0.01
CBF1	AAILACAAEYIQK	802.15	21.05	0.991420635	0.01
CCA1	FNEENCQDMDK	804.92	19.9	0.992021169	0.01
WRS1	AVFGFNDSDCIGK	805.48	19.52	0.977839062	0.01
SFA1	AFEDLHNGDCLR	809.26	12.4	0.992021169	0.01
YPR148C	AAVDCECEFQNLHNEK	812.37	13.13	0.978437859	0.01
YPR148C	AAVDCECEFQNLHNEK	818.12	14.47	0.974265871	0.01
SUI2	ADVEVSCFSYEGIDAIKDALK	834.94	26.26	0.975069796	0.01
SUI2	ADVEVSCFSYEGIDAIKDALK	837.91	26.13	0.975825022	0.01
CDC19	ACDDKIMYVDYK	846.46	14.8	0.971509758	0.01
NUG1	ACPVGNEAGVTTSLR	851.95	17.55	0.966763935	0.01
SLG1	ADSYNWQSSSHCNSECSAK	853.85	21.1	0.992021169	0.01
CDC19	ACDDKIMYVDYK	854.44	14.52	0.974265871	0.01
YOL007C	FLYQAHPNGTVFIAFAGCLGA	855.13	23.7	0.992021169	0.01
NUG1	ACPVGNEAGVTTSLR	856.39	16.89	0.975825022	0.01
CDC19	ACDDKIMYVDYK	858.85	14.74	0.973408379	0.01
DBP2	AEGFDKPTGIQCQGWPMAISGR	860.26	15.92	0.977206062	0.01
SLG1	ADSYNWQSSSHCNSECSAK	860.28	15.9	0.989070255	0.01
GAR1	CGDGVQATSFKEGDKFYIAADK	860.35	13.7	0.992021169	0.01
DBP2	AEGFDKPTGIQCQGWPMAISGR	862.97	20.63	0.971509758	0.01
DBP2	AEGFDKPTGIQCQGWPMAISGR	865.44	15.08	0.982270429	0.01
ILV1	ACSAGNHAQGVAFAAK	866.3	11.7	0.992021169	0.01
NOB1	AEHVVEEAGSKEQICNDENIK	867.52	16.09	0.938683832	0.01
LPD1	AAQLGFNTACVEKR	868.38	12.38	0.911526929	0.01
DBP2	AEGFDKPTGIQCQGWPMAISGR	868.53	16.03	0.969319243	0.01
BMH2	ACHLAK	869.46	15.7	0.992021169	0.01
TRM1	CFALYGGANMVSHESTHESALR	870.38	15.9	0.927563755	0.01
NOB1	AEHVVEEAGSKEQICNDENIK	870.63	16.41	0.981004262	0.01
TCI1	ACELDPEGQVGPPDK	871.88	15.94	0.970455038	0.01

LPD1	AAQLGFNTACVEKR	873.16	12.5	0.98647698	0.01
TRM1	CFALYGGANMVSHESTHESALR	873.39	16.25	0.927563755	0.01
TRM1	CFALYGGANMVSHESTHESALR	875.6	17.11	0.975069796	0.01
TCI1	ACELDPEGQVGGPDK	876.46	17.03	0.984355976	0.01
TRM1	CFALYGGANMVSHESTHESALR	878.65	17.63	0.975825022	0.01
PYC2	CSCSGSTYEIVR	880.39	18.43	0.980054669	0.01
DED1	ACVVYGGSPIGNQLR	881.62	16.77	0.980541042	0.01
LOS1	CFGNGTCLDNDDINKDPNLK	884.92	15.4	0.976535843	0.01
DED1	ACVVYGGSPIGNQLR	885.96	17.08	0.975825022	0.01
RPS21B	CSATNR	887.51	18.2	0.969319243	0.01
SLA2	ACIVYTWDHQSSK	888.28	21.4	0.976535843	0.01
PYC2	CSCSGSTYEIVR	889.28	17.81	0.970455038	0.01
LOS1	CFGNGTCLDNDDINKDPNLK	890.57	16.16	0.96201929	0.01
CAT5	CQNLSDAQAAFLDR	891.36	15.49	0.98647698	0.01
FAS1	CFGPIK	891.63	18.95	0.927563755	0.01
RAT1	AESECDLDAEIKDEIVADVNR	893.49	21.01	0.971509758	0.01
RAP1	ACCQSNLLNME	893.64	21.43	0.963744469	0.01
CAT5	CQNLSDAQAAFLDR	894.59	13.95	0.802584429	0.01
RAT1	AESECDLDAEIKDEIVADVNR	896.4	20.9	0.992021169	0.01
RRP5	ACQYMDSYTIHTK	899.2	15.6	0.992021169	0.01
PYK2	AEVSDVGNAVLDGADCVMLSGETAK	899.98	25.48	0.960121799	0.01
CDC19	AEVSDVGNAVLDGADCVMLSGETAK	901.75	26.94	0.975069796	0.01
PYK2	AEVSDVGNAVLDGADCVMLSGETAK	902.9	22.54	0.955695216	0.01
ARG80	ACINASDTPDATDTSP	903.87	23.1	0.992021169	0.01
EFT2	AEQLYEGPADDANCIAIKNCD	903.96	21.3	0.992021169	0.01
CDC19	AEVSDVGNAVLDGADCVMLSGETAK	904.14	25.19	0.975825022	0.01
CDC19	AEVSDVGNAVLDGADCVMLSGETAK	907.11	25.32	0.975825022	0.01
NAM9	CQPDELISLATEMMNPNETTKK	911.08	24.7	0.938683832	0.01
CCT6	AAAAQDEITGDGTTTVVCLVGELLR	911.42	29.78	0.953091973	0.01
CCT6	AAAAQDEITGDGTTTVVCLVGELLR	914.27	30.35	0.955695216	0.01
YBR096W	CGFHETVPLENLSQEYCSEI	919.51	20.2	0.992021169	0.01
YCL033C	CGGHLGHVFELEGWK	926.2	12.35	0.841478237	0.01
PEP5	ACYQQYEGFDEDR	927.07	18.5	0.992021169	0.01
ODC1	AAVDHYTGVMDCCLK	927.26	14	0.992021169	0.01
TRP5	AETGAGQHGVATATACAK	936.23	11.78	0.927563755	0.01
NPL4	CQPSAITLQQQEFR	939.72	14.3	0.988266653	0.01
TRP5	AETGAGQHGVATATACAK	940.73	14.2	0.867630377	0.01
NPL4	CQPSAITLQQQEFR	944.38	15.5	0.985493593	0.01
YBR025C	CFDDAEIIHVEGDVD	952.92	17.89	0.969319243	0.01
DLD1	AVAQLNHCNSFQFAK	953.82	14.82	0.988091541	0.01
YBR025C	CFDDAEIIHVEGDVD	957.77	18.32	0.986002536	0.01
SEC14	AAGHLVETSCTIMDLK	959.13	14.12	0.984043137	0.01

TUB1	AFHESNSVSEITNACFEPGNQMVK	959.61	17.91	0.968092654	0.01
TUB3	AVCMLSNTTAAIADAWK	961.65	18.5	0.992021169	0.01
TUB1	AFHESNSVSEITNACFEPGNQMVK	961.99	16.65	0.973408379	0.01
RPT1	ACIIFFEIDAVGGAR	963.26	28.9	0.992021169	0.01
SEC14	AAGHLVETSCTIMDLK	963.52	15.43	0.98733551	0.01
TUB1	AFHESNSVSEITNACFEPGNQMVK	965.02	16.71	0.974265871	0.01
SEC14	AAGHLVETSCTIMDLK	966.99	17.21	0.973408379	0.01
MEF1	AECALSTMFGFATSLR	971.3	26.1	0.992021169	0.01
UTP20	CREMASVLISTMLPK	975.23	25.1	0.992021169	0.01
TEF2	CGGIDKR	976.65	18.4	0.994534999	0.01
TEF2	ATVIVLNHPGQISAGYSPVLDCHTAH	977.14	19.87	0.973408379	0.01
TUB1	AVCMLSNTTISIAEAWK	977.51	16.6	0.992021169	0.01
7	AVCDLSTEEGEIIWELGSLQERPK	977.72	27.05	0.969319243	0.01
7	AVCDLSTEEGEIIWELGSLQERPK	980.84	26	0.955695216	0.01
DPP1	CQPVEGLPLDTLFTAK	980.9	24.93	0.981004262	0.01
ECM29	FPATNVTTILDEIFSGCDSTKPSLR	981.69	30.65	0.920343147	0.01
FBA1	AFGNCHGLYAGDIALRPEILAEHQK	984.89	22.59	0.975825022	0.01
DPP1	CQPVEGLPLDTLFTAK	985.22	25.12	0.987131262	0.01
TEF2	CGGIDKR	985.75	20.7	0.992177612	0.01
PIM1	CQTQNPLILIDEIDK	986.1	24.88	0.980541042	0.01
FBA1	AFGNCHGLYAGDIALRPEILAEHQK	987.84	23.51	0.943055829	0.01
PIM1	CQTQNPLILIDEIDK	990.85	28.58	0.976535843	0.01
YDR332W	ACVNSIR	991.59	15.9	0.992021169	0.01
CTT1	FNCYVQTMTPAQATK	995	13.76	0.970455038	0.01
GFA1	CGIFGYCNYLVER	996.63	17.92	0.958024835	0.01
CTT1	FNCYVQTMTPAQATK	999.42	13.38	0.977206062	0.01
MAP1	ACMLGR	444.46	19.4	0.992021169	0.01
KGD2	ACTLAAK	457.96	17.9	0.992021169	0.01
MVD1	ACVLVVSDIKK	471.53	15.96	0.968092654	0.01
EFT2	CFGPDGNGPNLVIDQTK	1002.06	18.21	0.983024762	0.01
CDC19	ACDDKIMYVDYK	564.93	14.51	0.969319243	0.01
RRP5	ACQYMDSYTIHTK	597.31	20.36	0.968092654	0.01
POL5	ACEEDSANR	612.06	16.5	0.992021169	0.01
NCL1	FNLQNCMR	635.18	10.5	0.992021169	0.01
MVD1	ACVLVVSDIK	637.93	21.97	0.975825022	0.01
MVD1	ACVLVVSDIK	642.56	21.77	0.981004262	0.01
CWC2	CEYLHHIPDEEDIGK	679.31	15.85	0.975825022	0.01
PPH21	CGNQAAIMEVDENHNR	680.31	17.7	0.972491784	0.01
PPH21	CGNQAAIMEVDENHNR	685.68	16.14	0.971509758	0.01
SCC2	ACSSCLSHLHPYINK	716.43	12.7	0.992021169	0.01
SHM2	CGAYLMVDMAH	720.06	13.83	0.984946245	0.01
RPL34A	CGDCGSALQGISTLRPR	737.06	17.6	0.867630377	0.01

ARO1	AALYALHSLGCK	742.43	17.48	0.977839062	0.01
ARO4	AVDACQAAAHSHHFMGVTK	745.43	26	0.992021169	0.01
CDC1	CQWSTWEDWPEGAESHR	778.56	17	0.992021169	0.01
YCP4	ACLSYLAHHGIIIFLPLGYK	785.43	33.27	0.983717531	0.01
TIF4632	ACDEPHWSSMYAQLCGK	794.68	16.57	0.973408379	0.01
DCG1	ADVSIVGLLDSSINYCNLVGK	806.68	12.2	0.992021169	0.01
CDC19	ACDDKIMYVDYK	850.93	15.31	0.982270429	0.01
NAM9	CQPDELISLATEMMNPNETTK	874.18	19.5	0.992021169	0.01
CDC19	AEVSDVGNAILDGADCVMLSGETAK	898.81	26.91	0.975825022	0.01
EFT2	AEQLYEGPADDANCIAIKNCD	909.93	21.3	0.992021169	0.01
YDR279W	AAYHNLLTFSPTMDSGCLNPDIK	913.06	19.8	0.992021169	0.01
IRS4	AAQAIFQNHSNEVSSPCPPVTVSR	923.31	11.1	0.992021169	0.01
DLD1	AVAQLNHCNSFQFAK	957.81	16.58	0.969319243	0.01
RIM11	FNALQCLCSPYFDELKLDDGK	965.06	22.25	0.927563755	0.01
YGR117C	AEYTHIACYSIIDAK	968.43	14.1	0.992021169	0.01
RPL34A	CGDCGSALQGISTLR	968.56	15.46	0.980541042	0.01
RPL34A	CGDCGSALQGISTLR	977.68	16.65	0.983024762	0.01
YBR005W	AAYVAPPPLVQECSSSVNSLERPPAAVV	1071.12	16.3	0.979005151	0.01
RPL21A	CRQEFLER	1307.62	19.85	0.955695216	0.01
CDC19	ACDDKIMYVDYK	1706.62	15.1	0.992021169	0.01
				0.974385656	
CTT1	FNCYVQTMTPAQATK	1002.95	12.47	0.730220003	0.1
KAP95	AESIDPQQHLPGVVQACLIGLQDHPK	1007.95	22	0.920343147	0.1
NEW1	FNVALDCISDKENTVK	1012.46	16.17	0.556367811	0.1
NOT5	CGNDFVYNEEDFEKL	1025.64	18.1	0.80730353	0.1
DED81	CSDDPRVTESDVLMPNVGEITGGSMR	1032	19.8	0.920343147	0.1
DED81	CSDDPRVTESDVLMPNVGEITGGSMR	1042.7	15.8	0.920343147	0.1
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1045.98	16.88	0.792425812	0.1
YNR046W	ACDTSNDNFPLQYDGSK	1051.88	17.49	0.730220003	0.1
YNR046W	ACDTSNDNFPLQYDGSK	1056.46	18.52	0.802584429	0.1
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1061.15	10	0.920343147	0.1
ILS1	CGLEATDDVLVEYELVK	1063.2	22.1	0.873879611	0.1
RPB4	ACDTADEAKTLIPSLNNK	1067	31.9	0.920343147	0.1
ILS1	CGLEATDDVLVEYELVK	1067.41	27.21	0.886401326	0.1
CDC19	AEVSDVGNAILDGADCVM	1069.38	26.1	0.920343147	0.1
EFT2	AEQLYEGPADDANCIAIK	1079.74	17.61	0.847498938	0.1
CDC19	ACDDKIMYVDYKNITK	1082.65	13	0.80730353	0.1
UTP7	AELFLNETCHSATYLNQEQYFAVAQK	1083.44	20.4	0.850342006	0.1
UTP7	AELFLNETCHSATYLNQEQYFAVAQK	1086.25	17	0.920343147	0.1
POM152	ACAANVDQISFLEPINLK	1087.51	22.77	0.802584429	0.1
BIO2	ACTGGILGLGESEDDHIGFIYTLNMSPH	1091.17	16.3	0.920343147	0.1

POM152	ACAAVNDQISFLEPINLK	1092.25	26.08	0.899269534	0.1
HIS7	ACEALGAGEILLNCIDK	1094.67	22.9	0.920343147	0.1
YNL087W	AENFICEVNIPTIELVR	1099.24	41.63	0.841478237	0.1
YJL055W	FNLNWSDEGHAHEDCAK	1101.43	12.05	0.89531579	0.1
RPC40	CFPPGVIGIDEGSDEAYVK	1112.63	19.05	0.831507026	0.1
RPC40	CFPPGVIGIDEGSDEAYVK	1117.17	19.72	0.838287316	0.1
SPT4	ACMLCGIVQTTNEFNR	1128.74	18.55	0.775093636	0.1
YBR025C	CFDDAEIIHVEGDVDPVR	1129.18	19.34	0.847498938	0.1
K1CJ_HUMAN	AETECQNTHEYQQLLDIK	1132.41	26.25	0.838287316	0.1
CCA1	FNEENCQDMDKINHVVNDNILNSHLK	1134.23	14.8	0.920343147	0.1
SPT4	ACMLCGIVQTTNEFNR	1136.15	13	0.920343147	0.1
ADE6	CGLSGFSVSDLLIPGNEQPWELNIGKPYH	1137.02	27.9	0.920343147	0.1
RHO5	CGFMGYTECSAATQAGVR	1162.5	14.9	0.920343147	0.1
YCL019W	AVCDNTPSIDTDPPEYRSSDHATPNIMPDK	1175.51	27.8	0.920343147	0.1
GPA2	FNVNLEPECELTQQDLR	1181.95	30	0.920343147	0.1
GPA2	FNVNLEPECELTQQDLR	1187.13	17.9	0.920343147	0.1
MYO3	FNSQFEP CAGNITNYLLEK	1208.52	19.95	0.897985133	0.1
FRS1	ATWVEVLPLTLCSHDENFK	1215.52	23.2	0.920343147	0.1
YPR148C	AAVDCECEFQNLHNEK	1217.2	11.1	0.920343147	0.1
MYO5	FNNQFEP CAGNITNYLLEK	1222.19	20.85	0.853081616	0.1
MYO5	FNNQFEP CAGNITNYLLEK	1226.67	26.24	0.896667649	0.1
GCN20	AALCLNNPHILVLDSPNHLDTTGLDALVEALK	1246.39	70	0.920343147	0.1
SUI2	ADVEVSCFSYEGIDAIKDALK	1251.7	29.6	0.918723075	0.1
ADE4	CGILGIVLANQTTPVAPEL CDGCIFLQHR	1255.65	23	0.920343147	0.1
SUI2	ADVEVSCFSYEGIDAIKDALK	1255.97	28.34	0.827900862	0.1
TCI1	ACELDPEGQVGGPDKFFTMTGQIMGGQDGVSIITR	1264.45	70	0.920343147	0.1
ADE4	CGILGIVLANQTTPVAPEL CDGCIFLQHR	1264.77	22.9	0.811804445	0.1
RAT1	AESECDLDAEIKDEIVADVNDRENSETTEVSR	1270.68	18.85	0.633933271	0.1
YHR029C	AFAPVINVYEDPVC GSGSVALAR	1282.96	18.1	0.920343147	0.1
YHR029C	AFAPVINVYEDPVC GSGSVALAR	1286.67	19.7	0.920343147	0.1
SLG1	ADSYNWQSSSHCNSECSAK	1288.77	21.1	0.920343147	0.1
DBP2	AEGFDKPTGIQCQGWP MALSGR	1289.65	16.8	0.879567578	0.1
DBP2	AEGFDKPTGIQCQGWP MALSGR	1293.65	17.5	0.920343147	0.1
DBP2	AEGFDKPTGIQCQGWP MALSGR	1296.95	13.85	0.531964138	0.1
NAM9	CQPDELISLATEMMNPNETTK	1297.44	26.9	0.920343147	0.1
RIM11	FNALQCLCSPYFDELKLDGKINQITTDLK	1301.46	22.4	0.920343147	0.1
YLR004C	AANADSCSVSTSSINVDDADVALR	1305.21	26.4	0.920343147	0.1
TRM1	CFALYGGANMVSHETHESALR	1317.18	13.8	0.920343147	0.1
ACS2	ACIIDPVTGVELEGNDVEGLAVK	1339.72	24.8	0.738878819	0.1
YEF3	AVDNIPVGPNFDDEEDEDLNCNCEFSLAYGAK	1344.63	23.46	0.761863246	0.1
URA2	AAYALGGLGSGFANNEKELVDLCNVAFSSSPQVLVEK	1346	26.23	0.754656935	0.1
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1347.26	26.41	0.838287316	0.1

YEF3	AVDNIPVGP NFDDEEDEDGDLNCNCEFSLAYGAK	1350.97	24.4	0.68915192	0.1
EFT2	AEQLYEGPADDANCIAIKNCD	1355.19	21.15	0.68915192	0.1
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1355.39	24.14	0.797631076	0.1
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1359.93	25.16	0.827900862	0.1
ADH1	AAHIPQGTDLAQVAPILCAGITVYK	1390.22	22.1	0.920343147	0.1
TUB1	AFHESNSVSEITNACFEPGNQMVK	1434.19	15.6	0.834966266	0.1
TUB1	AFHESNSVSEITNACFEPGNQMVK	1442.2	14.73	0.802584429	0.1
ARO1	AALYALHSLGCK	1482.7	14	0.920343147	0.1
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1552.22	16.6	0.920343147	0.1
YMR259C	AFCIRCQLEFPAILEELLSKSVK	1556.63	36.9	0.920343147	0.1
LPD1	AAQLGFNTACVEK	1578.7	16.8	0.920343147	0.1
LPD1	AAQLGFNTACVEK	1587.89	16.8	0.920343147	0.1
SPT15	AAPSEKDTSATSGIVPTLQNIVATVTLGCR	1684.49	29.2	0.920343147	0.1
CDC19	ACDDKIMYVDYK	1717.24	15.33	0.792425812	0.1
DED1	ACVVYGGSPIGNQLR	1769.91	15.35	0.834966266	0.1
ADE3	ACAQQFR	526.21	17.8	0.920343147	0.1
SPR3	CRNRDLPLLDNK	562.96	12.1	0.920343147	0.1
RRP5	ACQYMDSYTIHTK	605.69	16.13	0.834966266	0.1
YDR307W	CGLLGHDLR	611.08	16.2	0.920343147	0.1
PUS1	CGCPVER	618.94	18.4	0.867630377	0.1
YLR126C	CQNQGFYR	626.58	19.4	0.920343147	0.1
SEC14	AAGHLVETSCTIMDLK	645.21	15.25	0.633933271	0.1
PIM1	CQTQNPLILIDEIDK	660.57	18.9	0.920343147	0.1
GAR1	CGDGVQATSFK	670.96	19.95	0.754656935	0.1
GAR1	CGDGVQATSFK	675.33	19.8	0.781179715	0.1
MVD1	ACVLVVSDIKK	706.46	16.36	0.838287316	0.1
YOR175C	CGLGYNGYDSK	707.57	13.6	0.920343147	0.1
FBA1	CQYAYLTGIR	708.44	18.74	0.738878819	0.1
SCC2	ACSSCLSHLHPYINK	710.21	10.5	0.920343147	0.1
FBA1	CQYAYLTGIR	712.95	18.9	0.850342006	0.1
ARO1	CSAEAEFQALR	731.46	14.47	0.831507026	0.1
ARO4	AVDACQAAAHSHHFMGVTK	742.45	26	0.920343147	0.1
ACO1	ACQDATAQMAILQFMSAGLP	774.33	24.2	0.920343147	0.1
CDC19	ACDDKIMYVDYK	846.46	14.8	0.720980736	0.1
NUG1	ACPVGNEAGVTTSLR	851.95	17.55	0.676917461	0.1
DBP2	AEGFDKPTGIQCQGWPMALSGR	865.44	15.08	0.824138295	0.1
BMH2	ACHLAK	869.46	15.7	0.920343147	0.1
TCI1	ACELDPEGQVGGPDK	876.46	17.03	0.844546479	0.1
RRP5	ACQYMDSYTIHTK	899.2	15.6	0.920343147	0.1
PEP5	ACYQQYEGFDEDR	927.07	18.5	0.920343147	0.1
DLD1	AVAQLNHCNSFQFAK	953.82	14.82	0.881351668	0.1
GRX3	CGFSR	403.6	17.8	0.920343147	0.1

GCD10	CRPYQSIR	420.41	17.9	0.920343147	0.1
RPL21A	CRQEFLER	440.23	19.48	0.676917461	0.1
YJR124C	CFGPVR	458.22	21.05	0.475042763	0.1
TEF2	CGGIDKR	493.23	16.2	0.711102275	0.1
SML1	CQQQQAPSTLR	499.73	16.3	0.920343147	0.1
YNL247W	CQPWNK	506.66	19.1	0.920343147	0.1
UTP7	AELFLNETCHSATYLNQEQYFAVAQK	1086.25	17	0.920343147	0.1
EFT2	CFGPDGNGPNLVIDQTK	1002.06	18.21	0.831507026	0.1
CDC60	FMSSMAYPYMNGVMHAGHCFTLSK	1005.4	11.6	0.920343147	0.1
GFA1	CGIFGYCNYLVER	1005.42	19.65	0.633933271	0.1
EFT2	CFGPDGNGPNLVIDQTK	1006.54	18.05	0.838287316	0.1
CTT1	FNCYVQTMTPAQATK	1007.4	11.18	0.802584429	0.1
KAP95	AESIDPQQHLPGVVQACLIQLQDHPK	1010.9	21.15	0.68915192	0.1
NEW1	FNVALDCISDKENTVK	1016.85	15	0.920343147	0.1
CWC2	CEYLHHIPDEEDIGK	1017.78	11.85	0.6494311	0.1
YDL183C	AEQVDTQPLHVYYPGIISSPDECLR	1018.03	17.2	0.920343147	0.1
PPH21	CGNQAAIMEVDENHNR	1019.38	14.6	0.920343147	0.1
MAP1	ACMLGR	444.46	19.4	0.920343147	0.1
FAS1	CFGPIK	446.52	22.1	0.920343147	0.1
KGD2	ACTLAAK	457.96	17.9	0.920343147	0.1
NGR1	CFGFVR	483.08	24.6	0.920343147	0.1
ASN2	ADWGCAEDPSGR	498.75	17.3	0.920343147	0.1
YNL247W	CQPWNK	502.08	19	0.920343147	0.1
PDB1	CQMVFR	511.19	20.72	0.841478237	0.1
BUD3	ACSITIPYFYK	515.11	18.55	0.912495232	0.1
FAS1	CFGPIKVELPTK	521.23	17.55	0.441748075	0.1
CCT3	ACTIMLR	522.53	21.06	0.633933271	0.1
ADE3	ACAQQFR	530.77	17.7	0.860732955	0.1
MBR1	CQQTLNPLCK	535.67	21.3	0.920343147	0.1
ASN2	CGIFAAFK	542.59	16.65	0.633933271	0.1
ASN2	CGIFAAFK	547.13	28.1	0.404647962	0.1
ASN1	CGIFAAFR	561.28	19.47	0.730220003	0.1
CDC19	ACDDKIMYVDYK	564.93	14.51	0.700517965	0.1
CDC19	ACDDKIMYVDYK	567.78	15.16	0.754656935	0.1
CDC19	ACDDKIMYVDYK	570.35	13.19	0.761863246	0.1
ARG3	FMHCLPR	574.74	19.1	0.892503441	0.1
LPD1	AAQLGFNTACVEKR	579.59	12.52	0.663715257	0.1
LPD1	AAQLGFNTACVEKR	582.63	12.43	0.786949185	0.1
DED1	ACVVYGGSPIGNQLR	588.02	13.1	0.920343147	0.1
GPX2	CGFTPQYK	590.74	21.62	0.676917461	0.1
SLA2	ACIVYTDWDHQSSK	592.84	14	0.920343147	0.1
MES1	CGALLDPFELINPR	596.25	25.9	0.556367811	0.1

RRP5	ACQYMDSYTIHTK	597.31	20.36	0.68915192	0.1
CDD1	ACELSYSPYSHFR	597.53	17.4	0.920343147	0.1
CDD1	ACELSYSPYSHFR	599.88	17.4	0.738878819	0.1
RRP5	ACQYMDSYTIHTK	602.79	17.13	0.768664585	0.1
YDR307W	CGLLGHDLR	606.22	15.6	0.920343147	0.1
EMP24	CFFEDLSK	609.05	18.96	0.761863246	0.1
PUS1	CGCPVER	610.1	18.35	0.811804445	0.1
RGA1	CGENIADLR	610.36	15.3	0.920343147	0.1
POL5	ACEEDSANR	612.06	16.5	0.920343147	0.1
EMP24	CFFEDLSK	613.28	19.05	0.720980736	0.1
POL5	ACEEDSANR	616.27	16.5	0.920343147	0.1
ODC1	AAVDHYTGVMDCCLK	620.89	14.6	0.920343147	0.1
NCL1	FNLQNCMR	627.41	17.28	0.747009112	0.1
SLA2	ACSVEETAPK	631.61	17.9	0.920343147	0.1
NCL1	FNLQNCMR	632.11	12.6	0.899269534	0.1
NCL1	FNLQNCMR	635.18	10.5	0.920343147	0.1
MVD1	ACVLVVSIDK	637.93	21.97	0.761863246	0.1
SEC14	AAGHLVETSCTIMDLK	639.92	14.38	0.633933271	0.1
MVD1	ACVLVVSIDK	642.56	21.77	0.811804445	0.1
RPL34A	CGDCGSALQGISTLR	646.39	14.63	0.768664585	0.1
YMR031C	CEQDITEAR	646.99	19	0.920343147	0.1
SAM1	ACLAEDPHSK	649.4	17.7	0.920343147	0.1
RPL34A	CGDCGSALQGISTLR	652.15	14.53	0.663715257	0.1
RPL21A	CRQEFLER	654.77	19.53	0.761863246	0.1
RPL21A	CRQEFLER	659.37	19.52	0.786949185	0.1
PDR5	FPCAIEYVPR	659.92	16.58	0.834966266	0.1
IPI2	CGLSFFEGILSSIIEF	664.3	21.5	0.920343147	0.1
YDL193W	CFGLFRYQYQYNK	675.99	19	0.920343147	0.1
CWC2	CEYLHHIPDEEDIGK	679.31	15.85	0.761863246	0.1
HIF1	CQQTLDLSPK	685.76	14.65	0.91344261	0.1
DUS1	CQPYFRPVNGITGDKR	696.84	12.5	0.920343147	0.1
YJR149W	ACIAGAIASLPLSHLDFR	698.4	23.7	0.920343147	0.1
SEN1	FNDIVCQWR	704.91	13	0.920343147	0.1
SCC2	ACSSCLSHLHPYINK	716.43	12.7	0.920343147	0.1
EFT2	AEQLYEGPADDANCIAIK	717.37	16.22	0.730220003	0.1
CDC19	ACDDKIMYVDYKNITK	719.77	13.97	0.824138295	0.1
SHM2	CGAYLMVDMAH	720.06	13.83	0.850342006	0.1
CDC19	ACDDKIMYVDYKNITK	722.47	13.06	0.663715257	0.1
GCD11	CQRPGCPGR	723.49	16.9	0.920343147	0.1
APN1	CEQLGIGLYNLHPGSTLK	724.74	20.63	0.68915192	0.1
MIS1	ATVTVCHSHTR	724.85	16.4	0.920343147	0.1
CDC19	ACDDKIMYVDYKNITK	725.42	13.09	0.504977757	0.1

APN1	CEQLGIGLYNLHPGSTLK	727.65	19.86	0.761863246	0.1
SHM2	CGAYLMVDMAH	728.13	11.5	0.920343147	0.1
HIS7	ACEALGAGEILLNCIDK	730.24	22.97	0.738878819	0.1
RPT5	ACAAQTNATFLK	734.02	16.72	0.844546479	0.1
ADE12	CQNLLGNGVVIHVPSFFK	734.51	23.4	0.920343147	0.1
YJL055W	FNLNWSDEGHAHEDCAK	734.63	21.34	0.781179715	0.1
ARO1	AALYALHSLGCK	738.05	16.96	0.802584429	0.1
RPT5	ACAAQTNATFLK	738.48	16.19	0.781179715	0.1
ARO4	AVDACQAAAHSHHFMGVTK	745.43	26	0.920343147	0.1
SEN1	ACLMNSATALLR	746.35	18.1	0.920343147	0.1
ASN2	ADWGCAEDPSGR	750.65	20.29	0.68915192	0.1
TFB3	FLVNPECYHR	753.51	16.8	0.920343147	0.1
YBR025C	CFDDAEIIHVEGDVDPVR	756.36	20.56	0.775093636	0.1
YDR193W	FNDSLMSFCVK	764.41	25.1	0.920343147	0.1
CTL1	FNEYMCSFLNASDLIRK	766.39	21	0.920343147	0.1
YLR427W	CGNFPPANLGSIK	777.12	30.7	0.920343147	0.1
CDC1	CQWSTWEDWPEGAESHR	778.56	17	0.920343147	0.1
YCP4	ACLSYLAHHGIIIFLPLGYK	782.13	33.9	0.920343147	0.1
FAS1	CFGPIKVELPTK	785.17	17	0.786949185	0.1
YCP4	ACLSYLAHHGIIIFLPLGYK	785.43	33.27	0.838287316	0.1
YOR289W	CSCNILGNFK	786.02	14.8	0.920343147	0.1
TIF4632	ACDEPHWSSMYAQLCGK	800.04	14.26	0.786949185	0.1
CCA1	FNEENCQDMDK	800.53	19.9	0.920343147	0.1
CBF1	AAILACAAEYIQK	802.15	21.05	0.914369734	0.1
CCA1	FNEENCQDMDK	804.92	19.9	0.920343147	0.1
WRS1	AVFGFNDSDCIGK	805.48	19.52	0.781179715	0.1
DCG1	ADVSIVGLLDSSINYCNLVGK	806.68	12.2	0.920343147	0.1
SFA1	AFEDLHNGDCLR	809.26	12.4	0.920343147	0.1
YPR148C	AAVDCECEFQNLHNEK	812.37	13.13	0.786949185	0.1
YPR148C	AAVDCECEFQNLHNEK	818.12	14.47	0.747009112	0.1
SUI2	ADVEVSCFSYEGIDAIKDALK	837.91	26.13	0.761863246	0.1
SLG1	ADSYNWQSSSHCNSECSAK	853.85	21.1	0.920343147	0.1
YOL007C	FLYQAHPNGTVFIAFAGCLGA	855.13	23.7	0.920343147	0.1
NUG1	ACPVGNEAGVTTSLR	856.39	16.89	0.761863246	0.1
CDC19	ACDDKIMYVDYK	858.85	14.74	0.738878819	0.1
SLG1	ADSYNWQSSSHCNSECSAK	860.28	15.9	0.891040011	0.1
GAR1	CGDGVQATSFKEGDKFYIAADK	860.35	13.7	0.920343147	0.1
ILV1	ACSAGNHAQGVAFAAK	866.3	11.7	0.920343147	0.1
DBP2	AEGFDKPTGIQCQGWPMAISGR	868.53	16.03	0.700517965	0.1
NOB1	AEHVVEEAGSKEQICNDENIK	870.63	16.41	0.811804445	0.1
TCI1	ACELDPEGQVGGPDK	871.88	15.94	0.711102275	0.1
LPD1	AAQLGFNTACVEKR	873.16	12.5	0.865408047	0.1

NAM9	CQPDELISLATEMMNPNETTK	874.18	19.5	0.920343147	0.1
TRM1	CFALYGGANMVSHESTHESALR	875.6	17.11	0.754656935	0.1
TRM1	CFALYGGANMVSHESTHESALR	878.65	17.63	0.761863246	0.1
PYC2	CSCSGSTYEIVR	880.39	18.43	0.802584429	0.1
DED1	ACVVYGGSPIGNQLR	881.62	16.77	0.80730353	0.1
LOS1	CFGNGTCLDNDDINKDPNLK	884.92	15.4	0.768664585	0.1
SLA2	ACIVYTWDHQSSK	888.28	21.4	0.768664585	0.1
CAT5	CQNLSDAQAAFLDR	891.36	15.49	0.865408047	0.1
RAT1	AESECDLDAEIKDEIVADVNR	893.49	21.01	0.720980736	0.1
RAT1	AESECDLDAEIKDEIVADVNR	896.4	20.9	0.920343147	0.1
CDC19	AEVSDVGNAILDGADCVMLSGETAK	898.81	26.91	0.761863246	0.1
PYK2	AEVSDVGNAVLGDADCVMLSGETAK	899.98	25.48	0.617069415	0.1
CDC19	AEVSDVGNAILDGADCVMLSGETAK	901.75	26.94	0.754656935	0.1
PYK2	AEVSDVGNAVLGDADCVMLSGETAK	902.9	22.54	0.578508489	0.1
ARG80	ACINASDTPDATDTSP	903.87	23.1	0.920343147	0.1
CDC19	AEVSDVGNAILDGADCVMLSGETAK	904.14	25.19	0.761863246	0.1
EFT2	AEQLYEGPADDANCIAIKNCD	909.93	21.3	0.920343147	0.1
CCT6	AAAAQDEITGDGTTTVVCLVGELLR	911.42	29.78	0.556367811	0.1
YDR279W	AAYHNLLTFSPTMDSGCLNPDIK	913.06	19.8	0.920343147	0.1
CCT6	AAAAQDEITGDGTTTVVCLVGELLR	914.27	30.35	0.578508489	0.1
YBR096W	CGFHETVPLENLSQEYCSEI	919.51	20.2	0.920343147	0.1
IRS4	AAQAIFQNHSNEVSSPCPPVTVSR	923.31	11.1	0.920343147	0.1
ODC1	AAVDHYTGVMDCCLK	927.26	14	0.920343147	0.1
NPL4	CQPSAITLQQQEFR	939.72	14.3	0.883083861	0.1
NPL4	CQPSAITLQQQEFR	944.38	15.5	0.855723281	0.1
YBR025C	CFDDAEIIHVEGDVD	957.77	18.32	0.860732955	0.1
DLD1	AVAQLNHCNSFQFAK	957.81	16.58	0.700517965	0.1
SEC14	AAGHLVETSCTIMDLK	959.13	14.12	0.841478237	0.1
TUB1	AFHESNSVSEITNACFEPGNQMVK	959.61	17.91	0.68915192	0.1
TUB3	AVCMLSNTTIAIDAWK	961.65	18.5	0.920343147	0.1
RPT1	ACIIFFEIDAVGGAR	963.26	28.9	0.920343147	0.1
SEC14	AAGHLVETSCTIMDLK	963.52	15.43	0.873879611	0.1
TUB1	AFHESNSVSEITNACFEPGNQMVK	965.02	16.71	0.747009112	0.1
YGR117C	AEYTHIACYSIIDAK	968.43	14.1	0.920343147	0.1
MEF1	AECALSTMFGFATSLR	971.3	26.1	0.920343147	0.1
UTP20	CREMASVLISTMLPK	975.23	25.1	0.920343147	0.1
TEF2	CGGIDKR	976.65	18.4	0.945392265	0.1
TEF2	ATVIVLNHPGQISAGYSPVLDCHTAH	977.14	19.87	0.738878819	0.1
TUB1	AVCMLSNTTISIAEAWK	977.51	16.6	0.920343147	0.1
RPL34A	CGDCGSALQGISTLR	977.68	16.65	0.831507026	0.1
DPP1	CQPVEGLPLDTLFTAK	980.9	24.93	0.811804445	0.1
FBA1	AFGNCHGLYAGDIALRPEILAEHQK	984.89	22.59	0.761863246	0.1

DPP1	CQPVEGLPLDTLFTAK	985.22	25.12	0.87186285	0.1
TEF2	CGGIDKR	985.75	20.7	0.921899999	0.1
PIM1	CQTQNPLILIDEIDK	986.1	24.88	0.80730353	0.1
FBA1	AFGNCHGLYAGDIALRPEILAEHQK	987.84	23.51	0.475042763	0.1
YDR332W	ACVNSIR	991.59	15.9	0.920343147	0.1
CTT1	FNCYVQTMTPAQATK	995	13.76	0.711102275	0.1
CTT1	FNCYVQTMTPAQATK	999.42	13.38	0.775093636	0.1
FBA1	AAAFGNCHGLYAGDIALRPEILAEHQK	1032.36	23.89	0.738878819	0.1
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1035.11	16.2	0.700517965	0.1
FBA1	AAAFGNCHGLYAGDIALRPEILAEHQK	1035.31	23.15	0.747009112	0.1
SUI2	ADVEVSCFSYEGIDAIK	1037.79	19.11	0.87583413	0.1
RPO21	CQTCQEGMNECPGHFGHIDLAK	1039.86	10.5	0.738878819	0.1
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1040.57	15.01	0.781179715	0.1
SUI2	ADVEVSCFSYEGIDAIK	1042.05	21.1	0.775093636	0.1
RPO21	CQTCQEGMNECPGHFGHIDLAK	1049.06	10.5	0.920343147	0.1
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1063.59	10	0.920343147	0.1
NIT2	AVDTQCYVLM PGQVGMHDLSDPEWEK	1065.82	30.7	0.920343147	0.1
YBR005W	AAYVAPPPLVQECSSSESVNSLERPPAAVV	1071.12	16.3	0.792425812	0.1
CDC19	ACDDKIMYVDYKNITK	1074.28	14.03	0.711102275	0.1
EFT2	AEQLYEGPADDANCIAIK	1075.33	17.64	0.827900862	0.1
YML096W	CGKPVIELLNVSFENPR	1076.06	22	0.920343147	0.1
YNL087W	AENFICEVNIPTIELVR	1095.33	37.87	0.834966266	0.1
CDC43	FNGELCIPQEIFNDFSK	1115.61	26.4	0.927563755	0.1
SPT15	AAPSEKDTSATSGIVPTLQNIVATVTLGCR	1120.09	29.8	0.531964138	0.1
SPT15	AAPSEKDTSATSGIVPTLQNIVATVTLGCR	1123.29	29	0.877729233	0.1
YFL034W	ACLPGEDKEVESSNDFLGESHYKPPSTPK	1131.34	13.35	0.858272134	0.1
GCV2	AVDVLKNPDVSGCLVQYPATDGSILPPDSMK	1156.81	20	0.920343147	0.1
TIF4632	ACDEPHWSSMYAQLCGK	1191.06	15.2	0.797631076	0.1
TCI1	ACELDPEGQVGGPDKFFTMGQIMGGQDGVSIITR	1262.34	24	0.920343147	0.1
RAT1	AESECDLDAEIKDEIVADVNDRENSETTEVSR	1273.83	25.6	0.700517965	0.1
RPL21A	CRQEFLER	1307.62	19.85	0.578508489	0.1
ACS2	ACIIDPVTGVELEGNDVEGVLA VK	1334.58	23.15	0.504977757	0.1
URA2	AAYALGGLGSGFANNEKELVDLCNVA FSSSPQVLVEK	1343.07	24.11	0.747009112	0.1
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1352.07	26.57	0.853081616	0.1
EFT2	AEQLYEGPADDANCIAIKNCD	1363.82	21.3	0.920343147	0.1
YBR096W	CGFHETVPLENLSQEYCSEI	1377.33	21.54	0.738878819	0.1
STE20	CSDGDPSTKYANLVKIGQGASGGVYT	1413.29	11.6	0.920343147	0.1
TUB1	AFHESNSVSEITNACFEPGNQMVK	1438.81	18.88	0.738878819	0.1
ARD2	CSECHQHNVFVYLPVDDLT K	1446.79	20.63	0.920343147	0.1
MAL13	CQNALITLPISK	1529.28	22.3	0.920343147	0.1
CDC19	ACDDKIMYVDYK	1691.56	12.87	0.921899999	0.1
CDC19	ACDDKIMYVDYK	1700.06	14.68	0.901743936	0.1

CDC19	ACDDKIMYVDYK	1706.62	15.1	0.920343147 0.830332699	0.1
NOT5	CGNDFVYNEEDFEKL	1025.64	18.1	0.625682521	0.2
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1061.15	10	0.841478237	0.2
ILS1	CGLEATDDVLVEYELVK	1067.41	27.21	0.775093636	0.2
CDC19	AEVSDVGNAILDGADCVML	1069.38	26.1	0.841478237	0.2
CDC19	ACDDKIMYVDYKNITK	1082.65	13	0.625682521	0.2
BIO2	ACTGGILGLGESEDDHIGFIYTLSNMSPH	1091.17	16.3	0.841478237	0.2
RPC40	CFPPGVIGIDEGSDEAYVK	1112.63	19.05	0.670444088	0.2
K1CJ_HUMAN	AETECQNTHEYQQLLDIK	1132.41	26.25	0.68314913	0.2
SPT4	ACMLCGIVQTTNEFNR	1136.15	13	0.841478237	0.2
GPA2	FNVNLEPECELTQQDLNR	1187.13	17.9	0.841478237	0.2
MYO5	FNNQFEPACAGNITNYLLEK	1226.67	26.24	0.795061104	0.2
GCN20	AALCLNNPHILVLDEPSNHLDTTGLDALVEALK	1246.39	70	0.841478237	0.2
ADE4	CGILGIVLANQTTTPVAPELDCGICIFLQHR	1255.65	23	0.841478237	0.2
YHR029C	AFAPVINVYEDPVC GSGSVALAR	1286.67	19.7	0.841478237	0.2
DBP2	AEGFDKPTGIQCQGWPMALSGR	1289.65	16.8	0.761863246	0.2
DBP2	AEGFDKPTGIQCQGWPMALSGR	1293.65	17.5	0.841478237	0.2
YMR259C	AFCIRCQLEFPAILEELLSKSVK	1556.63	36.9	0.841478237	0.2
LPD1	AAQLGFNTACVEK	1587.89	16.8	0.841478237	0.2
DED1	ACVVYGGSPIGNQLR	1769.91	15.35	0.676917461	0.2
CTT1	FNCYVQTMTPAQATK	1002.95	12.47	0.490403529	0.2
KAP95	AESIDPQQHLPGVVQACLIGLQDHPK	1007.95	22	0.841478237	0.2
NEW1	FNVALDCISDKENTVK	1016.85	15	0.841478237	0.2
BUD3	ACSITIPYFYK	515.11	18.55	0.826039752	0.2
ADE3	ACAQQFR	526.21	17.8	0.841478237	0.2
SPR3	CRNRDLPLLDNK	562.96	12.1	0.841478237	0.2
CDC19	ACDDKIMYVDYK	570.35	13.19	0.544467774	0.2
LPD1	AAQLGFNTACVEKR	579.59	12.52	0.384528956	0.2
SLA2	ACIVYTWDHQSSK	592.84	14	0.841478237	0.2
RRP5	ACQYMDSYTIHTK	605.69	16.13	0.676917461	0.2
YDR307W	CGLLGHDLR	606.22	15.6	0.841478237	0.2
RGA1	CGENIADLR	610.36	15.3	0.841478237	0.2
YDR307W	CGLLGHDLR	611.08	16.2	0.841478237	0.2
YLR126C	CQNQGFYR	626.58	19.4	0.841478237	0.2
SLA2	ACSVEETAPK	631.61	17.9	0.841478237	0.2
NCL1	FNLQNCMR	632.11	12.6	0.800138098	0.2
PIM1	CQTQNPLILIDEIDK	660.57	18.9	0.841478237	0.2
GAR1	CGDGVQATSFK	675.33	19.8	0.578508489	0.2
DUS1	CQPYFRPVNGITGDKR	696.84	12.5	0.841478237	0.2
YOR175C	CGLGYNGYDSK	707.57	13.6	0.841478237	0.2

SCC2	ACSSCLSHLHPYINK	710.21	10.5	0.841478237	0.2
FBA1	CQYAYLTGIR	712.95	18.9	0.705902861	0.2
ARO1	CSAEAEFQALR	731.46	14.47	0.670444088	0.2
RPT5	ACAAQTNATFLK	738.48	16.19	0.578508489	0.2
ACO1	ACQDATAQMAILQFMSAGLP	774.33	24.2	0.841478237	0.2
SLG1	ADSYNWQSSSHCNSECSAK	853.85	21.1	0.841478237	0.2
GAR1	CGDGVQATSFKEGDKFYIAADK	860.35	13.7	0.841478237	0.2
DBP2	AEGFDKPTGIQCQGWPMALSGR	865.44	15.08	0.65671621	0.2
BMH2	ACHLAK	869.46	15.7	0.841478237	0.2
MET17	NTFGAGGYFCQPIK	870.78	15.9	0.841478237	0.2
TCI1	ACELDPEGQVGGPDK	876.46	17.03	0.694937804	0.2
RRP5	ACQYMDSYTIHTK	899.2	15.6	0.841478237	0.2
PYK2	AEVSDVGNAVLDGADCVMLSGETAK	899.98	25.48	0.317300419	0.2
CDC19	AEVSDVGNAILDGADCVMLSGETAK	907.11	25.32	0.544467774	0.2
NPL4	CQPSAITLQQQEFR	939.72	14.3	0.768664585	0.2
DLD1	AVAQLNHCNSFQFAK	953.82	14.82	0.76531241	0.2
UTP20	CREMASVLISTMLPK	975.23	25.1	0.841478237	0.2
DPP1	CQPVEGLPLDTLFTAK	985.22	25.12	0.747009112	0.2
PIM1	CQTQNPLILIDEIDK	986.1	24.88	0.625682521	0.2
YDR332W	ACVNSIR	991.59	15.9	0.841478237	0.2
GRX3	CGFSR	403.6	17.8	0.841478237	0.2
GCD10	CRPYQSIR	420.41	17.9	0.841478237	0.2
RPL21A	CRQEFLER	440.23	19.48	0.404647962	0.2
YJR124C	CFGPVR	458.22	21.05	0.153114961	0.2
NGR1	CFGFVR	483.08	24.6	0.841478237	0.2
TEF2	CGGIDKR	493.23	16.2	0.458842652	0.2
ASN2	ADWGCAEDPSGR	498.75	17.3	0.841478237	0.2
SML1	CQQQQAPSTLR	499.73	16.3	0.841478237	0.2
YNL247W	CQPWNK	502.08	19	0.841478237	0.2
YNL247W	CQPWNK	506.66	19.1	0.841478237	0.2
CDC60	FMSSMAYPYMNGVMHAGHCFTLSK	1005.4	11.6	0.841478237	0.2
EFT2	CFGPDGNGPNLVIDQTK	1006.54	18.05	0.68314913	0.2
CTT1	FNCYVQTMTPAQATK	1007.4	11.18	0.617069415	0.2
YDL183C	AEQVDTQPLHVYYPGIISSPDECLR	1018.03	17.2	0.841478237	0.2
PPH21	CGNQAAIMEVDENHNR	1019.38	14.6	0.841478237	0.2
DED81	CSDDPRVTESDVLMNVGEITGGSMR	1032	19.8	0.841478237	0.2
FBA1	AAAFGNCHGLYAGDIALRPEILAEHQK	1035.31	23.15	0.518815555	0.2
SUI2	ADVEVSCFSYEGIDAIK	1037.79	19.11	0.754656935	0.2
RPO21	CQTCQEGMNECPGHFGHIDLAK	1039.86	10.5	0.504977757	0.2
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1040.57	15.01	0.578508489	0.2
SUI2	ADVEVSCFSYEGIDAIK	1042.05	21.1	0.567702774	0.2
RPO21	CQTCQEGMNECPGHFGHIDLAK	1049.06	10.5	0.841478237	0.2

ILS1	CGLEATDDVLVEYELVK	1063.2	22.1	0.750890661	0.2
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1063.59	10	0.841478237	0.2
NIT2	AVDTQCYVLMPGQVGMHDLSDPEWEK	1065.82	30.7	0.841478237	0.2
RPB4	ACDTADEAKTLIPSLNNK	1067	31.9	0.841478237	0.2
YBR005W	AAYVAPPPLVQECSSSVNSLERPPAAVV	1071.12	16.3	0.59866288	0.2
CDC19	ACDDKIMYVDYKNITK	1074.28	14.03	0.458842652	0.2
EFT2	AEQLYEGPADDANCIAIK	1075.33	17.64	0.663715257	0.2
YML096W	CGKPVIELLNVSFENPR	1076.06	22	0.841478237	0.2
EFT2	AEQLYEGPADDANCIAIK	1079.74	17.61	0.700517965	0.2
UTP7	AELFLNETCHSATYQLONEQYFAVAQK	1086.25	17	0.841478237	0.2
POM152	ACAANVDQISFLEPINLK	1087.51	22.77	0.617069415	0.2
POM152	ACAANVDQISFLEPINLK	1092.25	26.08	0.800138098	0.2
YNL087W	AENFICEVNIPTIELVR	1095.33	37.87	0.676917461	0.2
YNL087W	AENFICEVNIPTIELVR	1099.24	41.63	0.68915192	0.2
YJL055W	FNLNWSDEGHAEHEDCAK	1101.43	12.05	0.792425812	0.2
CDC43	FNGELCIPQEIFNDFSK	1115.61	26.4	0.855723281	0.2
SPT15	AAPSEKDTSATSGIVPTLQNIIVATVTLGCR	1123.29	29	0.758312899	0.2
YBR025C	CFDDAEIIHVEGDVDPVR	1129.18	19.34	0.700517965	0.2
CCA1	FNEENCQDMDKINHVVNDNILNSHLK	1134.23	14.8	0.841478237	0.2
ADE6	CGLSGFSVSDLLIPGNEQPWELNIGKPYH	1137.02	27.9	0.841478237	0.2
GCV2	AVDVLKNPDVSGCLVQYPATDGSILPPDSMK	1156.81	20	0.841478237	0.2
RHO5	CGFMGYTECSAATQAGVR	1162.5	14.9	0.841478237	0.2
YCL019W	AVCDNTPSIDTDPPEYRSSDHATPNIMPK	1175.51	27.8	0.841478237	0.2
GPA2	FNVNLEPECELTQQDLR	1181.95	30	0.841478237	0.2
TIF4632	ACDEPHWSSMYAQLCGK	1191.06	15.2	0.608071084	0.2
MYO3	FNSQFEPKAGNITNYLLEK	1208.52	19.95	0.797631076	0.2
FRS1	ATWVEVLPLTLCSHDENFK	1215.52	23.2	0.841478237	0.2
YPR148C	AAVDCECEFQNLHNEK	1217.2	11.1	0.841478237	0.2
MYO5	FNNQFEPKAGNITNYLLEK	1222.19	20.85	0.711102275	0.2
SUI2	ADVEVSCFSYEGIDAIKDALK	1251.7	29.6	0.838287316	0.2
SUI2	ADVEVSCFSYEGIDAIKDALK	1255.97	28.34	0.663715257	0.2
TCI1	ACELDPEGQVGGPDKFFTMGQIMGGQDGVSIITR	1262.34	24	0.841478237	0.2
TCI1	ACELDPEGQVGGPDKFFTMGQIMGGQDGVSIITR	1264.45	70	0.841478237	0.2
ADE4	CGILGIVLANQTTTPVAPELDCGCIFLQHR	1264.77	22.9	0.633933271	0.2
YHR029C	AFAPVINVEDPVCGSGSVALAR	1282.96	18.1	0.841478237	0.2
SLG1	ADSYNWQSSSHCNSECSAK	1288.77	21.1	0.841478237	0.2
NAM9	CQPDELISLATEMMNPNETTK	1297.44	26.9	0.841478237	0.2
YLR004C	AANADSCSVSTSSINVDDADVALR	1305.21	26.4	0.841478237	0.2
TRM1	CFALYGGANMVSHETHESALR	1317.18	13.8	0.841478237	0.2
GAR1	CGDGVQATSFK	1339.59	20.45	0.664368423	0.2
ACS2	ACIIDPVTGVELEGNDVEGLVAVK	1339.72	24.8	0.504977757	0.2
URA2	AAYALGGLGSGFANNEKELVDLCNVAFSSSPQVLVEK	1343.07	24.11	0.518815555	0.2

CDC19	AEVSDVGNAILDGADCVMLSGETAK	1347.26	26.41	0.68314913	0.2
YEF3	AVDNIPVGP NFDDEEDEDLCNCEFSLAYGAK	1350.97	24.4	0.423702278	0.2
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1352.07	26.57	0.711102275	0.2
EFT2	AEQLYEGPADDANCIAIKNCD	1363.82	21.3	0.841478237	0.2
YBR096W	CGFHETVPLENLSQEYCSEI	1377.33	21.54	0.504977757	0.2
STE20	CSDGDPSTKYANLVKIGQGASGGVYT	1413.29	11.6	0.841478237	0.2
TUB1	AFHESNSVSEITNACFEPGNQMVK	1434.19	15.6	0.676917461	0.2
TUB1	AFHESNSVSEITNACFEPGNQMVK	1442.2	14.73	0.617069415	0.2
ARD2	CSECHQHN VFVYLPVDDLT	1446.79	20.63	0.841478237	0.2
ARO1	AALYALHSLGCK	1482.7	14	0.841478237	0.2
MAL13	CQNALITLPISK	1529.28	22.3	0.841478237	0.2
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1552.22	16.6	0.841478237	0.2
LPD1	AAQLGFNTACVEK	1578.7	16.8	0.841478237	0.2
SPT15	AAPSEKDT SATSGIVPTLQNIVATVTLGCR	1684.49	29.2	0.841478237	0.2
CDC19	ACDDKIMYVDYK	1691.56	12.87	0.844546479	0.2
CDC19	ACDDKIMYVDYK	1700.06	14.68	0.804972222	0.2
CDC19	ACDDKIMYVDYK	1706.62	15.1	0.841478237	0.2
CDC19	ACDDKIMYVDYK	1717.24	15.33	0.59866288	0.2
MAP1	ACMLGR	444.46	19.4	0.841478237	0.2
FAS1	CFGPIK	446.52	22.1	0.841478237	0.2
KGD2	ACTLAAK	457.96	17.9	0.841478237	0.2
CCT3	ACTIMLR	522.53	21.06	0.340894075	0.2
ADE3	ACAQQFR	530.77	17.7	0.725676425	0.2
MBR1	CQQT LNPLCK	535.67	21.3	0.841478237	0.2
ASN2	CGIFAAFK	547.13	28.1	0.09556777	0.2
CDC19	ACDDKIMYVDYK	567.78	15.16	0.531964138	0.2
ARG3	FMHCLPR	574.74	19.1	0.786949185	0.2
LPD1	AAQLGFNTACVEKR	582.63	12.43	0.588818231	0.2
DED1	ACVVYGGSPIGNQLR	588.02	13.1	0.841478237	0.2
RRP5	ACQYMSYTIHTK	597.31	20.36	0.423702278	0.2
CDD1	ACELSYSPYSHFR	597.53	17.4	0.841478237	0.2
POL5	ACEEDSANR	612.06	16.5	0.841478237	0.2
POL5	ACEEDSANR	616.27	16.5	0.841478237	0.2
ODC1	AAVDHYTGVMDCLT	620.89	14.6	0.841478237	0.2
NCL1	FNLQNCMR	635.18	10.5	0.841478237	0.2
SEC14	AAGHLVETSCTIMDLK	639.92	14.38	0.340894075	0.2
MVD1	ACVLVSDIK	642.56	21.77	0.633933271	0.2
YMR031C	CEQDITEAR	646.99	19	0.841478237	0.2
SAM1	ACLAEDPHSK	649.4	17.7	0.841478237	0.2
RPL21A	CRQEFLER	659.37	19.52	0.588818231	0.2
PDR5	FPCA EYVPR	659.92	16.58	0.676917461	0.2
IPI2	CGLSFFEGILSSI E F	664.3	21.5	0.841478237	0.2

YDL193W	CFGLFRYGQYQYNK	675.99	19	0.841478237	0.2
CWC2	CEYLHHIPDEEDIGK	679.31	15.85	0.544467774	0.2
HIF1	CQQTLDLSPK	685.76	14.65	0.827900862	0.2
YJR149W	ACIAGAIASLPLSHLDFR	698.4	23.7	0.841478237	0.2
SEN1	FNDIVCQWR	704.91	13	0.841478237	0.2
SCC2	ACSSCLSHLHPYINK	716.43	12.7	0.841478237	0.2
SHM2	CGAYLMVDMAH	720.06	13.83	0.705902861	0.2
GCD11	CQRP GCPGR	723.49	16.9	0.841478237	0.2
APN1	CEQLGIGLYNLHPGSTLK	727.65	19.86	0.544467774	0.2
SHM2	CGAYLMVDMAH	728.13	11.5	0.841478237	0.2
HIS7	ACEALGAGEILLNCIDK	730.24	22.97	0.504977757	0.2
ADE12	CQNLLGNGVVIHVPSFFK	734.51	23.4	0.841478237	0.2
YJL055W	FNLNWSDEGHAHEDCAK	734.63	21.34	0.578508489	0.2
RPL34A	CGDCGSALQGISTLRPR	737.06	17.6	0.664368423	0.2
ARO4	AVDACQAAAHSHHFMGVTK	745.43	26	0.841478237	0.2
ASN2	ADWGCAEDPSGR	750.65	20.29	0.423702278	0.2
TFB3	FLVNPECYHR	753.51	16.8	0.841478237	0.2
YDR193W	FNDSLMSFCVK	764.41	25.1	0.841478237	0.2
CTL1	FNEYMCSFLNASDLIRK	766.39	21	0.841478237	0.2
YLR427W	CGNFPPANLGSIK	777.12	30.7	0.841478237	0.2
CDC1	CQWSTWEDWPEGAESHR	778.56	17	0.841478237	0.2
YCP4	ACLSYLAHHGIIIFLPLGYK	782.13	33.9	0.841478237	0.2
YCP4	ACLSYLAHHGIIIFLPLGYK	785.43	33.27	0.68314913	0.2
YOR289W	CSCNILGNFK	786.02	14.8	0.841478237	0.2
CCA1	FNEENCQDMDK	800.53	19.9	0.841478237	0.2
CBF1	AAILACAAEYIQK	802.15	21.05	0.829722884	0.2
CCA1	FNEENCQDMDK	804.92	19.9	0.841478237	0.2
DCG1	ADVSIVGLLDSSINYCNLVGK	806.68	12.2	0.841478237	0.2
SFA1	AFEDLHNGDCLR	809.26	12.4	0.841478237	0.2
SUI2	ADVEVSCFSYEGIDAIDALK	837.91	26.13	0.544467774	0.2
YOL007C	FLYQAHHPNGTVFIAFAGCLGA	855.13	23.7	0.841478237	0.2
ILV1	ACSAGNHAQGVAFAAK	866.3	11.7	0.841478237	0.2
TCI1	ACELDPEGQVGGPDK	871.88	15.94	0.458842652	0.2
LPD1	AAQLGFNTACVEKR	873.16	12.5	0.734618574	0.2
NAM9	CQPDELISLATEMMNPNETTK	874.18	19.5	0.841478237	0.2
DED1	ACVVYGGSPIGNQLR	881.62	16.77	0.625682521	0.2
LOS1	CFGNGTCLDNDDINKDPNLK	884.92	15.4	0.556367811	0.2
RAT1	AESECDLDAEIKDEIVADVNR	896.4	20.9	0.841478237	0.2
CDC19	AEVSDVGNAILDGADCVMLSGETAK	898.81	26.91	0.544467774	0.2
ARG80	ACINASDTPDATDTSP	903.87	23.1	0.841478237	0.2
CDC19	AEVSDVGNAILDGADCVMLSGETAK	904.14	25.19	0.544467774	0.2
EFT2	AEQLYEGPADDANCIAIKNCD	909.93	21.3	0.841478237	0.2

YDR279W	AAYHNLLTFSPTMDSGCLNPDIK	913.06	19.8	0.841478237	0.2
YBR096W	CGFHETVPLENLSQEYCSEI	919.51	20.2	0.841478237	0.2
IRS4	AAQAIFQNHNSNEVSSPCPPVTVSR	923.31	11.1	0.841478237	0.2
ODC1	AAVDHYTGVMDCCLK	927.26	14	0.841478237	0.2
NPL4	CQPSAITLQQQEFR	944.38	15.5	0.716125371	0.2
YBR025C	CFDDAEIIHVEGDVD	957.77	18.32	0.725676425	0.2
DLD1	AVAQLNHCNSFQFAK	957.81	16.58	0.441748075	0.2
TUB3	AVCMLSNTTAIADAWK	961.65	18.5	0.841478237	0.2
RPT1	ACIIFFDEIDAVGGAR	963.26	28.9	0.841478237	0.2
SEC14	AAGHLVETSCTIMDLK	963.52	15.43	0.750890661	0.2
YGR117C	AEYTHIACYSIIDAK	968.43	14.1	0.841478237	0.2
MEF1	AECALSTMFGFATSLR	971.3	26.1	0.841478237	0.2
TEF2	CGGIDKR	976.65	18.4	0.891040011	0.2
DPP1	CQPVEGLPLDTLFTAK	980.9	24.93	0.633933271	0.2
FBA1	AFGNCHGLYAGDIALRPEILAEHQK	984.89	22.59	0.544467774	0.2
TEF2	CGGIDKR	985.75	20.7	0.844546479	0.2
CTT1	FNCYVQTMTPAQATK	999.42	13.38	0.567702774	0.2
				0.793757571	
CDC60	FMSSMAYPYMNGVMHAGHCFTLSK	1005.4	11.6	0.617069415	0.5
YDL183C	AEQVDTQPLHVYPPGISSPDECLR	1018.03	17.2	0.617069415	0.5
RPO21	CQTCQEGMNECPGHFGHIDLAK	1039.86	10.5	0.09556777	0.5
DED81	CSDDPRVTESVDVLMNVGEITGGSMR	1042.7	15.8	0.617069415	0.5
RPO21	CQTCQEGMNECPGHFGHIDLAK	1049.06	10.5	0.617069415	0.5
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1061.15	10	0.617069415	0.5
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1063.59	10	0.617069415	0.5
NIT2	AVDTQCYVLMPGQVGMHDLSDPEWEK	1065.82	30.7	0.617069415	0.5
YML096W	CGKPVIELLNVSFENPR	1072.05	19.4	0.617069415	0.5
UTP7	AELFLNETCHSATYLQNEQYFAVAQK	1086.25	17	0.617069415	0.5
POM152	ACAANVDQISFLEPINLK	1087.51	22.77	0.211287898	0.5
BIO2	ACTGGILGLGESEDDHIGFIYTLNMSPH	1091.17	16.3	0.617069415	0.5
POM152	ACAANVDQISFLEPINLK	1092.25	26.08	0.526784511	0.5
YNL087W	AENFICEVNIPTIELVR	1095.33	37.87	0.297555869	0.5
YNL087W	AENFICEVNIPTIELVR	1099.24	41.63	0.317300419	0.5
CDC43	FNGELCIPQEIFNDFSK	1115.61	26.4	0.6494311	0.5
CCA1	FNEENCQDMDKINHVVNDNILNSHLK	1134.23	14.8	0.617069415	0.5
SPT4	ACMLCGIVQTTNEFNR	1136.15	13	0.617069415	0.5
ADE6	CGLSGFSVSDLLIPGNEQPWELNIGKPYH	1137.02	27.9	0.617069415	0.5
RHO5	CGFMGYTECSAATQAGVR	1162.5	14.9	0.617069415	0.5
YCL019W	AVCDNTPSIDTDPPEYRSSDHATPNIMPK	1175.51	27.8	0.617069415	0.5
GPA2	FNVNLEPECELTQQDLR	1181.95	30	0.617069415	0.5
YPR148C	AAVDCECEFQNLHNEK	1217.2	11.1	0.617069415	0.5

MYO5	FNNQFEP CAGNITNYLLEK	1222.19	20.85	0.354474936	0.5
MYO5	FNNQFEP CAGNITNYLLEK	1226.67	26.24	0.516104601	0.5
GCN20	AALCLNNPHILVLDEPSNHLDTTGLDALVEALK	1246.39	70	0.617069415	0.5
SUI2	ADVEVSCFSYEGIDAIKDALK	1251.7	29.6	0.609902725	0.5
ADE4	CGILGIVLANQTTTPVAPELCDGCIFLQHR	1255.65	23	0.617069415	0.5
SUI2	ADVEVSCFSYEGIDAIKDALK	1255.97	28.34	0.277045343	0.5
TCI1	ACELDPEGQVGGPDKFFTMGQIMGGQDGVSIITR	1262.34	24	0.617069415	0.5
TCI1	ACELDPEGQVGGPDKFFTMGQIMGGQDGVSIITR	1264.45	70	0.617069415	0.5
YHR029C	AFAPVINVYEDPVC GSGSVALAR	1282.96	18.1	0.617069415	0.5
SLG1	ADSYNWQSSSHCNSECSAK	1288.77	21.1	0.617069415	0.5
DBP2	AEGFDKPTGIQCQGWPMALSGR	1289.65	16.8	0.448696848	0.5
NAM9	CQPDELISLATEMMNPNETTK	1297.44	26.9	0.617069415	0.5
YLR004C	AANADSCSVSTSSINVDDADVALR	1305.21	26.4	0.617069415	0.5
TRM1	CFALYGGANMVSHESTHESALR	1317.18	13.8	0.617069415	0.5
ACS2	ACIIDPVTGVELEGNDVEGLAVK	1334.58	23.15	0.664368423	0.5
CDC19	AEVSDVGNAILDGADCVMLSGETAK	1352.07	26.57	0.354474936	0.5
EFT2	AEQLYEGPADDANCIAIKNCD	1363.82	21.3	0.617069415	0.5
STE20	CSDGDPSTKYANLVKIGQGASGGVYT	1413.29	11.6	0.617069415	0.5
ARD2	CSECHQHNVFVYLPVDDLTk	1446.79	20.63	0.617069415	0.5
ARO1	AALYALHSLGCK	1482.7	14	0.617069415	0.5
MAL13	CQNALITLPISK	1529.28	22.3	0.617069415	0.5
ERG10	CGNADV VVAGGCESMTNAPYYMPAAR	1552.22	16.6	0.617069415	0.5
YMR259C	AFCIRCQLEFPAILEELLSKSVK	1556.63	36.9	0.617069415	0.5
LPD1	AAQLGFNTACVEK	1578.7	16.8	0.617069415	0.5
LPD1	AAQLGFNTACVEK	1587.89	16.8	0.617069415	0.5
SPT15	AAPSEKDT SATSGIVPTLQNIVATVTLGCR	1684.49	29.2	0.617069415	0.5
CDC19	ACDDKIMYVDYK	1691.56	12.87	0.623989595	0.5
CDC19	ACDDKIMYVDYK	1706.62	15.1	0.617069415	0.5
CDC19	ACDDKIMYVDYK	1717.24	15.33	0.188232726	0.5
GRX3	CGFSR	403.6	17.8	0.617069415	0.5
GCD10	CRPYQSIR	420.41	17.9	0.617069415	0.5
FAS1	CFGPIK	446.52	22.1	0.617069415	0.5
KGD2	ACTLAAK	457.96	17.9	0.617069415	0.5
NGR1	CFGFVR	483.08	24.6	0.617069415	0.5
ASN2	ADWGCAEDPSGR	498.75	17.3	0.617069415	0.5
YNL247W	CQPWNK	506.66	19.1	0.617069415	0.5
ADE3	ACAQQFR	526.21	17.8	0.617069415	0.5
MBR1	CQQT LNPLCK	535.67	21.3	0.617069415	0.5
SPR3	CRNRDLPLLDNK	562.96	12.1	0.617069415	0.5
SLA2	ACIVYTDWHQSSK	592.84	14	0.617069415	0.5
YDR307W	CGLLGHDLR	606.22	15.6	0.617069415	0.5
YDR307W	CGLLGHDLR	611.08	16.2	0.617069415	0.5

POL5	ACEEDSANR	612.06	16.5	0.617069415	0.5
NCL1	FNLQNCMR	635.18	10.5	0.617069415	0.5
SAM1	ACLAEDPHSK	649.4	17.7	0.617069415	0.5
IPI2	CGLSFFEGILSSI ELF	664.3	21.5	0.617069415	0.5
YDL193W	CFGLFRYGQYQYNK	675.99	19	0.617069415	0.5
DUS1	CQPYFRPVNGITGDKR	696.84	12.5	0.617069415	0.5
YJR149W	ACIAGAIASLPLSHLDFR	698.4	23.7	0.617069415	0.5
SEN1	FNDIVCQWR	704.91	13	0.617069415	0.5
SCC2	ACSSCLSHLHPYINK	710.21	10.5	0.617069415	0.5
SCC2	ACSSCLSHLHPYINK	716.43	12.7	0.617069415	0.5
CDC19	ACDDKIMYVDYKNITK	725.42	13.09	0.664368423	0.5
ARO4	AVDACQAAAHSHHFMGVTK	742.45	26	0.617069415	0.5
ARO4	AVDACQAAAHSHHFMGVTK	745.43	26	0.617069415	0.5
YLR427W	CGNFPPANLGSIK	777.12	30.7	0.617069415	0.5
YCP4	ACLSYLAHHGII FLPLGYK	782.13	33.9	0.617069415	0.5
DCG1	ADVSIVGLLDSSINYCNLVGK	806.68	12.2	0.617069415	0.5
SFA1	AFEDLHNGDCLR	809.26	12.4	0.617069415	0.5
SLG1	ADSYNWQSSSHCNSECSAK	853.85	21.1	0.617069415	0.5
BMH2	ACHLAK	869.46	15.7	0.617069415	0.5
LPD1	AAQLGFNTACVEKR	873.16	12.5	0.396731179	0.5
YDR279W	AAYHNLLTFSPTMDSGCLNPDIK	913.06	19.8	0.617069415	0.5
YBR096W	CGFHETVPLENLSQEYCSEI	919.51	20.2	0.617069415	0.5
IRS4	AAQAIFQNHNSNEVSSPCPPVTVSR	923.31	11.1	0.617069415	0.5
TUB3	AVCMLSNTTAIADAWK	961.65	18.5	0.617069415	0.5
RPT1	ACIIFFDEIDAVGGAR	963.26	28.9	0.617069415	0.5
UTP20	CREMASVLISTMLPK	975.23	25.1	0.617069415	0.5
TEF2	CGGIDKR	976.65	18.4	0.731996449	0.5
DPP1	CQPVEGLPLDTLFTAK	985.22	25.12	0.419973923	0.5
PIM1	CQTQNPLILIDEIDK	986.1	24.88	0.222638367	0.5
				0.576958114	
FBA1	AAAFGNCHGLYAGDIALRPEILAEHQK	1032.36	23.89	0.664368423	1
RPO21	CQTCQEGMNECPGHFGHIDLAK	1039.86	10.5	0.664368423	1
DED81	CSDDPRVTESVDVLMNVGEITGGSMR	1042.7	15.8	0.317300419	1
RPO21	CQTCQEGMNECPGHFGHIDLAK	1049.06	10.5	0.317300419	1
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1061.15	10	0.317300419	1
YLR431C	ACEELHSESTTAQDGSSALPSKPIDIHK	1063.59	10	0.317300419	1
NIT2	AVDTQCYVLMPGQVGMHDLSDPEWEK	1065.82	30.7	0.317300419	1
SPT4	ACMLCGIVQTTNEFNR	1136.15	13	0.317300419	1
YPR148C	AAVDCECEFQNL EHNK	1217.2	11.1	0.317300419	1
GCN20	AALCLNNPHILVLDEPSNHLDTTGLDALVEALK	1246.39	70	0.317300419	1
SUI2	ADVEVSCFSYEGIDA IKDALK	1251.7	29.6	0.307524691	1

ADE4	CGILGIVLANQTTTPVAPELCDGCIFLQHR	1255.65	23	0.317300419	1
TCI1	ACELDPEGQVGGPDKFFTMGQIMGGQDGVSIITR	1264.45	70	0.317300419	1
YHR029C	AFAPVINVYEDPVCSGSVALAR	1286.67	19.7	0.317300419	1
YLR004C	AANADSCSVSTSSINVDDADVALR	1305.21	26.4	0.317300419	1
ACS2	ACIIDPVTGVELEGNDVEGLVAVK	1339.72	24.8	0.664368423	1
ADH1	AAHIPQGTDLAQVAPILCAGITVYK	1390.22	22.1	0.317300419	1
STE20	CSDGDPSTKYANLVKIGQGASGGVYT	1413.29	11.6	0.317300419	1
TUB1	AFHESNSVSEITNACFEPGNQMVK	1438.81	18.88	0.664368423	1
ARO1	AALYALHSLGCK	1482.7	14	0.317300419	1
MAL13	CQNALITLPISK	1529.28	22.3	0.317300419	1
YMR259C	AFCIRCQLEFPAILEELLSKSVK	1556.63	36.9	0.317300419	1
LPD1	AAQLGFNTACVEK	1578.7	16.8	0.317300419	1
LPD1	AAQLGFNTACVEK	1587.89	16.8	0.317300419	1
SPT15	AAPSEKDTSATSGIVPTLQNIVATVTLGCR	1684.49	29.2	0.317300419	1
CDC19	ACDDKIMYVDYK	1691.56	12.87	0.326882632	1
CDC19	ACDDKIMYVDYK	1706.62	15.1	0.317300419	1
GRX3	CGFSR	403.6	17.8	0.317300419	1
GCD10	CRPYQSIR	420.41	17.9	0.317300419	1
NGR1	CFGFVR	483.08	24.6	0.317300419	1
CDD1	ACELSYSPYSHFR	599.88	17.4	0.664368423	1
NCL1	FNLQNCMR	635.18	10.5	0.317300419	1
SCC2	ACSSCLSHLHPYINK	710.21	10.5	0.317300419	1
HIS7	ACEALGAGEILLNCIDK	730.24	22.97	0.664368423	1
ARO4	AVDACQAAAHSHHFMGVTK	745.43	26	0.317300419	1
YLR427W	CGNFPPANLGSIK	777.12	30.7	0.317300419	1
YCP4	ACLSYLAHHGIIIFLPLGYK	782.13	33.9	0.317300419	1
DCG1	ADVSIVGLLDSSINYNLVGK	806.68	12.2	0.317300419	1
RRP5	ACQYMSYTIHTK	899.2	15.6	0.317300419	1
TUB1	AVCMLSNTTTSIAEAWK	977.51	16.6	0.317300419	1
TCI1	ACELDPEGQVGGPDKFFTMGQIMGGQDGVSIITR	1264.45	70	0.04550454	2
ARO1	AALYALHSLGCK	1482.7	14	0.04550454	2
YMR259C	AFCIRCQLEFPAILEELLSKSVK	1556.63	36.9	0.04550454	2
CDC19	ACDDKIMYVDYK	1706.62	15.1	0.04550454	2
GRX3	CGFSR	403.6	17.8	0.04550454	2
GCD10	CRPYQSIR	420.41	17.9	0.04550454	2
PUS1	CGCPVER	618.94	18.4	0.664368423	2
LPD1	AAQLGFNTACVEKR	873.16	12.5	0.93460116	2