

The list of the peptides discovered in the serum of control and ovarian cancer patients

Protein	Accession	Peptide	Unique	-10lgP	Mass	Length	ppm	m/z	z	RT	Scan	T1	T2	T3	Con1	Con2	Con3	Start	End	PTM
P00734	THRB_HUMAN	LEDKTERELLESY	Y	16.98	2082.13	13	3.4	695.1	3	96.2	F2:13367	8.33E-05	4.44E-05	5.49E-05	4.88E-04	4.83E-04	5.50E-04	347	359	TMT6plex
Q14624	ITIH4_HUMAN	QLGLPGPPDVPDH	Y	38.75	1323.65	13	0.5	662.8	2	110	F2:15972	1.09E-04	9.59E-05	9.51E-05	0.00E+00	0.00E+00	0.00E+00	669	681	Pyro-glu from Q
A7KAX9	RHG32_HUMAN	NHLLVH	Y	17.96	960.571	6	0.9	481.3	2	100	F2:14123	4.11E-05	4.88E-05	4.23E-05	0.00E+00	0.00E+00	0.00E+00	246	251	TMT6plex
P00488	F13A_HUMAN	NNSNAAEDDLPTVEL QGVVPR	Y	60.27	2466.26	21	4.1	1234	2	104	F1:15541	0.00E+00	0.00E+00	3.72E-04	9.91E-04	1.04E-03	1.21E-03	18	38	TMT6plex
P01833	PIGR_HUMAN	ADAAPDEKVLDSGFR EIEN	Y	30.7	2533.31	19	3	845.4	3	94.9	F1:13887	0.00E+00	1.21E-04	6.47E-05	4.08E-04	2.62E-04	3.25E-04	578	596	TMT6plex
P02671	FIBA_HUMAN	DEAGSEADHEGTHST	Y	57.11	1770.75	15	5.1	591.3	3	12.8	F1:784	0.00E+00	0.00E+00	0.00E+00	5.90E-05	4.58E-05	6.34E-05	605	619	TMT6plex
P00734	THRB_HUMAN	SLEDKTERELLESYID G	Y	38.17	2454.29	17	2.1	819.1	3	121	F1:18962	6.39E-04	3.58E-04	3.81E-04	8.86E-04	1.15E-03	1.01E-03	346	362	TMT6plex
P00734	THRB_HUMAN	SLEDKTERELLESY	Y	41.92	2169.16	14	1.6	724.1	3	102	F1:15206	3.17E-04	6.76E-05	1.58E-04	1.64E-03	1.99E-03	1.31E-03	346	359	TMT6plex
P00734	THRB_HUMAN	EDKTERELLESY	Y	37.31	1969.04	12	3.6	985.5	2	78.3	F1:11047	5.31E-04	6.53E-05	3.58E-04	2.61E-03	2.11E-03	1.67E-03	348	359	TMT6plex
P02765	FETUA_HUMAN	SLGSPSGEVSHPRKT	Y	42.26	1996.11	15	3.7	500	4	27.9	F1:3174	7.68E-05	6.12E-05	1.11E-04	2.41E-04	3.28E-04	3.53E-04	325	339	TMT6plex
P00734	THRB_HUMAN	GDGLDESDRAIEG	Y	18.82	1676.77	14	4.8	839.4	2	53	F2:6590	1.71E-04	2.43E-04	1.11E-04	3.44E-04	4.51E-04	4.91E-04	300	313	TMT6plex
O00161	SNP23_HUMAN	TNGQLQQPT	Y	36.62	1215.63	9	5.6	608.8	2	41.1	F1:5174	5.90E-04	5.39E-04	3.26E-04	1.04E-03	8.69E-04	8.91E-04	123	131	TMT6plex; Deamidation
P01024	CO3_HUMAN	TKENEGFTVTAEGK	Y	43.36	2197.22	14	1	733.4	3	56.4	F1:7570	2.72E-04	1.99E-04	2.28E-04	6.83E-04	7.73E-04	5.50E-04	1324	1337	TMT6plex
P00734	THRB_HUMAN	SLEDKTERELL	Y	22.01	1790.02	11	2.6	896	2	77.1	F1:10844	3.18E-04	1.96E-04	2.10E-04	9.37E-04	7.35E-04	6.36E-04	346	356	TMT6plex
P04632	CPNS1_HUMAN	GGGGGGLGGGLG	Y	31.92	1043.56	12	1.4	522.8	2	54	F1:7162	1.77E-03	1.31E-03	1.76E-03	7.47E-04	6.83E-04	9.81E-04	15	26	TMT6plex
P01024	CO3_HUMAN	SEETKENEGF	Y	41.89	1626.81	10	5.5	814.4	2	48.9	F1:6382	3.27E-03	3.26E-03	2.71E-03	5.09E-03	4.41E-03	5.66E-03	1321	1330	TMT6plex
Q14624	ITIH4_HUMAN	QGAKIPKPEAS	Y	27.9	1812.11	11	4.3	605	3	41.7	F1:5262	1.96E-04	1.72E-04	2.48E-04	5.35E-04	8.08E-04	6.90E-04	630	640	TMT6plex
P58215	LOXL3_HUMAN	AKYGGP	Y	17.44	1049.63	6	-8	525.8	2	81.6	F2:10930	6.06E-05	1.21E-04	9.40E-05	1.64E-04	1.63E-04	2.11E-04	98	103	TMT6plex
O60673	DPOLZ_HUMAN	PYLRQ	N	16.57	904.533	5	8.3	453.3	2	80.5	F1:11415	8.09E-05	8.75E-05	9.53E-05	1.53E-04	1.46E-04	1.88E-04	3121	3125	TMT6plex
P00734	THRB_HUMAN	DKTERELL	Y	15.04	1460.86	8	1.4	488	3	48	F1:6245	3.18E-04	3.20E-04	6.07E-04	8.45E-04	7.61E-04	1.05E-03	349	356	TMT6plex
P02671	FIBA_HUMAN	GDSTFESKS	Y	30.65	1414.73	9	-2.7	708.4	2	38.4	F2:4519	1.51E-03	1.52E-03	1.08E-03	5.76E-04	6.27E-04	4.86E-04	592	600	TMT6plex
P01024	CO3_HUMAN	SEETKENEGFTVTAE GK	Y	49.63	2542.34	17	-2.2	848.5	3	58.7	F2:7499	3.51E-04	1.09E-03	8.65E-04	1.68E-03	2.35E-03	2.82E-03	1321	1337	TMT6plex
P02671	FIBA_HUMAN	SYKMADEAGSEADH EGTHST	Y	57.37	2580.18	20	3.5	861.1	3	39.6	F1:4987	8.48E-04	2.34E-04	5.56E-04	2.56E-03	1.47E-03	1.95E-03	600	619	TMT6plex
P01024	CO3_HUMAN	NEGFTVTAE	Y	31.61	1195.59	9	-6.5	598.8	2	68.8	F1:9521	5.13E-04	4.32E-04	6.11E-04	9.71E-04	1.46E-03	1.32E-03	1327	1335	TMT6plex
P00734	THRB_HUMAN	DKTERELLESY	Y	35.11	1840	11	4.1	921	2	73.6	F1:10256	4.96E-04	1.93E-04	3.66E-04	1.93E-03	1.52E-03	1.11E-03	349	359	TMT6plex
Q9H4Q3	PRD13_HUMAN	GDPPPP	Y	21.33	807.433	6	1.9	404.7	2	28.7	F1:3326	1.80E-04	1.93E-04	1.66E-04	1.30E-04	8.06E-05	1.21E-04	370	375	TMT6plex
Q14624	ITIH4_HUMAN	NFRPG	Y	17.08	819.444	5	3.1	410.7	2	32.5	F1:3899	2.42E-04	3.14E-04	4.82E-04	1.04E-03	1.80E-03	1.54E-03	659	663	TMT6plex; Deamidation
P02775	CXCL7_HUMAN	NLAKGKEESLDS	Y	41.32	1863	13	2.9	622	3	41.7	F1:5253	1.85E-04	1.93E-04	1.38E-04	2.51E-04	2.81E-04	3.45E-04	44	56	TMT6plex
P00734	THRB_HUMAN	EDKTERELL	Y	30.88	1589.9	9	4.9	531	3	52.5	F1:6939	6.83E-04	1.13E-03	8.11E-04	2.13E-03	1.64E-03	2.60E-03	348	356	TMT6plex

Q8WZ42	TITIN_HUMAN	EEVVV	N	15.64	802.464	5	0.2	402.2	2	60.1	F1:8174	1.78E-04	1.10E-04	6.04E-04	8.56E-04	1.00E-03	1.11E-03	19117	19121	TMT6plex
Q96A19	C102A_HUMAN	NIEKL	N	20.58	1073.69	5	-5.5	537.8	2	53.3	F1:7058	2.18E-03	1.95E-03	2.94E-03	4.29E-03	3.98E-03	3.18E-03	279	283	TMT6plex
Q13402	MYO7A_HUMAN	NLEKL	N	20.58	1073.69	5	-5.5	537.8	2	53.3	F1:7058	2.18E-03	1.95E-03	2.94E-03	4.29E-03	3.98E-03	3.18E-03	1150	1154	TMT6plex
P00734	THRB_HUMAN	NIEKI	N	20.58	1073.69	5	-5.5	537.8	2	53.3	F1:7058	2.18E-03	1.95E-03	2.94E-03	4.29E-03	3.98E-03	3.18E-03	437	441	TMT6plex
P02671	FIBA_HUMAN	MADEAGSEADHEGTHST	Y	62.68	1972.83	17	2.4	658.6	3	22.7	F2:2245	1.69E-04	8.77E-05	1.04E-04	2.39E-04	2.02E-04	2.43E-04	603	619	TMT6plex
P02671	FIBA_HUMAN	DFLAEGGGV	Y	41.35	1092.57	9	2.9	547.3	2	101	F1:14966	5.54E-03	9.52E-03	6.35E-03	3.57E-03	2.13E-03	0.00E+00	26	34	TMT6plex
P02452	CO1A1_HUMAN	DDGEAGKPG	Y	36.6	1302.68	9	3.8	652.4	2	25.9	F1:2847	4.40E-04	7.07E-04	1.07E-03	1.46E-03	1.34E-03	1.95E-03	231	239	TMT6plex
P02461	CO3A1_HUMAN	DGVPGKDGPRGPT	Y	32.86	1709.95	13	2.3	571	3	34.8	F1:4250	2.76E-04	4.75E-04	2.72E-04	8.25E-04	6.02E-04	5.88E-04	752	764	TMT6plex
P02675	FIBB_HUMAN	DKKREEAPSLRPAPPPISGGGY	Y	46.44	3008.7	22	4.9	753.2	4	56.5	F2:7129	0.00E+00	0.00E+00	0.00E+00	4.37E-05	4.96E-05	7.95E-05	50	71	TMT6plex
P00734	THRB_HUMAN	FEKKSLEDKTERELLESY	Y	20.03	3159.78	18	4.6	1054	3	102	F1:15144	5.83E-05	0.00E+00	0.00E+00	3.79E-04	3.28E-04	1.76E-04	342	359	TMT6plex
Q9HCU4	CELR2_HUMAN	NDGDWHHAQLALGASGGPGHAIL	Y	16.12	2523.25	23	-0.4	842.1	3	22.8	F1:2373	0.00E+00	0.00E+00	0.00E+00	7.93E-05	3.88E-05	6.02E-05	1695	1717	TMT6plex; Deamidation
P01024	CO3_HUMAN	ENEGFTVTAEKG	Y	51.99	1738.91	12	0.8	870.5	2	63.5	F1:8689	1.06E-03	1.08E-03	6.65E-04	1.29E-03	1.53E-03	1.76E-03	1326	1337	TMT6plex
P60608	EFC2_HUMAN	PIAFLGLK	Y	18.3	1315.86	8	3.4	658.9	2	123	F2:18501	0.00E+00	6.60E-05	0.00E+00	9.40E-05	1.03E-04	1.30E-04	101	108	TMT6plex
Q9BXJ8	T120A_HUMAN	FKLYLTII	Y	19.69	1467.95	8	1.9	735	2	124	F1:19415	4.75E-05	4.96E-05	5.19E-05	1.70E-04	1.08E-04	1.71E-04	136	143	TMT6plex
P01024	CO3_HUMAN	TLDPER	Y	19.07	958.529	6	4.3	480.3	2	23.8	F2:2446	5.81E-04	6.38E-04	4.14E-04	1.12E-03	8.49E-04	7.99E-04	946	951	TMT6plex
P68363	TBA1B_HUMAN	DVVPK	N	17.22	1014.65	5	2.3	508.3	2	38.5	F1:4821	7.18E-04	7.54E-04	6.89E-04	9.77E-04	1.21E-03	1.31E-03	322	326	TMT6plex
Q15942	ZYX_HUMAN	VNPFPRPGDSEPPAPGAQRAQMG	Y	27.61	2604.31	23	1.5	869.1	3	65.3	F1:8972	0.00E+00	5.47E-05	4.00E-05	9.63E-05	1.10E-04	1.04E-04	36	58	TMT6plex
Q6UX71	PXDC2_HUMAN	DTNRASVQDSPEPR	Y	20.04	1856.92	15	2.1	620	3	19.8	F1:1887	1.23E-04	1.70E-04	2.12E-04	1.03E-04	5.92E-05	5.75E-05	76	90	TMT6plex
P02671	FIBA_HUMAN	DEAGSEADHEGTH	Y	50.87	1582.67	13	8.4	792.3	2	11.4	F2:598	1.10E-04	1.15E-04	5.04E-05	3.20E-04	1.89E-04	3.55E-04	605	617	TMT6plex
P02452	CO1A1_HUMAN	DGKTGPPGP	Y	30.37	1298.72	9	3.6	650.4	2	27.2	F1:3059	7.04E-04	1.17E-03	1.27E-03	1.87E-03	1.43E-03	1.82E-03	550	558	TMT6plex; Hydroxylation
P0C0L4	CO4A_HUMAN	QLNNRQI	Y	33.61	867.456	7	2.6	434.7	2	42.2	F2:5011	4.23E-04	3.44E-04	1.43E-03	1.61E-03	1.95E-03	2.53E-03	1345	1351	Pyro-glu from Q
P00734	THRB_HUMAN	DESDRAIEG	Y	20.01	1334.62	10	2.3	668.3	2	28.3	F1:3251	4.09E-04	6.99E-04	5.17E-04	9.05E-04	1.15E-03	1.51E-03	304	313	TMT6plex
P01024	CO3_HUMAN	EGFTVTAEKG	Y	47.15	1495.83	10	2.8	748.9	2	63.7	F1:8719	5.73E-04	6.89E-04	5.27E-04	9.37E-04	8.19E-04	1.17E-03	1328	1337	TMT6plex
P02671	FIBA_HUMAN	DGHKEVTKEVV	Y	34.61	1927.13	11	4.2	482.8	4	39.7	F1:4989	3.78E-05	0.00E+00	4.41E-05	7.41E-05	6.75E-05	9.09E-05	473	483	TMT6plex
Q13395	TARB1_HUMAN	GHDCAAN	Y	16.3	915.407	7	-5.6	458.7	2	105	F2:14938	9.69E-05	4.36E-05	8.19E-05	4.37E-05	0.00E+00	0.00E+00	1097	1103	TMT6plex
P52566	GDIR2_HUMAN	TEKAPEPHVEE	Y	23.2	1535.77	11	4.1	768.9	2	41.5	F1:5221	3.12E-04	4.75E-04	2.33E-04	5.18E-04	7.41E-04	8.85E-04	2	12	TMT6plex; Acetylation
P01024	CO3_HUMAN	TLDPERLG	Y	30.3	1128.63	8	4.8	565.3	2	56.7	F2:7172	3.54E-03	3.34E-03	2.78E-03	4.31E-03	3.90E-03	3.86E-03	946	953	TMT6plex
Q14624	ITI4_HUMAN	GPPDVPDHA	Y	48.82	1132.57	9	1.3	567.3	2	39.8	F1:5009	1.18E-03	5.05E-03	2.42E-03	6.90E-03	6.01E-03	1.04E-02	674	682	TMT6plex
P02671	FIBA_HUMAN	QFTSSTSYNRGDSTFESKS	Y	39.55	2586.26	19	5.9	863.1	3	59.8	F1:8133	3.56E-04	7.84E-04	5.49E-04	2.67E-04	1.22E-04	0.00E+00	582	600	TMT6plex

P01024	CO3_HUMAN	GDFLEAN	Y	21	975.487	7	6.3	488.8	2	97.5	F1:14353	1.37E-04	1.10E-04	1.50E-04	8.28E-05	5.54E-05	0.00E+00	1173	1179	TMT6plex; Dehydration
P01024	CO3_HUMAN	EETKENEGFTVTAEGK	Y	51.34	2455.3	16	0	819.4	3	58.5	F2:7473	2.20E-04	3.52E-04	4.11E-04	1.18E-03	1.09E-03	1.94E-03	1322	1337	TMT6plex
Q9Y5S2	MRCKB_HUMAN	DPELR	N	16.62	857.481	5	7	429.8	2	26.8	F2:2882	1.71E-04	2.00E-04	2.00E-04	4.37E-04	5.65E-04	7.71E-04	1575	1579	TMT6plex
Q15942	ZYX_HUMAN	QEKGHPVPPPAQ	Y	24.95	1566.84	12	3.6	784.4	2	28.5	F1:3293	0.00E+00	5.50E-05	5.53E-05	1.19E-04	1.01E-04	8.19E-05	326	337	Pyro-glu from Q; TMT6plex
Q9BXF3	CECR2_HUMAN	KNVSSI	N	17.81	875.528	6	-0.1	438.8	2	36.2	F1:4465	1.12E-04	1.48E-04	2.20E-04	2.80E-04	2.38E-04	3.65E-04	188	193	TMT6plex
O00443	P3C2A_HUMAN	KNVSSL	N	17.81	875.528	6	-0.1	438.8	2	36.2	F1:4465	1.12E-04	1.48E-04	2.20E-04	2.80E-04	2.38E-04	3.65E-04	293	298	TMT6plex
P0DJ18	SAA1_HUMAN	GGAWAAEAISDAREN IQ	Y	19	1987	17	1.9	663.3	3	112	F1:17118	0.00E+00	4.76E-05	0.00E+00	6.33E-05	8.66E-05	6.58E-05	68	84	TMT6plex; Mutation
Q7RTS9	DYM_HUMAN	QDLNV	N	17.9	816.454	5	6.7	409.2	2	57.9	F1:7824	1.79E-04	1.01E-04	2.43E-04	3.16E-04	5.62E-04	6.17E-04	523	527	TMT6plex
P02452	CO1A1_HUMAN	NGDDGEAGKPGRPG ERGPPGP	Y	15.15	2507.24	21	4.3	836.8	3	22.7	F2:2254	7.30E-05	1.43E-04	0.00E+00	2.39E-04	2.11E-04	2.38E-04	229	249	TMT6plex; Deamidation ; Dihydroxy
P0C0L4	CO4A_HUMAN	SLGSKINVKVGGNS	Y	43.66	2046.24	14	1.1	683.1	3	65.5	F1:9003	5.45E-04	1.24E-03	6.89E-04	1.51E-03	1.33E-03	1.78E-03	1361	1374	TMT6plex
Q96T58	MINT_HUMAN	TKEAR	N	17.08	1061.66	5	-4.4	531.8	2	95.1	F1:13920	1.89E-03	9.62E-04	2.03E-03	3.47E-04	2.53E-04	5.81E-04	2298	2302	TMT6plex
O15072	ATS3_HUMAN	PRSLVM	Y	18.42	930.552	6	8	466.3	2	90.4	F2:12346	0.00E+00	0.00E+00	0.00E+00	8.88E-05	5.13E-05	1.29E-04	1080	1085	TMT6plex
Q14624	ITIH4_HUMAN	QAGAAGSRMNFPRG EGDDESIMLEDSVSPK	Y	42.73	1401.66	14	1.4	701.8	2	43.5	F1:5546	1.68E-04	2.05E-04	1.29E-04	2.17E-04	2.56E-04	2.50E-04	650	663	Pyro-glu from Q
Q9Y490	TLN1_HUMAN		Y	32.99	2210.07	16	1	737.7	3	85	F1:12155	1.48E-04	2.80E-04	1.43E-04	3.13E-05	9.11E-05	0.00E+00	412	427	TMT6plex
Q14624	ITIH4_HUMAN	GPPDVPDHAAYHP	Y	38.98	1600.78	13	1.5	534.6	3	46.5	F1:6010	9.81E-05	1.44E-04	1.15E-04	1.65E-04	1.57E-04	1.76E-04	674	686	TMT6plex
P02461	CO3A1_HUMAN	DGVPGKDGPR	Y	28.76	1454.82	10	1.8	485.9	3	28.4	F1:3263	2.15E-04	3.71E-04	3.58E-04	8.15E-04	5.13E-04	5.53E-04	752	761	TMT6plex
Q15942	ZYX_HUMAN	VQEKGHPVPPPAQNQ NQV	Y	31.28	2495.37	18	1.8	832.8	3	38.8	F1:4867	4.78E-05	0.00E+00	0.00E+00	1.20E-04	1.63E-04	5.95E-05	325	342	TMT6plex
P01024	CO3_HUMAN	ETKENEGF	Y	19.63	1410.74	8	1	706.4	2	45.5	F1:5836	1.93E-03	1.59E-03	1.33E-03	2.93E-03	2.46E-03	3.99E-03	1323	1330	TMT6plex
Q9Y493	ZAN_HUMAN	ARLLSPDLW	Y	21.43	1298.75	9	2.3	650.4	2	65.7	F2:8491	3.68E-04	4.99E-04	4.17E-04	3.08E-04	2.64E-04	3.45E-04	102	110	TMT6plex
P01024	CO3_HUMAN	ETKENEGFTVTAEGK	Y	48.53	2326.26	15	4.7	776.4	3	56.9	F2:7211	6.30E-04	7.54E-04	9.67E-04	2.98E-03	2.77E-03	5.26E-03	1323	1337	TMT6plex
A9QM74	IMA8_HUMAN	LPALLHLLQ	Y	16.43	1245.8	9	7.6	623.9	2	106	F2:15116	4.85E-05	3.49E-05	0.00E+00	5.65E-05	7.72E-05	1.11E-04	243	251	TMT6plex
O15554	KCNN4_HUMAN	GLHPAPVR	Y	24.09	1074.65	8	0.7	538.3	2	77.2	F2:10226	0.00E+00	6.91E-05	7.52E-05	1.44E-04	1.29E-04	9.77E-05	116	123	TMT6plex
Q14624	ITIH4_HUMAN	YLQGAKIPKPEAS	Y	39.58	2088.26	13	1.2	697.1	3	69	F1:9552	3.14E-04	6.60E-04	5.58E-04	1.12E-03	2.20E-03	1.41E-03	628	640	TMT6plex
Q14624	ITIH4_HUMAN	LQGAKIPKPEAS	Y	28.49	1925.19	12	5.6	642.7	3	57.1	F2:7251	1.60E-04	1.80E-04	2.13E-04	4.12E-04	8.08E-04	5.30E-04	629	640	TMT6plex
Q14624	ITIH4_HUMAN	VLSSRQL	Y	24	1030.63	7	0.7	516.3	2	48.9	F1:6391	6.33E-04	7.23E-04	8.76E-04	1.36E-03	2.53E-03	1.73E-03	664	670	TMT6plex
P42684	ABL2_HUMAN	GENHVVK	Y	16.15	1240.72	7	5	414.6	3	23.3	F2:2371	5.62E-05	6.31E-05	6.71E-05	1.16E-04	9.81E-05	7.79E-05	418	424	TMT6plex; Deamidation
P02675	FIBB_HUMAN	NEEGF	Y	18.14	823.392	5	1.5	412.7	2	47.8	F1:6220	3.36E-04	1.27E-04	3.09E-04	7.08E-04	3.66E-04	7.07E-04	36	40	TMT6plex
P10124	SRGN_HUMAN	DSQDLGQHGLEED	Y	25.87	1670.76	13	1.9	836.4	2	48.7	F1:6358	1.31E-04	2.24E-04	1.66E-04	2.56E-04	3.09E-04	4.39E-04	143	155	TMT6plex
Q460N5	PAR14_HUMAN	THGNHSLI	Y	16.09	1106.6	8	8.7	554.3	2	62.1	F2:7918	1.21E-04	1.96E-04	2.24E-04	2.82E-04	2.89E-04	2.60E-04	1749	1756	TMT6plex

Q9Y490	TLN1_HUMAN	EGDEESTMLENSVSP K	Y	23.27	2209.08	16	7.9	737.4	3	84.2	F2:11365	8.26E-05	2.15E-04	1.13E-04	0.00E+00	3.78E-05	0.00E+00	412	427	TMT6plex; Mutation
P02671	FIBA_HUMAN	DEAGSEADHEGTHST KT	Y	29.73	1999.89	17	9.3	1001	2	17.3	F1:1472	6.06E-03	1.33E-03	3.49E-03	1.02E-02	1.07E-02	2.06E-02	605	621	TMT6plex; Mutation
P02461	CO3A1_HUMAN	NGEKGETGAPG	Y	15.98	1490.76	11	1	746.4	2	22.2	F1:2285	2.69E-04	6.23E-04	4.28E-04	9.13E-04	5.75E-04	8.54E-04	272	282	Deamidation ; Hydroxylation
P01024	CO3_HUMAN	EETKENEGF	Y	35.51	1539.78	9	5.2	770.9	2	47.5	F2:5804	4.42E-03	4.32E-03	3.04E-03	7.42E-03	5.54E-03	9.69E-03	1322	1330	TMT6plex
Q5T3U5	MRP7_HUMAN	GHVAVR	Y	15.16	866.529	6	-0.7	434.3	2	44.5	F1:5686	5.59E-04	4.08E-04	2.25E-03	2.26E-03	2.50E-03	3.77E-03	655	660	TMT6plex
P67936	TPM4_HUMAN	DRKYEEVA	N	15.03	1466.81	8	3.7	489.9	3	33.3	F1:4031	4.42E-04	2.74E-04	1.96E-04	5.37E-04	6.91E-04	4.21E-04	123	130	TMT6plex
P01024	CO3_HUMAN	ITHRIHWE	Y	20.49	1319.73	8	1.5	440.9	3	38.5	F1:4812	6.99E-05	9.61E-05	1.34E-04	1.69E-04	2.20E-04	1.33E-04	1307	1314	TMT6plex
P00734	THRB_HUMAN	ESYIDGR	Y	33.36	1067.55	7	1.9	534.8	2	36.5	F1:4519	8.91E-04	5.88E-04	1.25E-03	1.58E-03	1.46E-03	2.49E-03	357	363	TMT6plex
Q14624	ITIH4_HUMAN	DVPDH	Y	16.25	810.408	5	8.9	406.2	2	16	F2:1305	4.93E-05	8.60E-05	0.00E+00	8.08E-05	1.89E-04	2.09E-04	677	681	TMT6plex
Q96BY7	ATG2B_HUMAN	SAFKSA	Y	16.57	1067.64	6	2.7	534.8	2	33.5	F1:4061	1.16E-03	9.60E-04	1.02E-03	9.44E-04	5.68E-04	6.28E-04	1004	1009	TMT6plex
P02671	FIBA_HUMAN	DSTFESKS	Y	31.62	1357.71	8	2.9	679.9	2	41.9	F1:5295	2.27E-03	2.64E-03	1.33E-03	8.38E-04	7.69E-04	9.95E-04	593	600	TMT6plex
P01009	A1AT_HUMAN	EDPQGDAAQK	Y	47.02	1515.79	10	3.6	758.9	2	28	F1:3193	8.88E-04	1.53E-03	7.44E-04	3.67E-03	1.99E-03	2.13E-03	25	34	TMT6plex
Q15942	ZYX_HUMAN	FSPGAPGGSGSQPNQ KLGHPAL	Y	36.69	2690.42	23	3.2	897.8	3	68.9	F2:8963	1.23E-04	8.31E-05	0.00E+00	1.99E-04	3.40E-04	1.48E-04	280	302	TMT6plex
P02452	CO1A1_HUMAN	NGDDGEAGKPG	Y	27.61	1474.73	11	4	738.4	2	29.6	F1:3446	3.42E-04	4.39E-04	8.72E-04	1.21E-03	1.26E-03	2.35E-03	229	239	TMT6plex; Deamidation
Q96ES6	MFSD3_HUMAN	HTAHLR	Y	19.41	1075.65	7	8.8	538.8	2	79.5	F1:11249	1.49E-04	5.66E-04	1.44E-04	8.98E-04	4.40E-04	9.36E-04	201	207	TMT6plex
Q6NUI2	GPAT2_HUMAN	VQVGIVPDALLVPV	Y	16.45	1647.02	14	5.5	824.5	2	117	F1:18110	1.03E-04	1.26E-04	0.00E+00	1.71E-04	1.66E-04	2.18E-04	315	328	TMT6plex
P68363	TBA1B_HUMAN	QPPTVVPGGDL	N	22.64	1307.73	11	-1.2	654.9	2	86.6	F1:12433	2.05E-04	3.14E-04	2.65E-04	3.71E-04	3.21E-04	3.54E-04	358	368	TMT6plex
P02461	CO3A1_HUMAN	GSPGGPGSDGKPGP	Y	30.97	1408.71	14	6.5	705.4	2	28.1	F2:3046	1.06E-04	1.02E-04	5.50E-05	2.00E-04	2.21E-04	4.02E-04	540	553	Methyl ester; TMT6plex
Q7Z407	CSMD3_HUMAN	NHPLPR	Y	18.4	961.566	6	0.7	481.8	2	64.2	F1:8791	1.88E-04	1.90E-04	2.77E-04	2.79E-04	3.11E-04	3.11E-04	2273	2278	TMT6plex
P01024	CO3_HUMAN	IHWESA	Y	16.85	970.508	6	1.8	486.3	2	57.8	F1:7798	3.04E-04	4.13E-04	4.92E-04	5.52E-04	1.08E-03	8.81E-04	1311	1316	TMT6plex
P02671	FIBA_HUMAN	FLAEGGGV	Y	37.9	977.539	8	2.3	489.8	2	93	F1:13550	4.85E-04	7.57E-04	1.00E-03	4.72E-04	4.04E-04	1.37E-04	27	34	TMT6plex
Q9HB75	PIDD1_HUMAN	NSWGDLE	Y	16.75	1049.49	7	1.7	525.8	2	101	F1:15047	4.02E-04	6.44E-04	5.65E-04	4.60E-04	1.88E-04	1.50E-04	419	425	TMT6plex; Deamidation
P01024	CO3_HUMAN	SEETKENEGFTVTA	Y	15.98	1981	14	4.3	661.3	3	58.1	F2:7405	4.56E-05	8.00E-05	0.00E+00	7.99E-05	1.13E-04	1.22E-04	1321	1334	TMT6plex; Dehydration
O95810	SDPR_HUMAN	NETKSEDLP SSE	Y	30.61	1563.75	12	2.7	782.9	2	33	F1:3987	7.65E-05	2.37E-04	1.17E-04	2.14E-04	2.85E-04	3.86E-04	311	322	TMT6plex
P01024	CO3_HUMAN	SVQLTEK	Y	32.72	1261.76	7	3	631.9	2	48.8	F1:6370	1.27E-03	1.67E-03	1.49E-03	2.04E-03	2.30E-03	3.28E-03	672	678	TMT6plex
P0C0L4	CO4A_HUMAN	ALQLNNRQI	Y	35.38	1297.77	9	3	649.9	2	60.1	F1:8171	1.13E-03	1.84E-03	1.97E-03	1.20E-03	9.01E-04	7.22E-04	1343	1351	TMT6plex
P01042	KNG1_HUMAN	WGHEKQ	Y	22.47	1241.69	6	2.2	414.9	3	26.7	F1:2981	0.00E+00	2.57E-05	7.94E-05	9.61E-05	1.37E-04	7.10E-05	431	436	TMT6plex
Q15942	ZYX_HUMAN	EPPPAPGA	Y	22.03	963.523	8	1.7	482.8	2	35.6	F1:4384	4.36E-04	4.56E-04	3.42E-04	5.47E-04	4.50E-04	5.60E-04	45	52	TMT6plex
P01024	CO3_HUMAN	NEGFTVT	Y	31.66	995.513	7	-0.1	498.8	2	62.6	F1:8548	1.68E-04	2.61E-04	3.72E-04	5.02E-04	3.56E-04	4.28E-04	1327	1333	TMT6plex

P00734	THRB_HUMAN	DGLDEDSRAIEG	Y	22.25	1619.75	13	5.2	810.9	2	54.4	F2:6809	3.45E-04	3.66E-04	3.27E-04	4.77E-04	7.51E-04	8.94E-04	301	313	TMT6plex
P02671	FIBA_HUMAN	EGDFLAEGGGV	Y	45.29	1278.63	11	3.5	640.3	2	99.1	F1:14624	9.63E-04	1.51E-03	1.45E-03	1.03E-03	7.36E-04	2.50E-04	24	34	TMT6plex
Q9H2Y7	ZN106_HUMAN	DTEQDVLV	Y	16.7	1148.58	8	-4.2	575.3	2	69.1	F1:9563	7.32E-04	5.09E-04	6.27E-04	4.97E-04	3.43E-04	4.92E-04	1371	1378	TMT6plex
P68363	TBA1B_HUMAN	QPPTVVPGGDLAKV	N	43.24	1835.09	14	1.7	612.7	3	86.6	F1:12440	9.41E-05	6.59E-05	4.35E-05	5.34E-05	0.00E+00	0.00E+00	358	371	TMT6plex
Q15942	ZYX_HUMAN	AAPRPSPAISV	Y	30.75	1106.61	11	3.5	554.3	2	64.2	F1:8803	2.01E-04	2.70E-04	3.17E-04	3.72E-04	3.35E-04	3.60E-04	2	12	Acetylation
P25054	APC_HUMAN	SPPNK	N	16.91	999.612	5	7.2	500.8	2	88.4	F1:12739	7.34E-04	1.37E-03	1.07E-03	5.08E-04	4.34E-04	7.64E-04	2337	2341	TMT6plex
Q14624	ITIH4_HUMAN	GLPGPPDVPD	Y	36.63	1191.63	10	1.9	596.8	2	86.9	F1:12487	1.68E-04	2.18E-04	2.88E-04	3.20E-04	6.67E-04	5.12E-04	671	680	TMT6plex
P02671	FIBA_HUMAN	RGDSTFESKS	Y	34.37	1570.84	10	2.3	524.6	3	27.2	F1:3070	2.58E-04	4.80E-04	1.84E-04	1.09E-04	9.06E-05	0.00E+00	591	600	TMT6plex
Q4G0P3	HYDIN_HUMAN	MHGLPLV	Y	17.78	994.584	7	-4	498.3	2	77.3	F1:10880	5.49E-05	6.68E-05	1.16E-04	1.62E-04	1.71E-04	9.73E-05	2429	2435	TMT6plex
P02671	FIBA_HUMAN	SSSYSKQFTSSTSYN	Y	42.33	2131.05	15	2.9	711.4	3	58.1	F2:7408	1.15E-04	1.30E-04	6.82E-05	6.53E-05	6.54E-05	0.00E+00	576	590	TMT6plex
P02671	FIBA_HUMAN	SGSTGQWHSESGSFR PDSPGSGN	Y	39.26	2549.14	23	3.2	850.7	3	48.3	F1:6296	9.18E-05	4.51E-05	4.20E-05	1.20E-04	7.56E-05	1.36E-04	380	402	TMT6plex
A6NI72	NCF1B_HUMAN	NVHSIHQRS	Y	16.81	1306.69	9	0.7	436.6	3	34.8	F1:4252	2.52E-04	2.40E-04	4.90E-04	9.01E-04	1.04E-03	4.39E-04	308	316	TMT6plex; Deamidation
Q14624	ITIH4_HUMAN	QGAKIP	N	19.19	1070.69	6	-2.9	536.3	2	37.1	F1:4619	7.31E-04	7.83E-04	1.01E-03	1.54E-03	2.36E-03	1.26E-03	630	635	TMT6plex
Q14624	ITIH4_HUMAN	GPPDVPDHAAYHPF	Y	55.85	1747.85	14	-2.7	583.6	3	66.5	F2:8601	1.71E-04	0.00E+00	4.10E-04	1.48E-03	1.66E-03	4.39E-04	674	687	TMT6plex
P02671	FIBA_HUMAN	GDFLAEG	Y	29.56	936.476	7	1	469.2	2	80.8	F1:11448	1.43E-04	1.93E-04	2.56E-04	1.34E-04	1.06E-04	9.65E-05	25	31	TMT6plex
Q9UPS6	SET1B_HUMAN	FKARR	Y	16.18	1134.74	5	0.8	568.4	2	64.2	F1:8789	5.27E-04	5.91E-04	6.01E-04	7.66E-04	6.93E-04	1.00E-03	308	312	TMT6plex
Q14624	ITIH4_HUMAN	GLPGPPDVPDHA	Y	50.68	1399.73	12	3.2	700.9	2	70.9	F1:9845	4.48E-04	7.73E-04	5.81E-04	1.13E-03	3.14E-03	2.27E-03	671	682	TMT6plex
P00734	THRB_HUMAN	TERELLESY	Y	27.96	1367.71	9	0.3	684.9	2	74	F1:10323	6.99E-04	5.14E-04	5.82E-04	3.02E-03	2.04E-03	1.14E-03	351	359	TMT6plex
P0C0L4	CO4A_HUMAN	SHALQLNNRQI	Y	42.97	1521.86	11	4.2	508.3	3	36.4	F2:4218	2.90E-04	2.78E-04	1.91E-04	3.95E-04	2.88E-04	3.39E-04	1341	1351	TMT6plex
Q9ULI3	HEG1_HUMAN	DPPPSPA	Y	17.78	908.481	7	2.1	455.2	2	30.8	F1:3647	2.24E-04	3.25E-04	2.68E-04	2.30E-04	1.45E-04	2.09E-04	32	38	TMT6plex
P02671	FIBA_HUMAN	QFTSSTSYNRGD	Y	33.82	1344.56	12	4.3	673.3	2	55.2	F1:7367	1.03E-03	1.48E-03	1.04E-03	8.86E-04	7.02E-04	8.53E-04	582	593	Pyro-glu from Q
A8CG34	P121C_HUMAN	PTHRV	Y	15.56	837.502	5	-0.2	419.8	2	76	F1:10642	0.00E+00	0.00E+00	1.01E-04	1.50E-04	6.49E-05	1.50E-04	167	171	TMT6plex
P00488	F13A_HUMAN	QGVVPR	Y	19.57	883.544	6	4	442.8	2	20.9	F1:2077	4.29E-04	4.01E-04	5.61E-04	7.47E-04	6.03E-04	1.07E-03	33	38	TMT6plex
P02671	FIBA_HUMAN	ADSGEGDFLA	Y	26.78	1289.54	10	7.5	645.8	2	111	F1:16984	1.61E-04	1.81E-04	9.21E-05	6.93E-05	6.07E-05	1.08E-04	20	29	TMT6plex; Phosphorylation
Q14624	ITIH4_HUMAN	NRQAGAAGSRMNFR PGVLSS	Y	20.58	2344.2	20	0.8	587.1	4	56.4	F2:7118	0.00E+00	0.00E+00	5.84E-06	4.63E-05	1.65E-04	2.47E-04	648	667	TMT6plex; Glyoxal-derived hydroimiadazole ne
Q8WXH0	SYNE2_HUMAN	RAALPLQL	N	15.72	1110.7	8	-5.4	556.4	2	91	F2:12468	0.00E+00	6.24E-05	4.14E-05	8.56E-05	5.37E-05	1.03E-04	6834	6841	TMT6plex; Deamidation
Q7Z408	CSMD2_HUMAN	PPPTILPN	Y	20.47	1076.64	8	6.8	539.3	2	58.7	F1:7949	1.08E-03	1.41E-03	9.55E-04	1.80E-03	1.26E-03	1.62E-03	2295	2302	TMT6plex
P01042	KNG1_HUMAN	DDDLQHGGHVLDDH GHKH	Y	54.43	2503.24	18	6.4	835.4	3	27.9	F1:3178	1.28E-04	8.82E-05	1.42E-04	3.87E-04	1.02E-03	4.79E-04	480	497	TMT6plex
P0C0L4	CO4A_HUMAN	DAPLQPV	Y	27.57	967.554	7	8.3	484.8	2	62.1	F1:8483	4.27E-04	6.51E-04	9.22E-04	2.81E-03	1.29E-03	1.44E-03	1432	1438	TMT6plex
Q9Y6J0	CABIN_HUMAN	LPILSSQ	Y	20.19	985.601	7	4.6	493.8	2	88	F2:11985	3.82E-05	3.35E-05	4.91E-05	3.56E-05	0.00E+00	0.00E+00	1412	1418	TMT6plex

P02671	FIBA_HUMAN	GDFLAEGG	Y	30.41	993.497	8	0.8	497.8	2	84.9	F1:12149	0.00E+00	3.75E-04	3.87E-04	7.08E-04	4.82E-04	4.80E-04	25	32	TMT6plex
A8TX70	CO6A5_HUMAN	GDKGI	N	15.12	946.585	5	6	474.3	2	93.3	F2:12860	4.71E-05	0.00E+00	3.69E-05	5.51E-05	4.99E-05	8.26E-05	1437	1441	TMT6plex
Q17RW2	COOA1_HUMAN	GDKGL	N	15.12	946.585	5	6	474.3	2	93.3	F2:12860	4.71E-05	0.00E+00	3.69E-05	5.51E-05	4.99E-05	8.26E-05	567	571	TMT6plex
Q9H2X0	CHRD_HUMAN	PSCPHPVQA	Y	17.04	1163.6	9	-1.5	582.8	2	53.5	F2:6669	1.72E-04	2.47E-04	1.81E-04	2.28E-04	2.55E-04	2.93E-04	746	754	TMT6plex
Q14112	NID2_HUMAN	HTPVH	N	15.23	818.46	5	8.2	410.2	2	24.3	F1:2589	2.14E-04	2.55E-04	2.09E-04	3.91E-04	6.69E-04	3.55E-04	544	548	TMT6plex
P48634	PRC2A_HUMAN	GGFRPG	Y	23.3	818.46	6	8.2	410.2	2	24.3	F1:2590	2.14E-04	2.55E-04	2.09E-04	3.91E-04	6.69E-04	3.55E-04	1862	1867	TMT6plex
O15360	FANCA_HUMAN	FHQSSR	Y	20.7	989.525	6	3.2	495.8	2	49.2	F2:6097	1.94E-04	2.33E-04	2.32E-04	2.74E-04	3.55E-04	4.88E-04	991	996	TMT6plex
O95810	SDPR_HUMAN	ALTSEEAERSDGDV QPAVLQ	Y	30.69	2440.23	21	6	814.4	3	77.9	F2:10329	0.00E+00	7.12E-05	0.00E+00	7.20E-05	1.68E-04	6.74E-05	400	420	TMT6plex
Q96J65	MRP9_HUMAN	GNSALAP	Y	15.35	857.481	7	3.2	429.7	2	28.9	F1:3347	1.94E-04	3.18E-04	2.76E-04	4.58E-04	4.38E-04	8.48E-04	345	351	TMT6plex
Q9P107	GMIP_HUMAN	SGSRVRV	Y	17.76	988.598	7	0.2	495.3	2	72	F1:10030	1.14E-04	2.17E-04	1.77E-04	1.95E-04	2.56E-04	2.84E-04	589	595	TMT6plex
P02671	FIBA_HUMAN	GEGDFLAEGGGV	Y	40.48	1335.65	12	1.3	668.8	2	99.4	F1:14684	7.37E-04	5.27E-04	4.26E-04	5.02E-04	2.44E-04	1.95E-04	23	34	TMT6plex
Q01433	AMPD2_HUMAN	SAPYEFPEESPIEQL RRQ	Y	22.41	2662.31	20	0.4	888.4	3	104	F1:15623	5.71E-05	1.47E-04	0.00E+00	2.03E-04	3.33E-04	1.15E-04	142	161	TMT6plex
P00734	THRB_HUMAN	ERELLESY	Y	30.83	1266.67	8	4	634.3	2	67.9	F1:9394	1.56E-03	1.49E-03	9.34E-04	2.31E-03	2.10E-03	1.45E-03	352	359	TMT6plex
P01024	CO3_HUMAN	WESASLL	Y	29.75	1033.56	7	8.1	517.8	2	121	F1:18940	4.98E-04	3.96E-04	6.13E-04	8.60E-04	7.34E-04	5.50E-04	1313	1319	TMT6plex
P01042	KNG1_HUMAN	DWGHE	Y	21.03	871.403	5	3.5	436.7	2	34	F1:4130	3.60E-04	3.79E-04	8.45E-04	7.66E-04	1.11E-03	8.20E-04	430	434	TMT6plex
Q14696	MESD_HUMAN	ESILKM	Y	15.63	1177.71	6	-0.9	589.9	2	78.7	F1:11123	1.84E-04	3.92E-04	3.20E-04	3.42E-04	5.08E-04	6.05E-04	102	107	TMT6plex
P02671	FIBA_HUMAN	NRGDSTFESKS	Y	41.45	1684.88	11	2.9	562.6	3	26.7	F1:2984	5.97E-04	1.10E-03	3.14E-04	1.89E-04	2.06E-04	0.00E+00	590	600	TMT6plex
P10124	SRGN_HUMAN	DLFPK	Y	24.04	1076.66	5	-4	539.3	2	72.4	F1:10088	1.63E-02	2.51E-02	2.16E-02	1.32E-02	1.88E-02	1.26E-02	73	77	TMT6plex
P01042	KNG1_HUMAN	KNGKHNGW	Y	26.79	1628.92	8	0	408.2	4	37.5	F1:4662	0.00E+00	2.36E-05	9.48E-05	1.09E-04	1.55E-04	6.76E-05	512	519	TMT6plex; Deamidation
P00734	THRB_HUMAN	LEDKTERELLESYIDG	Y	31.32	2367.26	16	3.2	790.1	3	119	F1:18445	2.24E-04	1.21E-04	1.86E-04	3.80E-04	3.68E-04	1.94E-04	347	362	TMT6plex
P0C0L4	CO4A_HUMAN	SLGSKIN	Y	20.22	1175.73	7	3.7	588.9	2	42.3	F2:5021	7.20E-04	1.45E-03	1.02E-03	1.62E-03	1.45E-03	1.61E-03	1361	1367	TMT6plex
O15054	KDM6B_HUMAN	DFPPT	Y	20.31	804.422	5	1	403.2	2	100	F1:14873	7.56E-05	1.73E-04	1.53E-04	4.33E-05	1.12E-04	0.00E+00	672	676	TMT6plex
P02671	FIBA_HUMAN	SKQFTSST	Y	21.82	1342.75	8	4.3	672.4	2	31.9	F2:3573	3.20E-03	1.11E-03	1.96E-03	7.90E-04	6.53E-04	4.79E-04	580	587	TMT6plex
O15197	EPHB6_HUMAN	AQLGNR	Y	15.56	886.519	6	6.2	444.3	2	75.4	F1:10561	9.50E-05	1.82E-04	5.50E-05	3.60E-04	1.60E-04	5.18E-04	7	12	TMT6plex
P02671	FIBA_HUMAN	SSSYSKQFTSST	Y	29.06	1766.91	12	0.5	884.5	2	48.6	F2:5997	1.16E-03	9.12E-04	1.02E-03	9.57E-04	4.74E-04	2.75E-04	576	587	TMT6plex
Q15942	ZYX_HUMAN	DSEPPPAPGA	Y	23.79	1165.58	10	3.1	583.8	2	34.5	F2:3961	1.04E-04	2.09E-04	1.73E-04	2.25E-04	2.07E-04	2.61E-04	43	52	TMT6plex
Q14624	ITIH4_HUMAN	FRPGVLS	Y	24.45	1003.6	7	-0.1	502.8	2	57.5	F2:7310	1.07E-03	6.06E-04	2.16E-03	2.42E-03	3.84E-03	1.82E-03	660	666	TMT6plex
P02671	FIBA_HUMAN	EAGSEADHEGTHST	Y	56.41	1655.72	14	5.3	552.9	3	11.1	F1:547	6.51E-05	3.81E-05	0.00E+00	1.59E-04	5.38E-05	2.28E-04	606	619	TMT6plex
Q14624	ITIH4_HUMAN	PGPPDVPDH	Y	30.39	1158.59	9	2.9	580.3	2	38.9	F2:4587	1.68E-04	2.32E-04	1.61E-04	3.07E-04	7.81E-04	4.44E-04	673	681	TMT6plex
P02671	FIBA_HUMAN	EFVSETESRGSSESGIFT	Y	15.48	2090	17	6.8	697.7	3	91	F2:12467	6.83E-05	7.31E-05	0.00E+00	1.37E-04	8.79E-05	7.99E-05	539	555	TMT6plex
Q9BWT3	PAPOG_HUMAN	QRQKQH	Y	16.25	1281.77	6	9.7	641.9	2	92.1	F2:12654	1.87E-04	2.08E-04	2.02E-04	2.07E-04	2.20E-04	2.47E-04	13	18	TMT6plex
Q14624	ITIH4_HUMAN	QVAEKPMEGESRN	Y	23.15	1685.82	13	2.8	563	3	37.2	F2:4358	7.18E-05	7.26E-05	4.53E-05	8.79E-05	1.17E-04	7.26E-05	603	615	Pyro-glu from Q; TMT6plex
P49137	MAPK2_HUMAN	LGLGINGK	Y	23.08	1228.79	8	-2.5	615.4	2	113	F2:16431	1.31E-04	3.69E-05	1.05E-04	1.67E-04	1.47E-04	3.21E-04	70	77	TMT6plex

P01024	CO3_HUMAN	EGFTVTAE	Y	36.39	1081.55	8	4.4	541.8	2	71.7	F1:9974	2.40E-04	3.10E-04	2.10E-04	3.08E-04	3.56E-04	2.95E-04	1328	1335	TMT6plex
Q14624	ITIH4_HUMAN	SKQLGLPGPPDVPDH A	Y	49.45	1884.01	16	-1.3	629	3	66.5	F2:8604	9.80E-05	1.29E-04	7.56E-05	1.23E-04	2.78E-04	2.00E-04	667	682	TMT6plex
P01023	A2MG_HUMAN	HGPEGL	Y	17.4	837.455	6	7.3	419.7	2	24.2	F2:2501	1.16E-04	1.97E-04	2.07E-04	3.32E-04	2.02E-04	2.48E-04	698	703	TMT6plex
P02671	FIBA_HUMAN	SSSYSKQFTSSTS YNR GDST	Y	34.46	2647.28	20	2.5	883.4	3	50.6	F1:6659	3.41E-04	3.72E-04	2.57E-04	2.84E-04	2.45E-04	1.39E-04	576	595	TMT6plex
Q9BRB3	PIGQ_HUMAN	AHLPPPQL	Y	28.58	1100.65	8	7.6	551.3	2	76.3	F2:10078	6.40E-05	6.74E-05	1.13E-04	1.04E-04	1.18E-04	1.26E-04	521	528	TMT6plex
Q14624	ITIH4_HUMAN	QLGLPGPPDVPDHA A YHPF	Y	62.34	2256.15	19	5.1	753.1	3	102	F2:14321	0.00E+00	1.82E-04	1.58E-04	5.96E-04	8.83E-04	1.96E-04	669	687	TMT6plex
Q9ULK4	MED23_HUMAN	TALLR	N	18.7	801.528	5	4.3	401.8	2	45.8	F1:5889	3.95E-04	5.76E-04	8.27E-04	1.27E-03	7.25E-04	1.75E-03	267	271	TMT6plex
Q96RW7	HMCN1_HUMAN	LTHNGK	Y	16.06	1126.69	6	6.5	564.4	2	84.6	F1:12084	2.25E-04	1.76E-04	1.75E-04	2.04E-04	2.67E-04	3.13E-04	5463	5468	TMT6plex
Q3B7T1	EDRF1_HUMAN	HVNGIVQ	Y	17.15	994.576	7	-1.2	498.3	2	87.1	F1:12516	5.57E-05	7.07E-05	8.95E-05	1.49E-04	8.42E-05	1.94E-04	370	376	TMT6plex
A7E2V4	ZSWM8_HUMAN	LYEQT	N	15.28	881.47	5	2.2	441.7	2	65.4	F1:8978	1.50E-04	1.76E-04	2.12E-04	3.26E-04	1.92E-04	3.65E-04	1423	1427	TMT6plex
P01024	CO3_HUMAN	EGFTVT	Y	27.8	881.47	6	2.2	441.7	2	65.4	F1:8979	1.50E-04	1.76E-04	2.12E-04	3.26E-04	1.92E-04	3.65E-04	1328	1333	TMT6plex
Q15942	ZYX_HUMAN	QPQPKPQ	Y	23.98	1033.58	7	3.4	517.8	2	28.7	F1:3322	2.98E-04	3.61E-04	3.10E-04	3.68E-04	3.46E-04	3.80E-04	227	233	Pyro-glu from Q; TMT6plex
P02671	FIBA_HUMAN	SSYSKQFTS	Y	17.02	1491.8	9	2.8	746.9	2	50.6	F1:6660	2.72E-03	2.97E-03	1.93E-03	2.41E-03	1.31E-03	1.25E-03	577	585	TMT6plex
P02461	CO3A1_HUMAN	GAAGTPGLQGMPGE RG	Y	22.21	1496.7	16	5	749.4	2	25.8	F1:2844	1.07E-04	1.78E-04	1.51E-04	1.95E-04	2.80E-04	4.42E-04	717	732	Acetylation
P01024	CO3_HUMAN	ENEGFTV	Y	23.79	1023.51	7	3.4	512.8	2	71.6	F2:9388	4.50E-05	6.01E-05	1.01E-04	4.38E-04	1.80E-04	1.73E-04	1326	1332	TMT6plex
P02671	FIBA_HUMAN	SSSYSKQFT	Y	44.27	1491.8	9	1.9	746.9	2	48.4	F2:5963	3.63E-03	4.63E-03	2.86E-03	3.53E-03	1.48E-03	1.48E-03	576	584	TMT6plex
P01024	CO3_HUMAN	LDPERLG	Y	21.33	1027.59	7	4	514.8	2	57.4	F1:7734	1.02E-03	1.01E-03	9.36E-04	1.15E-03	1.06E-03	1.39E-03	947	953	TMT6plex
Q0P670	CQ074_HUMAN	PPASTSTLR	Y	15.22	1157.66	9	3.8	579.8	2	70	F2:9158	4.14E-04	1.77E-04	2.70E-04	4.62E-04	4.11E-04	4.46E-04	481	489	TMT6plex
P60709	ACTB_HUMAN	DEAQSKRGILT	Y	15.33	1674.97	11	4	559.3	3	41.5	F1:5230	1.09E-03	8.70E-04	2.86E-04	3.28E-04	1.99E-04	1.30E-04	56	66	TMT6plex
P02671	FIBA_HUMAN	SSYSKQFTSSTS Y	Y	31.75	1929.97	13	3.8	966	2	66.1	F1:9098	1.46E-03	3.88E-04	8.63E-04	3.18E-04	2.23E-04	1.05E-04	577	589	TMT6plex
Q9Y490	TLN1_HUMAN	NAAVQGHAS	Y	15.94	1082.57	9	-7.1	542.3	2	19.1	F1:1781	2.14E-04	1.62E-04	2.38E-04	7.38E-04	6.71E-04	2.43E-04	2412	2420	TMT6plex
Q14624	ITIH4_HUMAN	GPPDVPDHAAY	Y	39.32	1366.67	11	2.4	684.3	2	54.6	F1:7272	5.93E-04	5.06E-04	4.68E-04	7.95E-04	7.37E-04	5.37E-04	674	684	TMT6plex
P02671	FIBA_HUMAN	SSSYSKQFTSSTS	Y	36.92	1853.94	13	4.5	928	2	47.9	F2:5878	2.99E-03	1.06E-03	1.40E-03	6.82E-04	4.30E-04	3.87E-04	576	588	TMT6plex
P00734	THRB_HUMAN	LESYIDGR	Y	29.53	1180.63	8	4.1	591.3	2	74.6	F2:9815	3.87E-04	3.18E-04	7.24E-04	7.28E-04	6.69E-04	8.33E-04	356	363	TMT6plex
Q14624	ITIH4_HUMAN	GLPGPPDVPDHAAYH P	Y	49.66	1867.94	16	3.6	623.7	3	68.4	F2:8888	1.09E-04	1.86E-04	1.06E-04	1.48E-04	2.10E-04	2.28E-04	671	686	TMT6plex
Q14624	ITIH4_HUMAN	GSEMVVAGKLQ	Y	24.19	1575.91	11	5.2	526.3	3	69.1	F2:9002	4.35E-05	7.50E-05	8.89E-05	7.50E-05	1.55E-04	1.27E-04	488	498	TMT6plex
Q9C0C2	TB182_HUMAN	KEVLASP	Y	15.53	971.585	7	-0.5	486.8	2	86.5	F1:12420	8.30E-05	6.61E-05	0.00E+00	1.14E-04	7.80E-05	2.10E-04	173	179	TMT6plex
P00734	THRB_HUMAN	TERELLESYIDGR	Y	24.35	1808.95	13	4.4	604	3	92.6	F2:12741	8.39E-05	4.03E-05	1.59E-04	2.61E-04	1.32E-04	1.61E-04	351	363	TMT6plex
P01042	KNG1_HUMAN	DWGHEKQ	Y	33.14	1356.72	7	2.2	453.2	3	32.6	F1:3912	1.86E-04	1.29E-04	3.09E-04	2.83E-04	6.81E-04	4.01E-04	430	436	TMT6plex
Q7Z2Z2	ETUD1_HUMAN	VHLQR	N	15.27	880.545	5	2	441.3	2	41.5	F2:4919	7.38E-05	1.44E-04	1.25E-04	1.40E-04	1.95E-04	1.49E-04	665	669	TMT6plex
P52566	GDIR2_HUMAN	NYKPP	N	17.55	1075.64	5	-4.4	538.8	2	85.6	F1:12268	1.48E-04	1.34E-04	1.78E-04	1.26E-04	6.93E-05	1.35E-04	23	27	TMT6plex

Q14624	ITIH4_HUMAN	QAGAAGSRMNFPRG VLSS	Y	35.91	1787.87	18	3.4	894.9	2	71.7	F1:9972	6.23E-04	6.63E-04	6.17E-04	6.10E-04	5.28E-04	4.26E-04	650	667	Pyro-glu from Q
P02675	FIBB_HUMAN	EEGFFS	Y	26.6	943.449	6	2	472.7	2	90.6	F1:13122	3.17E-04	9.44E-04	5.36E-04	2.80E-04	2.01E-04	1.43E-04	37	42	TMT6plex
Q3MIN7	RGL3_HUMAN	PVPYL	N	18.37	816.495	5	0.9	409.3	2	77.8	F1:10967	4.11E-05	0.00E+00	0.00E+00	2.93E-05	5.31E-05	1.11E-04	420	424	TMT6plex
Q9Y6X0	SETBP_HUMAN	PVPYI	N	18.37	816.495	5	0.9	409.3	2	77.8	F1:10967	4.11E-05	0.00E+00	0.00E+00	2.93E-05	5.31E-05	1.11E-04	995	999	TMT6plex
Q16643	DREB_HUMAN	EDENAEPVGTTYQKT D	Y	36.28	2254.1	16	1.6	752.4	3	54.1	F1:7190	0.00E+00	7.77E-05	4.23E-05	9.03E-05	9.27E-05	8.17E-05	152	167	TMT6plex
Q14624	ITIH4_HUMAN	LGLPGPPDVPDHAAY HPF	Y	59.5	2128.09	18	0.8	710.4	3	105	F1:15682	1.14E-04	0.00E+00	0.00E+00	1.87E-04	3.95E-04	9.06E-05	670	687	TMT6plex
Q14624	ITIH4_HUMAN	QVAEKPMEGESRNR N	Y	24.33	1955.97	15	1.5	653	3	28.2	F1:3231	1.89E-04	2.21E-04	1.41E-04	2.86E-04	3.27E-04	6.32E-04	603	617	Pyro-glu from Q; TMT6plex
P02675	FIBB_HUMAN	VNDNEEGFFSA	Y	40.25	1457.65	11	1.9	729.8	2	115	F1:17693	6.50E-04	1.88E-04	7.41E-04	1.72E-04	1.42E-04	1.63E-04	33	43	TMT6plex; Deamidation
P02775	CXCL7_HUMAN	NLAKGKEESLSDSPLY	Y	41.24	2369.29	15	2.1	790.8	3	87.2	F1:12545	1.04E-03	1.17E-04	6.22E-04	1.84E-03	1.46E-03	6.98E-04	44	58	TMT6plex; Deamidation
Q9UPS6	SET1B_HUMAN	PMPPPL	N	15.79	879.509	6	8	440.8	2	84.5	F2:11407	1.65E-04	7.59E-05	4.31E-05	5.86E-05	0.00E+00	0.00E+00	704	709	TMT6plex
O95810	SDPR_HUMAN	EIAEEAAEKAT	Y	41.28	1618.88	11	4.4	810.5	2	69.2	F2:9015	1.19E-03	1.79E-03	3.63E-04	1.67E-03	2.95E-03	1.73E-03	350	360	TMT6plex
P0C0L4	CO4A_HUMAN	EEELQFSLGSK	Y	38.02	1723.94	11	5	575.7	3	94.1	F2:13003	0.00E+00	4.71E-05	0.00E+00	4.88E-05	5.07E-05	1.47E-04	1355	1365	TMT6plex
P01024	CO3_HUMAN	HRIHWESASLL	Y	27.18	1575.88	11	-2	788.9	2	66.2	F1:9103	8.13E-04	1.06E-03	5.67E-04	1.43E-03	3.70E-03	1.77E-03	1309	1319	TMT6plex; Amidation
Q9UHR5	S30BP_HUMAN	PAVVTVTT	Y	15.9	1015.61	8	0.6	508.8	2	108	F1:16288	0.00E+00	3.96E-05	8.00E-05	9.61E-05	7.02E-05	2.01E-04	279	286	TMT6plex
P01024	CO3_HUMAN	ETKENEGFTVTA	Y	15.31	1782.94	12	3.5	892.5	2	59.8	F2:7647	7.85E-05	1.35E-04	0.00E+00	5.20E-04	3.67E-04	9.50E-05	1323	1334	TMT6plex
P01024	CO3_HUMAN	THRIHWE	Y	28.02	1206.65	7	6.4	604.3	2	19.9	F2:1860	1.57E-04	5.63E-04	4.54E-04	8.45E-04	6.08E-04	5.18E-04	1308	1314	TMT6plex
Q8IZY2	ABCA7_HUMAN	EHPTPDLGPG	Y	15.49	1247.63	10	1.9	624.8	2	30.2	F1:3546	4.26E-04	5.44E-04	3.70E-04	3.57E-04	2.92E-04	3.81E-04	451	460	TMT6plex
O00151	PDLI1_HUMAN	QEKQELNEPPKQ	Y	31.02	1908.04	12	2.3	637	3	47	F1:6096	5.94E-05	1.51E-04	6.53E-05	1.40E-04	1.60E-04	1.58E-04	201	212	Pyro-glu from Q; TMT6plex
P02671	FIBA_HUMAN	SYSKQF	Y	35.27	1216.69	6	2.8	609.4	2	53.8	F1:7127	7.65E-03	4.80E-03	8.67E-03	6.64E-03	3.44E-03	2.11E-03	578	583	TMT6plex
P02461	CO3A1_HUMAN	TGPGGDKGDTGPPGP	Y	39.35	1782.92	15	1.9	892.5	2	36.6	F1:4526	6.44E-04	7.40E-04	1.03E-03	2.07E-03	1.43E-03	9.25E-04	623	637	TMT6plex; Hydroxylation
Q7Z407	CSMD3_HUMAN	LSHCEDPGIP	Y	15.71	1295.64	10	-1.1	648.8	2	17.8	F1:1553	7.19E-05	6.92E-05	1.21E-04	2.24E-04	1.01E-04	1.51E-04	1351	1360	TMT6plex
O95810	SDPR_HUMAN	ALTSEEAEERSDGPV QPAVLQVHQTS	Y	56.07	2992.49	26	-1	998.5	3	72.9	F1:10157	4.46E-05	1.06E-04	0.00E+00	9.40E-05	1.58E-04	9.10E-05	400	425	TMT6plex
P01024	CO3_HUMAN	NEGFTVTA	Y	33.87	1066.55	8	1.5	534.3	2	69.2	F1:9588	4.12E-04	3.18E-04	2.89E-04	5.40E-04	3.94E-04	3.94E-04	1327	1334	TMT6plex
P02671	FIBA_HUMAN	NRGDSTFES	Y	19.09	1240.59	9	6.9	621.3	2	20.2	F2:1907	1.57E-03	6.49E-04	6.28E-04	4.09E-04	2.71E-04	2.52E-04	590	598	TMT6plex
P10124	SRGN_HUMAN	ELLPGESNKIPR	Y	32.18	1810.07	12	3.1	604.4	3	65.2	F1:8945	3.56E-04	6.21E-04	5.63E-04	2.82E-04	3.28E-04	4.44E-04	58	69	TMT6plex
Q12996	CSTF3_HUMAN	PRHLAP	N	16.01	918.56	6	1.8	460.3	2	87.6	F2:11914	2.34E-04	6.01E-05	4.64E-04	4.20E-05	0.00E+00	0.00E+00	594	599	TMT6plex
Q15942	ZYX_HUMAN	HVQPQPQPKPQ	Y	47.09	1741	11	6.3	581.3	3	22	F1:2259	0.00E+00	1.05E-04	0.00E+00	1.25E-04	1.29E-04	6.17E-05	223	233	TMT6plex
Q5T4S7	UBR4_HUMAN	TSSPPDMS	Y	19.47	1049.49	8	3.5	525.8	2	25	F2:2623	2.26E-04	3.11E-04	4.00E-04	3.84E-04	4.76E-04	3.80E-04	3130	3137	TMT6plex
P02671	FIBA_HUMAN	GEGDFLAEGGGVR	Y	55.83	1491.75	13	3.5	746.9	2	68	F1:9406	4.41E-03	2.66E-03	8.76E-03	2.98E-03	1.32E-03	7.71E-04	23	35	TMT6plex



P02671	FIBA_HUMAN	QFTSSTSYNRGDSTFE SKSYKMA	Y	29.5	3062.47	23	1.3	1022	3	86.2	F1:12371	2.88E-03	3.43E-04	1.82E-03	4.52E-04	1.43E-04	0.00E+00	582	604	Pyro-glu from Q; TMT6plex
P00734	THRB_HUMAN	SLEDKTEREL	Y	20.57	1676.94	10	6.6	560	3	56.3	F2:7108	1.65E-04	2.66E-04	1.92E-04	4.33E-04	4.95E-04	1.21E-03	346	355	TMT6plex
P01024	CO3_HUMAN	HWESASLL	Y	37.95	1170.62	8	3.3	586.3	2	82.9	F1:11783	9.21E-04	1.21E-03	1.08E-03	1.24E-03	1.28E-03	1.85E-03	1312	1319	TMT6plex
P00488	F13A_HUMAN	RAVPPNNSNAEDDL PTVELQGVVPR	Y	60.51	2986.57	26	-0.4	996.5	3	91.8	F1:13342	4.09E-05	1.26E-04	4.56E-05	1.72E-04	8.66E-05	1.35E-04	13	38	TMT6plex
P0C0L4	CO4A_HUMAN	QLFEGR	N	21.66	977.55	6	0.7	489.8	2	47.2	F1:6127	3.46E-04	5.38E-04	7.48E-04	9.00E-04	6.51E-04	7.70E-04	1442	1447	TMT6plex
Q9NYQ8	FAT2_HUMAN	YTPII	N	15.59	834.505	5	2.2	418.3	2	77.7	F1:10954	4.96E-04	8.39E-04	1.01E-03	5.40E-04	5.03E-04	4.09E-04	2187	2191	TMT6plex
Q01484	ANK2_HUMAN	YTPLI	N	15.59	834.505	5	2.2	418.3	2	77.7	F1:10954	4.96E-04	8.39E-04	1.01E-03	5.40E-04	5.03E-04	4.09E-04	729	733	TMT6plex
P02775	CXCL7_HUMAN	KTTSGI	Y	16.17	834.501	6	7.1	418.3	2	77.7	F1:10955	4.96E-04	8.39E-04	1.01E-03	5.40E-04	5.03E-04	4.09E-04	67	72	TMT6plex
Q05682	CALD1_HUMAN	PTAAGTPNKETAGLK VG	Y	28.29	2069.19	17	5.7	690.7	3	45.4	F2:5484	6.64E-05	4.91E-05	0.00E+00	6.90E-05	2.04E-04	8.75E-05	725	741	TMT6plex
P02671	FIBA_HUMAN	ADEAGSEADHEGTHS TKRGHAKS	Y	22.72	2849.41	23	6.9	475.9	6	17.3	F1:1476	4.24E-05	0.00E+00	4.56E-05	0.00E+00	0.00E+00	0.00E+00	604	626	TMT6plex; Methyl ester
P02671	FIBA_HUMAN	YKMADEAGSEADHE GTHST	Y	24.85	2493.15	19	1.8	624.3	4	38.6	F1:4826	0.00E+00	0.00E+00	0.00E+00	6.35E-05	0.00E+00	5.61E-05	601	619	TMT6plex
Q9H4B7	TBB1_HUMAN	NVLEVV	Y	21.28	900.548	6	3.1	451.3	2	96.6	F2:13427	0.00E+00	0.00E+00	0.00E+00	3.78E-05	4.31E-05	0.00E+00	115	120	TMT6plex
P15088	CBPA3_HUMAN	PVGLIATT	Y	24.75	999.617	8	1	500.8	2	99.3	F1:14669	4.56E-05	0.00E+00	5.32E-05	0.00E+00	0.00E+00	0.00E+00	6	13	TMT6plex
Q5FWE3	PRRT3_HUMAN	DEAEWPGRPQSHPP APPVQAPST	Y	15.38	2809.35	24	-4.8	562.9	5	37.2	F1:4629	0.00E+00	0.00E+00	0.00E+00	1.64E-04	1.40E-04	0.00E+00	391	414	TMT6plex; Deamidation
Q99715	COCA1_HUMAN	GFSVVFV	N	16.17	883.501	6	8.2	442.8	2	76	F1:10646	2.93E-04	1.20E-04	1.62E-04	1.10E-04	0.00E+00	1.40E-04	2452	2457	TMT6plex
Q9Y566	SHAN1_HUMAN	RRSTLFLS	Y	18.06	1207.72	8	9.3	604.9	2	108	F1:16233	6.35E-05	8.36E-05	0.00E+00	1.04E-04	6.33E-05	1.45E-04	1252	1259	TMT6plex
Q14624	ITIH4_HUMAN	DVPDHAAYHPF	Y	43.82	1496.73	11	1.5	499.9	3	57.1	F1:7687	9.29E-05	9.70E-05	7.65E-05	1.36E-04	2.66E-04	1.27E-04	677	687	TMT6plex
P00734	THRB_HUMAN	TFGSGEADCGLR	Y	18.12	1462.66	12	-5	732.3	2	54.1	F1:7177	7.11E-04	1.18E-03	8.02E-04	1.35E-03	1.26E-03	2.64E-03	328	339	TMT6plex; Replacement of 2 protons by magnesium
O00624	NPT3_HUMAN	GISRGFGLIAGIISSTA TGFLISQVGP	Y	16.56	2847.61	27	-7.3	712.9	4	38.7	F1:4843	0.00E+00	0.00E+00	0.00E+00	6.27E-05	4.82E-05	0.00E+00	411	437	TMT6plex
Q15942	ZYX_HUMAN	NTQPRGPPASSPAPAP K	Y	38.98	1901.03	17	2.8	634.7	3	21.2	F1:2122	0.00E+00	1.09E-04	0.00E+00	8.79E-05	8.75E-05	1.40E-04	249	265	TMT6plex
A6NGR9	MROH6_HUMAN	GQPQGPSPA	Y	16.75	1066.56	9	3.5	534.3	2	23.7	F1:2510	3.20E-04	4.76E-04	3.06E-04	5.70E-04	4.39E-04	4.31E-04	33	41	TMT6plex
P60709	ACTB_HUMAN	DDMEKIWH	Y	23.63	1530.79	8	3.4	511.3	3	71.2	F2:9337	1.02E-04	2.48E-04	5.28E-05	3.43E-05	3.17E-05	0.00E+00	80	87	TMT6plex
P02671	FIBA_HUMAN	GDFLAEGGG	Y	34.64	1050.52	9	2.5	526.3	2	78.7	F1:11127	1.19E-04	4.66E-04	3.97E-04	1.91E-04	8.03E-05	1.07E-04	25	33	TMT6plex
P02671	FIBA_HUMAN	SSSYSKQFTSSTSY	Y	38.86	2017	14	7.6	1010	2	65.8	F1:9042	4.03E-03	9.59E-04	2.42E-03	1.30E-03	6.66E-04	4.06E-04	576	589	TMT6plex
P00734	THRB_HUMAN	TFGSGEAD	Y	31.67	1011.47	8	2.6	506.7	2	45.9	F1:5908	3.39E-04	5.20E-04	5.55E-04	7.08E-04	5.88E-04	1.23E-03	328	335	TMT6plex
P00488	F13A_HUMAN	EDDLPTVELQGVVPR	Y	38.73	1895.02	15	-2.5	632.7	3	108	F1:16353	0.00E+00	0.00E+00	0.00E+00	3.45E-05	0.00E+00	4.64E-05	24	38	TMT6plex
Q9Y6J8	STYL1_HUMAN	KTILGD	N	15.12	874.533	6	0	438.3	2	122	F2:18215	7.81E-05	5.80E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	298	303	TMT6plex
P52566	GDIR2_HUMAN	KTLLGD	N	15.12	874.533	6	0	438.3	2	122	F2:18215	7.81E-05	5.80E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	50	55	TMT6plex

Q9C0G6	DYH6_HUMAN	IRRAF	N	21.67	890.565	5	-0.2	446.3	2	116	F1:17940	5.21E-05	0.00E+00	3.85E-05	0.00E+00	0.00E+00	0.00E+00	3664	3668	TMT6plex
A8K8P3	SFI1_HUMAN	LRRAF	N	21.67	890.565	5	-0.2	446.3	2	116	F1:17940	5.21E-05	0.00E+00	3.85E-05	0.00E+00	0.00E+00	0.00E+00	352	356	TMT6plex
P02652	APOA2_HUMAN	ELGTQPA	Y	15.56	943.518	7	4.4	472.8	2	37.4	F2:4404	3.42E-04	4.76E-04	5.87E-04	6.35E-04	5.62E-04	1.03E-03	92	98	TMT6plex
P08123	CO1A2_HUMAN	DFGYDGD	Y	27.91	1016.43	7	0.9	509.2	2	77.3	F1:10878	5.12E-05	1.39E-04	1.44E-04	1.39E-04	1.88E-04	3.30E-04	1109	1115	TMT6plex
P02656	APOC3_HUMAN	DLDEVRPT	Y	23.17	1269.68	9	0.1	635.8	2	50.1	F1:6584	4.12E-04	4.36E-04	5.04E-04	8.77E-04	6.08E-04	1.64E-03	86	94	TMT6plex
P02671	FIBA_HUMAN	FLAEGGGVR	Y	36.73	1133.64	9	4.3	567.8	2	57.4	F1:7732	4.85E-03	1.11E-03	5.92E-03	2.03E-03	1.02E-03	6.24E-04	27	35	TMT6plex
P01024	CO3_HUMAN	IHWESASLLR	Y	30.22	1439.81	10	2.2	720.9	2	78.8	F2:10479	3.31E-04	6.31E-04	4.48E-04	6.67E-04	7.90E-04	1.61E-03	1311	1320	TMT6plex
P02675	FIBB_HUMAN	NDNEEGF	Y	32.99	1052.46	7	-1.4	527.2	2	49.9	F1:6549	5.12E-03	2.42E-03	7.30E-03	6.83E-03	7.56E-03	8.33E-03	34	40	TMT6plex
POC0L4	CO4A_HUMAN	FKSHALQLNNRQI	Y	26.38	2026.18	13	2.4	507.6	4	57.9	F1:7821	0.00E+00	5.63E-05	3.89E-05	0.00E+00	0.00E+00	0.00E+00	1339	1351	TMT6plex
P00734	THRB_HUMAN	SLEDKTERELLES	Y	29.3	2006.09	13	1.7	669.7	3	83.7	F1:11931	1.30E-04	2.96E-04	1.92E-04	3.91E-04	6.48E-04	1.53E-03	346	358	TMT6plex
Q9Y334	VWA7_HUMAN	ADDLFAAYF	Y	15.49	1260.62	9	-1.3	631.3	2	99.3	F1:14674	3.49E-03	4.93E-03	5.03E-03	4.51E-03	1.98E-03	5.83E-04	84	92	TMT6plex
O43497	CAC1G_HUMAN	DLERYYYQTEN	Y	17.09	1558.75	10	9.4	780.4	2	53.4	F1:7066	3.60E-04	5.63E-04	2.77E-04	4.79E-04	5.64E-04	6.28E-04	254	263	TMT6plex
O95810	SDPR_HUMAN	EEAERSDGDVPQPAV LQ	Y	32.44	2068.03	17	-4.2	690.3	3	61.3	F1:8360	1.36E-04	1.38E-04	6.05E-05	1.36E-04	2.28E-04	1.48E-04	404	420	TMT6plex
P00734	THRB_HUMAN	AHVRGLQ	Y	20.01	1008.6	7	8	505.3	2	98.5	F1:14528	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.99E-05	6.00E-05	2	8	TMT6plex
O95810	SDPR_HUMAN	GSVKG	N	15.64	904.575	5	7.5	453.3	2	122	F1:19181	5.58E-05	3.70E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	88	92	TMT6plex
Q9H4B7	TBB1_HUMAN	VLEEDDEVTEEAEME PEDKGH	Y	61.38	2901.35	21	0.4	968.1	3	91.6	F1:13321	5.17E-05	1.31E-04	4.32E-05	1.11E-04	3.58E-04	1.67E-04	431	451	TMT6plex
P51788	CLCN2_HUMAN	CCFAAP	Y	15.09	839.387	6	1.9	420.7	2	44.5	F1:5682	2.25E-04	2.29E-04	2.69E-04	1.54E-04	1.08E-04	2.43E-04	250	255	TMT6plex
Q9Y566	SHAN1_HUMAN	PRPLVH	Y	15.89	946.592	6	-0.9	474.3	2	96.5	F1:14159	0.00E+00	0.00E+00	0.00E+00	4.13E-05	0.00E+00	6.43E-05	1335	1340	TMT6plex
Q96AP7	ESAM_HUMAN	DGAHPQPI	Y	31.66	1062.57	8	4.8	532.3	2	23.2	F2:2335	3.32E-04	4.07E-04	2.46E-04	5.16E-04	3.72E-04	3.92E-04	351	358	TMT6plex
Q8WXI7	MUC16_HUMAN	FLVTT	N	16.37	808.49	5	-4.9	405.3	2	57.7	F2:7353	5.50E-05	1.50E-04	2.00E-04	4.69E-04	1.26E-04	3.62E-04	4461	4465	TMT6plex
Q15942	ZYX_HUMAN	EPPPAP	N	18.29	835.464	6	1.6	418.7	2	36	F1:4440	1.68E-04	3.12E-04	2.34E-04	2.33E-04	5.44E-04	4.36E-04	45	50	TMT6plex
O15294	OGT1_HUMAN	TLQMWANILKRVPN S VLW	Y	16.17	2627.5	18	8	657.9	4	82.2	F2:11028	0.00E+00	0.00E+00	0.00E+00	8.31E-05	1.31E-04	0.00E+00	857	874	TMT6plex; Deamidation
P60709	ACTB_HUMAN	EHPVLL	N	15.05	935.564	6	4.1	468.8	2	49.4	F2:6125	1.79E-04	1.90E-04	3.28E-04	3.46E-04	2.60E-04	5.26E-04	100	105	TMT6plex
P02671	FIBA_HUMAN	GDSTFESKSY	Y	38.45	1577.8	10	0.8	789.9	2	59.7	F1:8119	5.42E-03	1.20E-03	2.71E-03	8.84E-04	1.02E-03	5.64E-04	592	601	TMT6plex
P60709	ACTB_HUMAN	APEEHPVLL	Y	38.85	1232.7	9	2.6	617.4	2	65.2	F1:8951	4.28E-04	5.61E-04	3.62E-04	5.43E-04	7.08E-04	4.96E-04	97	105	TMT6plex
P01024	CO3_HUMAN	NEGFTVTAEGK	Y	42.77	1380.71	11	1	691.4	2	50.6	F1:6663	7.26E-04	9.53E-04	5.03E-04	8.78E-04	1.11E-03	9.01E-04	1327	1337	TMT6plex
P02656	APOC3_HUMAN	DYWSTVKD	Y	36.06	1470.78	8	3.8	736.4	2	78.8	F1:11133	4.15E-04	3.65E-04	2.78E-04	5.64E-04	5.86E-04	1.38E-03	72	79	TMT6plex
Q96HP0	DOCK6_HUMAN	MPFAW	N	15.62	879.452	5	5.2	440.7	2	83.3	F1:11854	9.02E-05	2.05E-04	2.23E-04	1.26E-04	6.34E-05	1.06E-04	392	396	TMT6plex
P02671	FIBA_HUMAN	DFLAEG	Y	22.25	879.454	6	2.5	440.7	2	83.3	F1:11855	9.02E-05	2.05E-04	2.23E-04	1.26E-04	6.34E-05	1.06E-04	26	31	TMT6plex
Q14624	ITI4_HUMAN	FRPGVLSSRQLGLPGP PDVPDHA	Y	41.92	2640.43	23	1.6	661.1	4	92	F2:12630	0.00E+00	0.00E+00	0.00E+00	3.79E-05	6.41E-05	0.00E+00	660	682	TMT6plex
Q9Y281	COF2_HUMAN	SLEGKPL	Y	20.56	1200.75	7	-8.4	601.4	2	61.2	F1:8352	6.09E-04	1.27E-03	4.69E-04	1.27E-03	1.32E-03	1.06E-03	160	166	TMT6plex
P02671	FIBA_HUMAN	GDFLAEGGGVR	Y	51.77	1305.69	11	2.2	653.9	2	70.7	F1:9808	1.04E-02	9.79E-04	1.48E-02	2.24E-03	1.15E-03	6.65E-04	25	35	TMT6plex
P04632	CPNS1_HUMAN	EPPPPRT	Y	27.83	1021.58	7	3.1	511.8	2	18.8	F1:1723	1.65E-03	2.10E-03	3.47E-04	8.53E-04	2.25E-04	2.24E-04	79	85	TMT6plex

Q14624	ITIH4_HUMAN	SSRKLGLPGPPDVDP HAAYHPF	Y	32.99	2586.35	22	-4	647.6	4	83	F2:11161	0.00E+00	0.00E+00	0.00E+00	3.55E-05	6.15E-05	0.00E+00	666	687	TMT6plex; Mutation
Q76MJ5	ERN2_HUMAN	LSGGSHPF	Y	15.16	1029.54	8	-8.3	515.8	2	39.8	F1:5016	1.46E-03	1.57E-03	1.63E-03	1.78E-03	1.65E-03	2.32E-03	717	724	TMT6plex
Q14624	ITIH4_HUMAN	GPPDVDP	Y	32.49	924.476	7	0.1	463.2	2	50	F1:6558	4.22E-04	1.65E-03	1.20E-03	2.35E-03	1.15E-03	2.03E-03	674	680	TMT6plex
P02675	FIBB_HUMAN	DNEEGFFS	Y	31.05	1172.52	8	2.8	587.3	2	90.1	F1:13027	4.03E-04	1.40E-03	7.91E-04	3.74E-04	2.70E-04	3.83E-04	35	42	TMT6plex
P02675	FIBB_HUMAN	GVNDNEEGF	Y	42.12	1208.55	9	0.3	605.3	2	62.4	F1:8516	5.36E-04	6.13E-04	7.35E-04	6.00E-04	5.14E-04	4.32E-04	32	40	TMT6plex
O95810	SDPR_HUMAN	SEEAERSDGDPPVQPA VLQ	Y	32.3	2155.06	18	2.7	1079	2	60.7	F1:8285	9.77E-05	6.34E-05	0.00E+00	1.30E-04	3.09E-04	8.43E-05	403	420	TMT6plex
Q86UX7	URP2_HUMAN	DEAPGDPIQQ	Y	38.18	1297.64	10	2.2	649.8	2	54.4	F1:7235	7.14E-04	1.24E-03	6.84E-04	1.64E-03	1.53E-03	8.44E-04	392	401	TMT6plex
P01024	CO3_HUMAN	HWESAS	Y	28.08	944.455	6	7.4	473.2	2	25.4	F1:2764	4.16E-04	7.12E-04	4.09E-04	5.03E-04	1.49E-03	1.04E-03	1312	1317	TMT6plex
P0C0L4	CO4A_HUMAN	TLEIPGN	Y	29.07	971.549	7	-0.1	486.8	2	77.8	F1:10972	2.93E-04	3.20E-04	1.98E-04	3.12E-04	3.35E-04	3.57E-04	957	963	TMT6plex
P42345	MTOR_HUMAN	HALIR	N	18.02	837.539	5	1.1	419.8	2	91.2	F1:13236	5.31E-05	0.00E+00	0.00E+00	6.14E-05	3.22E-05	1.57E-04	2247	2251	TMT6plex
P60709	ACTB_HUMAN	HAILR	N	18.02	837.539	5	1.1	419.8	2	91.2	F1:13236	5.31E-05	0.00E+00	0.00E+00	6.14E-05	3.22E-05	1.57E-04	173	177	TMT6plex
Q86UQ4	ABCAD_HUMAN	HAIIR	N	18.02	837.539	5	1.1	419.8	2	91.2	F1:13236	5.31E-05	0.00E+00	0.00E+00	6.14E-05	3.22E-05	1.57E-04	4777	4781	TMT6plex
P02461	CO3A1_HUMAN	GGDKGDTGPPGP	Y	27.54	1527.79	12	1.8	764.9	2	28.3	F1:3256	6.49E-04	5.18E-04	9.38E-04	1.72E-03	1.01E-03	8.09E-04	626	637	TMT6plex; Hydroxylation
P00734	THRB_HUMAN	YIDGR	N	18.87	851.47	5	3	426.7	2	27	F1:3029	6.03E-04	2.40E-04	6.47E-04	9.35E-04	2.85E-03	9.99E-04	359	363	TMT6plex
P60709	ACTB_HUMAN	DDAPRAVFPS	N	17.5	1302.68	10	2.1	652.3	2	60.2	F1:8195	1.39E-03	1.42E-03	4.95E-04	6.89E-04	6.02E-04	4.30E-04	24	33	TMT6plex
Q8IU A7	ABCA9_HUMAN	SIGYVSS	Y	17.92	940.507	7	8	471.3	2	63.2	F2:8096	3.34E-04	5.99E-04	2.63E-04	1.99E-04	1.77E-04	2.91E-04	1111	1117	TMT6plex
P02671	FIBA_HUMAN	MADEAGSEADHEGT HSTKT	Y	15.39	2201.97	19	9.8	551.5	4	29.2	F1:3393	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.23E-05	8.08E-05	603	621	TMT6plex; Mutation
Q15942	ZYX_HUMAN	HVQPQPQPKPVQ	Y	54.38	1968.13	13	1.7	657.1	3	30.4	F1:3572	4.03E-04	3.72E-04	7.43E-05	5.45E-04	1.04E-03	3.43E-04	223	235	TMT6plex
P04004	VTNC_HUMAN	EEEAPAPEVGASKPE GI	Y	43.79	2167.14	17	1.7	723.4	3	73.4	F1:10225	3.27E-04	2.33E-04	1.03E-04	2.82E-04	7.17E-04	3.59E-04	119	135	TMT6plex
P00734	THRB_HUMAN	EDKTERELLESYIDGR	Y	50.02	2410.27	16	5.8	804.4	3	93.5	F2:12910	1.01E-03	0.00E+00	2.16E-03	4.31E-03	3.02E-03	9.84E-04	348	363	TMT6plex
P05111	INHA_HUMAN	GVRRLPR	Y	16.01	1081.7	7	7.5	541.9	2	61.6	F1:8394	4.12E-04	5.54E-04	5.46E-04	6.45E-04	5.43E-04	9.44E-04	54	60	TMT6plex
Q14624	ITIH4_HUMAN	GVLSSRQLGLPGPPD VPDHA	Y	51.53	2240.21	20	0.8	747.7	3	90.4	F1:13090	4.96E-05	2.19E-04	1.57E-04	3.24E-04	6.45E-04	1.73E-04	663	682	TMT6plex
P01009	A1AT_HUMAN	EDPQGDAAQ	Y	19.81	1158.54	9	4.4	580.3	2	22.8	F1:2377	1.90E-04	2.15E-04	1.43E-04	2.31E-04	3.40E-04	1.99E-04	25	33	TMT6plex
P02671	FIBA_HUMAN	NRGDSTFESKSY	Y	44.61	1847.94	12	1.8	617	3	42.7	F1:5429	2.35E-03	6.69E-04	1.03E-03	5.41E-04	5.67E-04	2.90E-04	590	601	TMT6plex
P01024	CO3_HUMAN	RIHWESASLL	Y	37.94	1439.81	10	3.3	720.9	2	81.1	F1:11506	8.79E-04	1.74E-03	6.13E-04	6.19E-04	5.09E-04	3.52E-04	1310	1319	TMT6plex
P02671	FIBA_HUMAN	DFLAEGG	Y	24.85	936.476	7	3.2	469.2	2	85.1	F1:12185	4.56E-05	8.12E-05	1.15E-04	2.21E-04	7.90E-05	3.62E-04	26	32	TMT6plex
O00151	PDLI1_HUMAN	QEILESEEKGDPNKPS GF	Y	48.62	2444.25	18	4.7	815.8	3	96.2	F2:13356	9.78E-05	4.37E-05	0.00E+00	1.93E-04	4.83E-04	8.08E-05	220	237	Pyro-glu from Q; TMT6plex
P01024	CO3_HUMAN	EGVQKEDIPPADL	Y	31.14	1868.03	13	4.1	935	2	76.8	F1:10787	4.01E-04	5.98E-04	3.11E-04	6.24E-04	5.57E-04	1.25E-03	955	967	TMT6plex
P02452	CO1A1_HUMAN	DGKTGPPGPA	Y	37.39	1369.76	10	1.7	685.9	2	26.5	F1:2949	1.48E-03	1.76E-03	2.27E-03	1.56E-03	1.62E-03	7.64E-04	550	559	TMT6plex; Hydroxylation
P02671	FIBA_HUMAN	RGDSTFESKSY	Y	42.5	1733.9	11	1.6	579	3	43.8	F1:5581	8.32E-04	2.94E-04	5.66E-04	4.21E-04	2.44E-04	2.39E-04	591	601	TMT6plex

Q15942	ZYX_HUMAN	KPKVNPFRPGDSEPPP APGA	Y	27.73	2744.56	20	0.1	687.1	4	59.6	F1:8104	4.03E-05	8.26E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	33	52	TMT6plex
Q15942	ZYX_HUMAN	ASSPAPAPKFSVPTPK FTPVAS	Y	53.55	2870.65	22	3.2	957.9	3	88.7	F2:12113	1.25E-04	1.39E-04	0.00E+00	2.33E-04	5.52E-04	1.25E-04	257	278	TMT6plex
Q14204	DYHC1_HUMAN	KGRQN	Y	19.76	830.493	5	5.8	416.3	2	87.9	F1:12652	0.00E+00	3.37E-05	6.01E-05	4.83E-06	0.00E+00	0.00E+00	4228	4232	TMT6plex
P00734	THRB_HUMAN	EDKTERELLESYIDG	Y	45.57	2254.17	15	1.5	1128	2	105	F1:15708	1.52E-03	1.33E-03	1.92E-03	6.02E-03	3.67E-03	1.60E-03	348	362	TMT6plex
P04632	CPNS1_HUMAN	GGGGGGGGLG	Y	15.09	873.451	10	2.1	437.7	2	22.1	F1:2272	2.04E-04	1.82E-04	1.86E-04	1.62E-04	1.41E-04	1.93E-04	13	22	TMT6plex
P57740	NU107_HUMAN	PGHLLR	Y	15.9	920.576	6	3	461.3	2	98.4	F2:13755	4.16E-04	0.00E+00	3.68E-04	0.00E+00	0.00E+00	1.22E-04	543	548	TMT6plex
P60709	ACTB_HUMAN	DVDIRKD	N	16.6	1317.77	7	4.3	440.3	3	36.2	F2:4191	2.99E-04	3.09E-04	2.09E-04	2.03E-04	1.79E-04	2.62E-04	286	292	TMT6plex
P0DJ18	SAA1_HUMAN	NHFRPAGLPEKY	N	23.24	1656.89	12	-0.1	553.3	3	44.8	F1:5724	6.15E-05	1.52E-04	8.02E-05	2.50E-04	1.06E-04	1.57E-04	111	122	TMT6plex
P01024	CO3_HUMAN	HWESA	Y	18.6	857.424	5	3.2	429.7	2	27.2	F1:3053	5.71E-04	1.67E-03	5.93E-04	7.10E-04	5.13E-03	3.46E-03	1312	1316	TMT6plex
P01024	CO3_HUMAN	THRIHWESASLL	Y	39.91	1677.92	12	3.5	840	2	66.3	F1:9128	1.16E-03	2.40E-03	1.66E-03	1.39E-03	1.20E-03	8.22E-04	1308	1319	TMT6plex
O15234	CASC3_HUMAN	KGPKH	N	20.5	1023.66	5	3.7	512.8	2	61.1	F1:8343	2.29E-04	3.82E-04	5.10E-04	5.29E-04	4.39E-04	9.55E-04	165	169	TMT6plex
Q14624	ITI4_HUMAN	QLGLPGPPDVPDHA	Y	49.97	1640.87	14	2.7	821.4	2	88.8	F1:12811	1.79E-04	4.90E-04	1.71E-04	5.28E-04	1.25E-03	3.89E-04	669	682	TMT6plex
O43847	NRDC_HUMAN	DDEEGF	Y	15.66	939.402	6	3	470.7	2	60.7	F1:8279	2.39E-04	3.58E-04	4.71E-04	6.95E-04	5.90E-04	1.90E-03	166	171	TMT6plex
P01024	CO3_HUMAN	HWESASL	Y	30.8	1057.54	7	3.4	529.8	2	58.3	F1:7875	2.96E-04	7.15E-04	5.23E-04	4.24E-04	1.17E-03	1.35E-03	1312	1318	TMT6plex
P02671	FIBA_HUMAN	DSTFESK	Y	34.86	1270.68	7	3.1	636.3	2	42.6	F1:5400	6.29E-03	1.48E-03	4.83E-03	1.54E-03	1.63E-03	2.30E-03	593	599	TMT6plex
P10124	SRGN_HUMAN	TDLFPK	Y	23.78	1177.71	6	3.9	589.9	2	76.4	F1:10719	1.41E-03	2.09E-03	2.77E-03	1.25E-03	1.97E-03	9.40E-04	72	77	TMT6plex
P0C0L4	CO4A_HUMAN	DDPDAPL	Y	27.83	970.481	7	5.1	486.3	2	58.2	F2:7427	1.00E-04	1.74E-04	1.75E-04	2.23E-04	2.27E-04	5.68E-04	1429	1435	TMT6plex
P68363	TBA1B_HUMAN	DGALNVDLTFEQTN	N	48.48	1764.87	14	2.9	883.4	2	125	F2:18836	1.56E-04	1.33E-04	0.00E+00	4.92E-05	0.00E+00	0.00E+00	245	258	TMT6plex
P02671	FIBA_HUMAN	DFLAEGGGVR	Y	48.12	1248.67	10	-0.7	625.3	2	66.4	F2:8588	8.35E-03	8.53E-04	1.13E-02	3.56E-03	1.15E-03	4.44E-04	26	35	TMT6plex
Q14624	ITI4_HUMAN	SRQLGLPGPPDVPDH	Y	29.25	1812.97	15	2.9	605.3	3	64.9	F1:8895	5.78E-05	1.06E-04	1.29E-04	1.15E-04	1.65E-04	1.23E-04	667	681	TMT6plex
P52306	GDS1_HUMAN	ESNRLL	Y	17.57	959.56	6	2.6	480.8	2	36.7	F2:4274	1.12E-03	6.29E-04	9.22E-04	1.43E-03	9.45E-04	1.13E-03	465	470	TMT6plex
P00488	F13A_HUMAN	NSNAAEDDLPTVE	Y	30.52	1602.76	13	3.8	802.4	2	73.6	F1:10265	2.09E-04	3.87E-04	2.28E-04	3.08E-04	3.52E-04	4.95E-04	19	31	TMT6plex
Q92636	FAN_HUMAN	SSIITG	N	15.22	805.475	6	2.9	403.7	2	60.7	F1:8274	6.50E-05	8.00E-05	1.19E-04	2.20E-04	8.02E-05	3.54E-04	899	904	TMT6plex
P0C0L4	CO4A_HUMAN	LNNRQI	Y	18.49	985.587	6	2.6	493.8	2	32	F1:3825	8.01E-04	1.12E-03	1.18E-03	1.89E-03	1.16E-03	3.53E-03	1346	1351	TMT6plex
P0C0L4	CO4A_HUMAN	GLEEELQ	Y	27.91	1045.55	7	2.3	523.8	2	71.6	F1:9948	2.48E-04	4.13E-04	3.11E-04	3.31E-04	2.22E-03	1.14E-03	1353	1359	TMT6plex
Q8IZQ1	WDFY3_HUMAN	FLPKHT	Y	18.51	1199.74	6	-6.7	600.9	2	98.3	F1:14493	1.77E-04	1.45E-04	2.80E-04	2.37E-04	2.82E-04	5.28E-04	1762	1767	TMT6plex
O95810	SDPR_HUMAN	SEEAERSDGDVPVQPA VLQVHQTS	Y	53.31	2707.33	23	3.2	903.5	3	57.5	F1:7746	0.00E+00	1.05E-04	0.00E+00	6.16E-05	2.05E-04	7.73E-05	403	425	TMT6plex
Q12888	TP53B_HUMAN	LHRTSSGTSL	Y	20.05	1286.71	10	-5.9	429.9	3	55.3	F1:7381	8.07E-05	2.13E-04	1.88E-04	1.39E-04	3.23E-04	3.84E-04	1312	1321	TMT6plex
Q14624	ITI4_HUMAN	GLPGPPDVPDHAAYH PF	Y	67.52	2015.01	17	3.9	672.7	3	89.5	F2:12218	1.49E-04	1.69E-04	1.40E-04	5.73E-04	1.78E-03	3.26E-04	671	687	TMT6plex
Q14624	ITI4_HUMAN	FRPGVL	Y	16.17	916.57	6	0.2	459.3	2	65.7	F1:9027	2.12E-04	1.91E-04	5.63E-04	6.94E-04	1.10E-03	3.04E-04	660	665	TMT6plex
Q13315	ATM_HUMAN	KSL LTD	Y	16.42	904.543	6	1.3	453.3	2	78.6	F1:11108	0.00E+00	4.30E-05	8.64E-05	9.21E-05	6.23E-05	9.67E-05	1280	1285	TMT6plex
Q8NCH0	CHSTE_HUMAN	APPHVR	Y	18.39	904.545	6	-0.2	453.3	2	78.6	F1:11109	0.00E+00	4.30E-05	8.64E-05	9.21E-05	6.23E-05	9.67E-05	315	320	TMT6plex

O95810	SDPR_HUMAN	SEEAERSDGDVPVQPA VLQVHQ	Y	47.37	2519.25	21	-0.6	840.8	3	59.6	F1:8102	5.11E-05	1.37E-04	0.00E+00	1.36E-04	1.58E-04	8.91E-05	403	423	TMT6plex
Q14624	ITIH4_HUMAN	SRQLGLPGPPDVPDH AAYHPF	Y	63.31	2499.29	21	4.7	625.8	4	83.1	F2:11179	0.00E+00	0.00E+00	5.31E-05	1.85E-04	3.13E-04	0.00E+00	667	687	TMT6plex
P10124	SRGN_HUMAN	NLPSPDSQDLGQHGLE ED	Y	35.84	2081.97	17	-1.4	1042	2	70.1	F1:9708	1.31E-04	1.43E-04	1.06E-04	2.26E-04	6.50E-04	2.11E-04	139	155	TMT6plex
P01042	KNG1_HUMAN	HDWGHE	Y	27.31	1008.46	6	1.8	505.2	2	18.6	F1:1687	2.98E-04	4.04E-04	9.05E-04	9.99E-04	1.73E-03	5.58E-04	429	434	TMT6plex
Q86WK9	MPRA_HUMAN	THLLAALVL	Y	19.63	1178.76	9	8	590.4	2	62.7	F2:8018	2.65E-04	4.90E-04	7.09E-04	6.16E-04	6.05E-04	9.30E-04	77	85	TMT6plex
Q9BXM0	PRAX_HUMAN	KGPVPAA	Y	16.21	867.538	7	-0.6	434.8	2	94.6	F1:13829	9.43E-05	7.16E-05	1.22E-04	1.47E-04	1.44E-04	3.86E-04	176	182	TMT6plex
P00734	THRB_HUMAN	DFNSAVQL	Y	23.32	1121.59	8	3.6	561.8	2	98	F1:14442	1.21E-04	9.15E-05	9.75E-05	1.37E-04	1.29E-04	2.76E-04	250	257	TMT6plex
Q8WWM	ATX2L_HUMAN	GAPHPQVMLLH	Y	17.14	1524.84	12	-0.7	509.3	3	69	F1:9554	6.10E-05	4.57E-05	0.00E+00	5.07E-05	5.47E-05	1.01E-04	981	992	TMT6plex
P00488	F13A_HUMAN	NNSNAEEDDLPTVE	Y	37.22	1716.8	14	2.2	859.4	2	72.2	F1:10049	1.06E-04	2.96E-04	1.47E-04	1.83E-04	3.20E-04	4.92E-04	18	31	TMT6plex
P62328	TYB4_HUMAN	SDKPDM	Y	19.74	962.458	6	2.3	482.2	2	46	F1:5927	5.90E-04	2.39E-03	3.32E-04	7.47E-04	4.11E-03	3.68E-03	2	7	Acetylation ; TMT6plex
Q14624	ITIH4_HUMAN	GLPGPPDVPDH	Y	57.6	1328.69	11	4.9	665.4	2	67.2	F1:9274	5.81E-04	1.44E-03	7.49E-04	1.10E-03	3.29E-03	1.57E-03	671	681	TMT6plex
P00734	THRB_HUMAN	EDKTEREL	Y	29.9	1476.82	8	3.3	493.3	3	31.8	F1:3792	4.93E-04	5.97E-04	4.45E-04	1.28E-03	9.91E-04	4.17E-03	348	355	TMT6plex
P02671	FIBA_HUMAN	STFESKSY	Y	35.41	1405.75	8	5.4	703.9	2	56.3	F2:7103	7.30E-03	1.93E-03	2.55E-03	1.14E-03	1.47E-03	9.94E-04	594	601	TMT6plex
Q14767	LTBP2_HUMAN	PLRGH	N	16.85	807.492	5	0.3	404.8	2	66	F1:9069	1.54E-04	1.28E-04	2.03E-04	7.04E-05	9.21E-05	1.70E-04	1598	1602	TMT6plex
P02671	FIBA_HUMAN	VPPEWK	Y	26.71	1212.73	6	4.4	607.4	2	69	F2:8975	6.54E-04	1.07E-03	5.29E-04	5.36E-04	5.33E-04	4.08E-04	244	249	TMT6plex
O14924	RGS12_HUMAN	VLPEFLR	Y	15.08	1101.67	7	9.6	551.9	2	97.7	F1:14376	8.16E-05	5.48E-05	6.40E-05	8.58E-05	6.91E-05	1.27E-04	1215	1221	TMT6plex
P0DJ18	SAA1_HUMAN	DPNHFRPAGLPEK	N	26.15	1935.07	13	0.9	484.8	4	53.8	F1:7136	4.51E-05	2.03E-04	7.92E-05	4.48E-05	0.00E+00	5.68E-05	109	121	TMT6plex
Q14624	ITIH4_HUMAN	LPGPPDVPDHAAYHP F	Y	62.03	1957.99	16	4.1	653.7	3	91.1	F1:13226	3.11E-04	2.98E-04	4.14E-04	4.52E-04	7.59E-04	3.69E-04	672	687	TMT6plex
Q14624	ITIH4_HUMAN	NVHSGSTFF	Y	37.3	1223.61	9	3.4	612.8	2	62.7	F1:8564	6.18E-04	4.66E-04	4.12E-04	6.45E-04	5.55E-04	5.86E-04	617	625	TMT6plex
P02671	FIBA_HUMAN	SYNRGDSTFES	Y	31.27	1490.68	11	4.3	746.4	2	36.5	F2:4248	1.39E-03	9.16E-04	8.67E-04	1.10E-03	5.55E-04	4.85E-04	588	598	TMT6plex
O00151	PDLI1_HUMAN	QEKQELNEPPKQS	Y	33.92	1995.07	13	1.9	666	3	46.4	F1:5991	1.02E-04	1.37E-04	9.45E-05	1.23E-04	2.32E-04	1.38E-04	201	213	Pyro-glu from Q; TMT6plex
Q9BRK4	LZTS2_HUMAN	GGPAPPR	Y	17.23	879.513	7	3.4	440.8	2	92.2	F1:13421	2.20E-04	1.16E-04	5.44E-05	4.01E-05	4.79E-05	7.56E-05	40	46	TMT6plex
Q3MIN7	RGL3_HUMAN	LPPMPP	N	19.43	879.509	6	7.7	440.8	2	92.2	F1:13420	2.20E-04	1.16E-04	5.44E-05	4.01E-05	4.79E-05	7.56E-05	114	119	TMT6plex
P0C0L4	CO4A_HUMAN	SHALQLNNRQ	Y	24.8	1408.77	10	3.7	705.4	2	20.3	F1:1979	1.42E-04	2.21E-04	2.79E-04	2.80E-04	3.01E-04	7.00E-04	1341	1350	TMT6plex
Q86Y01	DTX1_HUMAN	NDGGAWTAYDMD	Y	19.03	1544.63	12	-5.5	773.3	2	85.4	F2:11563	3.08E-04	1.14E-04	0.00E+00	5.03E-04	1.16E-03	1.46E-04	113	124	TMT6plex; Deamidation
Q92932	PTPR2_HUMAN	LAENGVR	Y	22.96	986.571	7	2.8	494.3	2	26.4	F1:2925	5.51E-03	4.79E-04	7.54E-03	2.54E-03	9.33E-04	2.89E-04	848	854	TMT6plex
P02671	FIBA_HUMAN	LAEGGGVR	Y	29.21	986.571	8	2.8	494.3	2	26.4	F1:2926	5.51E-03	4.79E-04	7.54E-03	2.54E-03	9.33E-04	2.89E-04	28	35	TMT6plex
Q01484	ANK2_HUMAN	GNTALHI	N	15.45	953.55	7	-7.3	477.8	2	78.1	F1:11014	5.26E-05	1.21E-04	4.70E-04	4.17E-04	2.52E-04	7.72E-04	97	103	TMT6plex
Q495B1	AKD1A_HUMAN	GNTALHL	N	15.45	953.55	7	-7.3	477.8	2	78.1	F1:11014	5.26E-05	1.21E-04	4.70E-04	4.17E-04	2.52E-04	7.72E-04	192	198	TMT6plex
Q14624	ITIH4_HUMAN	LIIRYDV	Y	16.04	904.538	7	6.5	453.3	2	70.9	F1:9834	7.40E-05	1.76E-04	2.24E-04	2.50E-04	1.58E-04	3.48E-04	237	243	Methyl ester
P00734	THRB_HUMAN	SLEDKTERE	Y	32.25	1563.85	9	2.3	522.3	3	32.4	F1:3876	3.67E-04	3.88E-04	2.72E-04	7.91E-04	1.09E-03	4.07E-03	346	354	TMT6plex

O60303	K0556_HUMAN	ILFTT	N	17.32	822.505	5	4.9	412.3	2	80.4	F1:11398	0.00E+00	4.17E-05	6.56E-05	5.34E-05	5.12E-05	1.07E-04	1124	1128	TMT6plex
Q7Z407	CSMD3_HUMAN	LLFTT	N	17.32	822.505	5	4.9	412.3	2	80.4	F1:11398	0.00E+00	4.17E-05	6.56E-05	5.34E-05	5.12E-05	1.07E-04	983	987	TMT6plex
Q86UQ4	ABCAD_HUMAN	IIFTT	N	17.32	822.505	5	4.9	412.3	2	80.4	F1:11398	0.00E+00	4.17E-05	6.56E-05	5.34E-05	5.12E-05	1.07E-04	4027	4031	TMT6plex
P0C0L4	CO4A_HUMAN	DPDAPLQPVTP	Y	36.32	1377.73	11	1.6	689.9	2	81.1	F2:10842	5.74E-04	1.08E-03	2.55E-04	7.40E-04	1.04E-03	1.31E-03	1430	1440	TMT6plex
P02671	FIBA_HUMAN	STSYNRGDSTFES	Y	24.36	1678.76	13	1.1	840.4	2	36.8	F2:4289	1.52E-03	1.01E-03	9.40E-04	1.16E-03	7.75E-04	3.69E-04	586	598	TMT6plex
Q8NFU7	TET1_HUMAN	ATDMSCDHLK	Y	17.7	1577.79	10	5	789.9	2	63.7	F1:8728	3.24E-03	6.36E-04	1.48E-03	6.71E-04	6.49E-04	4.62E-04	808	817	TMT6plex
Q8IZQ1	WDFY3_HUMAN	FIYLYK	N	16.3	1303.79	6	0.1	652.9	2	124	F1:19487	0.00E+00	1.23E-04	5.24E-05	2.03E-04	4.66E-05	4.05E-04	769	774	TMT6plex
Q96EP0	RNF31_HUMAN	HFTIA	N	16.97	816.47	5	7	409.2	2	39.2	F1:4929	1.14E-04	1.67E-04	2.02E-04	4.75E-04	1.34E-04	3.31E-04	729	733	TMT6plex
Q9HCU4	CELR2_HUMAN	HFTLA	N	16.97	816.47	5	7	409.2	2	39.2	F1:4929	1.14E-04	1.67E-04	2.02E-04	4.75E-04	1.34E-04	3.31E-04	1388	1392	TMT6plex
P55291	CAD15_HUMAN	DELTGEIRTVQ	Y	15.6	1488.8	11	2.7	745.4	2	78.6	F1:11106	4.32E-04	5.39E-04	4.22E-04	4.25E-04	6.72E-04	6.93E-04	205	215	TMT6plex
P68363	TBA1B_HUMAN	EEGEFSEAREDM	N	29.19	1656.71	12	2.9	829.4	2	63.2	F1:8651	6.68E-04	1.06E-03	2.11E-04	2.60E-04	3.19E-04	2.23E-04	414	425	TMT6plex
Q9NV12	TM140_HUMAN	VIVVICLM	Y	15.7	1117.68	8	1.6	559.8	2	94.3	F2:13044	7.46E-05	1.05E-04	0.00E+00	1.72E-04	1.03E-04	7.25E-05	21	28	TMT6plex
P02671	FIBA_HUMAN	VSETESRGSSEG	Y	17.5	1452.69	12	2	727.4	2	18.4	F1:1659	2.74E-04	1.17E-04	9.63E-05	2.03E-04	2.34E-04	5.10E-04	541	552	TMT6plex
PODJI8	SAA1_HUMAN	FGHGAED	Y	25.13	960.45	7	2.6	481.2	2	24.8	F1:2667	2.07E-04	4.51E-04	2.71E-04	2.17E-04	2.18E-04	1.60E-04	87	93	TMT6plex
P00734	THRB_HUMAN	EETGDGLDESDRAI EG	Y	46.96	2035.9	17	2.6	1019	2	60	F1:8159	1.19E-04	1.70E-04	1.49E-04	1.26E-04	1.03E-03	2.57E-03	297	313	TMT6plex
P01042	KNG1_HUMAN	DDDLHQ	Y	24.93	1099.5	7	7.5	550.8	2	25.4	F1:2766	2.68E-04	4.80E-04	5.39E-04	6.21E-04	1.49E-03	5.51E-04	480	486	TMT6plex
Q14624	ITIH4_HUMAN	GVLSSRQLGLPGPPD VPDHAAYHPF	Y	58.33	2855.49	25	3.7	714.9	4	101	F1:14972	0.00E+00	0.00E+00	0.00E+00	3.17E-05	9.16E-05	0.00E+00	663	687	TMT6plex
Q05682	CALD1_HUMAN	QERYEIEETETVT	Y	21.68	1608.72	13	3.6	805.4	2	74.8	F1:10475	1.48E-03	5.98E-04	1.41E-03	1.03E-03	6.68E-04	4.66E-04	157	169	Pyro-glu from Q
Q8NDA8	MROH1_HUMAN	LAPLLLHLQ	Y	29.02	1245.8	9	4.2	623.9	2	74.5	F1:10432	3.36E-04	6.12E-04	3.08E-04	5.81E-04	4.34E-04	8.08E-04	1496	1504	TMT6plex
A8K8P3	SFI1_HUMAN	HWQKRRFL	Y	21.14	1628.97	8	-9	408.2	4	66.6	F1:9182	1.20E-03	1.05E-03	8.76E-04	1.39E-03	3.02E-03	1.28E-03	283	290	TMT6plex; Deamidation
P01024	CO3_HUMAN	ENEGFTVTAEG	Y	39.21	1381.66	11	3.4	691.8	2	70.4	F1:9755	6.79E-04	1.06E-03	4.17E-04	4.75E-04	4.91E-04	3.42E-04	1326	1336	TMT6plex
Q9P241	AT10D_HUMAN	QPPVPR	Y	15.22	922.544	6	2.5	462.3	2	26.8	F1:2986	5.40E-04	1.40E-03	4.76E-04	3.84E-04	2.32E-04	4.44E-04	984	989	TMT6plex; Deamidation
Q14624	ITIH4_HUMAN	NVHSATRERRLDYQE GP	Y	19.1	2256.16	17	9.3	565.1	4	48.2	F2:5930	0.00E+00	3.11E-05	0.00E+00	6.08E-05	8.17E-05	0.00E+00	902	918	TMT6plex; Mutation
P01024	CO3_HUMAN	ETKENEGFTVT	Y	20.83	1711.9	11	1.6	857	2	57.6	F1:7755	4.16E-04	1.27E-03	3.61E-04	9.68E-04	9.20E-04	1.59E-03	1323	1333	TMT6plex
P02675	FIBB_HUMAN	VNDNEEGFFS	Y	39.16	1386.61	10	3.9	694.3	2	110	F2:15863	1.30E-04	5.05E-04	6.27E-04	3.57E-04	1.47E-04	6.38E-05	33	42	TMT6plex; Deamidation
Q96QD5	DEPD7_HUMAN	ELLNLLKT	Y	15.72	1400.9	8	4.6	701.5	2	74.4	F2:9784	4.10E-04	6.01E-04	7.06E-04	6.83E-04	6.28E-04	1.11E-03	471	478	TMT6plex
P02675	FIBB_HUMAN	EAFSLRPAPPPISGGG V	Y	38.44	1894.02	17	5.4	632.3	3	75.9	F2:10025	7.91E-05	4.94E-05	5.34E-05	0.00E+00	7.25E-05	0.00E+00	55	71	TMT6plex
Q15942	ZYX_HUMAN	VNPFPRPGDSEPPAPG AQ	Y	45.07	2061.05	18	5.4	1032	2	69.6	F2:9090	7.77E-05	3.06E-04	5.87E-05	2.82E-04	2.85E-04	2.37E-04	36	53	TMT6plex
P04632	CPNS1_HUMAN	QYNPEPPPPR	Y	33.1	1176.56	10	3.8	589.3	2	43.4	F2:5186	5.19E-04	4.78E-04	2.18E-04	2.44E-04	3.44E-04	2.00E-04	75	84	Pyro-glu from Q
O15294	OGT1_HUMAN	KLAYM	N	17.5	853.493	5	4.6	427.8	2	69.3	F1:9597	7.58E-05	8.23E-05	2.99E-04	2.74E-04	1.82E-04	3.44E-04	695	699	TMT6plex

P02452	CO1A1_HUMAN	DGATGAAGPPGP	Y	26.4	1211.6	12	1.4	606.8	2	33.4	F1:4046	4.04E-04	3.51E-04	4.97E-04	5.37E-04	4.03E-04	6.98E-04	325	336	TMT6plex; Hydroxylation
P0C0L4	CO4A_HUMAN	DPDAPLQPVTPL	Y	46.07	1490.82	12	2.8	746.4	2	106	F1:16022	1.01E-04	2.38E-04	1.44E-04	4.06E-04	3.38E-04	1.24E-04	1430	1441	TMT6plex
P00734	THRB_HUMAN	SLEDKTERELLESYID GR	Y	48.63	2610.39	18	2.6	871.1	3	109	F1:16570	6.35E-04	1.07E-04	9.29E-04	8.01E-04	1.47E-03	7.03E-04	346	363	TMT6plex
Q8WZ42	TITIN_HUMAN	GPCQNLK	Y	18.28	988.521	7	5.1	495.3	2	72.6	F1:10106	1.26E-04	2.94E-04	2.32E-04	1.97E-04	1.61E-03	7.01E-04	18930	18936	TMT6plex; Deamidation
Q8WUY3	PRUN2_HUMAN	IEEEIQ	N	20.62	988.528	6	-1.5	495.3	2	72.6	F1:10107	1.26E-04	2.94E-04	2.32E-04	1.97E-04	1.61E-03	7.01E-04	1698	1703	TMT6plex
P0C0L4	CO4A_HUMAN	LEEEELQ	N	20.62	988.528	6	-1.5	495.3	2	72.6	F1:10107	1.26E-04	2.94E-04	2.32E-04	1.97E-04	1.61E-03	7.01E-04	1354	1359	TMT6plex
P0C0L4	CO4A_HUMAN	SHALQLNRRQIR	Y	28.22	1677.96	12	2.1	560.3	3	24.5	F1:2628	1.59E-04	2.07E-04	1.84E-04	2.12E-04	1.86E-04	2.84E-04	1341	1352	TMT6plex
Q8WZ42	TITIN_HUMAN	HLVSLQIL	Y	17.01	1156.74	8	-2.2	579.4	2	96.4	F2:13406	6.16E-05	8.99E-05	7.26E-05	1.31E-04	1.59E-04	5.68E-04	5373	5380	TMT6plex; Replacement of proton by lithium
P02671	FIBA_HUMAN	DEAGSEADHEGTHST K	Y	27.53	2128.01	16	3.6	533	4	15.7	F1:1247	0.00E+00	0.00E+00	0.00E+00	3.12E-05	0.00E+00	9.67E-05	605	620	TMT6plex
Q05682	CALD1_HUMAN	KPTKPAASDLPVPAE GVRNI	Y	23.37	2746.63	20	-1.3	687.7	4	72.4	F1:10085	0.00E+00	0.00E+00	0.00E+00	3.37E-05	1.05E-04	0.00E+00	693	712	TMT6plex
P0C0L4	CO4A_HUMAN	DDPDAPLQPV	Y	38.47	1294.66	10	0.2	648.3	2	73.6	F2:9655	2.42E-04	3.85E-04	1.74E-04	4.20E-04	3.00E-04	3.64E-04	1429	1438	TMT6plex
Q86UX7	URP2_HUMAN	TGSGGPGNHPHPDA SAEGLNP	Y	36.7	2254.06	22	1.2	752.4	3	36.2	F1:4471	0.00E+00	7.15E-05	0.00E+00	4.13E-05	5.41E-05	8.35E-05	482	503	TMT6plex
Q14624	ITIH4_HUMAN	FRPGVLSSRQLGLPGP PDVPDHAA	Y	39.05	2711.47	24	0.9	904.8	3	91.6	F2:12556	1.08E-04	7.39E-05	0.00E+00	6.60E-05	1.63E-04	1.14E-04	660	683	TMT6plex
P02671	FIBA_HUMAN	DSTFESKSY	Y	42.5	1520.78	9	-1.9	761.4	2	58.6	F2:7477	3.98E-02	4.74E-03	1.18E-02	2.59E-03	2.86E-03	3.30E-03	593	601	TMT6plex
P67936	TPM4_HUMAN	HIAEEADRKYEEVA	N	40.84	2117.12	14	-0.2	706.7	3	62.5	F1:8531	3.93E-04	2.53E-04	1.15E-04	8.69E-04	1.25E-03	1.14E-04	117	130	TMT6plex
P0DJ18	SAA1_HUMAN	DPNHFRPAG	N	36.21	1238.64	9	3.2	413.9	3	25.7	F1:2822	6.76E-05	1.07E-04	0.00E+00	0.00E+00	3.70E-05	0.00E+00	109	117	TMT6plex
P00734	THRB_HUMAN	EDKTERELLES	Y	26.12	1805.98	11	3.1	904	2	56.7	F1:7620	3.91E-04	1.01E-03	3.59E-04	8.46E-04	1.25E-03	3.98E-03	348	358	TMT6plex
Q96DM3	MIC1_HUMAN	RLRGSPN	Y	15.58	1027.61	7	1.8	514.8	2	81.3	F2:10867	6.39E-05	8.62E-05	1.10E-04	1.62E-04	6.88E-05	1.93E-04	622	628	TMT6plex
Q6ZRS2	SRCAP_HUMAN	PPSPRPS	Y	16.3	965.55	7	2.2	483.8	2	20.2	F1:1961	2.06E-04	3.12E-04	1.18E-04	1.16E-04	1.04E-04	1.71E-04	3014	3020	TMT6plex
Q5JPB2	ZN831_HUMAN	PWDSAPMASPGLP	Y	15.32	1553.78	13	-6.9	777.9	2	25.4	F1:2776	9.88E-05	3.27E-04	2.18E-04	4.19E-04	3.01E-04	2.41E-04	279	291	TMT6plex
P63241	IF5A1_HUMAN	QDSGEVREDLRLPEG DLG	Y	23.93	1966.92	18	3.3	984.5	2	94.4	F1:13798	6.71E-05	7.68E-05	0.00E+00	8.59E-05	6.75E-05	9.56E-05	103	120	Pyro-glu from Q
P02671	FIBA_HUMAN	SSSYSKQFTS	Y	51.81	1578.83	10	4.1	790.4	2	47.7	F2:5844	2.04E-03	2.89E-03	1.66E-03	2.36E-03	9.05E-04	1.13E-03	576	585	TMT6plex
P34995	PE2R1_HUMAN	QLLRLLPP	Y	17.69	1178.76	8	7.7	590.4	2	56	F2:7062	5.01E-04	9.08E-04	6.85E-04	6.91E-04	1.01E-03	9.67E-04	361	368	TMT6plex; Deamidation
O75469	NR112_HUMAN	NFRLPGV	Y	16.79	1030.61	7	3.1	516.3	2	64.6	F1:8857	4.01E-04	3.84E-04	5.23E-04	7.01E-04	1.10E-03	3.91E-04	171	177	TMT6plex
P01024	CO3_HUMAN	ETKENEGFTVTAEG	Y	26.3	1969	14	0	985.5	2	60.3	F2:7695	2.22E-04	3.97E-04	1.69E-04	1.15E-03	7.71E-04	1.38E-04	1323	1336	TMT6plex
Q5T011	SZT2_HUMAN	PALHRAA	Y	16.53	963.582	7	-1.4	482.8	2	94.8	F1:13867	6.39E-05	3.16E-05	2.41E-04	0.00E+00	5.69E-05	0.00E+00	1718	1724	TMT6plex
P01024	CO3_HUMAN	EETKENEGFTVTA	Y	28.47	1911.98	13	2.9	957	2	64.9	F1:8902	2.76E-04	4.75E-04	1.69E-04	1.24E-03	7.52E-04	2.06E-04	1322	1334	TMT6plex

P68363	TBA1B_HUMAN	QLITGKEDAANN	N	38.13	1484.77	12	1.7	743.4	2	69.4	F1:9610	1.46E-03	3.29E-03	1.02E-03	9.53E-04	1.39E-03	4.34E-04	91	102	Pyro-glu from Q; TMT6plex
Q9H4B7	TBB1_HUMAN	DLAGSDR	Y	23.18	961.503	7	2.6	481.8	2	19.8	F1:1902	7.46E-04	7.20E-04	2.59E-04	3.02E-04	4.35E-04	3.11E-04	31	37	TMT6plex
P02656	APOC3_HUMAN	DALSSVQESQVAQQA	Y	36.86	1788.91	15	-4.6	597.3	3	75.7	F1:10600	8.53E-05	4.97E-05	6.01E-05	1.41E-04	5.93E-05	9.65E-05	45	59	TMT6plex
P00488	F13A_HUMAN	DDLPTVELQGVVPR	Y	46.5	1765.98	14	1.4	589.7	3	106	F1:15942	0.00E+00	3.19E-05	0.00E+00	7.53E-05	0.00E+00	5.32E-05	25	38	TMT6plex
Q15758	AAAT_HUMAN	AAGGYCGS	Y	16.88	913.417	8	7.5	457.7	2	38.7	F2:4554	3.20E-04	9.00E-04	5.40E-04	2.81E-04	1.53E-04	5.55E-04	34	41	TMT6plex
P02671	FIBA_HUMAN	DSTFES	Y	18.72	913.423	6	0.3	457.7	2	38.7	F2:4555	3.20E-04	9.00E-04	5.40E-04	2.81E-04	1.53E-04	5.55E-04	593	598	TMT6plex
P00734	THRB_HUMAN	DKTERELLESYIDGR	Y	47.5	2281.23	15	1.9	761.4	3	91.9	F2:12609	3.93E-04	2.94E-04	6.76E-04	1.02E-03	7.24E-04	4.09E-04	349	363	TMT6plex
P02675	FIBB_HUMAN	QGVNDNEEG	Y	18.92	943.352	9	2.6	472.7	2	28.8	F1:3331	2.36E-04	3.25E-04	2.08E-04	2.59E-04	1.04E-04	1.96E-04	31	39	Pyro-glu from Q
P00734	THRB_HUMAN	DKTERELLESYIDG	Y	44.15	2125.13	14	2	1064	2	102	F1:15242	1.05E-03	8.53E-04	1.04E-03	3.89E-03	1.96E-03	8.70E-04	349	362	TMT6plex
Q9NYQ8	FAT2_HUMAN	HGTFR	N	17.74	845.471	5	6.2	423.7	2	53.1	F2:6595	8.28E-04	1.14E-03	4.05E-03	6.03E-04	4.54E-04	5.67E-04	969	973	TMT6plex
Q9Y4H2	IRS2_HUMAN	LHHGPG	Y	18.5	845.471	6	6.2	423.7	2	53.1	F2:6594	8.28E-04	1.14E-03	4.05E-03	6.03E-04	4.54E-04	5.67E-04	473	478	TMT6plex
Q8WXH0	SYNE2_HUMAN	FTLPGR	N	17.38	918.549	6	3	460.3	2	87.8	F1:12646	1.78E-04	0.00E+00	6.48E-04	0.00E+00	0.00E+00	0.00E+00	2373	2378	TMT6plex
P02671	FIBA_HUMAN	EFVSETESRGSSESG	Y	34.05	1728.8	14	2.1	865.4	2	46.3	F1:5978	1.08E-03	1.08E-03	3.10E-04	7.72E-04	1.32E-03	1.88E-03	539	552	TMT6plex
O75074	LRP3_HUMAN	GVCNRPPP	Y	18.21	1067.57	8	7.8	534.8	2	68.4	F1:9471	1.49E-04	2.85E-04	1.61E-04	1.05E-04	1.38E-04	1.68E-04	746	753	TMT6plex
Q05682	CALD1_HUMAN	ERQKEFDPTITDASLS LPS	Y	24.65	2591.38	19	2.7	864.8	3	95.8	F1:14055	6.88E-05	1.45E-04	0.00E+00	2.24E-04	7.70E-05	1.31E-04	116	134	TMT6plex
Q8N2C7	UNC80_HUMAN	ITAIPITQ	Y	15.84	1084.67	8	2.2	543.3	2	108	F2:15491	2.04E-04	3.86E-05	4.64E-05	6.14E-05	0.00E+00	0.00E+00	1753	1760	TMT6plex
Q9H799	CE042_HUMAN	ATLIR	N	15.22	801.528	5	7.9	401.8	2	48.4	F2:5971	3.59E-04	5.02E-04	1.11E-03	1.48E-03	4.92E-04	1.46E-03	309	313	TMT6plex
Q8IZQ1	WDFY3_HUMAN	ATLLR	N	15.22	801.528	5	7.9	401.8	2	48.4	F2:5971	3.59E-04	5.02E-04	1.11E-03	1.48E-03	4.92E-04	1.46E-03	2524	2528	TMT6plex
P02671	FIBA_HUMAN	DEAAFFDTASTG	Y	23.1	1459.67	12	2	730.8	2	104	F1:15615	1.08E-03	4.13E-04	3.11E-04	1.92E-04	3.52E-04	2.47E-04	515	526	TMT6plex
Q86UQ4	ABCAD_HUMAN	ELILF	N	17.37	862.537	5	-4	432.3	2	100	F1:14807	0.00E+00	1.01E-04	6.49E-05	0.00E+00	4.06E-05	0.00E+00	824	828	TMT6plex
Q9P225	DYH2_HUMAN	EILF	N	17.37	862.537	5	-4	432.3	2	100	F1:14807	0.00E+00	1.01E-04	6.49E-05	0.00E+00	4.06E-05	0.00E+00	1938	1942	TMT6plex
Q9Y566	SHAN1_HUMAN	ELLLF	N	17.37	862.537	5	-4	432.3	2	100	F1:14807	0.00E+00	1.01E-04	6.49E-05	0.00E+00	4.06E-05	0.00E+00	298	302	TMT6plex
O00443	P3C2A_HUMAN	ELIIF	N	17.37	862.537	5	-4	432.3	2	100	F1:14807	0.00E+00	1.01E-04	6.49E-05	0.00E+00	4.06E-05	0.00E+00	743	747	TMT6plex
P01042	KNG1_HUMAN	HDWGHEKQ	Y	37.1	1493.78	8	4.3	498.9	3	20.7	F1:2046	1.06E-04	7.21E-05	2.80E-04	2.46E-04	7.79E-04	2.07E-04	429	436	TMT6plex
Q14624	ITIH4_HUMAN	GLPGPPDVPDHAA	Y	48.91	1470.77	13	-1.1	736.4	2	67.2	F1:9276	6.99E-04	1.35E-03	5.09E-04	1.03E-03	1.63E-03	1.07E-03	671	683	TMT6plex
Q8WZ42	TITIN_HUMAN	SENVCT	Y	15.17	881.4	6	2.5	441.7	2	21.2	F1:2137	4.15E-04	2.45E-04	3.90E-04	3.06E-04	1.29E-04	3.21E-04	7719	7724	TMT6plex; Deamidation
P0C0L4	CO4A_HUMAN	LGSKINVKVGNS	Y	19.1	1959.21	13	5.4	654.1	3	63.8	F2:8188	2.54E-04	3.07E-04	2.77E-04	4.25E-04	3.84E-04	1.35E-03	1362	1374	TMT6plex
Q9UBW5	BIN2_HUMAN	TAPEPQEEVSTSENPO L	Y	33.67	2084.01	17	4.5	1043	2	76.2	F1:10685	3.93E-05	0.00E+00	0.00E+00	6.42E-05	1.20E-04	0.00E+00	549	565	TMT6plex
O00151	PDLI1_HUMAN	QEILESEEKGDPNKPS G	Y	30.89	2297.18	17	5.2	766.7	3	69.6	F2:9092	3.57E-05	1.09E-04	0.00E+00	4.20E-05	1.57E-04	1.12E-04	220	236	Pyro-glu from Q; TMT6plex
P09493	TPM1_HUMAN	DEEKMEIQEIQI	N	19.08	1962.04	12	2.7	982	2	112	F1:17071	6.43E-04	1.08E-04	0.00E+00	8.85E-04	9.33E-04	1.24E-04	137	148	TMT6plex
P06753	TPM3_HUMAN	DEEKMELQEIQI	N	19.08	1962.04	12	2.7	982	2	112	F1:17071	6.43E-04	1.08E-04	0.00E+00	8.85E-04	9.33E-04	1.24E-04	138	149	TMT6plex
P02671	FIBA_HUMAN	TFESKSY	Y	24.57	1318.72	7	7.6	660.4	2	56.2	F1:7528	7.96E-03	1.55E-03	2.50E-03	1.28E-03	1.10E-03	1.29E-03	595	601	TMT6plex



O00151	PDLII_HUMAN	EKGDPNKPSGF	Y	15.75	1862.05	11	3.3	621.7	3	49	F1:6410	4.38E-04	1.67E-04	7.06E-05	4.76E-04	7.38E-04	1.76E-04	227	237	TMT6plex
Q8WZ42	TITIN_HUMAN	DRFGP	N	15.83	819.444	5	4.2	410.7	2	27.1	F2:2922	8.48E-05	1.17E-04	2.16E-04	1.05E-04	2.70E-04	3.96E-04	21494	21498	TMT6plex
P01024	CO3_HUMAN	SEETKENEGFTVT	Y	15.52	1927.98	13	5.9	965	2	57.8	F2:7358	1.53E-04	4.44E-04	1.50E-04	3.28E-04	3.04E-04	6.11E-04	1321	1333	TMT6plex
P02675	FIBB_HUMAN	VNDNEEGF	Y	33.77	1152.51	8	-1.2	577.3	2	73.6	F2:9653	9.71E-04	3.31E-04	1.86E-03	2.43E-03	2.22E-03	1.22E-02	33	40	TMT6plex; Deamidation
P02649	APOE_HUMAN	TVGSLAGQPLQERAQ AWGERL	Y	50.74	2495.34	21	2.1	832.8	3	98.7	F1:14546	0.00E+00	6.84E-05	1.04E-04	2.80E-04	1.35E-03	1.34E-04	212	232	TMT6plex
P02671	FIBA_HUMAN	DSGEGDFLAEGGGV	Y	51.74	1537.71	14	-4.1	769.9	2	105	F1:15787	2.98E-04	6.08E-04	4.40E-04	7.53E-04	5.61E-04	4.68E-04	21	34	TMT6plex
P10124	SRGN_HUMAN	SLDRNLPSDSQDLGQ HG	Y	56.24	2067.02	17	4.9	690	3	52.4	F1:6937	2.20E-04	4.37E-04	3.38E-04	2.65E-04	5.85E-04	6.44E-04	135	151	TMT6plex
P15822	ZEP1_HUMAN	HAHTI	N	15.21	806.46	5	2.7	404.2	2	72.8	F1:10134	7.33E-05	0.00E+00	7.28E-05	4.22E-05	0.00E+00	0.00E+00	456	460	TMT6plex
P02671	FIBA_HUMAN	ELERPGGNEIT	Y	22.62	1442.76	11	1.9	722.4	2	46.6	F1:6025	1.89E-03	6.56E-04	5.44E-04	5.02E-04	5.65E-04	2.45E-04	260	270	TMT6plex
Q8NBP7	PCSK9_HUMAN	NLERITPPR	Y	24.44	1323.78	9	3.8	442.3	3	37.6	F1:4690	2.23E-04	1.16E-04	2.09E-04	1.59E-04	1.13E-04	1.37E-04	157	165	TMT6plex
Q7Z478	DHX29_HUMAN	NDKIL	N	15.01	1059.67	5	7.8	530.8	2	112	F2:16396	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.25E-04	1.32E-03	1353	1357	TMT6plex
Q13459	MYO9B_HUMAN	NDKLI	N	15.01	1059.67	5	7.8	530.8	2	112	F2:16396	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.25E-04	1.32E-03	462	466	TMT6plex
Q5CZC0	FSIP2_HUMAN	NDKII	N	15.01	1059.67	5	7.8	530.8	2	112	F2:16396	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.25E-04	1.32E-03	1260	1264	TMT6plex
O95180	CAC1H_HUMAN	VFFCLGQTT	Y	17.67	1244.63	9	-5.7	623.3	2	65.5	F1:9000	2.65E-04	4.53E-04	2.84E-04	4.37E-04	4.23E-04	3.88E-04	79	87	TMT6plex; Deamidation
Q9ULI3	HEG1_HUMAN	SRKRN	N	15.95	1117.71	5	9.8	559.9	2	117	F1:18179	4.85E-04	5.37E-05	5.44E-05	0.00E+00	0.00E+00	0.00E+00	275	279	TMT6plex
P04632	CPNS1_HUMAN	GGGGGGGLGGGLG	Y	34.28	1100.58	13	-2.1	551.3	2	53.5	F1:7085	8.90E-04	9.17E-04	7.84E-04	7.73E-04	6.51E-04	8.82E-04	14	26	TMT6plex
Q96J65	MRP9_HUMAN	FRRSAI	N	15.53	977.597	6	5.6	489.8	2	74.8	F2:9849	5.15E-05	4.94E-05	9.14E-05	7.99E-05	6.70E-05	1.24E-04	287	292	TMT6plex
P02647	APOA1_HUMAN	HFQQ	Y	27.96	973.497	5	-5.5	487.8	2	53.4	F1:7069	8.35E-04	8.95E-04	9.43E-04	9.95E-04	2.61E-03	1.17E-03	20	24	TMT6plex
O00391	QSOX1_HUMAN	EPPEHMAELQ	Y	22.32	1408.69	10	5.4	705.4	2	49.2	F2:6100	1.56E-04	1.51E-04	1.77E-04	1.69E-04	1.70E-04	2.36E-04	620	629	TMT6plex
Q96FT7	ASIC4_HUMAN	GPHPVPV	Y	21.06	930.549	7	9.1	466.3	2	80.5	F1:11413	1.54E-04	3.67E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	78	84	TMT6plex
Q3KP44	ANR55_HUMAN	GNRIL	N	16.97	800.507	5	6.1	401.3	2	105	F2:14936	0.00E+00	5.83E-05	9.79E-05	0.00E+00	3.92E-05	0.00E+00	206	210	TMT6plex
Q86XX4	FRAS1_HUMAN	GNRLI	N	16.97	800.507	5	6.1	401.3	2	105	F2:14936	0.00E+00	5.83E-05	9.79E-05	0.00E+00	3.92E-05	0.00E+00	2181	2185	TMT6plex
Q9Y4F3	MARF1_HUMAN	GNRII	N	16.97	800.507	5	6.1	401.3	2	105	F2:14936	0.00E+00	5.83E-05	9.79E-05	0.00E+00	3.92E-05	0.00E+00	575	579	TMT6plex
P0C0L4	CO4A_HUMAN	NGFKSHALQLN <sup>NGFKSHALQLN</sup> NNKQIP	Y	54.89	2124.19	16	4.3	425.8	5	35.6	F2:4089	0.00E+00	4.53E-04	1.84E-04	1.04E-04	0.00E+00	0.00E+00	1337	1352	TMT6plex
P0C0L4	CO4A_HUMAN	SHALQL	Y	26.25	896.528	6	2.3	449.3	2	42	F1:5317	6.35E-04	8.49E-04	5.46E-04	7.17E-04	7.54E-04	1.01E-03	1341	1346	TMT6plex
P01024	CO3_HUMAN	RIHWESASLLR	Y	40.07	1595.91	11	-0.4	533	3	62.5	F1:8535	1.08E-04	2.04E-04	1.54E-04	1.74E-04	1.77E-04	3.35E-04	1310	1320	TMT6plex
P10124	SRGN_HUMAN	DRNLPSDSQDLGQH	Y	40.69	1809.88	14	4.9	604.3	3	33.5	F2:3813	3.48E-04	2.08E-04	2.56E-04	2.16E-04	2.69E-04	1.10E-04	137	150	TMT6plex
P42658	DPP6_HUMAN	TKVAH	N	15.37	1012.64	5	7.2	507.3	2	88.3	F2:12041	3.57E-04	2.86E-04	3.78E-04	4.33E-04	4.27E-04	1.21E-03	770	774	TMT6plex
P02671	FIBA_HUMAN	DEAGSEADHEG	Y	46.08	1344.56	11	1.8	673.3	2	15.4	F1:1186	2.45E-04	2.04E-04	1.45E-04	4.12E-04	4.49E-04	2.47E-03	605	615	TMT6plex
P68363	TBA1B_HUMAN	DKTIGGGDDSFNT	N	43.5	1783.9	13	1.7	893	2	62.8	F1:8573	1.19E-03	2.11E-03	3.91E-04	5.42E-04	8.36E-04	3.16E-04	39	51	TMT6plex
O95466	FMNL_HUMAN	PPAAYIQ	Y	15.52	988.543	7	-3.9	495.3	2	84.2	F1:12026	7.48E-05	7.74E-05	1.06E-04	1.10E-04	1.06E-04	3.08E-04	79	85	TMT6plex; Deamidation

P02671	FIBA_HUMAN	SYKMADEAGSEADH EGTHSTKRGHAKSRP	Y	32.62	4155.17	30	1.6	520.4	8	36.7	F1:4544	9.59E-05	0.00E+00	5.90E-05	1.11E-04	3.85E-05	1.73E-04	600	629	TMT6plex
P00488	F13A_HUMAN	v NNSNAAEDDLPTVEL QG	Y	35.76	2014.96	17	3	1008	2	96.6	F1:14177	4.25E-05	1.18E-04	0.00E+00	1.04E-04	8.96E-05	4.93E-04	18	34	TMT6plex
Q5T4S7	UBR4_HUMAN	DVHTSNRLH	Y	17.51	1306.69	9	3	654.4	2	32.7	F2:3691	3.41E-04	2.32E-04	4.35E-04	5.13E-04	1.18E-03	3.36E-04	2963	2971	TMT6plex
Q8NFW1	COMA1_HUMAN	GFLGPR	N	18.68	874.523	6	8.3	438.3	2	86.2	F1:12362	9.55E-05	0.00E+00	0.00E+00	6.80E-05	8.62E-05	6.79E-05	1360	1365	TMT6plex
Q92508	PIEZ1_HUMAN	FLVEL	N	15.5	848.521	5	-3.3	425.3	2	91	F1:13202	2.29E-04	4.81E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2114	2118	TMT6plex
Q96J17	SPTCS_HUMAN	FLVEI	N	15.5	848.521	5	-3.3	425.3	2	91	F1:13202	2.29E-04	4.81E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	771	775	TMT6plex
P0C0L4	CO4A_HUMAN	DKGQAGLQ	Y	28.2	1273.74	8	1.7	637.9	2	30.5	F1:3588	9.41E-04	1.21E-03	2.03E-03	1.57E-03	1.78E-03	2.16E-03	748	755	TMT6plex
P50552	VASP_HUMAN	KTPKDESANQEEPEA RVPAQ	Y	36.67	2910.57	20	2.9	728.7	4	39.7	F1:5002	0.00E+00	4.17E-05	0.00E+00	6.47E-05	1.57E-04	0.00E+00	283	302	TMT6plex
P02649	APOE_HUMAN	KVEQAVETEPEPELR	Y	44.82	2211.22	15	2.4	738.1	3	59.3	F1:8056	2.10E-04	4.00E-04	4.22E-04	3.51E-04	5.12E-04	4.55E-04	19	33	TMT6plex
P0DJ18	SAA1_HUMAN	GNYDAAKRGPGGVW AAEAISDAREN	Y	37.07	3032.55	25	1.2	759.1	4	83.8	F1:11951	0.00E+00	2.17E-04	4.39E-05	0.00E+00	0.00E+00	0.00E+00	58	82	TMT6plex
Q8WZ42	TITIN_HUMAN	VVAPPIPLLLP	Y	24.71	1170.74	11	3.3	586.4	2	117	F1:18029	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.00E-03	9.90E-03	9887	9897	Carbamylation
P02671	FIBA_HUMAN	ADEAGSEADHEGTHS T	Y	60.65	1841.79	16	5.7	614.9	3	13.3	F2:907	2.05E-04	4.46E-05	7.52E-05	2.32E-04	1.82E-04	1.17E-04	604	619	TMT6plex
P01042	KNG1_HUMAN	EQQHGLGHGHKF	Y	40.35	1831.98	12	2	459	4	21	F1:2104	0.00E+00	0.00E+00	0.00E+00	3.65E-05	1.81E-04	0.00E+00	466	477	TMT6plex
Q96RW7	HMCN1_HUMAN	YVRPR	N	17.65	918.56	5	0.9	460.3	2	85.3	F1:12212	2.59E-04	5.70E-05	6.65E-04	8.20E-05	4.26E-05	1.57E-04	1069	1073	TMT6plex
Q86UX7	URP2_HUMAN	HRPVI	Y	17.7	848.555	5	2.4	425.3	2	44.7	F2:5383	4.31E-04	8.00E-04	9.22E-04	1.27E-03	3.84E-03	7.66E-04	97	101	TMT6plex; Amidation
P68363	TBA1B_HUMAN	QPPTVVPGDLAKVQ	N	51.03	1963.15	15	2.6	655.4	3	78.9	F2:10496	1.45E-04	5.00E-04	1.11E-04	8.72E-05	1.79E-04	0.00E+00	358	372	TMT6plex
P62328	TYB4_HUMAN	SDKPDMAE	Y	31.57	1162.54	8	2.6	582.3	2	48.1	F1:6252	8.05E-04	7.78E-04	5.95E-04	9.07E-04	6.84E-04	9.40E-04	2	9	Acetylation ; TMT6plex
Q05682	CALD1_HUMAN	NDTAENETTEKEEKS ES	Y	30.46	2398.14	17	3.2	800.4	3	31.2	F1:3698	0.00E+00	4.30E-05	0.00E+00	0.00E+00	8.44E-05	5.98E-05	139	155	TMT6plex
P46095	GPR6_HUMAN	APPHLAA	Y	17.49	904.533	7	6.9	453.3	2	81.7	F1:11601	1.12E-04	7.03E-05	2.09E-04	9.68E-05	6.06E-05	7.38E-05	267	273	TMT6plex
Q7Z7G8	VP13B_HUMAN	GCLLLTSEV	Y	15.51	1162.65	9	0.7	582.3	2	80	F2:10657	1.54E-04	1.37E-04	1.48E-04	2.17E-04	1.51E-04	5.34E-04	3886	3894	TMT6plex
O95196	CSPG5_HUMAN	GRGPPPLL	Y	21.02	1034.64	8	8.7	518.3	2	91.8	F1:13352	6.91E-05	8.63E-05	1.11E-04	1.85E-04	8.22E-05	1.18E-04	10	17	TMT6plex
P02649	APOE_HUMAN	AATVGSLAGQPLQER AQAWGERL	Y	40.44	2637.42	23	2.4	880.1	3	102	F2:14395	0.00E+00	9.73E-05	1.64E-04	2.36E-04	1.16E-03	1.36E-04	210	232	TMT6plex
P02671	FIBA_HUMAN	STSYNRGDSTFESKS	Y	23.61	2123.05	15	-2	708.7	3	40.8	F1:5118	2.48E-04	7.80E-04	2.38E-04	2.40E-04	1.68E-04	1.61E-04	586	600	TMT6plex
Q04637	IF4G1_HUMAN	APSPGLPQPA	Y	18.35	1162.65	10	-6.3	582.3	2	75.9	F1:10637	2.64E-04	3.77E-04	2.53E-04	3.55E-04	2.92E-04	4.58E-04	13	22	TMT6plex
Q15942	ZYX_HUMAN	HVQPQPQPKPQVQLH V	Y	47.56	2317.34	16	4.7	580.3	4	47.6	F2:5812	4.70E-05	7.63E-05	0.00E+00	0.00E+00	3.49E-05	0.00E+00	223	238	TMT6plex
P10124	SRGN_HUMAN	SLDRNLPSDSQDLGQ HGLEEDFM	Y	54.1	2847.32	23	4.3	950.1	3	91.7	F2:12574	1.32E-04	6.74E-05	1.98E-04	2.93E-04	4.00E-04	7.52E-05	135	157	TMT6plex; Oxidation
P01024	CO3_HUMAN	EETKENEGFT	Y	29.63	1640.83	10	1.6	821.4	2	46.6	F1:6032	6.79E-04	1.76E-03	4.42E-04	9.83E-04	1.48E-03	3.70E-03	1322	1331	TMT6plex
P02671	FIBA_HUMAN	EILRGDFS	Y	18.74	1164.63	8	3.6	583.3	2	69.6	F2:9098	2.95E-03	6.61E-04	2.53E-04	2.08E-04	1.74E-04	2.48E-04	111	118	TMT6plex

P02671	FIBA_HUMAN	ADSGEGDFL	Y	34.59	1218.5	9	2.4	610.3	2	119	F1:18414	7.78E-04	3.15E-05	4.29E-04	2.00E-04	2.10E-04	0.00E+00	20	28	TMT6plex; Phosphorylation
Q9UQP3	TENN_HUMAN	EYTVH	N	17.47	876.454	5	-0.7	439.2	2	62.7	F1:8561	1.30E-04	1.63E-04	3.16E-04	3.08E-04	2.31E-04	2.92E-04	595	599	TMT6plex
P01024	CO3_HUMAN	HWESASLLR	Y	42.04	1326.72	9	5	664.4	2	56.5	F2:7127	1.85E-03	3.11E-03	2.47E-03	2.96E-03	3.42E-03	1.08E-02	1312	1320	TMT6plex
Q05682	CALD1_HUMAN	DDKKPF	Y	18.02	1435.86	6	2.1	479.6	3	50.5	F1:6641	1.54E-03	1.80E-03	4.74E-04	1.53E-03	4.29E-03	1.55E-03	629	634	TMT6plex
Q6PJ69	TRI65_HUMAN	LEQVDEQTFLQESQL LQPPGPLGP	Y	20.84	2892.5	24	-8.1	724.1	4	40.6	F1:5088	0.00E+00	0.00E+00	0.00E+00	4.58E-05	0.00E+00	8.32E-06	238	261	TMT6plex; Deamidation
P62328	TYB4_HUMAN	SDKPDMAEIEKFDKS KL	Y	52.42	2938.65	17	3	980.6	3	102	F1:15267	1.01E-03	1.42E-04	0.00E+00	1.05E-03	3.61E-03	3.20E-04	2	18	Acetylation ; TMT6plex
P02775	CXCL7_HUMAN	NLAKGKKEESLSDLY A	Y	21.09	2439.35	16	-2	814.1	3	82.1	F1:11657	2.14E-04	1.19E-04	1.57E-04	9.10E-04	3.47E-04	1.26E-04	44	59	TMT6plex
Q96BJ8	ELMO3_HUMAN	GLSADRR	Y	25.68	1002.58	7	8.3	502.3	2	38.4	F1:4806	5.84E-04	7.86E-04	7.78E-04	1.05E-03	1.07E-03	4.75E-03	330	336	TMT6plex
P01042	KNG1_HUMAN	DDDLHQQGGHVLHDH GH	Y	59.97	2008.92	16	3.4	503.2	4	32.4	F1:3880	0.00E+00	3.78E-05	0.00E+00	5.43E-05	1.43E-04	0.00E+00	480	495	TMT6plex
O95810	SDPR_HUMAN	EGEIAEEAAEKAT	Y	53.41	1804.95	13	3.1	903.5	2	77.9	F1:10983	2.41E-03	5.03E-03	6.27E-04	3.99E-03	7.39E-03	2.88E-03	348	360	TMT6plex
P0C0L4	CO4A_HUMAN	DPDAPLQP	Y	29.37	1080.57	8	6.2	541.3	2	61.8	F2:7879	1.63E-04	1.73E-04	2.07E-04	2.30E-04	1.76E-04	4.23E-04	1430	1437	TMT6plex
P04632	CPNS1_HUMAN	EPPPPR	Y	25.57	920.528	6	3.9	461.3	2	15.5	F1:1199	8.04E-04	4.21E-03	5.14E-04	4.93E-04	2.11E-04	3.07E-04	79	84	TMT6plex
P0C0L4	CO4A_HUMAN	DPDAPLQPV	Y	16.01	1179.63	9	0.5	590.8	2	74.1	F1:10342	4.16E-04	5.69E-04	2.98E-04	6.55E-04	5.50E-04	4.22E-04	1430	1438	TMT6plex
P01009	A1AT_HUMAN	EDPQGDAAQKT	Y	34.18	1616.84	11	3.7	540	3	30.8	F1:3643	2.07E-04	2.33E-04	1.07E-04	2.00E-04	2.65E-04	2.29E-04	25	35	TMT6plex
P02671	FIBA_HUMAN	HRHPDEAAFFDTAST GKTFPG	Y	45	2746.39	21	4.7	916.5	3	74.9	F1:10484	3.37E-04	1.19E-04	0.00E+00	8.12E-05	0.00E+00	0.00E+00	511	531	TMT6plex
Q01518	CAP1_HUMAN	SGPKPFSAPKPQ	Y	38.75	1927.15	12	1.5	643.4	3	50.7	F1:6685	1.76E-03	9.29E-04	1.30E-04	5.18E-04	3.72E-04	1.47E-04	295	306	TMT6plex
O95810	SDPR_HUMAN	VEGEIAEEAAEKA	Y	54.18	1802.97	13	3.5	902.5	2	92.5	F2:12715	2.69E-03	2.46E-03	3.46E-04	9.45E-04	1.41E-03	2.76E-04	347	359	TMT6plex
O00151	PDLI1_HUMAN	QEKQELNEPPK	Y	35.3	1779.98	11	3.4	594.3	3	49.3	F1:6450	1.45E-04	1.30E-04	1.23E-04	8.63E-05	1.01E-04	1.44E-04	201	211	Pyro-glu from Q; TMT6plex
O95810	SDPR_HUMAN	DGDPVQPA	Y	30.08	1026.52	8	2.2	514.3	2	36.1	F1:4462	4.27E-04	6.06E-04	4.73E-04	7.09E-04	4.24E-04	8.62E-04	410	417	TMT6plex
Q14624	ITIH4_HUMAN	SFSR	Y	20.24	821.46	5	3.1	411.7	2	24.9	F1:2699	1.15E-03	5.66E-04	7.15E-04	1.22E-03	2.55E-03	7.22E-04	640	644	TMT6plex
P02671	FIBA_HUMAN	TASTGKTFPG	Y	19.56	1439.8	10	4.8	720.9	2	36.5	F2:4243	1.80E-03	7.84E-04	3.07E-04	5.16E-04	4.68E-04	2.52E-04	522	531	TMT6plex; Hydroxylation
P0C0L4	CO4A_HUMAN	EEELQFS	Y	25.7	1109.54	7	-6.1	555.8	2	80.1	F1:11349	2.41E-04	3.54E-04	5.39E-04	4.21E-04	4.26E-04	8.79E-04	1355	1361	TMT6plex
P02671	FIBA_HUMAN	SYKMADEAGSEADH EGTHSTKRGHAKS	Y	28.78	3587.8	27	6.9	513.6	7	30.3	F1:3567	6.37E-05	0.00E+00	0.00E+00	8.67E-05	0.00E+00	1.08E-04	600	626	TMT6plex; Methyl ester
P0DJ18	SAA1_HUMAN	SGKDPNHF <sup>z</sup> K <sup>z</sup> AGL <sup>z</sup> PE <sup>z</sup>	Y	28.57	2436.38	16	4.4	488.3	5	49.7	F1:6522	0.00E+00	3.04E-04	4.89E-05	0.00E+00	0.00E+00	0.00E+00	106	121	TMT6plex
P50552	VASP_HUMAN	KVSKQEEASGGPTAP KAE	Y	28.41	2729.57	18	1.1	683.4	4	38.1	F1:4754	8.40E-05	4.90E-05	0.00E+00	3.91E-05	0.00E+00	0.00E+00	237	254	TMT6plex
Q6ZRS2	SRCAP_HUMAN	GHPLLLAP	Y	15.41	1045.65	8	9.3	523.8	2	102	F1:15212	0.00E+00	5.75E-05	8.54E-05	5.29E-05	6.78E-05	1.81E-04	1522	1529	TMT6plex
Q8WXG9	GPR98_HUMAN	HGEQRKGVFL	Y	17.13	1628.94	10	5.4	408.2	4	66.4	F2:8592	2.10E-04	5.57E-04	3.76E-04	3.69E-04	8.80E-04	5.01E-04	4952	4961	TMT6plex; Deamidation
Q9Y490	TLN1_HUMAN	QQYNRVGKVE	Y	27.39	1431.77	10	2.2	716.9	2	39	F1:4888	2.37E-03	3.26E-03	5.59E-04	1.56E-03	1.01E-03	6.55E-04	434	443	Pyro-glu from Q; TMT6plex

P67936	TPM4_HUMAN	QLKEAKHIAEE	N	37.97	1735.99	11	2	579.7	3	59.9	F1:8149	1.50E-04	1.65E-04	1.03E-04	2.08E-04	1.70E-04	1.33E-04	111	121	Pyro-glu from Q; TMT6plex
Q8WZ42	TITIN_HUMAN	KYDIISKGAVRILVIN	Y	15.04	2259.41	16	6	565.9	4	178	F1:29822	0.00E+00	0.00E+00	0.00E+00	3.20E-05	0.00E+00	2.08E-04	13345	13360	TMT6plex
Q9NQC3	RTN4_HUMAN	APPVAPERQPSWDPS PVS	Y	25.21	2145.11	18	2	716	3	78.6	F1:11099	6.02E-05	1.78E-04	6.24E-05	3.70E-05	1.03E-04	0.00E+00	97	114	TMT6plex
Q562E7	WDR81_HUMAN	TFGYKL	Y	16.75	1185.72	6	0.2	593.9	2	95.9	F1:14070	6.35E-05	5.81E-05	1.38E-04	1.17E-04	1.30E-04	6.05E-04	548	553	TMT6plex
P0C0L4	CO4A_HUMAN	NGFKSHALQLNRRQI	Y	53.5	2197.25	15	4.2	733.4	3	56.6	F2:7159	1.38E-03	1.87E-03	1.70E-03	1.86E-03	1.07E-03	9.53E-04	1337	1351	TMT6plex
P68363	TBA1B_HUMAN	DLAKVQ	N	18.24	1130.71	6	0.6	566.4	2	43.4	F1:5530	2.35E-03	6.26E-04	2.02E-04	2.39E-04	1.87E-04	3.32E-04	367	372	TMT6plex
P01024	CO3_HUMAN	WESASLLR	Y	35.86	1189.67	8	0.6	595.8	2	83.1	F1:11817	5.94E-04	8.82E-04	8.55E-04	9.06E-04	1.11E-03	4.06E-03	1313	1320	TMT6plex
P49286	MTR1B_HUMAN	LQSPAPPIIGVQH	Y	29.34	1397.77	13	-4.4	699.9	2	25.1	F1:2716	5.55E-04	7.07E-04	8.07E-04	1.26E-03	1.08E-03	5.33E-04	345	357	Acetylation
P68363	TBA1B_HUMAN	DVVPKD	N	19.85	1129.67	6	-4.8	565.8	2	40.6	F1:5090	2.72E-03	1.72E-03	4.23E-04	6.63E-04	1.07E-03	6.92E-04	322	327	TMT6plex
P01024	CO3_HUMAN	THRIHWESASLLR	Y	39.55	1834.02	13	1.7	459.5	4	54.2	F1:7203	0.00E+00	6.45E-05	1.04E-04	5.94E-05	1.51E-04	8.86E-05	1308	1320	TMT6plex
Q86VR7	VS10L_HUMAN	AAVPAGSRLLLP	Y	16.06	1392.87	12	9.6	697.4	2	138	F1:22324	0.00E+00	0.00E+00	0.00E+00	1.78E-05	1.34E-04	1.09E-03	448	459	TMT6plex
Q9Y490	TLN1_HUMAN	QQYNRVGKVEH	Y	38.43	1568.83	11	2.5	524	3	26.3	F1:2913	7.03E-04	3.28E-04	6.18E-05	1.95E-04	1.24E-04	9.87E-05	434	444	Pyro-glu from Q; TMT6plex
Q8WZ42	TITIN_HUMAN	QKVEPI	Y	18.95	924.548	6	3.7	463.3	2	64.9	F1:8893	2.68E-04	2.93E-04	5.21E-04	4.41E-04	4.74E-04	4.58E-04	4197	4202	Pyro-glu from Q; TMT6plex
P01024	CO3_HUMAN	EETKENEGFTVTAEG	Y	50.68	2098.05	15	3.5	1050	2	65.3	F1:8965	1.46E-03	2.40E-03	1.04E-03	4.70E-03	3.38E-03	8.93E-04	1322	1336	TMT6plex
P02671	FIBA_HUMAN	DSGEGDFL	Y	36.57	1067.5	8	0.4	534.8	2	88	F1:12667	2.30E-04	1.36E-04	1.10E-04	2.02E-04	1.98E-04	7.94E-04	21	28	TMT6plex
P0C0L4	CO4A_HUMAN	ELQFSLG	Y	21.35	1021.56	7	3.1	511.8	2	113	F1:17387	9.19E-05	4.29E-05	5.23E-05	8.33E-05	5.80E-05	1.21E-04	1357	1363	TMT6plex
P02679	FIBG_HUMAN	DESSKPNM	Y	20.13	1364.7	8	5.3	683.4	2	37.4	F1:4650	6.77E-03	1.06E-03	3.41E-04	2.79E-04	2.86E-04	2.56E-04	97	104	TMT6plex
O75369	FLNB_HUMAN	N	Y	17.7	3143.77	19	0.1	787	4	61.5	F1:8387	0.00E+00	7.30E-05	0.00E+00	1.21E-04	9.38E-05	0.00E+00	1	19	TMT6plex; Deamidation
P52566	GDIR2_HUMAN	TEKAPEPHVEEDDDD ELDSKLNLY	Y	66.93	3187.51	23	1.5	797.9	4	90.9	F1:13185	0.00E+00	6.08E-05	0.00E+00	7.02E-05	1.51E-04	0.00E+00	2	24	TMT6plex; Acetylation
Q93063	EXT2_HUMAN	EKGPGP	Y	17.77	1041.62	6	6.8	521.8	2	99.2	F1:14653	1.64E-04	5.91E-05	1.39E-04	4.98E-05	0.00E+00	1.44E-04	244	249	TMT6plex
P02671	FIBA_HUMAN	KMADEAGSEADHEG THST	Y	38.71	2346.08	18	2.3	587.5	4	18.4	F1:1651	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.17E-05	5.46E-06	602	619	TMT6plex; Oxidation
Q86UX7	URP2_HUMAN	GGPGNHPHGPDAE GLNPYG	Y	44.29	2229.04	21	3.4	744	3	49.5	F1:6490	8.36E-05	1.98E-04	5.25E-05	8.18E-05	8.39E-05	0.00E+00	485	505	TMT6plex
P02461	CO3A1_HUMAN	PGEPPQAGPSG	Y	16.86	1195.6	11	-3.6	598.8	2	63.7	F2:8178	1.73E-04	3.20E-04	2.28E-04	2.48E-04	2.75E-04	5.51E-04	203	213	TMT6plex; Methyl ester
Q96L91	EP400_HUMAN	AVHGALG	Y	16.25	852.502	7	6.8	427.3	2	68.7	F1:9498	4.35E-05	9.88E-05	1.88E-04	1.64E-04	1.10E-04	2.27E-04	1685	1691	TMT6plex
P00734	THRB_HUMAN	SLEDKTE	Y	17.21	1278.71	7	-4.4	640.4	2	38	F2:4475	1.20E-03	5.78E-04	1.24E-03	1.07E-03	1.17E-03	2.74E-03	346	352	TMT6plex
P0C0L4	CO4A_HUMAN	EELQFSLGSKIN	Y	25.66	1822.02	12	5.7	912	2	103	F2:14551	2.36E-04	4.06E-04	3.92E-04	8.11E-04	4.24E-04	3.30E-04	1356	1367	TMT6plex
Q14624	ITIH4_HUMAN	GVLSSRQLGLPGLPD VPDHAA	Y	64.35	2311.25	21	2.8	771.4	3	88.2	F1:12716	1.10E-04	1.21E-04	4.96E-04	8.10E-04	1.12E-03	0.00E+00	663	683	TMT6plex
Q86Y34	GPR97_HUMAN	GNRSVVR	Y	23.8	1015.61	7	2.6	508.8	2	80.7	F1:11434	1.03E-04	9.21E-05	8.54E-05	8.85E-05	1.08E-04	1.61E-04	143	149	TMT6plex
P68363	TBA1B_HUMAN	DVVPKDVNAAIA	N	22.17	1668.98	12	3.6	835.5	2	78.4	F1:11069	1.80E-03	6.55E-04	1.84E-04	3.11E-04	3.63E-04	2.62E-04	322	333	TMT6plex

Q96RP8	KCNA7_HUMAN	GNPPRLP	Y	15.92	978.581	7	7.5	490.3	2	90.1	F1:13039	0.00E+00	3.04E-05	2.92E-04	1.88E-04	1.29E-04	3.78E-04	198	204	TMT6plex
P07437	TBB5_HUMAN	EEEEDFGEEAEEEE	Y	20.18	1869.75	14	1.7	935.9	2	85.7	F2:11606	4.40E-05	1.44E-04	0.00E+00	6.25E-05	1.80E-04	1.15E-04	431	444	TMT6plex
Q14624	ITIH4_HUMAN	GPPDVPDH	Y	44.16	1061.53	8	4.5	531.8	2	31.1	F2:3456	2.27E-04	9.16E-04	5.66E-04	8.98E-04	6.66E-04	8.51E-04	674	681	TMT6plex
P0C0L4	CO4A_HUMAN	DDPDAPLQPVTPLQL FEGR	Y	44.28	2336.22	19	5.4	1169	2	145	F1:23642	0.00E+00	8.44E-05	4.29E-04	3.36E-04	1.15E-03	1.35E-04	1429	1447	TMT6plex
P02671	FIBA_HUMAN	DSGEGDFLAEGGGVR	Y	60.88	1693.81	15	5	847.9	2	71.2	F1:9884	1.18E-01	5.80E-02	1.42E-01	8.07E-02	9.20E-02	5.59E-02	21	35	TMT6plex
P0C0L4	CO4A_HUMAN	EEELQ	N	16.45	875.444	5	5.1	438.7	2	33.2	F2:3772	9.21E-05	1.01E-04	1.33E-04	3.60E-05	2.92E-04	3.04E-04	1355	1359	TMT6plex
Q8WUY3	PRUN2_HUMAN	EEEIQ	N	16.45	875.444	5	5.1	438.7	2	33.2	F2:3772	9.21E-05	1.01E-04	1.33E-04	3.60E-05	2.92E-04	3.04E-04	1699	1703	TMT6plex
Q9Y2Q0	AT8A1_HUMAN	AVPER	N	17.03	799.476	5	2.9	400.7	2	21	F1:2098	3.03E-04	5.01E-04	2.94E-04	2.59E-04	2.39E-04	3.56E-04	490	494	TMT6plex
O00151	PDL1_HUMAN	QEILESEEKGDPNKPS GFR	Y	18.41	2600.35	19	5.5	867.8	3	74.1	F2:9735	1.16E-04	5.30E-05	0.00E+00	1.88E-04	2.45E-04	0.00E+00	220	238	Pyro-glu from Q; TMT6plex
P02671	FIBA_HUMAN	HPDEAAF	Y	35.12	1014.5	7	-1.2	508.3	2	36.9	F1:4589	8.99E-04	4.99E-04	5.00E-04	9.57E-04	6.16E-04	8.42E-04	513	519	TMT6plex
Q9UBW5	BIN2_HUMAN	APPSRPPPPR	Y	41.42	1299.76	10	8.4	434.3	3	13.2	F2:886	3.71E-04	1.67E-03	2.57E-04	2.84E-04	3.00E-04	1.30E-04	412	421	TMT6plex
P02671	FIBA_HUMAN	FESKSY	Y	21.89	1217.67	6	8.2	609.8	2	56.2	F1:7530	7.38E-03	1.32E-03	2.00E-03	1.07E-03	1.13E-03	1.81E-03	596	601	TMT6plex
P0DJ18	SAA1_HUMAN	DAAKRGPGGVWAAE AISDA	Y	38.69	2299.23	19	7.2	767.4	3	83.7	F1:11938	6.26E-05	8.10E-04	1.59E-04	1.48E-04	6.42E-05	0.00E+00	61	79	TMT6plex
P00734	THRB_HUMAN	LEDKTERELLESYIDG R	Y	50.12	2523.36	17	-0.2	842.1	3	107	F1:16155	2.35E-04	5.27E-05	6.01E-04	6.20E-04	6.23E-04	2.66E-04	347	363	TMT6plex
Q96QU1	PCD15_HUMAN	SMTQLS	Y	21.47	894.468	6	-2.3	448.2	2	70.9	F1:9839	7.42E-05	3.23E-05	6.09E-05	3.34E-05	0.00E+00	6.44E-05	1861	1866	TMT6plex
Q14624	ITIH4_HUMAN	VVAGKLQ	Y	18.45	1171.77	7	3.3	586.9	2	48	F2:5895	4.98E-04	8.86E-04	1.20E-03	1.41E-03	4.04E-03	6.80E-04	492	498	TMT6plex
Q14624	ITIH4_HUMAN	DVPDHA	Y	24.6	881.445	6	6.6	441.7	2	21.1	F2:2019	1.86E-04	2.17E-04	1.50E-04	1.36E-04	2.92E-04	3.34E-04	677	682	TMT6plex
Q9UBW5	BIN2_HUMAN	APPSRPPPP	Y	37.55	1143.66	9	3.1	572.8	2	26.2	F1:2895	3.19E-04	3.95E-03	5.46E-04	2.06E-04	1.99E-04	3.22E-04	412	420	TMT6plex
P68363	TBA1B_HUMAN	QLFHPEQLITGKED	N	26.05	1865.97	14	4.3	934	2	118	F1:18324	7.42E-04	9.37E-04	2.06E-04	4.30E-04	5.66E-04	6.37E-05	85	98	Pyro-glu from Q; TMT6plex
Q8WZ42	TITIN_HUMAN	STAQLKVL	Y	19.75	1315.86	8	4.4	658.9	2	119	F1:18582	2.36E-04	1.68E-04	0.00E+00	1.70E-04	2.70E-04	2.11E-04	12579	12586	TMT6plex; Amidation
P21333	FLNA_HUMAN	QQGPVGVNV	Y	18.99	1126.62	9	0	564.3	2	57.1	F1:7681	2.58E-03	4.60E-03	1.85E-03	2.64E-03	2.34E-03	1.05E-03	941	949	TMT6plex; Deamidation
P02675	FIBB_HUMAN	QGVNDNEEGFFS	Y	28.32	1324.52	12	-0.7	663.3	2	129	F1:20517	0.00E+00	0.00E+00	0.00E+00	6.57E-05	6.73E-06	0.00E+00	31	42	Pyro-glu from Q
P62328	TYB4_HUMAN	ETIEQEKGAGES	Y	40.96	1805.94	12	2.1	603	3	46.3	F1:5982	2.68E-04	6.52E-04	2.20E-04	2.83E-04	1.87E-04	1.96E-04	33	44	TMT6plex
Q562R1	ACTBL_HUMAN	GPPIVHR	Y	23.14	1017.63	7	1.2	509.8	2	100	F2:14113	1.45E-04	4.32E-05	1.38E-03	0.00E+00	0.00E+00	8.35E-05	367	373	TMT6plex; Methyl ester
P0DJ19	SAA2_HUMAN	DAAKRGPGGA	Y	15.3	1356.79	10	5.8	453.3	3	13.3	F2:905	8.74E-05	1.96E-03	1.95E-04	8.41E-05	6.36E-05	0.00E+00	61	70	TMT6plex
O14745	NHRF1_HUMAN	EPPAAAQVQAGNE	Y	33.69	1567.77	14	1.2	784.9	2	56	F1:7493	3.90E-04	4.95E-04	2.88E-04	5.18E-04	5.49E-04	3.60E-04	121	134	TMT6plex
Q15942	ZYX_HUMAN	VNPFPRGDSEPPAPG AQRA	Y	39.31	2288.19	20	3.8	763.7	3	58.6	F1:7923	1.55E-04	5.45E-04	1.36E-04	9.95E-05	1.24E-04	1.54E-04	36	55	TMT6plex
O15438	MRP3_HUMAN	VDPNNV	Y	17.66	885.476	6	5.3	443.7	2	27.4	F2:2952	6.56E-04	2.02E-04	8.69E-05	1.35E-04	9.13E-05	1.20E-04	557	562	TMT6plex
Q14624	ITIH4_HUMAN	QAGAAGSRMNFPRG VL	Y	39.03	1613.81	16	3.7	807.9	2	76.4	F1:10721	2.78E-04	4.23E-04	1.52E-04	3.71E-04	4.22E-04	3.31E-04	650	665	Pyro-glu from Q

Q15942	ZYX_HUMAN	VNPFPRPGDSEPPAPG AQRAQ	Y	51.52	2416.24	21	5.8	806.4	3	56.9	F2:7215	5.74E-04	6.23E-04	1.36E-04	6.63E-04	1.04E-03	3.80E-04	36	56	TMT6plex
P50552	VASP_HUMAN	DESANQEEPEARVPA	Y	19.19	1869.89	15	2.8	624.3	3	41.8	F1:5279	1.34E-04	2.10E-04	1.39E-04	2.18E-04	1.34E-04	3.14E-04	287	301	TMT6plex
P02671	FIBA_HUMAN	TFESK	N	18.81	1068.62	5	2.6	535.3	2	38.4	F1:4799	2.08E-03	6.88E-04	1.70E-03	9.68E-04	8.80E-04	1.19E-03	595	599	TMT6plex
Q14624	ITIH4_HUMAN	PGPPDVPDHAAYHPF	Y	50.5	1844.9	15	2	616	3	72.1	F1:10045	9.48E-05	7.28E-05	7.69E-05	1.11E-04	1.24E-03	1.60E-04	673	687	TMT6plex
PODJI8	SAA1_HUMAN	DGARDMW	N	28.06	1078.51	7	3.1	540.3	2	56.1	F1:7517	2.63E-04	1.39E-03	3.33E-04	3.58E-04	1.52E-04	2.25E-04	30	36	TMT6plex
PODJI8	SAA1_HUMAN	SGKDPNHFRPAGLPE	Y	35.45	2079.13	15	3	520.8	4	50.5	F1:6652	0.00E+00	4.86E-04	4.52E-05	0.00E+00	0.00E+00	0.00E+00	106	120	TMT6plex
P01042	KNG1_HUMAN	NGKHNGW	Y	32.14	1271.67	7	4.1	424.9	3	38.2	F1:4769	2.19E-04	7.42E-04	3.80E-04	5.97E-04	3.30E-03	5.55E-04	513	519	TMT6plex; Deamidation
Q05682	CALD1_HUMAN	TSPTKV	Y	25.29	940.483	6	2.8	471.3	2	22.9	F1:2393	1.48E-04	1.60E-04	7.65E-05	1.47E-04	3.43E-04	1.30E-04	788	793	Phosphorylation ; TMT6plex
Q9HBX8	LGR6_HUMAN	PYAPPEGQPAALGFT	Y	15.42	1743.9	15	1.9	582.3	3	56.7	F2:7167	3.16E-04	2.15E-04	8.11E-05	3.12E-04	2.19E-04	3.19E-04	719	733	TMT6plex
Q14624	ITIH4_HUMAN	SRQLGLPGPPDVPDH AA	Y	48.24	1955.04	17	4.1	652.7	3	64.7	F1:8871	1.55E-04	2.60E-04	2.11E-04	1.60E-04	2.19E-04	1.21E-04	667	683	TMT6plex
P02671	FIBA_HUMAN	RGSESGIFT	Y	18.61	1181.62	9	2.9	591.8	2	43.1	F1:5479	4.97E-04	7.25E-04	5.72E-04	4.46E-04	4.20E-04	6.38E-04	547	555	TMT6plex
P62328	TYB4_HUMAN	SDKPDMAEIEKF	Y	52.52	1908.99	12	0.8	955.5	2	107	F1:16163	2.20E-03	3.67E-04	1.88E-04	2.12E-03	7.72E-03	4.14E-04	2	13	Acetylation ; TMT6plex
PODJI8	SAA1_HUMAN	FFGHGAEDSLADQAA NEWG	Y	45.73	2250.02	19	2.1	1126	2	124	F1:19470	0.00E+00	9.57E-04	1.41E-04	4.29E-05	4.89E-05	0.00E+00	86	104	TMT6plex
P02675	FIBB_HUMAN	QGVNDNEEGF	Y	35.91	1337.59	10	5	669.8	2	64.4	F2:8285	3.12E-04	8.42E-04	6.32E-04	3.18E-04	3.12E-04	6.03E-04	31	40	TMT6plex; Deamidation
P00488	F13A_HUMAN	DLPTVE	N	26.5	901.496	6	2.7	451.8	2	67.5	F1:9334	1.52E-04	1.79E-04	2.46E-04	2.64E-04	1.59E-04	5.95E-04	26	31	TMT6plex
O75022	LIRB3_HUMAN	AHPPLRL	Y	21.43	1031.64	7	-0.4	516.8	2	99.4	F1:14693	1.90E-04	5.59E-05	1.44E-03	1.06E-04	0.00E+00	1.01E-04	362	368	TMT6plex
P02671	FIBA_HUMAN	SGEGDFLAEGGGVR	Y	58.29	1578.78	14	4.2	790.4	2	66.7	F1:9193	2.69E-02	3.34E-03	5.33E-02	2.07E-02	1.04E-02	3.83E-03	22	35	TMT6plex
PODJI8	SAA1_HUMAN	FGHGAEDS	Y	34.42	1047.48	8	2.2	524.7	2	24.3	F1:2599	2.14E-04	5.65E-04	2.06E-04	1.94E-04	1.75E-04	2.21E-04	87	94	TMT6plex
Q05682	CALD1_HUMAN	DEEAKTTTTNTQ	Y	47.76	1795.92	12	4.7	899	2	23.1	F2:2329	1.82E-03	1.04E-03	1.30E-04	1.32E-03	3.12E-03	9.96E-04	76	87	TMT6plex
Q9NQC3	RTN4_HUMAN	GNDFVPPAPR	Y	34.21	1298.68	10	1.5	650.3	2	55.8	F2:7028	2.68E-04	6.83E-04	2.63E-04	5.08E-04	6.33E-04	5.40E-04	82	91	TMT6plex; Deamidation
P00734	THRB_HUMAN	ERELLESYIDG	Y	31.29	1551.8	11	1.9	776.9	2	100	F1:14824	3.44E-04	5.23E-04	2.94E-04	8.82E-04	5.84E-04	2.80E-04	352	362	TMT6plex
P02671	FIBA_HUMAN	SRGSESGIFT	Y	25.26	1268.66	10	2.8	635.3	2	39	F2:4597	1.70E-04	1.65E-04	1.18E-04	2.42E-04	1.04E-04	3.03E-04	546	555	TMT6plex
P01024	CO3_HUMAN	IHWESASL	Y	34.86	1170.62	8	2.1	586.3	2	84.7	F1:12103	9.70E-05	6.20E-04	3.82E-04	3.64E-04	4.78E-04	9.32E-04	1311	1318	TMT6plex
P42858	HD_HUMAN	HLVRPQ	Y	16.56	977.597	6	-2.3	489.8	2	86.4	F1:12410	2.47E-04	8.42E-05	1.51E-04	2.09E-04	1.46E-04	5.95E-04	195	200	TMT6plex
PODJI8	SAA1_HUMAN	GNYDAAKRGPGGVW AAEAISDA	Y	36.87	2633.36	22	2.3	878.8	3	92.7	F1:13504	7.48E-05	1.05E-03	1.48E-04	1.48E-04	0.00E+00	8.82E-05	58	79	TMT6plex
P01024	CO3_HUMAN	FTVTAEGK	Y	43.4	1309.76	8	-0.5	655.9	2	62.4	F1:8523	1.15E-03	1.27E-03	8.47E-04	1.17E-03	1.76E-03	1.29E-02	1330	1337	TMT6plex
P0C0L4	CO4A_HUMAN	NVKVGGNS	Y	26.26	1231.73	8	4.6	616.9	2	23.3	F2:2361	1.08E-03	7.93E-03	2.00E-03	6.22E-03	2.65E-03	1.37E-02	1367	1374	TMT6plex
Q96S97	MYADM_HUMA	PVTVTRTTTT	Y	38.82	1417.83	11	3	709.9	2	54.1	F1:7186	1.73E-03	2.10E-03	5.45E-04	1.24E-03	7.54E-04	8.37E-04	2	12	TMT6plex
Q9NQC3	RTN4_HUMAN	VPPAPR	Y	18.16	864.538	6	4.6	433.3	2	22.4	F2:2203	3.21E-04	1.65E-03	3.38E-04	3.70E-04	2.29E-04	2.67E-04	86	91	TMT6plex

P0DJ18	SAA1_HUMAN	EAISDAREN	Y	34.36	1232.62	9	1.9	617.3	2	23.4	F1:2474	4.08E-04	2.59E-03	3.82E-04	3.80E-04	2.58E-04	3.42E-04	74	82	TMT6plex
P01024	CO3_HUMAN	ESASLLR	Y	27.05	1003.59	7	2.6	502.8	2	38.3	F1:4794	8.05E-04	9.86E-04	8.47E-04	9.68E-04	1.07E-03	5.54E-03	1314	1320	TMT6plex
P57086	SCND1_HUMAN	PAAVPE	Y	15.25	908.517	7	2.9	455.3	2	37.8	F1:4711	3.01E-04	1.63E-04	2.48E-04	3.42E-04	2.05E-04	3.44E-04	14	20	TMT6plex
P02671	FIBA_HUMAN	GIAEFPSRG	Y	30.86	1161.63	9	2.6	581.8	2	54.4	F1:7241	1.46E-03	6.96E-04	7.63E-04	6.96E-04	5.74E-04	8.44E-04	566	574	TMT6plex
P0C0L4	CO4A_HUMAN	DDPDAPLQPVTPLQ	Y	41.22	1733.9	14	3.4	579	3	98.3	F1:14489	0.00E+00	5.12E-05	0.00E+00	6.09E-05	4.36E-04	0.00E+00	1429	1442	TMT6plex
Q96RW7	HMCN1_HUMAN	EGASK	N	16.95	948.565	5	4	475.3	2	75.1	F1:10528	9.78E-05	8.09E-05	1.08E-03	8.21E-04	5.01E-04	8.64E-03	61	65	TMT6plex
O95810	SDPR_HUMAN	ERSDGDVPVQPA	Y	24.33	1398.69	11	5.7	700.4	2	22.2	F2:2175	3.91E-04	6.17E-04	2.96E-04	6.22E-04	5.03E-04	4.95E-04	407	417	TMT6plex
P62328	TYB4_HUMAN	SDKPDMAEIEKFDKS	Y	52.38	2468.31	15	3.3	823.8	3	95.2	F2:13193	1.42E-04	4.32E-03	4.80E-04	1.73E-04	4.06E-04	0.00E+00	2	16	Acetylation ; TMT6plex
P0DJ18	SAA1_HUMAN	DAAKRGGP	N	21.23	1228.73	8	3.1	410.6	3	13.5	F1:895	0.00E+00	8.83E-04	4.93E-05	0.00E+00	0.00E+00	0.00E+00	61	68	TMT6plex
P02671	FIBA_HUMAN	GDSFESK	Y	33.68	1327.7	8	3.9	664.9	2	42.1	F1:5319	2.23E-03	7.89E-04	2.24E-03	1.26E-03	1.24E-03	1.19E-03	592	599	TMT6plex
P62328	TYB4_HUMAN	QEKNPSPKET	Y	37.35	1710.96	11	4.1	856.5	2	53.1	F1:7028	8.58E-04	3.47E-03	4.64E-04	8.03E-04	3.04E-03	8.66E-03	24	34	Pyro-glu from Q; TMT6plex
O95810	SDPR_HUMAN	DPVQPA	Y	21.75	854.47	6	2.2	428.2	2	34.2	F1:4154	1.75E-04	1.41E-04	2.31E-04	2.08E-04	2.12E-04	2.11E-04	412	417	TMT6plex
P20908	CO5A1_HUMAN	SSKGP	N	16.71	932.57	5	5.7	467.3	2	96.6	F1:14183	1.80E-04	0.00E+00	1.05E-04	4.62E-05	0.00E+00	6.67E-05	67	71	TMT6plex
Q5H8C1	FREM1_HUMAN	KGLFH	N	19.04	829.501	5	3.7	415.8	2	39.6	F1:4979	1.43E-04	4.49E-04	2.56E-04	1.59E-04	1.66E-04	2.32E-04	2018	2022	TMT6plex
P29274	AA2AR_HUMAN	DCSHAPL	Y	16.03	970.475	7	5.8	486.2	2	59.8	F1:8125	6.43E-04	3.71E-04	4.40E-04	4.81E-04	5.36E-04	1.33E-03	261	267	TMT6plex
P68363	TBA1B_HUMAN	QLITGKED	N	30.34	1114.61	8	1.9	558.3	2	68.8	F2:8943	7.06E-04	1.27E-03	2.43E-04	3.14E-04	6.04E-04	3.33E-04	91	98	Pyro-glu from Q; TMT6plex
P0DJ18	SAA1_HUMAN	GAEDSLADQAANEWC	Y	18.56	1761.8	15	3.1	881.9	2	107	F2:15418	1.35E-04	1.62E-04	0.00E+00	7.17E-05	6.01E-05	0.00E+00	90	104	TMT6plex
P52565	GDIR1_HUMAN	NEEDEHSVNYKPPA	Y	50.88	2086.04	14	5.8	696.4	3	41.7	F1:5255	8.85E-05	2.58E-04	7.71E-05	1.14E-04	1.07E-04	0.00E+00	18	31	TMT6plex
P02671	FIBA_HUMAN	IAEFPSRG	Y	20.09	1104.61	8	5.2	553.3	2	54.1	F2:6749	5.27E-04	4.09E-04	3.04E-04	4.61E-04	3.96E-04	8.94E-04	567	574	TMT6plex
P00734	THRB_HUMAN	DKTEREL	Y	26.69	1347.78	7	3.1	450.3	3	26.9	F1:3019	4.06E-04	4.20E-04	1.76E-03	7.85E-04	1.15E-03	4.67E-03	349	355	TMT6plex
Q8NI35	INADL_HUMAN	EVGIK	N	15.87	1002.65	5	1.6	502.3	2	59.3	F1:8046	6.06E-04	3.95E-04	2.03E-03	1.16E-03	1.18E-03	2.83E-03	1361	1365	TMT6plex
Q8TDY2	RBCC1_HUMAN	DGLIK	N	19.64	1002.65	5	1.6	502.3	2	59.3	F1:8047	6.06E-04	3.95E-04	2.03E-03	1.16E-03	1.18E-03	2.83E-03	879	883	TMT6plex
Q9Y4A5	TRRAP_HUMAN	DGILK	N	19.64	1002.65	5	1.6	502.3	2	59.3	F1:8047	6.06E-04	3.95E-04	2.03E-03	1.16E-03	1.18E-03	2.83E-03	3767	3771	TMT6plex
Q8NCM8	DYHC2_HUMAN	DGLLK	N	19.64	1002.65	5	1.6	502.3	2	59.3	F1:8047	6.06E-04	3.95E-04	2.03E-03	1.16E-03	1.18E-03	2.83E-03	568	572	TMT6plex
Q86UP3	ZFHX4_HUMAN	EVGLK	N	15.87	1002.65	5	1.6	502.3	2	59.3	F1:8046	6.06E-04	3.95E-04	2.03E-03	1.16E-03	1.18E-03	2.83E-03	2596	2600	TMT6plex
Q6ZN44	UNC5A_HUMAN	VPALVGPSAFK	Y	19.77	1542.95	11	2.4	772.5	2	127	F1:20109	7.68E-05	6.24E-05	6.86E-05	7.16E-05	7.55E-05	2.65E-04	744	754	TMT6plex
Q8WZ42	TITIN_HUMAN	KPIPDVV	Y	16.28	1206.77	7	1.6	604.4	2	48.6	F2:6003	3.36E-04	1.38E-03	4.26E-04	4.43E-04	2.70E-04	3.62E-04	25661	25667	TMT6plex; Dehydration
P52566	GDIR2_HUMAN	TEKAPEPHVEEDDDD ELDS	Y	26.3	2440.06	19	4.5	1221	2	65.1	F1:8930	0.00E+00	5.54E-04	5.62E-05	0.00E+00	5.08E-05	0.00E+00	2	20	TMT6plex; Acetylation
P02671	FIBA_HUMAN	GEFVSETESRGSSESGI FTNT	Y	33.87	2362.11	20	3.2	1182	2	90.8	F1:13170	1.28E-03	2.64E-04	2.53E-04	3.26E-04	2.86E-04	1.01E-04	538	557	TMT6plex
Q8WZ42	TITIN_HUMAN	PVEIGPILAV	Y	16.85	1020.62	10	-4.1	511.3	2	69.4	F1:9621	1.31E-04	1.34E-04	1.66E-04	1.71E-04	8.59E-05	7.94E-05	16207	16216	Methyl ester
P21359	NF1_HUMAN	HAIQI	N	17.3	809.496	5	2.3	405.8	2	42.2	F1:5341	3.00E-04	1.62E-04	6.19E-04	1.03E-03	2.31E-04	5.93E-04	1007	1011	TMT6plex

P0C0L4	CO4A_HUMAN	HALQL	N	17.3	809.496	5	2.3	405.8	2	42.2	F1:5341	3.00E-04	1.62E-04	6.19E-04	1.03E-03	2.31E-04	5.93E-04	1342	1346	TMT6plex
Q7Z6J9	SEN54_HUMAN	VVRRF	N	16.65	904.581	5	-1.6	453.3	2	111	F1:17004	1.45E-03	5.35E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	167	171	TMT6plex
P19113	DCHS_HUMAN	KLWV	N	20.27	920.569	5	5.7	461.3	2	95.8	F1:14057	2.73E-04	0.00E+00	3.08E-03	0.00E+00	0.00E+00	2.36E-04	361	365	TMT6plex
P02671	FIBA_HUMAN	ADSGEGDFLAEGGGV	Y	58.16	1608.75	15	-2.4	805.4	2	103	F1:15272	1.52E-03	2.52E-03	2.85E-03	4.13E-03	1.46E-03	4.26E-03	20	34	TMT6plex
Q8WZ42	TITIN_HUMAN	PKSRS	N	16.11	1031.65	5	-5.1	516.8	2	107	F1:16062	1.26E-04	0.00E+00	1.23E-03	6.60E-05	0.00E+00	5.35E-05	261	265	TMT6plex
Q9Y490	TLN1_HUMAN	DDELNWLHDHG	Y	45.53	1441.67	10	0.8	721.8	2	103	F1:15423	5.62E-04	1.49E-03	3.68E-04	4.85E-04	4.80E-04	3.59E-04	168	177	TMT6plex
P0DJ18	SAA1_HUMAN	YDAAKRGPGGAWAA EAISDA	Y	24.58	2434.26	20	1.9	812.4	3	91.7	F2:12588	6.50E-05	1.23E-03	1.81E-04	1.26E-04	7.22E-05	1.08E-04	60	79	TMT6plex; Mutation
Q14624	ITI4_HUMAN	GLPGPPDVPDHAAY	Y	43.79	1633.83	14	-2.3	817.9	2	81.6	F1:11577	3.16E-04	6.57E-04	2.28E-04	4.95E-04	1.01E-03	3.67E-04	671	684	TMT6plex
Q9NQ36	SCUB2_HUMAN	RSFIR	N	16.34	906.56	5	-3.4	454.3	2	81.6	F1:11581	1.54E-04	8.96E-05	5.95E-04	1.68E-04	7.43E-05	9.65E-05	981	985	TMT6plex
P0C0L4	CO4A_HUMAN	GLEEELQF	Y	30.45	1192.62	8	2.7	597.3	2	123	F1:19213	2.08E-04	1.42E-04	3.08E-04	3.63E-04	2.25E-04	2.49E-04	1353	1360	TMT6plex
Q14624	ITI4_HUMAN	EMVVAGKLQ	Y	41.09	1431.85	9	-2.4	716.9	2	70.1	F1:9717	7.50E-04	6.14E-04	7.49E-04	1.14E-03	3.72E-03	4.11E-04	490	498	TMT6plex
Q6ZU65	UBN2_HUMAN	STPHRPSTASGSSVVT	Y	18.43	1798.94	16	2.7	900.5	2	49.5	F1:6485	2.91E-04	4.13E-04	1.84E-04	2.58E-04	4.53E-04	4.26E-04	1204	1219	TMT6plex
P02649	APOE_HUMAN	KVEQAVETEPEPEL	Y	40.22	2055.11	14	1	1029	2	78	F1:11011	1.51E-04	1.73E-04	3.74E-04	2.92E-04	6.76E-04	2.01E-04	19	32	TMT6plex
P0DJ18	SAA1_HUMAN	DAAKRPGGVWA	Y	20.79	1641.94	12	4.5	548.3	3	47.1	F2:5733	2.05E-04	1.37E-03	1.90E-04	2.55E-04	1.25E-04	1.60E-04	61	72	TMT6plex
P0DJ18	SAA1_HUMAN	FGHGAEDSLADQAA NEWG	Y	50.42	2102.95	18	1.2	1052	2	103	F1:15318	0.00E+00	1.72E-03	2.60E-04	1.43E-04	1.65E-04	0.00E+00	87	104	TMT6plex
P67936	TPM4_HUMAN	ELERAEEAEVSE	Y	17.51	1774.89	13	1.5	592.6	3	44.3	F1:5664	0.00E+00	2.35E-04	8.56E-05	5.25E-05	0.00E+00	5.29E-05	139	151	TMT6plex
P02671	FIBA_HUMAN	EGDFLAEGGGVR	Y	54.69	1434.73	12	3.4	718.4	2	69.7	F2:9105	1.42E-03	6.27E-04	3.85E-03	1.74E-03	7.84E-04	2.75E-04	24	35	TMT6plex
P02679	FIBG_HUMAN	DESSKPNMIDAATL	Y	49.2	1949.02	14	-0.7	975.5	2	88	F1:12665	6.68E-03	2.93E-04	4.06E-04	4.84E-04	2.02E-04	1.10E-04	97	110	TMT6plex
P01024	CO3_HUMAN	IHWESAS	Y	32.49	1057.54	7	2.7	529.8	2	55	F1:7328	3.05E-04	6.20E-04	4.52E-04	4.51E-04	4.94E-04	1.31E-03	1311	1317	TMT6plex
P62328	TYB4_HUMAN	EKNPLPSKETIEQE	Y	36.46	2328.31	14	0.8	777.1	3	65.5	F1:9005	2.24E-04	6.10E-04	9.44E-05	7.82E-05	3.30E-04	0.00E+00	25	38	TMT6plex
O43194	GPR39_HUMAN	IGFVWVT	Y	19.4	1049.61	7	7.8	525.8	2	87.4	F1:12567	7.77E-05	5.81E-05	3.89E-05	5.25E-05	6.82E-05	1.26E-04	156	162	TMT6plex
P02675	FIBB_HUMAN	EEAPSLRPAPPISGG GY	Y	44.94	2023.06	18	-1.6	675.4	3	79.1	F1:11177	3.02E-04	1.82E-04	1.25E-04	2.08E-04	1.50E-04	6.65E-05	54	71	TMT6plex
Q9H4B7	TBB1_HUMAN	EEDEEVTEEAEMEPE DKGH	Y	57.17	2705.19	19	2.8	902.7	3	58.3	F1:7882	1.68E-04	3.55E-04	0.00E+00	1.31E-04	4.25E-04	3.41E-04	433	451	TMT6plex; Oxidation
Q8WZ42	TITIN_HUMAN	PVVISGV	Y	17.04	904.577	7	6.5	453.3	2	131	F2:19988	1.31E-03	3.03E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	23570	23576	Replacement of proton by lithium
P0DJ19	SAA2_HUMAN	TGHGAEDSLADQAA NKWG	Y	50.61	2285.14	18	8.5	762.7	3	76.6	F1:10751	0.00E+00	2.16E-03	3.22E-04	3.05E-04	8.84E-05	0.00E+00	87	104	TMT6plex; Mutation
P02775	CXCL7_HUMAN	EESLSDLY	Y	17.99	1298.61	9	1.1	650.3	2	92.6	F1:13479	3.09E-04	4.40E-04	3.02E-04	4.44E-04	5.41E-04	3.00E-04	50	58	TMT6plex
Q7Z5J4	RAI1_HUMAN	VDMMS	Y	15.79	913.391	6	2.4	457.7	2	25	F2:2632	2.40E-04	7.15E-04	3.29E-04	3.42E-04	5.81E-04	1.17E-03	1853	1858	TMT6plex
P37840	SYUA_HUMAN	NVGGAVVTG	Y	28.39	1001.57	9	4.5	501.8	2	44.8	F2:5396	2.52E-04	3.49E-04	7.01E-04	4.52E-04	5.07E-04	8.55E-04	65	73	TMT6plex
O14646	CHD1_HUMAN	RPEKG	N	15.1	1043.65	5	-4.6	522.8	2	99.5	F1:14712	8.83E-05	2.98E-05	8.09E-05	0.00E+00	5.76E-05	6.53E-05	1433	1437	TMT6plex
Q711Q0	CJ071_HUMAN	ARARTQ	N	16.03	930.556	6	0.7	466.3	2	86.5	F1:12426	7.14E-05	8.17E-05	4.94E-05	1.01E-04	6.14E-05	8.10E-05	1370	1375	TMT6plex



P0C0L4	CO4A_HUMAN	DDPDAPLQPVTP	Y	50.32	1605.85	13	1.6	536.3	3	106	F2:15150	3.99E-05	2.82E-05	0.00E+00	8.04E-05	6.67E-05	0.00E+00	1429	1441	TMT6plex
P02675	FIBB_HUMAN	DNEEGFF	Y	34.38	1085.49	7	1.9	543.8	2	98.4	F1:14500	6.41E-04	1.59E-04	7.13E-04	3.68E-04	2.72E-04	3.39E-04	35	41	TMT6plex
P60709	ACTB_HUMAN	QKDSYVVGDEAQS KRG	Y	44.51	2108.09	15	3.2	703.7	3	41.7	F1:5249	1.28E-03	3.39E-03	4.98E-04	8.29E-04	1.42E-03	2.20E-04	49	63	Pyro-glu from Q; TMT6plex
Q9H4B7	TBB1_HUMAN	LEEDEEVTEEAEMEP EDKGH	Y	55.45	2802.28	20	2.8	935.1	3	84.4	F1:12054	0.00E+00	1.87E-04	0.00E+00	9.43E-05	2.97E-04	6.00E-05	432	451	TMT6plex
Q9H992	MARH7_HUMAN	PGSLFR	Y	18.39	904.533	6	6.5	453.3	2	77	F1:10815	5.66E-05	7.70E-05	1.18E-04	1.40E-04	6.34E-05	1.31E-04	480	485	TMT6plex
P57053	H2BFS_HUMAN	PEPAKSAPAPK	Y	33.9	1779.09	11	1.8	445.8	4	34.7	F1:4239	4.34E-04	4.52E-05	1.51E-04	1.26E-04	8.83E-05	6.24E-05	2	12	TMT6plex
P62328	TYB4_HUMAN	SKETIEQEQKAGES	Y	55.92	2250.23	14	5.9	751.1	3	48.9	F1:6380	9.11E-04	1.99E-03	2.47E-04	3.99E-04	1.01E-03	1.30E-04	31	44	TMT6plex
P04632	CPNS1_HUMAN	EPPPPRTHYSNIE	Y	28.1	1764.9	13	3.1	589.3	3	33.8	F1:4097	7.10E-05	9.40E-05	0.00E+00	6.89E-05	5.17E-05	1.76E-04	79	91	TMT6plex
P0DJ18	SAA1_HUMAN	EAISDARENIQ	Y	25.82	1473.76	11	2.2	737.9	2	46	F1:5920	2.65E-04	1.31E-03	2.80E-04	3.23E-04	2.12E-04	2.70E-04	74	84	TMT6plex
P02775	CXCL7_HUMAN	NLAKGKEESLDS	Y	24.46	1977.14	12	3.7	660.1	3	48.8	F2:6034	2.46E-04	4.64E-04	3.64E-04	1.00E-03	3.67E-04	3.56E-04	44	55	TMT6plex
P18505	GBRB1_HUMAN	PSTLIT	N	17.21	859.522	6	-8.7	430.8	2	36.7	F1:4549	4.49E-04	1.66E-03	3.90E-04	3.71E-04	2.94E-04	5.84E-04	253	258	TMT6plex
Q92932	PTPR2_HUMAN	YDRGV	N	15.08	837.455	5	4.5	419.7	2	22.9	F2:2290	8.40E-04	1.83E-03	4.31E-04	1.24E-03	2.00E-03	1.20E-03	912	916	TMT6plex
Q96S97	MYADM_HUMAN	LAAIAILLN	Y	16.45	1139.75	9	-8.2	570.9	2	69.5	F2:9069	5.03E-04	4.54E-04	7.36E-04	5.21E-04	3.69E-04	5.24E-04	216	224	TMT6plex
P02775	CXCL7_HUMAN	PLHALQVL	Y	15.29	1117.72	8	-3	559.9	2	109	F1:16522	2.08E-02	1.28E-04	0.00E+00	1.56E-04	0.00E+00	0.00E+00	16	23	TMT6plex; Amidation
Q15942	ZYX_HUMAN	DDMTKNDPFGKARVS	Y	20.4	2310.26	14	1.5	578.6	4	62.3	F1:8504	1.74E-04	4.51E-04	6.44E-05	1.58E-04	1.23E-04	6.03E-05	156	169	TMT6plex
P01024	CO3_HUMAN	TKENEGFTVTAEG	Y	42.64	1839.96	13	0.4	921	2	59.6	F1:8106	8.15E-04	6.00E-04	4.18E-04	1.61E-03	1.24E-03	2.29E-04	1324	1336	TMT6plex
P01024	CO3_HUMAN	GRLKGPLLN	Y	15.1	1223.76	9	-4.3	408.9	3	138	F2:21426	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.68E-05	1200	1208	Formylation; TMT6plex
O43432	IF4G3_HUMAN	PASPPHTP	Y	15.14	1031.56	8	8	516.8	2	16.7	F2:1401	0.00E+00	4.65E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	422	429	TMT6plex
Q92903	CDS1_HUMAN	FKRAFKIKDF	Y	15.15	2215.4	10	-3.7	554.9	4	177	F1:29606	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.39E-04	377	386	TMT6plex
O76024	WFS1_HUMAN	PVGHLLV	Y	15.17	948.596	7	5.5	475.3	2	105	F1:15783	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.10E-03	492	498	TMT6plex
Q01668	CAC1D_HUMAN	GVPSLQVVLNSIHKAM VPLLIALLV	N	15.19	3195	26	-6	640	5	193	F1:31658	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.00E-03	253	278	TMT6plex
Q9NR48	ASH1L_HUMAN	NQILLN	N	15.25	942.57	6	-4.7	472.3	2	118	F2:17576	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.05E-05	2925	2930	TMT6plex
B8ZZ34	SHSA8_HUMAN	GLLGGR	N	15.44	800.507	6	5.5	401.3	2	106	F1:15933	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.11E-04	8	13	TMT6plex
Q8WXH0	SYNE2_HUMAN	MYRKN	Y	15.51	1168.68	5	4.7	585.3	2	166	F2:26743	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.86E-04	569	573	TMT6plex
O15438	MRP3_HUMAN	IPLNGAVAVKMR	Y	15.56	1726.07	12	8.9	864	2	140	F2:21753	1.64E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	463	474	TMT6plex
Q8N3K9	CMYA5_HUMAN	V TSADEHSVLA EEDKVA	Y	15.59	2257.18	17	1	565.3	4	56.3	F2:7095	0.00E+00	0.00E+00	0.00E+00	5.80E-05	0.00E+00	0.00E+00	1404	1420	TMT6plex
Q14008	CKAP5_HUMAN	PNIKQHVKNLGIPITV LGDSKNNVR	Y	15.7	3784.29	26	8.4	947.1	4	194	F1:31927	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	8.53E-04	933	958	TMT6plex; Deamidation
Q02817	MUC2_HUMAN	GSVLLN	N	15.71	830.507	6	-2.1	416.3	2	120	F1:18616	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.13E-04	464	469	TMT6plex
Q8TE82	S3TC1_HUMAN	ALPLAVTT	Y	15.73	1013.63	8	1.9	507.8	2	117	F2:17208	4.96E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1138	1145	TMT6plex
P13747	HLAE_HUMAN	EQEGSEYWDRETRSA	Y	15.77	2070.94	15	5	518.7	4	19.4	F1:1823	0.00E+00	0.00E+00	0.00E+00	6.60E-05	0.00E+00	0.00E+00	74	88	TMT6plex
O95613	PCNT_HUMAN	AAIEK	N	15.81	988.632	5	6.6	495.3	2	99.1	F2:13871	0.00E+00	2.81E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	414	418	TMT6plex

O15018	PDZD2_HUMAN	MNRGDFLLSVNGASL AGLAH	Y	15.85	2273.17	20	-4.1	569.3	4	43.2	F1:5500	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.27E-05	2665	2684	TMT6plex; Deamidation
O14646	CHD1_HUMAN	KTLID	N	15.88	817.511	5	1	409.8	2	84.9	F2:11478	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.24E-05	0.00E+00	628	632	TMT6plex
Q8WXG9	GPR98_HUMAN	KTILD	N	15.88	817.511	5	1	409.8	2	84.9	F2:11478	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.24E-05	0.00E+00	5737	5741	TMT6plex
Q5JPF3	AN36C_HUMAN	GRSALI	N	15.91	844.533	6	4.1	423.3	2	109	F1:16460	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.44E-03	197	202	TMT6plex
Q8NDA2	HMCN2_HUMAN	GRSALL	N	15.91	844.533	6	4.1	423.3	2	109	F1:16460	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.44E-03	800	805	TMT6plex
Q9BQC3	DPH2_HUMAN	HYADL	N	15.92	846.444	5	4.9	424.2	2	86.4	F2:11712	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.86E-05	0.00E+00	383	387	TMT6plex
Q5T3U5	MRP7_HUMAN	GPLALALVALLPAPA	Y	15.96	1615.03	15	-6.8	808.5	2	127	F1:20045	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.37E-03	132	146	TMT6plex
O95714	HERC2_HUMAN	PVPALPIVVQL	Y	16.06	1374.87	11	3.9	459.3	3	133	F1:21326	4.36E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2455	2465	TMT6plex; Deamidation
Q8WZ42	TITIN_HUMAN	GVEVK	N	16.1	988.632	5	4.6	495.3	2	98.5	F1:14519	0.00E+00	0.00E+00	7.26E-05	0.00E+00	0.00E+00	0.00E+00	895	899	TMT6plex
O75369	FLNB_HUMAN	KSGCIV	Y	16.11	834.484	6	-5.1	418.2	2	51.6	F1:6807	0.00E+00	0.00E+00	9.23E-05	0.00E+00	0.00E+00	0.00E+00	657	662	TMT6plex
P98164	LRP2_HUMAN	PRHIVV	Y	16.32	948.607	6	1.2	475.3	2	102	F2:14494	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.70E-04	2192	2197	TMT6plex
Q8WZ42	TITIN_HUMAN	VTKLLPGN	Y	16.56	1298.83	8	3.2	650.4	2	132	F1:21166	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.31E-04	25790	25797	TMT6plex
Q9NZR1	TMOD2_HUMAN	PIPTLREFAKAL	Y	16.82	1813.12	12	2.6	454.3	4	169	F1:28272	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.68E-04	211	222	TMT6plex
Q8NEN9	PDZD8_HUMAN	LLYRR	N	16.87	948.607	5	1.1	475.3	2	119	F2:17588	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.61E-04	25	29	TMT6plex
Q5VST9	OBSCN_HUMAN	LIYRR	N	16.87	948.607	5	1.1	475.3	2	119	F2:17588	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.61E-04	2257	2261	TMT6plex
Q9UBG0	MRC2_HUMAN	ILYRR	N	16.87	948.607	5	1.1	475.3	2	119	F2:17588	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.61E-04	1434	1438	TMT6plex
Q9Y2D5	AKAP2_HUMAN	GLLVQN	N	16.91	871.533	6	5.6	436.8	2	112	F1:17093	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.59E-04	571	576	TMT6plex
Q9GZZ9	UBA5_HUMAN	GILVQN	N	16.91	871.533	6	5.6	436.8	2	112	F1:17093	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.59E-04	263	268	TMT6plex
Q9Y490	TLN1_HUMAN	ALPAIMR	Y	16.92	999.61	7	8.8	500.8	2	119	F2:17766	4.32E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	448	454	TMT6plex
Q14624	ITIH4_HUMAN	PPRPVRTCSKVLVLL	Y	17.07	1920.19	15	3.9	641.1	3	143	F1:23270	0.00E+00	0.00E+00	2.61E-04	0.00E+00	0.00E+00	0.00E+00	3	17	TMT6plex; Methyl ester
Q14146	URB2_HUMAN	VSLTVVGPV	Y	17.08	1098.69	9	1.9	550.4	2	125	F2:18938	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	6.19E-05	1314	1322	TMT6plex
Q4G0P3	HYDIN_HUMAN	LILKNNG	Y	17.16	1228.79	7	-5.9	615.4	2	115	F1:17627	0.00E+00	0.00E+00	0.00E+00	1.07E-04	0.00E+00	0.00E+00	3508	3514	TMT6plex
Q13402	MYO7A_HUMAN	NGILR	N	17.16	800.507	5	6.8	401.3	2	104	F2:14725	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.21E-04	1160	1164	TMT6plex
Q8IWI9	MGAP_HUMAN	SFIIE	N	17.2	836.485	5	0.6	419.2	2	63.8	F1:8740	0.00E+00	7.27E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1371	1375	TMT6plex
Q96ER9	CCD51_HUMAN	SFLLE	N	17.2	836.485	5	0.6	419.2	2	63.8	F1:8740	0.00E+00	7.27E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	359	363	TMT6plex
Q7Z407	CSMD3_HUMAN	SFILE	N	17.2	836.485	5	0.6	419.2	2	63.8	F1:8740	0.00E+00	7.27E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2699	2703	TMT6plex
Q8NEY1	NAV1_HUMAN	GKTPP	N	17.31	956.606	5	7.9	479.3	2	104	F2:14806	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.33E-05	532	536	TMT6plex
A6NKB5	PCX2_HUMAN	LMVAR	N	17.37	817.505	5	1.4	409.8	2	129	F1:20572	0.00E+00	0.00E+00	0.00E+00	3.39E-05	0.00E+00	0.00E+00	774	778	TMT6plex
P14618	KPYM_HUMAN	IMVAR	N	17.37	817.505	5	1.4	409.8	2	129	F1:20572	0.00E+00	0.00E+00	0.00E+00	3.39E-05	0.00E+00	0.00E+00	290	294	TMT6plex
Q9NYU2	UGGG1_HUMAN	NGRII	N	17.66	800.507	5	7.2	401.3	2	102	F2:14313	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.43E-04	896	900	TMT6plex
Q8WZ42	TITIN_HUMAN	NGRIL	N	17.66	800.507	5	7.2	401.3	2	102	F2:14313	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.43E-04	9707	9711	TMT6plex
Q5VWG9	TAF3_HUMAN	SAKAPVRSVVT	Y	17.67	1571.98	11	8.1	787	2	131	F1:20821	0.00E+00	0.00E+00	5.32E-05	0.00E+00	0.00E+00	0.00E+00	839	849	TMT6plex

P68363	TBA1B_HUMAN	QPPTVVPGGDLAKVQ RAVCMLS	N	17.81	2740.55	22	-3.6	686.1	4	88.2	F1:12711	0.00E+00	1.40E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	358	379	TMT6plex; Replacement of proton with ammonium ion
P84550	SKOR1_HUMAN	PPPPPAR	N	18	959.576	7	-2.3	480.8	2	31.7	F1:3770	0.00E+00	0.00E+00	0.00E+00	4.12E-05	0.00E+00	0.00E+00	581	587	TMT6plex
P02671	FIBA_HUMAN	TNTKESSSHHPG	Y	18.04	1739.88	12	4.7	581	3	11.5	F1:607	0.00E+00	3.76E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	555	566	TMT6plex; Deamidation
Q92616	GCN1L_HUMAN	PALLARM	Y	18.29	999.61	7	8	500.8	2	106	F1:15860	0.00E+00	0.00E+00	4.18E-05	0.00E+00	0.00E+00	0.00E+00	688	694	TMT6plex
Q9Y646	CBPQ_HUMAN	PHTGIQEYQDGVPKIP TACITV	Y	18.36	2826.49	22	6.7	707.6	4	94.9	F1:13893	0.00E+00	2.48E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	215	236	TMT6plex; Deamidation
O95866	G6B_HUMAN	TEPQRPVKEEPPKIPG DLDQEPS	Y	18.53	3304.78	23	2.9	827.2	4	65	F1:8927	0.00E+00	3.10E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	186	208	TMT6plex
Q03001	DYST_HUMAN	ILNGR	N	18.9	800.507	5	4.5	401.3	2	103	F1:15354	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.34E-04	1889	1893	TMT6plex
Q96RW7	HMCN1_HUMAN	LLNGR	N	18.9	800.507	5	4.5	401.3	2	103	F1:15354	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.34E-04	1784	1788	TMT6plex
P0C0L4	CO4A_HUMAN	GSKINVKV	Y	18.96	1315.86	8	8.8	658.9	2	130	F2:19915	4.83E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1363	1370	TMT6plex; Methyl ester
Q9Y6X0	SETBP_HUMAN	LYLRR	N	19.13	948.607	5	2.4	475.3	2	122	F1:19118	4.10E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1005	1009	TMT6plex
Q8WZ42	TITIN_HUMAN	RVTKVNK	Y	19.2	1317.85	7	8.9	659.9	2	82.1	F1:11662	0.00E+00	0.00E+00	0.00E+00	3.20E-05	0.00E+00	0.00E+00	20026	20032	Hydroxylation; TMT6plex
Q9UBW5	BIN2_HUMAN	TEVVLTR	Y	19.22	986.587	8	2.9	494.3	2	124	F1:19424	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.70E-04	385	392	Methyl ester
Q9UQD0	SCN8A_HUMAN	KFANTF	Y	19.96	955.533	6	9.2	478.8	2	138	F1:22298	0.00E+00	0.00E+00	0.00E+00	3.56E-05	0.00E+00	0.00E+00	725	730	TMT6plex
Q8WZ42	TITIN_HUMAN	KVAVVPVA	Y	21.44	920.57	9	3.4	461.3	2	104	F1:15466	0.00E+00	0.00E+00	1.06E-03	0.00E+00	0.00E+00	0.00E+00	10366	10374	Acetylation
Q99466	NOTC4_HUMAN	LGLGAARELRDQAGL APADVAHQ	Y	21.79	2559.36	23	2.3	640.8	4	61	F1:8322	0.00E+00	2.47E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1787	1809	TMT6plex; Deamidation
Q9UKN1	MUC12_HUMAN	METTALPGSTTTPGLS ERSTTFHSSPRSPATT LSPASTT	Y	21.88	4192.08	39	6.4	699.7	6	57	F1:7662	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.23E-05	948	986	TMT6plex
Q14624	ITIH4_HUMAN	NFRPGVLSSRQLGLP GPPDVPDHAA	Y	26.78	2826.5	25	3.2	707.6	4	94.9	F1:13894	0.00E+00	2.48E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	659	683	TMT6plex; Deamidation
P02671	FIBA_HUMAN	LGEFVSETESRGSESG IFTNTKESSSHHPGIAE FPSRGKS	Y	26.81	4737.37	40	7.3	677.8	7	95.3	F1:13958	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.59E-05	0.00E+00	537	576	TMT6plex; Methyl ester
P50552	VASP_HUMAN	SVPNGPSPEEVEQKQ RQQPGPSEHIE	Y	27.05	3340.71	26	5	836.2	4	60.6	F1:8263	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.31E-05	0.00E+00	128	153	TMT6plex
PODJ19	SAA2_HUMAN	RLTGPGAEDSLADQA ANKWG	Y	29.04	2514.32	20	-7.2	629.6	4	69.8	F1:9677	0.00E+00	3.44E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	85	104	TMT6plex; Mutation
P02671	FIBA_HUMAN	ADEAGSEADHEGTHS TKRGHA	Y	29.46	2620.26	21	3.7	525.1	5	13.6	F1:916	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.87E-05	604	624	TMT6plex
P02671	FIBA_HUMAN	DEAGSEADHEGTHST KRGHAKS	Y	30.27	2778.37	22	9.2	464.1	6	17.8	F1:1560	8.98E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	605	626	TMT6plex; Methyl ester

P02671	FIBA_HUMAN	MADEAGSEADHEGT HSTKRGHAKS	Y	32.96	2980.45	24	7	497.8	6	21.3	F1:2147	0.00E+00	0.00E+00	5.68E-05	0.00E+00	0.00E+00	0.00E+00	603	626	TMT6plex; Methyl ester
O00151	PDLI1_HUMAN	EILESEEEKGDPNKPSG	Y	33.41	2415.31	16	2.2	604.8	4	60.1	F1:8169	0.00E+00	7.52E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	221	236	TMT6plex
Q01518	CAP1_HUMAN	THKNPALKAQSGPV	Y	33.58	2134.28	14	2.4	534.6	4	34.2	F1:4159	0.00E+00	0.00E+00	0.00E+00	3.00E-05	0.00E+00	0.00E+00	280	293	TMT6plex
Q86UX7	URP2_HUMAN	DEAPGDPIQQLNLKG CEVV	Y	35.31	2632.36	19	-3.4	659.1	4	96.1	F1:14101	0.00E+00	6.25E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	392	410	TMT6plex; S- guanylation-2
P02671	FIBA_HUMAN	SYKMADEAGSEADH EGTHSTKRG	Y	36.34	3166.56	23	4.5	528.8	6	22.2	F2:2173	0.00E+00	3.50E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	600	622	TMT6plex; Oxidation
P02671	FIBA_HUMAN	ADEAGSEADHEGTHS GAEDSLADQAANEW	Y	37.32	1740.74	15	3.7	581.3	3	15.6	F1:1225	0.00E+00	7.01E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	604	618	TMT6plex
P0DJ18	SAA1_HUMAN	GRSGKDPNHF <sup>DE</sup> FRPAGL	Y	38.19	3749.86	31	1.1	751	5	96.4	F1:14145	0.00E+00	2.64E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	90	120	TMT6plex
P02671	FIBA_HUMAN	DEAGSEADHEGTHST KRGHAKSRPV	Y	38.28	3345.74	25	3.2	479	7	22.2	F1:2276	0.00E+00	3.08E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	605	629	TMT6plex
P01024	CO3_HUMAN	SSK11HKIHWESASLL R	Y	38.55	2478.42	17	1.9	496.7	5	66.9	F1:9224	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.19E-04	0.00E+00	1304	1320	TMT6plex
P02679	FIBG_HUMAN	AIQLTYNPDESSKPN MIDAATL	Y	38.95	2849.49	22	1.3	950.8	3	125	F1:19618	2.36E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	89	110	TMT6plex
Q15942	ZYX_HUMAN	TQPRGPPASSPAPAPK	Y	39.72	2016.15	16	2.1	505	4	29.2	F1:3396	0.00E+00	1.17E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	250	265	TMT6plex
Q9H4B7	TBB1_HUMAN	AKAVLEEDVEEVTEEA EMEPEDKGH	Y	41.06	3400.68	24	2	851.2	4	94.1	F1:13738	0.00E+00	0.00E+00	0.00E+00	3.38E-05	0.00E+00	0.00E+00	428	451	TMT6plex
P02671	FIBA_HUMAN	NTKESSSHHPGIAEFP SRG	Y	42.05	2266.13	19	2.1	567.5	4	24.7	F1:2661	0.00E+00	0.00E+00	0.00E+00	3.95E-05	0.00E+00	0.00E+00	556	574	TMT6plex
P02671	FIBA_HUMAN	EEVSGNVSPGTRREY HTE	Y	43.16	2275.1	18	4.2	569.8	4	26.2	F1:2899	0.00E+00	2.84E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	414	431	TMT6plex
P02671	FIBA_HUMAN	MADEAGSEADHEGT HSTKRGHA	Y	43.53	2751.3	22	2.1	551.3	5	18.5	F1:1675	0.00E+00	0.00E+00	0.00E+00	0.00E+00	6.10E-05	0.00E+00	603	624	TMT6plex
P62328	TYB4_HUMAN	KNPLPSKETIEQEKQA GES	Y	44.49	3028.72	19	-3.1	606.7	5	70	F1:9699	0.00E+00	0.00E+00	0.00E+00	1.12E-04	0.00E+00	0.00E+00	26	44	TMT6plex
P0DJ18	SAA1_HUMAN	GAEDSLADQAANEW GRSGKDPNH	Y	46.17	2882.39	23	2.4	721.6	4	77.2	F1:10853	0.00E+00	9.07E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	90	112	TMT6plex
P02671	FIBA_HUMAN	MLGEFVSETESRGSE SGIFTNTKESSSHHPGI AEFPSRG	Y	46.36	4639.27	39	2.6	774.2	6	106	F1:15906	0.00E+00	0.00E+00	7.19E-05	0.00E+00	0.00E+00	0.00E+00	536	574	TMT6plex
P00488	F13A_HUMAN	TAFGGRRVPPNNSN AAEDDLPTVELQGVV PR	Y	47.65	3575.86	32	4.2	895	4	90.1	F2:12316	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.14E-05	7	38	TMT6plex
P02675	FIBB_HUMAN	GHRPLDKKREEAPSL RPAPPISGGGY	Y	51.56	3569.02	27	4.4	595.8	6	56.6	F2:7161	0.00E+00	5.75E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	45	71	TMT6plex
Q14624	ITIH4_HUMAN	SSRQLGLPGPPDVPD HAAYHPF	Y	53.62	2586.32	22	3.4	647.6	4	85.2	F1:12205	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.87E-05	0.00E+00	666	687	TMT6plex
P00488	F13A_HUMAN	VPPNNSNAEEDDLPT VELQGVVPR	Y	59.88	2759.43	24	4.1	920.8	3	110	F1:16769	0.00E+00	0.00E+00	4.35E-05	0.00E+00	0.00E+00	0.00E+00	15	38	TMT6plex

P02671	FIBA_HUMAN	SGSTGQWHSESGSFR PDSPGSGNARPNPD WGTF	Y	48.06	3804.71	34	2.5	952.2	4	80.5	F2:10729	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.69E-05	0.00E+00	380	413	TMT6plex
O00151	PDLI1_HUMAN	EILESEEKGDPNKPSG F	Y	46.09	2562.38	17	0.3	641.6	4	80.9	F2:10802	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.14E-05	0.00E+00	221	237	TMT6plex
P62328	TYB4_HUMAN	QEKNPPLPSKETIEQEK QAGES	Y	39.43	3039.63	21	1.3	760.9	4	77.5	F2:10266	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.43E-05	0.00E+00	24	44	Pyro-glu from Q; TMT6plex
P60709	ACTB_HUMAN	DDDIAALVVDNG	Y	33.6	1257.57	12	7.3	629.8	2	161	F1:26888	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.37E-05	0.00E+00	2	13	Acetylation
P02671	FIBA_HUMAN	DGHKEVTKEV	Y	30.44	1828.07	10	1.3	458	4	31.3	F1:3720	0.00E+00	4.73E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	473	482	TMT6plex
Q8WZ42	TITIN_HUMAN	AVPLKFFV	Y	24.87	1015.66	7	-9.3	508.8	2	137	F2:21131	5.01E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	12039	12045	TMT6plex; Methyl ester
P04632	CPNS1_HUMAN	FRRLFAQ	Y	23.74	936.529	7	7.4	469.3	2	130	F2:19846	5.22E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	101	107	
P02671	FIBA_HUMAN	SYKMADEAGSEADH EGTHSTKT	Y	21.27	2809.32	22	2.3	562.9	5	40.2	F1:5054	0.00E+00	0.00E+00	0.00E+00	6.26E-05	0.00E+00	0.00E+00	600	621	TMT6plex; Mutation
P02671	FIBA_HUMAN	DEAGSEADHEGTHST KR	Y	21.17	2284.11	17	4.6	457.8	5	11.8	F1:653	0.00E+00	3.86E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	605	621	TMT6plex
P02671	FIBA_HUMAN	HRHPDEAAF	Y	21.09	1307.66	9	6.8	436.9	3	14.1	F2:1032	4.80E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	511	519	TMT6plex
PODJ18	SAA1_HUMAN	SGKDPNHFPA	Y	19.25	1682.93	11	3.5	421.7	4	26.1	F1:2870	0.00E+00	4.42E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	106	116	TMT6plex
P25391	LAMA1_HUMAN	LINGR	N	18.9	800.507	5	4.5	401.3	2	103	F1:15354	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.34E-04	201	205	TMT6plex
Q9Y4K4	M4K5_HUMAN	KRAIPPP	Y	18.7	1006.65	7	-1.1	504.3	2	111	F1:16968	1.08E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	385	391	TMT6plex
Q8N697	S15A4_HUMAN	APLLGARRA	Y	18.27	1152.73	9	2	577.4	2	116	F1:17954	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.27E-03	12	20	TMT6plex
Q17RW2	COOA1_HUMAN	ITIHCLNTPRWSTQT SGPGLP	Y	17.92	2722.43	23	-3.6	681.6	4	34.3	F1:4174	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.42E-05	0.00E+00	1617	1639	TMT6plex; Deamidation Carbamidometh ylation ; TMT6plex
P52565	GDIR1_HUMAN	IKISFRVNR	Y	17.8	1417.87	9	1.9	709.9	2	124	F1:19399	0.00E+00	0.00E+00	0.00E+00	5.29E-05	0.00E+00	0.00E+00	112	120	
Q9NYQ6	CELR1_HUMAN	NGRLL	N	17.66	800.507	5	7.2	401.3	2	102	F2:14313	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.43E-04	924	928	TMT6plex
Q658Y4	F91A1_HUMAN	SFLIE	N	17.2	836.485	5	0.6	419.2	2	63.8	F1:8740	0.00E+00	7.27E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	419	423	TMT6plex
Q13332	PTPRS_HUMAN	NGLIR	N	17.16	800.507	5	6.8	401.3	2	104	F2:14725	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.21E-04	454	458	TMT6plex
Q9NYQ6	CELR1_HUMAN	PAGRRTT	Y	16.9	986.582	7	7.9	494.3	2	124	F1:19423	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.70E-04	2301	2307	TMT6plex
Q6NUI2	GPAT2_HUMAN	KTLDD	N	15.88	817.511	5	1	409.8	2	84.9	F2:11478	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.24E-05	0.00E+00	206	210	TMT6plex
P68363	TBA1B_HUMAN	AALEK	N	15.81	988.632	5	6.6	495.3	2	99.1	F2:13871	0.00E+00	2.81E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	426	430	TMT6plex
Q9HC84	MUC5B_HUMAN	ANGSVLIN	N	15.71	830.507	6	-2.1	416.3	2	120	F1:18616	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.13E-04	146	151	TMT6plex
Q05682	CALD1_HUMAN	GKRLE	N	15.57	1059.68	5	-5.9	530.8	2	106	F1:15993	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.14E-02	533	537	TMT6plex
Q5K4L6	S27A3_HUMAN	LPALRAM	Y	15.41	999.61	7	8.6	500.8	2	110	F1:16755	6.97E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	279	285	TMT6plex
P11509	CP2A6_HUMAN	GKLPPGPTP	Y	15.3	1320.82	9	5	661.4	2	117	F2:17302	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.98E-05	0.00E+00	31	39	TMT6plex
Q8WZ42	TITIN_HUMAN	FTKKLTKM	Y	15.23	1912.24	8	1.2	957.1	2	135	F2:20896	0.00E+00	0.00E+00	0.00E+00	5.19E-05	0.00E+00	0.00E+00	6166	6173	TMT6plex
PODJ19	SAA2_HUMAN	SGRDPNHFPAAGLPE	Y	15.33	1877.97	15	6.8	470.5	4	36.5	F2:4239	0.00E+00	5.29E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	106	120	TMT6plex
A7E2Y1	MYH7B_HUMAN	EALRLKKKMEGDL	N	15.4	2446.51	13	9.1	490.3	5	186	F2:29563	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.21E-04	1617	1629	TMT6plex

Q86WI1	PKHL1_HUMAN	VERSAFPVHHVAFVS SLLVITQPVAAQPGQP FPQQ	Y	16.4	4013.13	35	7.1	803.6	5	81.4	F2:10897	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.30E-05	0.00E+00	4067	4101	TMT6plex; Deamidation
Q6V1X1	DPP8_HUMAN	APHDFM	Y	16.45	945.458	6	9.7	473.7	2	120	F2:17971	4.86E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	79	84	TMT6plex
Q9H3T3	SEM6B_HUMAN	ASSSLLLLAPARAPEQ PPAPGEPTPD	Y	16.69	2810.5	26	-5.9	937.8	3	65.7	F2:8483	0.00E+00	4.79E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	746	771	TMT6plex
Q9C0J8	WDR33_HUMAN	SFRRGAPP	Y	16.89	1115.64	8	0.3	558.8	2	167	F1:28047	7.09E-06	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1103	1110	TMT6plex
P35749	MYH11_HUMAN	SKIFF	N	17.81	1098.68	5	2.8	550.4	2	120	F1:18602	0.00E+00	2.88E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	766	770	TMT6plex
O95996	APC2_HUMAN	LPPLRHL	Y	19.15	1073.69	7	3.7	537.9	2	151	F1:24776	0.00E+00	0.00E+00	5.97E-05	0.00E+00	0.00E+00	0.00E+00	758	764	TMT6plex
P68363	TBA1B_HUMAN	PTVVPGG	N	19.79	854.507	7	4.8	428.3	2	112	F1:17110	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.34E-04	360	366	TMT6plex
Q92502	STAR8_HUMAN	GVPLIHV	Y	21.19	1059.66	8	8.3	530.8	2	117	F1:18027	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.43E-03	571	578	TMT6plex
Q8WZ42	TITIN_HUMAN	GVYSVIAR	Y	22.26	1073.68	8	9.6	537.9	2	151	F1:24775	0.00E+00	0.00E+00	5.97E-05	0.00E+00	0.00E+00	0.00E+00	9828	9835	Myristoylation
P0DJ18	SAA1_HUMAN	SGKDPNHF	Y	22.96	1358.73	8	6.8	453.9	3	24.1	F2:2486	0.00E+00	2.31E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	106	113	TMT6plex
P02671	FIBA_HUMAN	DEAGSEADHEGTHST KRGHA	Y	34.83	2549.23	20	6.6	425.9	6	10.7	F2:490	0.00E+00	4.89E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	605	624	TMT6plex
O95810	SDPR_HUMAN	GAVEGKEELPDENKS LEE	Y	30.6	2659.42	18	1.2	665.9	4	68.3	F2:8866	0.00E+00	5.39E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	178	195	TMT6plex
P02671	FIBA_HUMAN	SESGIFTNTKESSSHH PG	Y	19.46	2359.18	18	-1.4	590.8	4	41	F1:5158	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.88E-05	549	566	TMT6plex
P0C0L4	CO4A_HUMAN	DDPDAPLQPVTPLKL FEG	Y	18.33	2180.16	18	-4.8	727.7	3	175	F2:28184	0.00E+00	5.37E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1429	1446	TMT6plex; Mutation
Q4G0P3	HYDIN_HUMAN	SKLFF	N	17.81	1098.68	5	2.8	550.4	2	120	F1:18602	0.00E+00	2.88E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	396	400	TMT6plex
Q8TEM1	PO210_HUMAN	TLSVLLAA	Y	15.2	1015.65	8	5.5	508.8	2	135	F2:20864	8.63E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	12	19	TMT6plex
P02675	FIBB_HUMAN	GVNDNEEGFF	Y	46.14	1355.62	10	0.8	678.8	2	103	F1:15417	2.73E-04	2.77E-04	4.23E-04	2.86E-04	2.08E-04	3.17E-04	32	41	TMT6plex
Q58FF3	ENPLL_HUMAN	DEDDKTVLDL	Y	16.8	1619.87	10	3.6	810.9	2	94.9	F1:13885	1.65E-04	2.91E-03	3.26E-04	3.10E-04	2.37E-04	1.90E-04	343	352	TMT6plex
Q8WZ42	TITIN_HUMAN	VVIGRPGPV	Y	20.06	906.565	9	-3.7	454.3	2	86.2	F2:11680	3.69E-04	0.00E+00	2.54E-03	0.00E+00	0.00E+00	5.28E-04	29663	29671	Methyl ester
P02671	FIBA_HUMAN	ELERPGGNEITRGGST SY	Y	18.64	2151.08	18	2.6	718	3	49.1	F1:6419	4.63E-04	4.98E-05	1.02E-04	1.09E-04	1.16E-04	0.00E+00	260	277	TMT6plex
O43749	OR1F1_HUMAN	LNVLHTLL	Y	18.26	1263.81	9	-8.3	632.9	2	116	F1:17971	7.36E-05	0.00E+00	0.00E+00	4.12E-05	0.00E+00	2.29E-03	154	162	TMT6plex
Q6ZVN8	RGMC_HUMAN	GRFSR	N	16.22	850.498	5	1.5	426.3	2	57.6	F1:7769	8.19E-04	1.48E-04	3.40E-04	2.34E-04	1.55E-04	3.20E-04	152	156	TMT6plex
P14618	KPYM_HUMAN	GIMVAR	Y	17.34	874.526	6	8.1	438.3	2	88.7	F1:12802	1.56E-04	1.25E-04	0.00E+00	4.17E-05	0.00E+00	9.03E-05	289	294	TMT6plex
P02675	FIBB_HUMAN	NDNEEGFF	Y	40.85	1199.53	8	3.9	600.8	2	95.2	F2:13206	1.43E-03	1.30E-04	1.82E-03	1.15E-03	3.92E-04	2.32E-04	34	41	TMT6plex
P02675	FIBB_HUMAN	EEAPSLRPAPPISGG G	Y	41.01	1875.99	17	2.3	939	2	56.1	F1:7507	2.54E-04	2.02E-03	3.31E-04	2.29E-04	2.72E-04	3.92E-04	54	70	TMT6plex; Hydroxylation
Q14957	NMDE3_HUMAN	RVHPPGV	Y	15.69	989.597	7	2.4	495.8	2	90.8	F2:12419	1.59E-04	0.00E+00	4.12E-05	0.00E+00	5.62E-05	0.00E+00	318	324	TMT6plex
P07437	TBB5_HUMAN	DEHGIDPT	Y	27.49	1111.53	8	4.6	556.8	2	24.7	F2:2583	2.58E-04	5.97E-04	2.11E-04	2.51E-04	2.24E-04	2.31E-04	26	33	TMT6plex
P02671	FIBA_HUMAN	FTSSTSYNRGDSTFES KS	Y	39.52	2458.2	18	1.6	820.4	3	61.9	F1:8453	3.32E-04	1.05E-03	0.00E+00	1.85E-04	1.98E-04	8.40E-05	583	600	TMT6plex
Q9H6A9	PCX3_HUMAN	GHLPRV	Y	17.53	906.56	6	1.1	454.3	2	86.8	F1:12463	2.18E-04	0.00E+00	1.97E-03	0.00E+00	0.00E+00	3.46E-04	1433	1438	TMT6plex

O14514	BAI1_HUMAN	LGPDSKP	Y	18.71	1170.7	7	4.5	586.4	2	103	F1:15383	1.02E-04	2.39E-04	1.48E-04	2.03E-04	1.50E-04	2.84E-04	1514	1520	TMT6plex
Q9Y286	SIGL7_HUMAN	RDRFHLL	Y	16.25	1184.7	7	-1.4	593.4	2	84.2	F1:12019	1.93E-04	2.44E-04	2.87E-03	2.73E-04	1.93E-04	2.42E-04	92	98	TMT6plex
Q9NQ36	SCUB2_HUMAN	GKCSL	N	15.59	964.578	5	-9.8	483.3	2	80.6	F1:11426	1.00E-04	4.52E-05	5.21E-04	7.45E-05	4.39E-06	1.43E-04	498	502	TMT6plex
Q8IZS8	CA2D3_HUMAN	GKCSI	N	15.59	964.578	5	-9.8	483.3	2	80.6	F1:11426	1.00E-04	4.52E-05	5.21E-04	7.45E-05	4.39E-06	1.43E-04	843	847	TMT6plex
P08582	TRFM_HUMAN	APLLPLLLPA	Y	27.33	1245.83	10	-9.8	623.9	2	110	F2:16029	5.95E-05	2.83E-05	7.63E-05	5.56E-05	5.54E-05	1.31E-04	719	728	TMT6plex
P52566	GDIR2_HUMAN	NYKPPP	Y	20.46	1173.68	6	3.4	587.8	2	37	F2:4330	5.92E-04	1.03E-03	1.02E-03	8.74E-04	9.18E-04	1.56E-03	23	28	TMT6plex; Deamidation
O95810	SDPR_HUMAN	QEKPSPPMPSPSTPS PSLNLG	Y	34.67	2436.2	22	4.5	813.1	3	98.6	F2:13783	0.00E+00	4.97E-05	0.00E+00	5.78E-05	0.00E+00	5.93E-05	20	41	Pyro-glu from Q; TMT6plex
Q5HYW3	RGAG4_HUMAN	GHRAAR	Y	17.41	895.53	6	1.9	448.8	2	35.8	F2:4132	4.10E-04	1.28E-03	5.36E-04	4.68E-04	3.37E-04	6.20E-04	559	564	TMT6plex
P12259	FA5_HUMAN	SQFLIKT	Y	26.69	1293.81	7	0.8	647.9	2	76.7	F1:10768	1.60E-03	1.13E-03	1.83E-03	1.87E-03	9.95E-04	4.28E-04	1023	1029	TMT6plex
P01024	CO3_HUMAN	IHWESASLL	Y	41.49	1283.71	9	2.1	642.9	2	107	F1:16037	2.79E-04	5.03E-04	6.13E-04	4.74E-04	1.29E-03	4.50E-04	1311	1319	TMT6plex
P0DJJ8	SAA1_HUMAN	DMREANYIGSD	N	32.75	1498.69	11	1.6	750.4	2	56.4	F1:7572	2.40E-04	2.74E-03	3.80E-04	3.42E-04	2.86E-04	3.62E-04	41	51	TMT6plex
P02656	APOC3_HUMAN	SEAEDASLL	Y	27.29	1162.59	9	2.1	582.3	2	80.8	F1:11453	2.06E-04	2.71E-04	2.51E-04	2.77E-04	2.13E-04	3.95E-04	21	29	TMT6plex
P0C0L4	CO4A_HUMAN	GFKSHALQLNNRQI	Y	44.9	2083.21	14	3.7	521.8	4	58.2	F1:7869	4.50E-05	9.72E-05	1.05E-04	1.06E-04	4.22E-05	5.87E-06	1338	1351	TMT6plex
Q9UL54	TAOK2_HUMAN	PTHLRP	Y	21.31	948.571	6	0.4	475.3	2	86.1	F1:12347	6.83E-05	1.22E-04	2.79E-04	6.30E-05	1.03E-04	1.18E-04	932	937	TMT6plex
P02452	CO1A1_HUMAN	DGPAGAPGTPGPQG	Y	23.92	1422.69	14	2	712.4	2	36	F1:4447	3.26E-04	6.54E-04	2.82E-04	5.36E-04	4.83E-04	5.87E-04	940	953	TMT6plex; Hydroxylation
P49281	NRAM2_HUMAN	ILVLIICS	Y	17.39	1101.7	8	-9.4	551.9	2	153	F2:24400	3.31E-06	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.12E-04	482	489	TMT6plex
P02452	CO1A1_HUMAN	GERGFPGERGVQGGP GPA	Y	20.83	2010.01	18	-0.2	671	3	34.9	F1:4266	7.49E-05	1.33E-04	8.00E-05	1.29E-04	1.04E-04	1.09E-04	677	694	TMT6plex; Deamidation ; Hydroxylation
Q2LD37	K1109_HUMAN	EGSAK	N	17.97	948.565	5	2.2	475.3	2	73	F1:10175	9.85E-05	8.86E-05	4.29E-04	1.05E-04	7.58E-05	1.10E-04	794	798	TMT6plex
Q8N3K9	CMYA5_HUMAN	VPTNK	Y	16.08	1015.64	5	8.8	508.8	2	136	F1:21815	1.04E-03	0.00E+00	0.00E+00	0.00E+00	3.56E-05	0.00E+00	161	165	TMT6plex
Q9BT22	ALG1_HUMAN	GPRVF	N	18.13	803.486	5	5.4	402.8	2	127	F1:20162	2.02E-03	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.03E-05	97	101	TMT6plex
O75914	PAK3_HUMAN	KPPAPPLR	Y	29.76	1103.7	8	3.3	552.9	2	98.5	F2:13767	0.00E+00	3.56E-05	0.00E+00	5.33E-05	3.33E-05	0.00E+00	10	17	TMT6plex
P68363	TBA1B_HUMAN	NVDLTEFQ	N	32.99	1193.61	8	1.3	597.8	2	100	F1:14834	2.32E-04	1.57E-04	1.06E-04	1.59E-04	3.26E-04	1.79E-04	249	256	TMT6plex
P0C0L4	CO4A_HUMAN	EELQFS	Y	23.58	980.502	6	1.9	491.3	2	77	F1:10827	1.50E-04	2.86E-04	2.43E-04	2.30E-04	2.19E-04	5.25E-04	1356	1361	TMT6plex
P02671	FIBA_HUMAN	KQFTSSTSYNRGDSTF ES	Y	32.79	2499.23	18	7.5	834.1	3	56.3	F2:7094	4.67E-04	2.24E-04	5.58E-04	5.04E-04	2.42E-04	1.07E-04	581	598	TMT6plex
P02671	FIBA_HUMAN	EGDFLAEGG	Y	29.4	1122.54	9	-2.7	562.3	2	81.9	F1:11636	1.66E-04	2.80E-04	2.59E-04	2.66E-04	1.73E-04	1.30E-04	24	32	TMT6plex
P0C0L4	CO4A_HUMAN	FSLGSKINV	Y	35.38	1421.86	9	2.4	711.9	2	102	F1:15080	1.81E-03	1.87E-03	2.03E-03	2.48E-03	1.02E-03	5.30E-04	1360	1368	TMT6plex
P10124	SRGN_HUMAN	DRNLPSDSQDLGQHG	Y	39.12	1866.9	15	0.4	623.3	3	34.9	F1:4279	1.17E-04	1.70E-04	9.80E-05	1.39E-04	1.05E-04	5.72E-04	137	151	TMT6plex
P01009	A1AT_HUMAN	EDPQGDAAQKTD	Y	37.62	1731.87	12	5.4	578.3	3	32.1	F1:3834	2.77E-04	4.25E-04	5.68E-04	4.53E-04	4.40E-04	6.58E-04	25	36	TMT6plex
P14618	KPYM_HUMAN	SKPHSEAGTAFIQT	Y	35.38	1743.9	14	1.6	873	2	57.7	F1:7781	5.74E-04	4.52E-04	1.28E-04	3.53E-04	2.18E-04	1.98E-04	2	15	Acetylation ; TMT6plex
P0DJJ8	SAA1_HUMAN	DPNHFRPAGLPE	N	41.97	1577.82	12	3.1	789.9	2	55.6	F2:7000	1.55E-04	6.22E-03	5.55E-04	1.09E-03	1.57E-04	9.62E-05	109	120	TMT6plex
P00488	F13A_HUMAN	EDDLPTVE	Y	34.08	1145.57	8	3	573.8	2	74.9	F1:10482	2.33E-04	3.58E-04	2.30E-04	2.39E-04	3.00E-04	6.53E-04	24	31	TMT6plex

P02675	FIBB_HUMAN	NDNEEGFFSA	Y	36.03	1357.6	10	2.8	679.8	2	94.4	F1:13794	4.17E-04	3.79E-04	1.49E-04	2.21E-04	2.17E-04	2.68E-04	34	43	TMT6plex
Q96MT0	YJ006_HUMAN	GRSASVRV	Y	16.61	1059.64	8	6.5	530.8	2	74.2	F2:9760	5.06E-05	1.08E-04	4.50E-05	3.72E-05	1.23E-04	1.42E-04	16	23	TMT6plex
PODJ18	SAA1_HUMAN	NHFRPA	N	28.32	970.519	6	2.1	486.3	2	18.7	F1:1700	2.57E-04	3.30E-03	4.28E-04	8.12E-04	1.55E-04	2.11E-04	111	116	TMT6plex; Deamidation
PODJ19	SAA2_HUMAN	DQAANKWG	Y	30.58	1346.73	8	4	674.4	2	48.6	F1:6333	8.36E-04	8.49E-03	1.04E-03	1.77E-03	7.78E-04	6.84E-04	97	104	TMT6plex
P13611	CSPG2_HUMAN	RLGEPNYGAEIRGFST GFPLEEDF	Y	18.53	2929.44	24	3.8	733.4	4	87.3	F1:12563	0.00E+00	8.96E-05	0.00E+00	5.19E-06	0.00E+00	0.00E+00	1911	1934	TMT6plex
Q14624	ITIH4_HUMAN	QGAKIPKPEASFSR	Y	15.68	2299.36	15	4.4	767.5	3	55.4	F1:7392	1.33E-04	9.66E-05	3.54E-04	2.90E-04	3.65E-04	1.78E-04	630	644	TMT6plex
Q5QNW6	H2B2F_HUMAN	PDKAKSAPAPK	Y	16.79	1765.07	11	-1.6	589.4	3	37	F1:4606	9.93E-04	2.95E-04	3.39E-04	4.68E-04	3.29E-04	1.82E-04	2	12	TMT6plex
Q8IVU1	IGDC3_HUMAN	TPPVRT	Y	17.62	1011.63	7	2.6	506.8	2	59.1	F1:8007	4.01E-04	6.79E-04	1.26E-03	7.75E-04	9.25E-04	1.48E-03	68	74	TMT6plex
Q9NZJ4	SACS_HUMAN	YATLI	N	18.17	808.49	5	-5.2	405.3	2	60.2	F1:8199	1.43E-04	2.40E-04	2.82E-04	2.93E-04	1.58E-04	5.05E-04	505	509	TMT6plex
Q9Y4A5	TRRAP_HUMAN	YATLL	N	18.17	808.49	5	-5.2	405.3	2	60.2	F1:8199	1.43E-04	2.40E-04	2.82E-04	2.93E-04	1.58E-04	5.05E-04	1835	1839	TMT6plex
Q9C0A6	SETD5_HUMAN	YATII	N	18.17	808.49	5	-5.2	405.3	2	60.2	F1:8199	1.43E-04	2.40E-04	2.82E-04	2.93E-04	1.58E-04	5.05E-04	58	62	TMT6plex
P02671	FIBA_HUMAN	DEAGSEADHEGTHST KRG	Y	33.6	2341.13	18	5.2	586.3	4	12.4	F1:729	0.00E+00	6.03E-05	0.00E+00	3.85E-05	0.00E+00	1.63E-04	605	622	TMT6plex
P68363	TBA1B_HUMAN	VDSVEGEGEEEEGEE	Y	24.06	1721.73	14	5	861.9	2	58.3	F1:7879	2.98E-04	4.62E-04	3.35E-04	6.11E-04	4.07E-04	3.29E-04	437	450	TMT6plex
Q9NR99	MXRA5_HUMAN	GSRSLPRG	Y	19.38	1057.62	8	1.4	529.8	2	75.7	F1:10605	0.00E+00	1.01E-04	1.47E-04	1.04E-04	1.14E-04	1.54E-04	1582	1589	TMT6plex
Q5H8C1	FREM1_HUMAN	YHGIV	N	15.03	816.47	5	8.9	409.2	2	31.9	F1:3805	1.28E-04	1.56E-04	4.22E-04	6.72E-04	1.94E-04	2.83E-04	1949	1953	TMT6plex
O15061	SYNEM_HUMAN	YHGLV	N	15.03	816.47	5	8.9	409.2	2	31.9	F1:3805	1.28E-04	1.56E-04	4.22E-04	6.72E-04	1.94E-04	2.83E-04	1326	1330	TMT6plex
P02671	FIBA_HUMAN	NRGDSTFESK	Y	32.14	1597.85	10	4.6	533.6	3	23.5	F2:2401	6.36E-04	2.68E-04	6.85E-04	5.10E-04	3.78E-04	3.25E-04	590	599	TMT6plex
Q9H7N4	SFR19_HUMAN	AATSDK	N	15.91	1049.61	6	7.5	525.8	2	85.3	F1:12217	5.76E-05	8.15E-05	7.44E-05	1.06E-04	4.88E-05	1.21E-04	1186	1191	TMT6plex
P55198	AF17_HUMAN	SKSPPG	N	16.3	1029.62	6	9.3	515.8	2	88	F2:11999	7.13E-05	7.08E-05	5.44E-05	4.76E-05	8.24E-05	0.00E+00	794	799	TMT6plex
Q9Y520	PRC2C_HUMAN	PPPHRPL	Y	21.93	1041.63	7	0.3	521.8	2	86	F1:12336	5.47E-05	5.65E-05	1.17E-04	1.29E-04	4.56E-05	1.49E-04	711	717	TMT6plex
Q14191	WRN_HUMAN	LGSLK	N	20.11	974.653	5	3.9	488.3	2	55.2	F1:7362	1.03E-03	1.30E-03	1.98E-03	4.11E-03	1.73E-03	1.06E-03	687	691	TMT6plex
P21359	NF1_HUMAN	LGSIK	N	20.11	974.653	5	3.9	488.3	2	55.2	F1:7362	1.03E-03	1.30E-03	1.98E-03	4.11E-03	1.73E-03	1.06E-03	2023	2027	TMT6plex
Q01484	ANK2_HUMAN	IGSIK	N	20.11	974.653	5	3.9	488.3	2	55.2	F1:7362	1.03E-03	1.30E-03	1.98E-03	4.11E-03	1.73E-03	1.06E-03	1763	1767	TMT6plex
Q9Y6X0	SETBP_HUMAN	IGSLK	N	20.11	974.653	5	3.9	488.3	2	55.2	F1:7362	1.03E-03	1.30E-03	1.98E-03	4.11E-03	1.73E-03	1.06E-03	845	849	TMT6plex
PODJ18	SAA1_HUMAN	DAAKKGF <sup>GGV</sup> WAAE A	Y	33.44	1913.05	15	7.8	638.7	3	56.2	F1:7526	1.39E-04	1.28E-03	2.19E-04	1.84E-04	1.92E-04	2.44E-04	61	75	TMT6plex
P0C0L4	CO4A_HUMAN	DDPDAPLQPVTP	Y	50.23	1492.76	12	9.1	747.4	2	83	F1:11798	1.37E-04	5.89E-04	2.37E-04	3.23E-04	3.72E-04	7.41E-04	1429	1440	TMT6plex
P63241	IF5A1_HUMAN	DSGEVREDLRLPEGD LG	Y	50.19	2085.05	17	-3.2	696	3	81.7	F1:11594	3.75E-04	5.31E-04	1.68E-04	3.60E-04	8.83E-04	3.51E-04	104	120	TMT6plex
P35749	MYH11_HUMAN	STVEAL	N	20.04	847.485	6	3.6	424.8	2	69.1	F1:9571	1.89E-04	2.32E-04	3.86E-04	2.93E-04	2.60E-04	4.82E-04	1385	1390	TMT6plex
P01024	CO3_HUMAN	ESASLL	N	21.61	847.485	6	3.6	424.8	2	69.2	F1:9572	1.89E-04	2.32E-04	3.86E-04	2.93E-04	2.60E-04	4.82E-04	1314	1319	TMT6plex
P62328	TYB4_HUMAN	SDKPDMAEIEKFD	Y	46.45	2024.02	13	1.8	1013	2	106	F1:15912	1.55E-03	5.99E-03	7.82E-04	9.87E-04	2.47E-03	2.91E-04	2	14	Acetylation ; TMT6plex
P0C0L4	CO4A_HUMAN	DDPDAPLQP	Y	38.97	1195.59	9	4.9	598.8	2	62.7	F2:8017	2.22E-04	3.25E-04	2.70E-04	2.60E-04	2.47E-04	9.51E-04	1429	1437	TMT6plex
P02675	FIBB_HUMAN	DNEEGFFSA	Y	34.9	1243.56	9	1.9	622.8	2	97	F1:14259	5.95E-04	2.63E-04	1.82E-04	2.48E-04	2.70E-04	1.74E-04	35	43	TMT6plex



Q9Y3L3	3BP1_HUMAN	VPTPAT	Y	15.98	813.48	6	-3.5	407.7	2	119	F1:18540	0.00E+00	3.31E-05	0.00E+00	0.00E+00	2.83E-06	0.00E+00	504	509	TMT6plex
P00488	F13A_HUMAN	AEDDLPTVELQGVVPR	Y	44.35	1966.06	16	-2.6	656.4	3	108	F1:16344	0.00E+00	5.59E-05	7.57E-05	5.80E-05	0.00E+00	0.00E+00	23	38	TMT6plex
P02671	FIBA_HUMAN	SKQFTSSTSYNRGDSTFES	Y	34.68	2586.26	19	1.2	863.1	3	55.9	F1:7480	4.06E-04	2.21E-04	3.26E-04	4.23E-04	1.85E-04	0.00E+00	580	598	TMT6plex
Q5VZ19	TDR10_HUMAN	TSKRPP	Y	15.82	1142.72	6	-2.7	572.4	2	117	F1:18094	0.00E+00	0.00E+00	1.35E-03	3.97E-05	3.19E-05	4.94E-05	104	109	TMT6plex
Q76KX8	ZN534_HUMAN	TAHLVIH	Y	15.51	1018.61	7	-2.9	510.3	2	37	F2:4327	1.65E-03	1.19E-03	6.49E-04	8.66E-04	1.02E-03	8.08E-04	327	333	TMT6plex
Q00973	B4GN1_HUMAN	AHIPVR	Y	15.26	920.576	6	-0.4	461.3	2	107	F1:16086	7.03E-05	0.00E+00	4.33E-04	5.03E-05	8.68E-05	0.00E+00	61	66	TMT6plex
Q14669	TRIPC_HUMAN	SSTVPPGA	Y	15.07	943.518	8	0	472.8	2	38.7	F2:4557	2.61E-04	4.66E-04	3.64E-04	3.48E-04	6.19E-04	3.82E-04	213	220	TMT6plex
P07951	TPM2_HUMAN	VKEAQ	N	15.23	1031.64	5	6.2	516.8	2	95.9	F2:13310	5.69E-06	0.00E+00	1.26E-03	0.00E+00	0.00E+00	1.27E-04	64	68	TMT6plex
Q8WXI7	MUC16_HUMAN	PVSKPG	Y	17.05	1041.66	6	7.1	521.8	2	113	F1:17408	2.19E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.30E-03	21266	21271	TMT6plex
A4UGR9	XIRP2_HUMAN	KSNRR	N	15.47	888.546	5	1.2	445.3	2	90	F1:13011	7.05E-05	3.35E-05	0.00E+00	5.24E-04	3.71E-05	0.00E+00	3174	3178	TMT6plex
Q15942	ZYX_HUMAN	HVQPQPQPKPQVQLHVQSQT	Y	46.7	2761.54	20	3.2	921.5	3	42.5	F2:5051	0.00E+00	7.02E-05	0.00E+00	6.04E-05	1.02E-04	0.00E+00	223	242	TMT6plex
Q14624	ITIH4_HUMAN	QLGLPGPPDVPD	Y	21.08	1186.59	12	1.6	594.3	2	145	F1:23658	2.66E-04	2.88E-05	0.00E+00	0.00E+00	0.00E+00	6.53E-05	669	680	Pyro-glu from Q
P62328	TYB4_HUMAN	TQEKNPLPSKETIEQEKQAGES	Y	45.73	3387.85	22	6.1	678.6	5	73.1	F1:10187	0.00E+00	3.41E-05	0.00E+00	3.35E-06	0.00E+00	0.00E+00	23	44	TMT6plex; Deamidation
P68363	TBA1B_HUMAN	QLFHPEQLITGKEDANN	N	44.29	2236.13	18	2.9	746.4	3	116	F1:17845	1.28E-04	4.31E-04	0.00E+00	9.53E-05	1.15E-04	0.00E+00	85	102	Pyro-glu from Q; TMT6plex
O00763	ACACB_HUMAN	DLKAN	N	16.31	1017.62	5	6.8	509.8	2	94.2	F2:13020	0.00E+00	0.00E+00	2.78E-03	0.00E+00	0.00E+00	2.77E-04	303	307	TMT6plex
Q96RW7	HMCN1_HUMAN	YVRPRV	Y	17.3	1017.63	6	0.7	509.8	2	94.2	F2:13021	0.00E+00	0.00E+00	2.78E-03	0.00E+00	0.00E+00	2.77E-04	1069	1074	TMT6plex
P02671	FIBA_HUMAN	TSSTSYNRGDSTFES	Y	30.73	1866.84	15	3	934.4	2	41.9	F1:5284	9.15E-04	9.79E-04	7.72E-04	1.06E-03	7.19E-04	2.47E-04	584	598	TMT6plex
Q15942	ZYX_HUMAN	NFRPGDSEPPAPGAQRAQ	Y	29.8	2317.18	20	4.4	773.4	3	47.3	F2:5767	1.31E-04	1.57E-04	8.84E-05	1.68E-04	2.57E-04	8.67E-05	37	56	TMT6plex
Q5VST9	OBSCN_HUMAN	PGRHLPL	Y	15.23	1017.63	7	2	509.8	2	93.2	F2:12841	5.37E-05	5.34E-05	6.60E-04	3.55E-05	4.24E-05	1.44E-04	7400	7406	TMT6plex
P02671	FIBA_HUMAN	SYSKQFTSSTSYNRGDSTFES	Y	58.15	2836.36	21	4.6	946.5	3	66.6	F1:9171	1.45E-03	7.65E-04	1.68E-03	1.77E-03	6.77E-04	0.00E+00	578	598	TMT6plex
P56945	BCAR1_HUMAN	PRHLLAP	Y	17.18	1031.64	7	-3.2	516.8	2	104	F1:15463	0.00E+00	0.00E+00	3.31E-03	0.00E+00	0.00E+00	3.47E-04	237	243	TMT6plex
Q14624	ITIH4_HUMAN	QLGLPGPPDVPDHAA	Y	41.43	1711.91	15	0.7	857	2	85.6	F1:12264	3.50E-04	3.85E-04	4.78E-04	4.08E-04	6.56E-04	3.88E-04	669	683	TMT6plex
Q9Y490	TLN1_HUMAN	DDSKTVTDM	Y	21.92	1468.75	9	3.3	735.4	2	48.8	F2:6046	8.87E-04	5.02E-03	4.43E-04	7.40E-04	1.41E-03	2.72E-04	103	111	TMT6plex
Q8TAQ2	SMRC2_HUMAN	PPNLPVSMANPLHPN	Y	18.7	1825.97	15	4.7	609.7	3	76	F2:10037	4.55E-05	1.20E-04	0.00E+00	0.00E+00	0.00E+00	6.46E-05	1132	1146	TMT6plex
P54886	P5CS_HUMAN	DHVVSDF	Y	16.84	1046.52	7	0.9	524.3	2	57.4	F2:7293	7.08E-04	1.25E-03	4.58E-04	8.91E-04	1.09E-03	1.07E-03	768	774	TMT6plex
P51788	CLCN2_HUMAN	GSPPEAA	Y	20.08	953.502	8	-6.6	477.8	2	55.5	F1:7415	3.45E-04	3.30E-04	6.45E-04	4.83E-04	4.09E-04	8.27E-04	730	737	TMT6plex
Q14624	ITIH4_HUMAN	NFRPGVLS	Y	21.63	1117.64	8	4.1	559.8	2	57.2	F2:7270	2.21E-03	8.52E-04	1.20E-03	1.84E-03	3.15E-03	1.06E-03	659	666	TMT6plex
Q15942	ZYX_HUMAN	EPPPAPG	Y	24.16	892.486	7	2.8	447.3	2	30.7	F1:3629	3.05E-04	9.37E-04	3.23E-04	3.32E-04	2.26E-04	4.47E-04	45	51	TMT6plex
P60709	ACTB_HUMAN	VAPEEHPVLLTEAPLNP	Y	56.43	2411.38	18	4.3	804.8	3	83.4	F2:11241	3.90E-04	8.75E-04	1.22E-04	2.60E-04	4.88E-04	0.00E+00	96	113	TMT6plex

Q9NQC3	RTN4_HUMAN	DSPPRPQPAFKYQ	Y	15.34	2068.05	13	2.1	690.4	3	66.2	F1:9107	1.89E-04	4.87E-04	1.36E-04	3.21E-04	6.70E-04	2.36E-04	14	26	TMT6plex; Phosphorylation
P0DJJ8	SAA1_HUMAN	FGHGAEDSL	Y	38.25	1160.57	9	2.6	581.3	2	56	F1:7488	4.16E-04	1.54E-03	6.06E-04	9.17E-04	1.07E-03	1.56E-03	87	95	TMT6plex
Q9H0E3	SP130_HUMAN	QQHVI	N	15.1	852.502	5	6.1	427.3	2	75.5	F1:10578	1.17E-04	1.72E-04	3.88E-04	3.69E-04	1.53E-04	4.43E-04	839	843	TMT6plex
P42858	HD_HUMAN	QQHVL	N	15.1	852.502	5	6.1	427.3	2	75.5	F1:10578	1.17E-04	1.72E-04	3.88E-04	3.69E-04	1.53E-04	4.43E-04	2826	2830	TMT6plex
P26006	ITA3_HUMAN	PVINIVH	Y	16.41	1020.62	7	1.9	511.3	2	66.4	F1:9138	4.45E-04	2.60E-04	3.43E-04	4.51E-04	3.68E-04	3.77E-04	464	470	TMT6plex; Deamidation
P48634	PRC2A_HUMAN	EPPRRPPP	Y	19	1173.68	8	1.5	587.8	2	41.5	F1:5223	9.94E-04	2.02E-03	1.21E-03	1.45E-03	1.72E-03	1.90E-03	1705	1712	TMT6plex
P02671	FIBA_HUMAN	YNRGDSTFESKSY	Y	20.02	2011.01	13	1.3	671.3	3	54.2	F1:7194	5.84E-04	2.27E-04	2.92E-04	2.67E-04	3.68E-04	1.60E-04	589	601	TMT6plex
P0DJJ8	SAA1_HUMAN	HGAEDSLADQA	Y	41.06	1341.64	11	3.4	671.8	2	31.9	F1:3803	4.41E-04	8.47E-04	3.75E-04	5.11E-04	3.65E-04	3.90E-04	89	99	TMT6plex
O95235	KI20A_HUMAN	YLRVR	N	15.13	934.592	5	-1.1	468.3	2	97	F1:14256	6.65E-05	0.00E+00	1.51E-04	2.72E-05	0.00E+00	7.05E-05	68	72	TMT6plex
Q8TDW7	FAT3_HUMAN	YIRVR	N	15.13	934.592	5	-1.1	468.3	2	97	F1:14256	6.65E-05	0.00E+00	1.51E-04	2.72E-05	0.00E+00	7.05E-05	3536	3540	TMT6plex
P02671	FIBA_HUMAN	HTEKLVTSKGDKEL	Y	46.03	2500.5	14	5.1	501.1	5	47.3	F2:5754	1.57E-04	3.56E-05	0.00E+00	6.31E-05	0.00E+00	0.00E+00	429	442	TMT6plex
P42858	HD_HUMAN	LRNVH	N	16.13	866.529	5	-0.7	434.3	2	71.9	F1:10003	6.29E-04	5.92E-04	8.99E-04	3.96E-04	3.48E-04	8.91E-04	3133	3137	TMT6plex
Q86U10	LPP60_HUMAN	LHAAAR	N	17.24	866.529	6	-0.7	434.3	2	71.9	F1:10002	6.29E-04	5.92E-04	8.99E-04	3.96E-04	3.48E-04	8.91E-04	438	443	TMT6plex
Q8WZ42	TITIN_HUMAN	IRNVH	N	16.13	866.529	5	-0.7	434.3	2	71.9	F1:10003	6.29E-04	5.92E-04	8.99E-04	3.96E-04	3.48E-04	8.91E-04	3027	3031	TMT6plex
P07437	TBB5_HUMAN	DEHGIDPTG	Y	35.44	1168.56	9	0.4	585.3	2	30.3	F1:3560	4.72E-04	2.90E-04	2.26E-04	4.23E-04	3.72E-04	3.87E-04	26	34	TMT6plex
Q14624	ITIH4_HUMAN	YLQGAKIPKPEASFS P R	Y	39.14	2575.51	17	3.4	859.5	3	77.1	F1:10840	7.59E-05	9.23E-05	3.43E-04	4.26E-04	5.39E-04	0.00E+00	628	644	TMT6plex
Q05682	CALD1_HUMAN	DEEAKTTTTNT	Y	36.11	1667.86	11	3.4	834.9	2	26.6	F1:2964	8.90E-04	4.96E-03	4.80E-04	6.27E-04	1.44E-03	5.04E-04	76	86	TMT6plex
P0DJJ9	SAA2_HUMAN	DAAKRGGGAWAAE VISNA	Y	31.81	2298.25	19	2.1	767.1	3	90.3	F1:13077	1.09E-04	4.70E-04	0.00E+00	1.04E-04	1.01E-04	0.00E+00	61	79	TMT6plex
Q9HCU4	CELR2_HUMAN	SITLRLE	Y	15.46	1059.65	7	-9	530.8	2	76.1	F1:10674	5.86E-05	9.67E-05	2.40E-04	1.09E-04	1.94E-04	2.61E-04	1128	1134	TMT6plex
P02768	ALBU_HUMAN	DETYVPK	Y	31.56	1308.73	7	4.9	655.4	2	48.9	F1:6386	8.69E-04	1.37E-03	1.41E-03	1.93E-03	1.27E-03	1.15E-03	518	524	TMT6plex
P0DJJ9	SAA2_HUMAN	EDSLADQAANKWG	Y	50.88	1861.96	13	1.5	932	2	90.6	F1:13126	1.85E-04	4.20E-03	8.12E-04	1.46E-03	2.67E-04	1.68E-04	92	104	TMT6plex
P60709	ACTB_HUMAN	DESGPSIVH	Y	35.28	1168.59	9	3.7	585.3	2	34.5	F1:4209	9.31E-04	1.01E-03	3.61E-04	6.60E-04	5.76E-04	5.28E-04	363	371	TMT6plex
P02671	FIBA_HUMAN	DEAGSEADHEGT	Y	44.46	1445.61	12	3.7	723.8	2	17.6	F1:1517	1.35E-04	9.31E-04	1.28E-04	1.97E-04	1.52E-04	1.51E-04	605	616	TMT6plex
P51587	BRCA2_HUMAN	NIDKI	N	16.87	1059.67	5	1.2	530.8	2	55.8	F1:7456	5.08E-04	1.36E-03	1.51E-03	1.45E-03	2.31E-03	8.60E-04	978	982	TMT6plex
P42356	PI4KA_HUMAN	NDIKI	N	17.09	1059.67	5	1.2	530.8	2	55.8	F1:7455	5.08E-04	1.36E-03	1.51E-03	1.45E-03	2.31E-03	8.60E-04	476	480	TMT6plex
Q9UBG0	MRC2_HUMAN	NDLKL	N	17.09	1059.67	5	1.2	530.8	2	55.8	F1:7455	5.08E-04	1.36E-03	1.51E-03	1.45E-03	2.31E-03	8.60E-04	445	449	TMT6plex
P23634	AT2B4_HUMAN	NDLKI	N	17.09	1059.67	5	1.2	530.8	2	55.8	F1:7455	5.08E-04	1.36E-03	1.51E-03	1.45E-03	2.31E-03	8.60E-04	230	234	TMT6plex
Q6P3X3	TTC27_HUMAN	NDIKL	N	17.09	1059.67	5	1.2	530.8	2	55.8	F1:7455	5.08E-04	1.36E-03	1.51E-03	1.45E-03	2.31E-03	8.60E-04	324	328	TMT6plex
Q9P225	DYH2_HUMAN	NLDKL	N	16.87	1059.67	5	1.2	530.8	2	55.8	F1:7456	5.08E-04	1.36E-03	1.51E-03	1.45E-03	2.31E-03	8.60E-04	3905	3909	TMT6plex
Q8TDW7	FAT3_HUMAN	NLDKI	N	16.87	1059.67	5	1.2	530.8	2	55.8	F1:7456	5.08E-04	1.36E-03	1.51E-03	1.45E-03	2.31E-03	8.60E-04	4248	4252	TMT6plex
P01024	CO3_HUMAN	NEGFTVTAEG	Y	27.81	1252.61	10	-1.5	627.3	2	68.7	F1:9496	3.46E-04	3.36E-04	3.29E-04	3.88E-04	2.87E-04	4.89E-04	1327	1336	TMT6plex
P02671	FIBA_HUMAN	DSGEGDF	Y	19.25	954.413	7	-0.5	478.2	2	52.6	F2:6527	3.57E-04	4.17E-04	6.93E-04	5.29E-04	3.89E-04	1.29E-03	21	27	TMT6plex

Q8WZ42	TITIN_HUMAN	PGPPGKPMI	Y	16.29	1317.85	9	7.9	659.9	2	80.9	F1:11475	3.86E-04	5.55E-04	3.52E-04	3.83E-04	5.15E-04	6.09E-04	28684	28692	TMT6plex; Amidation
Q14624	ITIH4_HUMAN	NVHSGSTF	Y	46.48	1077.53	8	3.3	539.8	2	33	F1:3985	3.05E-04	3.34E-04	5.58E-04	4.80E-04	7.47E-04	3.21E-04	617	624	TMT6plex; Deamidation
P0DJ18	SAA1_HUMAN	DPNHF	N	18.85	857.424	5	2	429.7	2	28.2	F1:3236	2.53E-04	2.33E-03	4.21E-04	4.36E-04	2.13E-04	6.23E-04	109	113	TMT6plex
P07951	TPM2_HUMAN	NDITSL	Y	24.36	891.475	6	1.5	446.7	2	80	F1:11330	1.72E-04	5.65E-05	4.46E-04	2.72E-04	2.06E-04	5.72E-04	279	284	TMT6plex; Deamidation
P50552	VASP_HUMAN	DESANQEEPEARVPA Q	Y	42.2	1997.95	16	3.3	667	3	36.8	F2:4293	0.00E+00	7.73E-05	0.00E+00	7.96E-05	8.56E-05	0.00E+00	287	302	TMT6plex
P78415	IRX3_HUMAN	PHLLGLPG	Y	21.92	1031.63	8	6.2	516.8	2	103	F1:15275	0.00E+00	0.00E+00	1.54E-03	0.00E+00	2.17E-04	0.00E+00	433	440	TMT6plex
P02452	CO1A1_HUMAN	DGEAGAQQPPGP	Y	44.04	1296.61	12	5.1	649.3	2	33.1	F1:3998	3.98E-04	7.56E-04	2.82E-04	4.48E-04	8.24E-04	5.85E-04	613	624	TMT6plex; Hydroxylation
O00151	PDLI1_HUMAN	EEKGDPNKPSG	Y	22.42	1844.02	11	2.9	615.7	3	27.1	F1:3041	1.69E-04	1.83E-03	1.78E-04	3.01E-04	1.59E-04	2.97E-04	226	236	TMT6plex
P07437	TBB5_HUMAN	DEQMLNVQN	Y	30.18	1318.64	9	5.3	660.3	2	65	F2:8381	3.93E-04	5.33E-04	2.54E-04	2.86E-04	3.05E-04	3.78E-04	327	335	TMT6plex
P02671	FIBA_HUMAN	DTASTGKTFFPGF	Y	38.8	1685.9	12	0.2	844	2	89.2	F1:12878	2.79E-03	9.18E-04	6.27E-04	8.79E-04	9.65E-04	7.59E-04	521	532	TMT6plex
P60709	ACTB_HUMAN	DMEKIWH	Y	15.34	1431.76	7	1.4	478.3	3	46.4	F1:5993	1.63E-04	8.38E-04	1.56E-04	2.51E-04	1.77E-04	1.52E-04	81	87	TMT6plex; Oxidation
Q8IZY2	ABCA7_HUMAN	LGPGHVR	Y	19.82	963.582	7	1.5	482.8	2	63	F1:8615	2.20E-04	2.69E-04	4.72E-04	5.12E-04	2.62E-04	4.32E-04	457	463	TMT6plex
Q15942	ZYX_HUMAN	EGGPEAIPPPPQPRE KVSS	Y	31.03	2526.38	20	5.3	843.1	3	56.5	F2:7135	9.78E-05	3.08E-04	1.05E-04	1.56E-04	2.59E-04	2.83E-04	124	143	TMT6plex
O95810	SDPR_HUMAN	GEDAAQAEKFQHPG	Y	52.77	1754.84	14	4	878.4	2	55.5	F1:7405	1.54E-03	3.02E-03	5.46E-04	1.81E-03	3.29E-03	2.00E-03	2	15	Acetylation ; TMT6plex
P01042	KNG1_HUMAN	DDDLEH	Y	17.87	971.44	6	8	486.7	2	21.3	F2:2058	5.82E-04	1.93E-04	1.11E-04	2.27E-04	1.49E-04	1.43E-04	480	485	TMT6plex
P68363	TBA1B_HUMAN	QPPTVVPGDLA	N	34.41	1378.77	12	8.4	690.4	2	83	F1:11804	5.96E-04	1.44E-03	3.32E-04	7.37E-04	1.24E-03	1.29E-03	358	369	TMT6plex
P02675	FIBB_HUMAN	REEAPSLRPAPPISG GG	Y	28.19	2032.09	18	5.1	678.4	3	43	F1:5467	7.57E-05	1.06E-04	7.86E-05	8.56E-05	7.09E-05	7.88E-05	53	70	TMT6plex; Hydroxylation
P00488	F13A_HUMAN	DDLPTVE	Y	28.07	1016.52	7	3.4	509.3	2	71.5	F1:9939	1.22E-04	1.50E-04	1.33E-04	1.38E-04	1.04E-04	3.85E-04	25	31	TMT6plex
P60709	ACTB_HUMAN	APEEHPVLLTEAPLNP K	Y	51.75	2312.31	17	0	771.8	3	80	F1:11334	1.58E-04	2.48E-04	6.21E-05	8.76E-05	1.74E-04	5.95E-05	97	113	TMT6plex
P0DJ18	SAA1_HUMAN	DAAKRGGPGGAWAAE AISDA	Y	21.55	2271.2	19	-0.1	758.1	3	80.2	F1:11364	6.54E-05	1.03E-03	7.11E-05	1.36E-04	1.22E-04	1.08E-04	61	79	TMT6plex; Mutation
P02671	FIBA_HUMAN	FVSETESRGSESGIFT NT	Y	40.37	2176.05	18	3.2	1089	2	88.3	F1:12726	1.02E-03	1.92E-04	3.14E-04	5.60E-04	1.82E-04	1.00E-04	540	557	TMT6plex
P67936	TPM4_HUMAN	ELERAEEAEVSEL	Y	43.3	1887.97	14	3.4	630.3	3	67.6	F1:9347	4.41E-04	7.41E-04	1.30E-04	8.65E-04	6.03E-04	3.62E-04	139	152	TMT6plex
Q92903	CDS1_HUMAN	VPISSV	N	16.06	829.511	6	-8.4	415.8	2	36.4	F2:4229	3.36E-04	9.87E-04	5.29E-04	4.82E-04	3.48E-04	5.35E-04	244	249	TMT6plex
Q9NYQ8	FAT2_HUMAN	VPLSSV	N	16.06	829.511	6	-8.4	415.8	2	36.4	F2:4229	3.36E-04	9.87E-04	5.29E-04	4.82E-04	3.48E-04	5.35E-04	1115	1120	TMT6plex
Q13395	TARB1_HUMAN	ILILHKFPQFL	Y	15.59	1826.16	11	-0.8	914.1	2	135	F1:21649	0.00E+00	0.00E+00	7.54E-05	0.00E+00	3.66E-05	1.82E-04	1216	1226	TMT6plex
P02671	FIBA_HUMAN	YSKQFTSSTSYNRGD STFES	Y	53.31	2749.32	20	2.6	917.5	3	66.4	F1:9146	9.05E-04	3.01E-04	6.74E-04	8.37E-04	3.63E-04	0.00E+00	579	598	TMT6plex
P68363	TBA1B_HUMAN	EEGEGFSEAKEDMAAL F	N	41.33	2040.91	16	1.5	1021	2	104	F1:15512	6.67E-04	1.13E-03	2.10E-04	4.73E-04	7.33E-04	5.25E-05	414	429	TMT6plex

Q9ULL5	PRR12_HUMAN	PPPLVAP	Y	21.08	918.574	7	-9.7	460.3	2	77.8	F1:10963	9.99E-05	6.48E-05	3.42E-04	7.83E-05	7.00E-05	1.41E-04	664	670	TMT6plex
Q05682	CALD1_HUMAN	DTKEAEGAPQVE	Y	42.07	1730.91	12	3	866.5	2	42	F1:5310	5.32E-04	1.59E-03	1.58E-04	3.03E-04	7.80E-04	9.13E-05	520	531	TMT6plex
P01009	A1AT_HUMAN	EDPQGDAAQKTDTS	Y	46.91	2057.01	15	3.2	686.7	3	28.5	F1:3281	6.98E-05	1.74E-04	1.22E-04	1.81E-04	9.15E-05	1.92E-04	25	39	TMT6plex
P01024	CO3_HUMAN	KENEGFTVTAE	Y	32.05	1738.91	11	1	870.5	2	59.5	F1:8092	9.10E-04	8.27E-04	5.76E-04	1.68E-03	1.41E-03	2.84E-04	1325	1335	TMT6plex; Carbamidomethylation
P02671	FIBA_HUMAN	QFTSSTSYNRGDSTFE SKSY	Y	18.54	2503.13	20	-0.2	1253	2	85.8	F1:12293	3.67E-03	2.82E-04	2.63E-03	1.92E-03	1.87E-03	1.43E-04	582	601	Pyro-glu from Q; TMT6plex
P02671	FIBA_HUMAN	EVSGNVSPGT	Y	32.24	1174.6	10	5.2	588.3	2	36.4	F2:4228	8.86E-04	9.51E-04	5.77E-04	6.67E-04	7.34E-04	7.27E-04	415	424	TMT6plex
P62328	TYB4_HUMAN	LPSKETIEQEKQAGES	Y	23.65	2460.37	16	4.7	821.1	3	76.9	F2:10175	9.39E-05	3.82E-04	8.95E-05	1.11E-04	1.98E-04	0.00E+00	29	44	TMT6plex
O95810	SDPR_HUMAN	GAVEGKEELPDENK SLE	Y	42.43	2530.37	17	-3.9	844.5	3	68.5	F1:9477	6.04E-04	1.44E-03	1.42E-04	5.26E-04	6.75E-04	0.00E+00	178	194	TMT6plex
P0C0L4	CO4A_HUMAN	HALQLNN	Y	29.99	1037.58	7	5.5	519.8	2	27.8	F2:3004	1.88E-04	2.52E-04	2.53E-04	2.24E-04	2.18E-04	3.98E-04	1342	1348	TMT6plex
O95810	SDPR_HUMAN	EEAERSDGDVPQPA	Y	29.97	1727.82	14	3.8	864.9	2	32.3	F1:3860	1.01E-04	6.99E-04	1.94E-04	1.85E-04	1.55E-04	2.02E-04	404	417	TMT6plex
Q96PD5	PGRP2_HUMAN	EPPRRTLPAIDLQ	Y	16.76	1662.91	13	4.8	832.5	2	56.8	F2:7182	1.01E-03	6.35E-04	1.60E-03	9.64E-04	6.52E-04	9.38E-04	564	576	TMT6plex
P02671	FIBA_HUMAN	EEVSGNVSPGT	Y	20.72	1303.65	11	2.7	652.8	2	42.7	F1:5421	4.94E-04	5.28E-04	5.28E-04	5.40E-04	4.77E-04	6.83E-04	414	424	TMT6plex
P0C0L4	CO4A_HUMAN	TPLQLFEGRRN	Y	28.66	1558.88	11	-0.7	520.6	3	75.1	F1:10518	1.45E-04	1.77E-04	1.45E-04	3.88E-04	0.00E+00	3.98E-04	1439	1449	TMT6plex
P01024	CO3_HUMAN	ASHLGLA	Y	27.72	896.528	7	0.2	449.3	2	36.7	F1:4559	5.50E-04	6.27E-04	1.04E-03	1.15E-03	5.46E-04	1.05E-03	741	747	TMT6plex
P15822	ZEP1_HUMAN	PPPHPLR	Y	22.18	1041.63	7	0.4	521.8	2	90.9	F1:13177	5.21E-05	1.04E-04	8.37E-05	1.00E-04	5.37E-05	1.72E-04	856	862	TMT6plex
Q8WWR&	NEUR4_HUMAN	TLLAFVEQR	Y	21.27	1304.77	9	-2.7	653.4	2	50.7	F1:6687	1.92E-03	4.11E-03	6.41E-04	1.02E-03	2.10E-03	1.08E-03	35	43	TMT6plex
Q9H4B7	TBB1_HUMAN	AVLEEDDEVTEEAEM EPEDKGH	Y	69.61	2988.38	22	5.7	997.1	3	87.7	F2:11939	6.66E-05	1.02E-04	0.00E+00	6.59E-05	5.59E-05	1.30E-04	430	451	TMT6plex; Oxidation
P52565	GDIR1_HUMAN	DEHSVNYKPPA	Y	38.9	1713.91	11	2.7	572.3	3	35.8	F2:4122	4.50E-04	8.18E-04	2.91E-04	2.88E-04	6.16E-04	2.22E-04	21	31	TMT6plex
O43312	MTSS1_HUMAN	TPVIPVK	Y	17.44	1210.81	7	3.3	606.4	2	72	F1:10019	6.71E-04	7.32E-04	1.04E-03	7.74E-04	7.60E-04	1.59E-03	613	619	TMT6plex
Q9BXF3	CECR2_HUMAN	GFPRY	N	15.86	867.481	5	6.4	434.8	2	129	F2:19734	2.08E-04	1.09E-04	2.38E-04	1.80E-04	9.62E-05	1.75E-04	1192	1196	TMT6plex
Q8WZ42	TITIN_HUMAN	VEAVK	N	16.96	1002.65	5	3.2	502.3	2	47.6	F2:5824	6.07E-03	7.57E-04	4.88E-04	1.23E-03	1.01E-03	7.63E-04	2704	2708	TMT6plex
O15294	OGT1_HUMAN	DIAVK	Y	20.96	1002.65	5	3.2	502.3	2	47.6	F2:5825	6.07E-03	7.57E-04	4.88E-04	1.23E-03	1.01E-03	7.63E-04	978	982	TMT6plex
Q99973	TEP1_HUMAN	DLAVK	Y	20.96	1002.65	5	3.2	502.3	2	47.6	F2:5825	6.07E-03	7.57E-04	4.88E-04	1.23E-03	1.01E-03	7.63E-04	220	224	TMT6plex
P0C0L4	CO4A_HUMAN	LQLNNRQ	Y	16.24	1113.65	7	2.4	557.8	2	34.2	F1:4150	5.43E-04	5.94E-04	6.84E-04	5.35E-04	4.86E-04	1.88E-03	1344	1350	TMT6plex
Q8WZ42	TITIN_HUMAN	DEEVPR	N	18.77	972.508	6	3.4	487.3	2	22.7	F1:2357	3.35E-04	6.51E-04	2.36E-04	2.72E-04	4.31E-04	2.07E-04	33404	33409	TMT6plex
P01042	KNG1_HUMAN	DLEHQGGHVL	Y	21.91	1332.7	10	1.3	667.4	2	38.5	F1:4816	6.83E-04	5.94E-04	3.18E-04	5.15E-04	8.09E-04	5.76E-04	482	491	TMT6plex
P60709	ACTB_HUMAN	DSYVGDEAQS KR G	Y	22.58	1868.96	13	1.6	624	3	36.3	F1:4486	2.26E-04	3.74E-04	9.49E-05	1.42E-04	1.84E-04	1.77E-04	51	63	TMT6plex
P02671	FIBA_HUMAN	DSGEGDFLAEGGG	Y	49.04	1438.64	13	1.9	720.3	2	84.1	F1:12000	2.43E-04	6.54E-04	2.17E-04	2.76E-04	2.54E-04	2.51E-04	21	33	TMT6plex
Q58EX7	PKHG4_HUMAN	PRPPAGAT	Y	18.56	994.576	8	5.5	498.3	2	73.7	F1:10275	5.95E-05	7.10E-05	1.53E-04	1.56E-04	5.83E-05	1.66E-04	49	56	TMT6plex
Q9H4B7	TBB1_HUMAN	DEEVTEEAEMEPEDK GH	Y	40.64	2431.11	17	4.4	811.4	3	58.1	F2:7418	0.00E+00	7.77E-05	0.00E+00	4.41E-05	1.40E-04	0.00E+00	435	451	TMT6plex
P0C0L4	CO4A_HUMAN	NGFKSHALQL	Y	30.85	1571.92	10	3.8	525	3	63.1	F1:8628	1.38E-04	1.76E-04	1.87E-04	1.96E-04	1.27E-04	2.88E-04	1337	1346	TMT6plex

O00391	QSOX1_HUMAN	ASMHR	N	15.45	829.443	5	-1.5	415.7	2	57.6	F1:7767	2.08E-04	2.34E-04	4.88E-04	3.04E-04	2.87E-04	6.69E-04	462	466	TMT6plex
O00570	SOX1_HUMAN	GGAQAPT	Y	15.46	829.45	7	-9.4	415.7	2	57.6	F1:7768	2.08E-04	2.34E-04	4.88E-04	3.04E-04	2.87E-04	6.69E-04	14	20	TMT6plex
P0C0L4	CO4A_HUMAN	EEELQF	N	24.54	1022.51	6	2.5	512.3	2	92.7	F1:13507	3.08E-04	1.30E-04	2.42E-04	3.23E-04	2.34E-04	2.51E-04	1355	1360	TMT6plex
P02675	FIBB_HUMAN	VNDNEEG	Y	20.54	1004.46	7	7.8	503.2	2	20.6	F2:1957	1.10E-04	2.35E-04	1.47E-04	1.99E-04	1.25E-04	3.05E-04	33	39	TMT6plex
P15822	ZEP1_HUMAN	AGLTYST	Y	16.48	940.507	7	6.4	471.3	2	66	F1:9068	1.51E-04	2.09E-04	2.47E-04	1.89E-04	1.83E-04	4.30E-04	2409	2415	TMT6plex
Q8WZ42	TITIN_HUMAN	PAIRGVPVP	Y	34.76	1245.81	10	-1.7	623.9	2	112	F1:17208	3.76E-05	9.03E-05	6.99E-05	7.96E-05	4.24E-05	1.59E-04	18458	18467	TMT6plex; Amidation
Q05682	CALD1_HUMAN	QERYEIEETE	Y	31.13	1307.55	10	3.2	654.8	2	58	F1:7839	4.28E-04	6.04E-04	3.30E-04	4.04E-04	6.17E-04	5.58E-04	157	166	Pyro-glu from Q
O95810	SDPR_HUMAN	TSEEAERSDGDVPVQP AVLQ	Y	26.49	2256.11	19	2.9	753	3	61.7	F1:8424	1.14E-04	1.55E-04	7.65E-05	1.20E-04	7.40E-05	9.51E-05	402	420	TMT6plex
P0DJ9	SAA2_HUMAN	EVISNAREN	Y	19.06	1259.67	9	2.9	630.8	2	25.1	F1:2729	3.03E-04	1.29E-03	3.63E-04	4.92E-04	3.43E-04	3.85E-04	74	82	TMT6plex
O00151	PDL1_HUMAN	QEKLQELNEPPKQSTS	Y	29.22	2330.22	16	-0.3	777.7	3	69.6	F1:9637	1.23E-04	1.73E-04	4.72E-05	1.11E-04	2.54E-04	1.07E-04	201	216	Pyro-glu from Q; TMT6plex
Q9Y6V0	PCLO_HUMAN	RPHGPLL	Y	16.19	1017.63	7	1.1	509.8	2	88.3	F1:12731	5.56E-04	5.52E-04	1.87E-03	9.59E-04	2.70E-04	5.75E-03	1692	1698	TMT6plex
Q9HCU4	CELR2_HUMAN	RLHGLH	Y	18.11	960.582	6	-0.6	481.3	2	39.1	F1:4906	1.05E-03	3.18E-03	9.47E-04	1.72E-03	7.86E-04	9.50E-04	1733	1738	TMT6plex
Q14624	ITIH4_HUMAN	VPDHAAYHPF	Y	39.14	1381.7	10	2	691.9	2	56.3	F1:7556	4.07E-04	6.22E-04	4.25E-04	5.54E-04	6.88E-04	4.25E-04	678	687	TMT6plex
P14618	KPYM_HUMAN	SKPHSEAGTAF	Y	31.14	1401.71	11	-3.8	701.9	2	38	F2:4472	4.39E-04	3.84E-04	1.38E-04	4.44E-04	7.00E-04	1.86E-04	2	12	Acetylation ; TMT6plex
P0C0L4	CO4A_HUMAN	GLEEELQFS	Y	29.98	1279.65	9	1.2	640.8	2	112	F1:17078	2.98E-04	2.22E-04	5.12E-04	2.54E-04	3.77E-04	7.90E-04	1353	1361	TMT6plex
P62328	TYB4_HUMAN	TIEQEKQAGES	Y	34.82	1676.9	11	1.1	560	3	37.5	F2:4417	1.47E-04	2.91E-04	4.86E-05	1.55E-04	9.67E-05	7.37E-05	34	44	TMT6plex
Q7Z2Z2	ETUD1_HUMAN	AVLSK	N	16.73	974.653	5	3	488.3	2	53.3	F2:6631	5.09E-04	7.83E-04	1.14E-03	2.05E-03	9.13E-04	5.24E-04	1001	1005	TMT6plex
Q86XA9	HTR5A_HUMAN	AVISK	N	16.73	974.653	5	3	488.3	2	53.3	F2:6631	5.09E-04	7.83E-04	1.14E-03	2.05E-03	9.13E-04	5.24E-04	243	247	TMT6plex
P48634	PRC2A_HUMAN	NLSPAPRLR	Y	15.24	1251.76	9	6.4	626.9	2	94.6	F2:13097	9.96E-05	8.99E-05	2.00E-04	6.67E-05	6.62E-05	1.60E-04	1002	1010	TMT6plex
P68366	TBA4A_HUMAN	EEVVGIDSYEDEDEGE E	Y	36.79	2071.84	16	4.8	1037	2	85.3	F2:11545	0.00E+00	1.82E-04	6.54E-06	0.00E+00	5.29E-05	0.00E+00	433	448	TMT6plex
P0C0L4	CO4A_HUMAN	SLGSKI	Y	20.3	1061.69	6	2.6	531.9	2	54.2	F1:7201	2.05E-03	2.95E-03	4.31E-03	6.50E-03	3.27E-03	2.47E-03	1361	1366	TMT6plex
P01023	A2MG_HUMAN	FYESDVMG	Y	18.89	1175.54	8	4.5	588.8	2	99.7	F2:13993	1.10E-04	1.33E-04	2.94E-04	1.48E-04	1.07E-04	1.51E-04	707	714	TMT6plex
Q8WZ42	TITIN_HUMAN	SGINPFLAETNQ	Y	15.03	1518.79	12	-2.3	760.4	2	55.9	F2:7049	1.74E-04	3.23E-04	1.05E-04	2.78E-04	2.42E-04	2.27E-04	32369	32380	TMT6plex
Q9Y2N7	HIF3A_HUMAN	LGLQRAR	Y	17.77	1041.66	7	2.4	521.8	2	104	F1:15551	6.20E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.49E-04	3	9	TMT6plex
P02452	CO1A1_HUMAN	GPPGARG	N	15.75	839.482	7	-0.6	420.7	2	78.6	F1:11113	1.21E-04	1.02E-04	5.04E-04	3.33E-04	1.22E-04	7.18E-04	569	575	TMT6plex
Q8WUY3	PRUN2_HUMAN	ESIHK	N	20	1046.67	5	4.9	524.3	2	60.7	F1:8271	1.01E-03	5.31E-04	3.61E-04	9.35E-04	8.82E-04	5.52E-04	3046	3050	TMT6plex
Q8WXH0	SYNE2_HUMAN	ESLLK	N	20	1046.67	5	4.9	524.3	2	60.7	F1:8271	1.01E-03	5.31E-04	3.61E-04	9.35E-04	8.82E-04	5.52E-04	1765	1769	TMT6plex
P52566	GDIR2_HUMAN	ESLIK	N	20	1046.67	5	4.9	524.3	2	60.7	F1:8271	1.01E-03	5.31E-04	3.61E-04	9.35E-04	8.82E-04	5.52E-04	43	47	TMT6plex
Q27J81	INF2_HUMAN	ESILK	N	20	1046.67	5	4.9	524.3	2	60.7	F1:8271	1.01E-03	5.31E-04	3.61E-04	9.35E-04	8.82E-04	5.52E-04	403	407	TMT6plex
P37802	TAGL2_HUMAN	ANRGPAYGLSREV	Y	31.65	1430.73	13	5.4	716.4	2	53.7	F2:6690	1.24E-04	1.85E-04	8.90E-05	1.14E-04	1.73E-04	1.82E-04	2	14	Acetylation
Q86W11	PKHL1_HUMAN	AAFVVTNPN	Y	16.86	1247.65	9	-3.3	624.8	2	27.4	F2:2956	1.41E-04	1.77E-04	1.29E-04	1.79E-04	6.82E-05	1.25E-04	2560	2568	TMT6plex
Q8TF74	WIPF2_HUMAN	PPPLRNG	Y	23.47	978.581	7	1.5	490.3	2	88	F1:12677	4.19E-05	5.29E-05	4.99E-05	4.89E-05	0.00E+00	3.03E-04	375	381	TMT6plex
P60709	ACTB_HUMAN	DDAPRAVFPISIVG	Y	24.92	1571.85	13	2.2	786.9	2	96.3	F1:14140	1.34E-03	7.06E-04	1.66E-04	6.87E-04	5.72E-04	1.72E-04	24	36	TMT6plex

Q8IZY2	ABCA7_HUMAN	VVFLDEPTT	Y	15.09	1248.68	9	8.1	625.4	2	78.2	F2:10394	1.95E-04	4.64E-04	2.56E-04	3.64E-04	7.70E-04	1.81E-04	1946	1954	TMT6plex
P02671	FIBA_HUMAN	SSYSKQF	Y	36.59	1303.72	7	4.3	652.9	2	53.1	F1:7026	8.53E-03	1.98E-03	8.19E-03	6.92E-03	4.68E-03	1.89E-03	577	583	TMT6plex
Q9Y490	TLN1_HUMAN	QKLHTDDELNWLHDH G	Y	52.68	2031.99	15	6	678.3	3	94.8	F1:13877	8.36E-05	2.59E-04	0.00E+00	1.59E-04	3.44E-04	6.26E-05	163	177	Pyro-glu from Q; TMT6plex
O95810	SDPR_HUMAN	EGKEELPDENKSLEET	Y	24.11	2533.34	16	4.7	845.5	3	62.8	F2:8028	0.00E+00	5.01E-04	6.18E-05	0.00E+00	8.52E-05	1.31E-04	181	196	TMT6plex
Q8IZQ1	WDFY3_HUMAN	SSLTVAR	N	16.43	961.576	7	0.7	481.8	2	36.8	F2:4291	6.44E-04	3.56E-03	9.38E-04	1.43E-03	6.94E-04	9.84E-04	1332	1338	TMT6plex
O95810	SDPR_HUMAN	EGEIAEEAAE	Y	33.68	1275.6	10	2.6	638.8	2	55.7	F1:7439	7.77E-04	1.71E-03	7.84E-04	7.70E-04	9.29E-04	8.95E-04	348	357	TMT6plex
O95810	SDPR_HUMAN	DGDPVQPAVLQVHQ	Y	53.21	1730.92	14	2.8	866.5	2	68.5	F2:8902	1.84E-04	6.26E-04	2.67E-04	4.49E-04	7.73E-04	2.57E-04	410	423	TMT6plex
Q9HCU4	CELR2_HUMAN	PPPRPPP	N	16.2	985.591	7	8.1	493.8	2	92.8	F1:13524	1.09E-04	6.93E-05	1.38E-04	2.41E-04	6.97E-05	1.19E-04	2878	2884	TMT6plex
P10071	GLI3_HUMAN	GHSPLI	N	16.7	948.56	7	8.9	475.3	2	66.7	F2:8624	1.08E-04	1.32E-04	1.25E-04	1.33E-04	9.83E-05	1.98E-04	375	381	TMT6plex
O14924	RGS12_HUMAN	VPGPSRPG	Y	16.76	994.576	8	2.2	498.3	2	77.8	F2:10304	0.00E+00	8.32E-05	1.17E-04	1.18E-04	1.01E-04	6.02E-05	1365	1372	TMT6plex
Q9H4B7	TBB1_HUMAN	DINEFGEAENNIHD	Y	21.33	1844.84	14	5.1	923.4	2	79.8	F2:10638	8.45E-05	2.01E-04	0.00E+00	5.21E-05	5.01E-05	5.87E-05	404	417	TMT6plex
P0DJ18	SAA1_HUMAN	HGAEDSLADQAANET WG	Y	44.89	1898.86	16	-3.9	950.4	2	81.8	F1:11622	8.04E-05	4.59E-04	4.64E-05	1.76E-04	1.18E-04	0.00E+00	89	104	TMT6plex
P0DJ18	SAA1_HUMAN	EDSLADQA	N	25.91	1076.52	8	4.6	539.3	2	45.5	F2:5492	3.01E-04	5.06E-04	2.08E-04	4.88E-04	2.83E-04	4.59E-04	92	99	TMT6plex
P98160	PGBM_HUMAN	GDQVVSVV	Y	17.38	1031.57	8	2.1	516.8	2	80.9	F1:11473	7.35E-05	1.24E-04	9.27E-05	4.26E-05	5.19E-05	1.32E-04	128	135	TMT6plex; Deamidation
Q8TF50	ZN526_HUMAN	QLCQAALG	Y	17.46	1031.56	8	8.5	516.8	2	80.9	F1:11472	7.35E-05	1.24E-04	9.27E-05	4.26E-05	5.19E-05	1.32E-04	648	655	TMT6plex
P00734	THRB_HUMAN	ERELLESYIDGR	Y	25.29	1707.9	12	3.1	570.3	3	86	F2:11653	0.00E+00	2.75E-05	8.83E-05	1.24E-04	7.91E-05	0.00E+00	352	363	TMT6plex
P02671	FIBA_HUMAN	ETESRGSESIGFTNT	Y	47.9	1842.88	15	-5.4	922.4	2	53.3	F1:7052	1.94E-03	4.01E-04	4.67E-04	8.25E-04	4.98E-04	4.05E-04	543	557	TMT6plex
Q96RP7	G3ST4_HUMAN	GAGPRAQ	Y	15.3	884.503	7	8.7	443.3	2	79	F1:11166	0.00E+00	5.06E-05	7.44E-05	7.53E-05	0.00E+00	1.43E-04	246	252	TMT6plex
P02675	FIBB_HUMAN	NEEGFF	Y	25.49	970.46	6	3.4	486.2	2	95	F1:13910	1.02E-03	4.15E-05	1.12E-03	8.53E-04	3.62E-04	1.82E-04	36	41	TMT6plex
P02671	FIBA_HUMAN	EGDFLAEGGG	Y	27.17	1179.56	10	5	590.8	2	81	F1:11480	1.47E-04	3.03E-04	2.66E-04	2.07E-04	3.62E-04	2.74E-04	24	33	TMT6plex
P0DJ18	SAA1_HUMAN	KDPNHFRPAGLPEKY	Y	16.08	2455.39	15	3	614.9	4	59	F1:8004	6.07E-05	1.89E-04	7.29E-05	1.80E-04	0.00E+00	0.00E+00	108	122	TMT6plex
P0DJ19	SAA2_HUMAN	DSLADQAANKWG	Y	45.6	1732.91	12	4.8	867.5	2	87.6	F2:11926	1.36E-04	2.32E-03	1.36E-04	7.32E-04	9.93E-05	2.07E-04	93	104	TMT6plex
Q3L8U1	CHD9_HUMAN	QAIITT	N	19.12	874.533	6	-0.6	438.3	2	80.5	F1:11408	7.96E-05	8.80E-05	1.47E-04	1.35E-04	8.24E-05	1.55E-04	970	975	TMT6plex
P52566	GDIR2_HUMAN	DDESLIKY	Y	33.44	1439.79	8	-5.5	720.9	2	80.1	F1:11351	3.31E-03	8.72E-04	2.80E-04	2.06E-03	4.24E-03	7.89E-04	41	48	TMT6plex
P10124	SRGN_HUMAN	SLDRNLPSPDSDLGQ HGLEEDF	Y	52.76	2700.28	22	1	901.1	3	93.5	F1:13640	0.00E+00	3.45E-04	6.63E-05	9.83E-05	8.85E-05	0.00E+00	135	156	TMT6plex
Q8TER5	ARH40_HUMAN	GPYLPR	Y	22.67	930.549	6	9.4	466.3	2	91.8	F1:13348	5.09E-05	7.15E-05	9.58E-05	6.64E-05	4.11E-05	7.81E-05	1197	1202	TMT6plex
Q92750	TAF4B_HUMAN	KPVVSGT	Y	22.51	915.559	7	5.8	458.8	2	116	F1:17902	1.48E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.03E-04	454	460	TMT6plex
P01042	KNG1_HUMAN	HGHQR	Y	18.73	878.467	5	5.3	440.2	2	53.4	F1:7074	1.29E-03	1.22E-03	2.65E-03	1.45E-03	1.05E-03	1.66E-03	453	457	TMT6plex; Oxidation
Q8WZ42	TITIN_HUMAN	GSKDVL	Y	18.07	1074.68	6	3.3	538.3	2	41.7	F1:5258	3.04E-03	6.48E-03	4.08E-03	5.10E-03	3.24E-03	2.89E-03	5140	5145	TMT6plex; Amidation
P02671	FIBA_HUMAN	FTSSTSYNRGDSTFES	Y	51.92	2013.91	16	2.3	1008	2	66.8	F1:9213	3.65E-03	1.77E-03	2.71E-03	3.62E-03	1.91E-03	5.81E-04	583	598	TMT6plex
Q9Y666	S12A7_HUMAN	EVLTEGLN	Y	16.51	1102.61	8	7.2	552.3	2	77	F2:10197	8.38E-05	2.33E-04	9.98E-05	1.38E-04	3.95E-05	1.30E-04	1059	1066	TMT6plex

Q15056	IF4H_HUMAN	GGARPREEVVQKEQE	Y	30.54	2169.19	15	2.8	543.3	4	25.6	F1:2804	0.00E+00	6.09E-05	0.00E+00	6.62E-05	4.86E-05	0.00E+00	234	248	TMT6plex
P02671	FIBA_HUMAN	EKVTSGSTTTT	Y	43.08	1568.87	11	2.8	785.4	2	25.6	F1:2806	1.61E-03	6.63E-04	4.52E-04	6.36E-04	9.80E-04	3.25E-04	447	457	TMT6plex
Q9Y490	TLN1_HUMAN	EEKKEEITGTL	Y	23.15	1963.14	11	3.4	655.4	3	67	F1:9246	8.37E-04	1.13E-04	4.91E-05	2.32E-04	1.74E-04	6.89E-05	135	145	TMT6plex
P50552	VASP_HUMAN	QEEASGGPTAPKAE	Y	16.44	1582.77	14	4.3	792.4	2	42.3	F1:5369	2.12E-04	3.69E-04	1.20E-04	2.35E-04	3.09E-04	3.11E-04	241	254	Pyro-glu from Q; TMT6plex
Q96AQ8	MCUR1_HUMAN	QRTQRLP	Y	16.53	1126.68	7	4.7	564.3	2	94.8	F1:13866	5.42E-05	1.08E-04	3.09E-04	1.45E-04	1.30E-04	4.35E-04	9	15	TMT6plex
Q14624	ITIH4_HUMAN	GPPDVDPHAA	Y	37.18	1203.61	10	3.1	602.8	2	36.9	F1:4578	1.18E-03	1.00E-03	5.60E-04	9.15E-04	8.71E-04	1.44E-03	674	683	TMT6plex
P01023	A2MG_HUMAN	YESDVMG	Y	27.55	1028.47	7	2.8	515.2	2	63.5	F1:8699	3.23E-04	1.25E-03	7.78E-04	5.92E-04	3.09E-04	8.62E-04	708	714	TMT6plex
O95810	SDPR_HUMAN	DENKSLEETLH	Y	18.67	1771.94	11	2.6	591.7	3	48.2	F2:5923	1.30E-04	3.09E-04	7.46E-05	1.30E-04	2.64E-04	2.81E-04	188	198	TMT6plex
P02671	FIBA_HUMAN	DEAAFFDTASTGK	Y	48.41	1816.92	13	5.3	606.7	3	91.3	F1:13249	1.31E-04	1.29E-04	1.48E-04	1.51E-04	1.32E-04	8.44E-05	515	527	TMT6plex
Q14624	ITIH4_HUMAN	QAGAAGSRMNFPRG VLS	Y	41.95	1700.84	17	0.7	851.4	2	71.4	F1:9915	4.04E-04	4.89E-04	4.13E-04	6.62E-04	5.75E-04	2.95E-04	650	666	Pyro-glu from Q
Q9P2K9	PTHD2_HUMAN	FWSTLGW	Y	15.02	1124.59	7	9.7	563.3	2	54.1	F2:6751	3.63E-04	6.26E-04	3.40E-04	4.26E-04	4.06E-04	7.80E-04	60	66	TMT6plex
P02671	FIBA_HUMAN	GDSTFE	Y	21.43	883.413	6	6.3	442.7	2	44	F2:5287	2.16E-04	2.05E-04	4.61E-04	3.33E-04	2.84E-04	4.47E-04	592	597	TMT6plex
P62328	TYB4_HUMAN	PLPSKETIEQEKQAGE S	Y	53.96	2557.42	17	1.2	853.5	3	77	F1:10821	4.97E-04	1.22E-03	1.49E-04	5.39E-04	1.27E-03	7.80E-04	28	44	TMT6plex
P02649	APOE_HUMAN	EQAVETEPEPEL	Y	36.61	1598.79	12	3.2	800.4	2	79	F2:10518	1.31E-04	4.23E-04	1.54E-04	3.16E-04	3.57E-04	2.29E-04	21	32	TMT6plex
P43121	MUC18_HUMAN	RVHIQ	N	15.09	880.545	5	-2.2	441.3	2	44.8	F1:5720	2.02E-04	7.41E-04	1.90E-04	2.97E-04	2.39E-04	2.31E-04	187	191	TMT6plex
Q9P225	DYH2_HUMAN	MIRLDR	N	15.29	1031.61	6	7.5	516.8	2	48.1	F1:6263	9.13E-04	1.30E-03	2.39E-03	1.30E-03	1.58E-03	2.95E-03	825	830	TMT6plex
P01024	CO3_HUMAN	WESASL	Y	21.15	902.47	6	2.6	452.2	2	122	F1:19006	3.47E-05	3.06E-05	0.00E+00	6.48E-05	4.14E-05	0.00E+00	1313	1318	TMT6plex; Dehydration
Q8WTX9	ZDHC1_HUMAN	RSPLLL	N	16.24	926.612	6	7.2	464.3	2	63	F1:8612	5.09E-04	5.55E-04	9.59E-04	7.25E-04	5.13E-04	1.30E-03	371	376	TMT6plex
A6NKX4	S22AV_HUMAN	PPHRLA	Y	17.69	918.56	6	2.2	460.3	2	77.8	F2:10312	5.40E-05	0.00E+00	7.31E-05	0.00E+00	6.93E-05	0.00E+00	211	216	TMT6plex
Q7Z6E9	RBBP6_HUMAN	DNKIL	N	18.83	1059.67	5	3.9	530.8	2	103	F1:15401	0.00E+00	1.23E-04	1.49E-04	1.69E-04	0.00E+00	2.73E-04	433	437	TMT6plex
Q14204	DYHC1_HUMAN	DNKLL	N	18.83	1059.67	5	3.9	530.8	2	103	F1:15401	0.00E+00	1.23E-04	1.49E-04	1.69E-04	0.00E+00	2.73E-04	2321	2325	TMT6plex
Q9UBW5	BIN2_HUMAN	DNKLI	N	18.83	1059.67	5	3.9	530.8	2	103	F1:15401	0.00E+00	1.23E-04	1.49E-04	1.69E-04	0.00E+00	2.73E-04	522	526	TMT6plex
P00734	THRB_HUMAN	ATSEYQTFNPR	Y	23.39	1688.84	12	1.8	845.4	2	88.7	F1:12804	3.84E-04	5.36E-04	5.38E-04	6.22E-04	4.68E-04	4.96E-04	316	327	TMT6plex
P00488	F13A_HUMAN	AEDDLPTVE	Y	22.19	1216.6	9	-1.6	609.3	2	75.8	F1:10617	2.38E-04	3.28E-04	4.21E-04	3.43E-04	2.93E-04	5.01E-04	23	31	TMT6plex
Q14767	LTBP2_HUMAN	QRDPVGRYEPAGGD ANRL	Y	41.17	1952.95	18	3.9	652	3	47.9	F2:5872	1.36E-04	1.34E-04	8.85E-05	1.47E-04	8.70E-05	1.85E-04	36	53	Pyro-glu from Q
P0DJJ9	SAA2_HUMAN	NIQRLT	Y	23.94	972.592	6	2.2	487.3	2	33.5	F1:4051	2.60E-04	2.13E-03	5.12E-04	1.10E-03	2.51E-04	3.45E-04	82	87	TMT6plex
Q08828	ADCY1_HUMAN	VVTNVRSLQ	Y	16.68	1243.75	9	8.1	622.9	2	38.7	F1:4848	8.03E-04	9.73E-04	2.48E-03	1.83E-03	2.14E-03	1.38E-03	107	115	TMT6plex
P0DJJ8	SAA1_HUMAN	YIGSDKY	N	19.5	1302.72	7	2.3	652.4	2	62.2	F1:8492	5.14E-04	2.24E-03	6.96E-04	1.12E-03	6.94E-04	5.40E-04	47	53	TMT6plex
Q15942	ZYX_HUMAN	NDPFKA	Y	27.75	1148.66	6	3.2	575.3	2	53.8	F1:7131	5.50E-03	3.31E-03	1.09E-03	3.88E-03	7.05E-03	2.35E-03	161	166	TMT6plex
Q68D10	SPT2_HUMAN	DGKLPP	Y	17.54	1083.67	6	-2.8	542.8	2	37.1	F1:4616	4.87E-04	2.09E-03	1.00E-03	8.37E-04	1.43E-03	2.54E-03	220	225	TMT6plex
Q6IA86	ELP2_HUMAN	LNHVLCNQDSLPEG AT	Y	16.57	2055.96	17	-8.5	1029	2	81.4	F2:10888	0.00E+00	5.69E-05	5.31E-05	1.17E-04	6.36E-05	0.00E+00	482	498	TMT6plex; Deamidation

P0DJ18	SAA1_HUMAN	EDSLADQAANEWG	Y	45.43	1633.74	13	-0.2	817.9	2	104	F1:15476	2.61E-04	1.04E-03	1.11E-04	3.14E-04	2.84E-04	2.52E-04	92	104	TMT6plex
Q9H4B7	TBB1_HUMAN	DLEPGTMD	N	18.57	1105.52	8	4.3	553.8	2	67.4	F1:9322	2.72E-04	2.84E-04	1.96E-04	3.14E-04	2.18E-04	2.93E-04	67	74	TMT6plex
P10745	RET3_HUMAN	VPTVLQT	Y	16.12	985.601	7	3.7	493.8	2	89	F2:12150	0.00E+00	4.61E-05	6.70E-05	3.91E-05	5.73E-05	5.58E-05	937	943	TMT6plex
O95613	PCNT_HUMAN	ELHKT	N	16.05	1084.66	5	5.2	543.3	2	105	F1:15768	6.08E-05	1.29E-04	3.19E-04	4.16E-04	2.20E-04	9.12E-05	1329	1333	TMT6plex
Q8WZ42	TITIN_HUMAN	EIHKT	N	16.05	1084.66	5	5.2	543.3	2	105	F1:15768	6.08E-05	1.29E-04	3.19E-04	4.16E-04	2.20E-04	9.12E-05	33837	33841	TMT6plex
P0C0L4	CO4A_HUMAN	NGFKSHAL	Y	22.86	1331.76	8	2.8	444.9	3	47.7	F1:6203	7.49E-05	9.12E-05	2.01E-04	1.12E-04	5.24E-05	1.20E-04	1337	1344	TMT6plex; Deamidation
P60709	ACTB_HUMAN	EAPLNPK	N	29.97	1225.74	7	4.3	613.9	2	37.1	F2:4341	1.10E-03	2.73E-03	7.60E-04	8.62E-04	1.64E-03	8.66E-04	107	113	TMT6plex
P01024	CO3_HUMAN	KENEGFTVTAEG	Y	26.76	1738.91	12	0.2	870.5	2	57.4	F2:7305	5.19E-04	4.78E-04	3.92E-04	9.53E-04	7.63E-04	1.45E-04	1325	1336	TMT6plex
P0DJ18	SAA1_HUMAN	GGAWAAEAI SDAREN	Y	24.38	1745.85	15	0.3	583	3	86.4	F1:12402	0.00E+00	7.72E-05	0.00E+00	5.61E-05	8.44E-05	0.00E+00	68	82	TMT6plex; Mutation
Q14624	ITIH4_HUMAN	VVVTRN	Y	15.37	915.57	6	-6.1	458.8	2	119	F2:17644	8.44E-05	0.00E+00	0.00E+00	2.90E-05	0.00E+00	0.00E+00	801	806	TMT6plex
P0DJ18	SAA1_HUMAN	DPNHFRPAGLPEKY	N	43.84	2098.14	14	6.7	525.5	4	63.2	F2:8092	0.00E+00	2.04E-04	0.00E+00	2.77E-04	3.63E-05	7.03E-05	109	122	TMT6plex
P02671	FIBA_HUMAN	SSSYSKQFTSSTSYNR GDSTF	Y	43.66	2794.35	21	-1	932.5	3	68.8	F1:9515	1.71E-03	6.07E-04	8.64E-04	1.37E-03	8.02E-04	1.61E-04	576	596	TMT6plex
Q6P3X3	TTC27_HUMAN	QVPPHW	Y	18.43	991.544	6	-0.9	496.8	2	40.9	F2:4841	4.76E-04	2.83E-04	1.52E-04	2.99E-04	2.47E-04	1.80E-04	435	440	TMT6plex
P07951	TPM2_HUMAN	DEEKMELQ	N	30.23	1478.77	8	1.7	740.4	2	54.6	F1:7281	8.37E-04	4.94E-03	7.38E-04	1.26E-03	1.48E-03	1.14E-03	137	144	TMT6plex
P67936	TPM4_HUMAN	DEEKMEIQ	N	30.23	1478.77	8	1.7	740.4	2	54.6	F1:7281	8.37E-04	4.94E-03	7.38E-04	1.26E-03	1.48E-03	1.14E-03	101	108	TMT6plex
Q15942	ZYX_HUMAN	SQPNQKLGHPPEALSA GTGSPQPPS	Y	34.43	2842.5	24	2	948.5	3	54.2	F1:7205	0.00E+00	9.79E-05	0.00E+00	0.00E+00	3.42E-05	0.00E+00	290	313	TMT6plex
Q15942	ZYX_HUMAN	RSPGAPGPLTLKEVEE LE	Y	56.62	2379.34	18	1.4	794.1	3	100	F1:14806	3.14E-04	5.79E-04	7.78E-05	2.44E-04	4.02E-04	0.00E+00	343	360	TMT6plex
P50552	VASP_HUMAN	KNSTTLP	Y	21.45	1218.72	7	2.8	610.4	2	48.7	F1:6350	9.63E-04	2.28E-03	5.43E-04	1.07E-03	2.36E-03	1.50E-03	312	318	TMT6plex; Deamidation
P02675	FIBB_HUMAN	NDNEEGFFS	Y	41.98	1286.56	9	0.5	644.3	2	87.1	F1:12511	1.64E-04	6.18E-04	3.09E-04	4.93E-04	4.10E-04	4.43E-04	34	42	TMT6plex
P02671	FIBA_HUMAN	EFVSETESRGSSESGIFT NT	Y	45.16	2305.09	19	1.1	1154	2	90.7	F1:13143	1.97E-03	3.96E-04	3.66E-04	9.99E-04	5.44E-04	1.38E-04	539	557	TMT6plex
Q15942	ZYX_HUMAN	QPQPQPKPQVQ	Y	32.56	1485.81	11	1.5	743.9	2	46.5	F1:6006	2.03E-04	4.63E-04	2.50E-04	3.02E-04	3.70E-04	3.99E-04	225	235	Pyro-glu from Q; TMT6plex
Q9Y490	TLN1_HUMAN	QENETVVVKE	Y	32.37	1385.72	10	2.1	693.9	2	60.9	F1:8317	5.30E-04	8.90E-04	4.80E-04	6.92E-04	9.24E-04	5.71E-04	2483	2492	Pyro-glu from Q; TMT6plex
O14939	PLD2_HUMAN	LVFAPGVPV	Y	16.92	1126.7	9	-2.6	564.4	2	92.3	F2:12683	8.99E-05	9.48E-05	3.09E-04	2.61E-04	1.03E-04	2.91E-04	57	65	TMT6plex
Q15942	ZYX_HUMAN	AAPRPSPAISVSV	Y	33.51	1292.71	13	-1.2	647.4	2	79.2	F1:11199	2.19E-04	2.18E-04	8.30E-05	2.67E-04	2.48E-04	1.18E-04	2	14	Acetylation
P0DJ18	SAA1_HUMAN	GKDPNHFRPAGLPE	Y	23.62	1992.09	14	1.2	499	4	50.8	F1:6695	0.00E+00	1.22E-04	0.00E+00	4.36E-05	0.00E+00	0.00E+00	107	120	TMT6plex
P68363	TBA1B_HUMAN	QMPSDKTIGGGDDS	N	31.34	1618.73	14	1.3	810.4	2	69.7	F1:9659	4.59E-04	6.81E-04	3.19E-04	4.50E-04	4.69E-04	3.37E-04	35	48	Pyro-glu from Q; TMT6plex
P60709	ACTB_HUMAN	QKDSYVGD	Y	33.4	1122.54	8	3.3	562.3	2	48.3	F1:6294	4.51E-04	1.16E-03	3.34E-04	5.40E-04	5.32E-04	3.90E-04	49	56	Pyro-glu from Q; TMT6plex



P07437	TBB5_HUMAN	SVVPSPKVSDTVVEP YN	Y	38.5	2274.25	17	0.1	759.1	3	85.4	F1:12238	1.81E-04	1.93E-04	0.00E+00	8.35E-05	1.57E-04	0.00E+00	168	184	TMT6plex
Q5VX71	SUSD4_HUMAN	QQQPQSP	Y	26.97	854.377	7	2.3	428.2	2	89.5	F1:12929	7.99E-05	3.41E-05	0.00E+00	6.13E-05	0.00E+00	0.00E+00	20	26	Acetylation ; Deamidation
P25940	CO5A3_HUMAN	STFRR	N	18.66	894.524	5	8	448.3	2	47.1	F2:5724	4.70E-04	9.03E-04	1.70E-03	1.20E-03	8.83E-04	1.74E-03	1610	1614	TMT6plex
Q9HAB3	S52A2_HUMAN	LSHLPPR	Y	16.84	1047.64	7	-2.7	524.8	2	85.8	F1:12298	5.29E-05	7.48E-05	3.16E-04	7.21E-05	8.44E-05	1.31E-04	136	142	TMT6plex
P02671	FIBA_HUMAN	FLAEGGG	Y	23.91	878.47	7	-0.5	440.2	2	72.8	F1:10150	9.23E-05	8.01E-05	3.04E-04	1.46E-04	7.16E-05	1.23E-04	27	33	TMT6plex
Q86UX7	URP2_HUMAN	TGSGGPGNHPHPDA SAEGLNPYG	Y	38.06	2474.14	24	3.5	825.7	3	47.7	F2:5846	6.29E-05	2.61E-04	0.00E+00	3.98E-05	6.20E-05	7.74E-05	482	505	TMT6plex
Q9H4B7	TBB1_HUMAN	EDEEVTEEA	Y	25.57	1407.61	10	2.6	704.8	2	48	F1:6236	1.74E-04	3.36E-04	2.39E-04	2.71E-04	2.86E-04	2.78E-04	434	443	TMT6plex
P07951	TPM2_HUMAN	DEEKMELQEMQL	N	40.84	1980	12	4.1	991	2	104	F2:14738	1.66E-03	1.04E-04	0.00E+00	1.56E-03	1.27E-03	1.04E-04	137	148	TMT6plex
P67936	TPM4_HUMAN	DEEKMEIQEMQL	N	40.84	1980	12	4.1	991	2	104	F2:14738	1.66E-03	1.04E-04	0.00E+00	1.56E-03	1.27E-03	1.04E-04	101	112	TMT6plex
Q9UPN6	SCAF8_HUMAN	SGPWNRG	Y	16.54	1001.52	7	-3.7	501.8	2	99.5	F2:13942	1.11E-04	3.52E-05	0.00E+00	3.36E-05	5.04E-05	0.00E+00	1134	1140	TMT6plex
Q5K4L6	S27A3_HUMAN	GFLRF	N	15.57	867.517	5	3.1	434.8	2	89.1	F1:12864	1.94E-04	1.81E-04	3.30E-04	2.63E-04	1.27E-04	5.46E-04	583	587	TMT6plex
Q8N6L0	KASH5_HUMAN	RHPLIPA	Y	17.18	1031.64	7	2.2	516.8	2	104	F2:14829	0.00E+00	7.18E-05	2.90E-03	1.62E-04	0.00E+00	1.04E-03	519	525	TMT6plex
Q15942	ZYX_HUMAN	GGSGSQPNQKLG	Y	30.13	1586.88	12	3	530	3	28.8	F1:3333	0.00E+00	8.19E-05	3.93E-05	6.09E-05	1.40E-04	0.00E+00	286	297	TMT6plex
P26045	PTN3_HUMAN	KLPQN	N	15.17	827.507	5	4.1	414.8	2	112	F1:17192	1.01E-04	0.00E+00	5.24E-05	0.00E+00	0.00E+00	8.57E-05	666	670	TMT6plex
Q15942	ZYX_HUMAN	LANTQPR	Y	25.03	1107.56	7	-5.3	554.8	2	44.6	F2:5370	2.98E-04	3.36E-04	1.44E-04	1.96E-04	3.60E-04	3.52E-04	247	253	TMT6plex; Phosphorylation
P02768	ALBU_HUMAN	DAHKSEVA	Y	23.56	1313.73	8	4.4	438.9	3	17.7	F1:1547	0.00E+00	0.00E+00	6.14E-05	6.26E-05	4.43E-05	0.00E+00	25	32	TMT6plex
P50552	VASP_HUMAN	EEASGGPTAPKAE	Y	28.12	1700.9	13	4.2	568	3	31.7	F2:3541	1.98E-04	1.54E-04	0.00E+00	1.15E-04	1.18E-04	0.00E+00	242	254	TMT6plex
Q04671	P_HUMAN	STLLQVDLAGALVAS GPSR	Y	15.34	2084.17	19	2	522.1	4	41.6	F2:4937	0.00E+00	5.14E-05	0.00E+00	4.04E-05	0.00E+00	4.83E-05	225	243	TMT6plex; Deamidation
Q8IZL8	PELP1_HUMAN	LTHPRVP	Y	15.03	1047.64	7	3.1	524.8	2	87.5	F1:12590	7.21E-05	9.07E-05	3.16E-04	9.08E-05	1.44E-04	1.05E-04	630	636	TMT6plex
Q96RP8	KCNA7_HUMAN	QAARKVLA <sup>Q</sup> VSVLV <sup>L</sup> LV <sup>L</sup> V <sup>S</sup>	Y	17.51	1965.26	17	-0.5	656.1	3	138	F2:21394	0.00E+00	5.96E-05	0.00E+00	0.00E+00	1.52E-04	0.00E+00	140	156	TMT6plex
O95810	SDPR_HUMAN	SDGDPVQPA	Y	24.88	1113.55	9	-3	557.8	2	37.2	F1:4633	4.05E-04	5.16E-04	3.65E-04	4.47E-04	4.68E-04	4.51E-04	409	417	TMT6plex
PODJ19	SAA2_HUMAN	TGHGAEDSLADQA	Y	38.2	1499.71	13	2.4	750.9	2	34.8	F1:4254	2.90E-04	7.01E-04	2.80E-04	4.00E-04	2.20E-04	3.97E-04	87	99	TMT6plex; Mutation
Q15942	ZYX_HUMAN	VQPQPQPKPVQ	Y	16.52	1831.07	12	8.4	611.4	3	40.9	F2:4839	5.57E-05	4.85E-05	0.00E+00	7.55E-05	7.99E-05	0.00E+00	224	235	TMT6plex
P00488	F13A_HUMAN	EDDLPT	Y	19	917.455	6	-4.3	459.7	2	53.2	F1:7049	9.35E-04	9.23E-04	2.13E-03	1.36E-03	9.42E-04	2.82E-03	24	29	TMT6plex
P42858	HD_HUMAN	ISAVHR	Y	15.82	910.555	6	3	456.3	2	77.2	F1:10864	2.56E-04	6.03E-05	1.36E-04	1.32E-04	9.97E-05	1.21E-04	1940	1945	TMT6plex
Q9Y5A9	YTHD2_HUMAN	KHGRVF	Y	19.83	971.587	6	1.5	486.8	2	85.7	F2:11608	4.11E-05	6.48E-05	0.00E+00	3.04E-05	3.79E-05	7.57E-05	408	413	TMT6plex
P62328	TYB4_HUMAN	IEQEKGAGES	Y	20.18	1575.85	10	2.6	788.9	2	38	F1:4741	8.79E-04	1.54E-03	4.27E-04	1.14E-03	1.19E-03	1.08E-03	35	44	TMT6plex
P01024	CO3_HUMAN	SEETKENE <sup>G</sup> FTV <sup>T</sup> AE GKGG <sup>T</sup> LS	Y	52	3085.6	23	4.2	1030	3	68.8	F2:8954	8.51E-05	8.48E-04	9.73E-05	2.48E-04	2.07E-04	1.40E-04	1321	1343	TMT6plex
PODJ18	SAA1_HUMAN	FRPAGLPE	N	16.43	1114.63	8	1.9	558.3	2	63.7	F1:8724	3.00E-04	1.63E-03	2.69E-04	7.83E-04	3.49E-04	2.80E-04	113	120	TMT6plex
Q8IVF4	DYH10_HUMAN	FLKNII	N	19.4	1204.79	6	2.4	603.4	2	119	F1:18506	0.00E+00	2.54E-05	0.00E+00	0.00E+00	0.00E+00	6.22E-05	139	144	TMT6plex

P0C0L4	CO4A_HUMAN	NGFKSHA	Y	27.49	1218.68	7	4.1	407.2	3	27.9	F1:3180	1.44E-04	1.35E-04	1.34E-04	1.20E-04	6.58E-05	4.09E-04	1337	1343	TMT6plex; Deamidation
P0DJJ8	SAA1_HUMAN	NHFRPAGLPE	N	33.12	1365.74	10	-3.5	683.9	2	40.8	F1:5120	1.97E-04	2.55E-03	4.10E-04	1.10E-03	3.82E-04	3.57E-04	111	120	TMT6plex
Q6P2D8	XARRA1_HUMAN	IPPPPK	Y	24.26	1218.81	7	5.1	610.4	2	75.2	F2:9910	8.58E-05	6.72E-04	1.25E-04	1.76E-04	1.75E-04	2.11E-04	677	683	TMT6plex
Q702N8	XIRP1_HUMAN	LPLPPPK	Y	24.26	1218.81	7	5.1	610.4	2	75.2	F2:9910	8.58E-05	6.72E-04	1.25E-04	1.76E-04	1.75E-04	2.11E-04	33	39	TMT6plex
P01024	CO3_HUMAN	EETKENEGFTVTAE	Y	29.85	2023.02	14	7.3	675.4	3	63.5	F2:8139	5.75E-05	2.42E-04	5.95E-05	3.09E-04	2.25E-04	0.00E+00	1322	1335	TMT6plex; Dehydration
O60610	DIAP1_HUMAN	DELPSAGDGGKS	Y	17.56	1646.85	13	1.2	824.4	2	47.4	F1:6152	9.50E-05	5.68E-04	8.99E-05	9.14E-05	2.55E-04	1.35E-04	24	36	TMT6plex
P02671	FIBA_HUMAN	QF1SS1SYNKGDS1FE	Y	33.28	2141.97	17	3.5	1072	2	63.7	F1:8722	9.07E-04	4.51E-04	8.30E-04	1.16E-03	3.73E-04	8.10E-05	582	598	TMT6plex
P0DJJ8	SAA1_HUMAN	DPNHFRPA	N	31.73	1181.61	8	3.1	591.8	2	25	F1:2711	2.11E-04	1.38E-03	2.50E-04	5.59E-04	2.31E-04	4.00E-04	109	116	TMT6plex
O95810	SDPR_HUMAN	VEGEIAEEAAEKAT	Y	49.65	1904.01	14	4.7	953	2	93.8	F2:12949	6.24E-04	8.57E-04	1.29E-04	6.60E-04	1.29E-03	2.40E-04	347	360	TMT6plex
Q15772	SPEG_HUMAN	PIPELLRAPP	Y	19.28	1330.82	10	3.7	666.4	2	97.4	F1:14338	1.44E-04	2.60E-04	1.81E-04	1.61E-04	2.51E-04	2.43E-04	1892	1901	TMT6plex
P0C0L4	CO4A_HUMAN	HALQLNNRQI	Y	34.16	1434.83	10	0.9	479.3	3	38.9	F1:4879	6.51E-05	1.63E-04	1.17E-04	1.22E-04	6.51E-05	2.59E-04	1342	1351	TMT6plex
Q8IVF4	DYH10_HUMAN	HVVLVH	Y	24.63	931.581	6	7.5	466.8	2	48.2	F1:6280	4.78E-04	8.38E-04	7.14E-04	7.17E-04	4.20E-04	6.78E-04	2992	2997	TMT6plex
Q6PIF6	MYO7B_HUMAN	TILIR	N	15.05	843.575	5	8.3	422.8	2	69.3	F2:9040	2.12E-04	8.43E-05	1.79E-04	1.34E-04	1.10E-04	3.80E-04	374	378	TMT6plex
P98160	PGBM_HUMAN	TLIIR	N	15.05	843.575	5	8.3	422.8	2	69.3	F2:9040	2.12E-04	8.43E-05	1.79E-04	1.34E-04	1.10E-04	3.80E-04	463	467	TMT6plex
O15020	SPTN2_HUMAN	TIILR	N	15.05	843.575	5	8.3	422.8	2	69.3	F2:9040	2.12E-04	8.43E-05	1.79E-04	1.34E-04	1.10E-04	3.80E-04	155	159	TMT6plex
Q8WZ42	TITIN_HUMAN	TLILR	N	15.05	843.575	5	8.3	422.8	2	69.3	F2:9040	2.12E-04	8.43E-05	1.79E-04	1.34E-04	1.10E-04	3.80E-04	20629	20633	TMT6plex
Q9Y490	TLN1_HUMAN	TLLLR	N	15.05	843.575	5	8.3	422.8	2	69.3	F2:9040	2.12E-04	8.43E-05	1.79E-04	1.34E-04	1.10E-04	3.80E-04	190	194	TMT6plex
Q6ZVN8	RGMC_HUMAN	THIR	N	15.05	843.575	5	8.3	422.8	2	69.3	F2:9040	2.12E-04	8.43E-05	1.79E-04	1.34E-04	1.10E-04	3.80E-04	284	288	TMT6plex
Q8WZ42	TITIN_HUMAN	GPPVEI	N	15.08	839.496	6	-2.6	420.8	2	119	F2:17748	4.39E-05	0.00E+00	5.18E-05	6.55E-05	0.00E+00	7.33E-05	16205	16210	TMT6plex
P02671	FIBA_HUMAN	SYKMADEAGSEADH EGTHSTKRGHHA	Y	42.13	3374.65	25	2.8	483.1	7	22.3	F1:2297	0.00E+00	4.26E-05	0.00E+00	9.85E-05	0.00E+00	0.00E+00	600	624	TMT6plex; Oxidation
O75112	LDB3_HUMAN	PVIPHQ	Y	15.82	918.549	6	8.9	460.3	2	124	F1:19474	1.12E-04	4.68E-05	0.00E+00	3.42E-05	5.00E-05	1.47E-04	101	106	TMT6plex
O95810	SDPR_HUMAN	GEIAEAAEKAT	Y	28.93	1675.9	12	1	559.6	3	70.5	F2:9228	5.75E-05	5.90E-05	8.93E-05	6.70E-05	9.26E-05	0.00E+00	349	360	TMT6plex
O95810	SDPR_HUMAN	GEDAAQAEKF	Y	35.45	1335.65	10	4.2	668.8	2	70	F2:9164	5.64E-04	1.21E-03	3.59E-04	6.11E-04	1.16E-03	8.19E-04	2	11	Acetylation ; TMT6plex
P02671	FIBA_HUMAN	SSSYSKQF	Y	41.3	1390.75	8	-4.3	696.4	2	52.5	F1:6953	3.47E-03	3.98E-03	3.86E-03	4.90E-03	2.86E-03	2.26E-03	576	583	TMT6plex
Q99490	AGAP2_HUMAN	EPLGRQL	Y	21.88	1040.62	7	1.6	521.3	2	45.4	F1:5825	7.78E-04	9.81E-04	2.46E-03	1.31E-03	1.10E-03	9.56E-04	1052	1058	TMT6plex
P52566	GDIR2_HUMAN	TEKAPEPHVEEDDDD ELDSKLN	Y	59.51	3024.45	22	6.5	1009	3	78.1	F2:10362	6.17E-05	2.19E-04	0.00E+00	7.53E-05	1.76E-04	1.39E-04	2	23	Acetylation ; TMT6plex
P02452	CO1A1_HUMAN	GQRGERGFPLPGP	Y	15.25	1652.89	14	-8.6	552	3	32.6	F1:3919	8.45E-04	4.18E-04	5.21E-04	5.50E-04	4.31E-04	5.91E-04	965	978	TMT6plex
P02675	FIBB_HUMAN	DNEEGF	Y	23.81	938.418	6	-5.4	470.2	2	51.6	F1:6812	2.15E-03	1.09E-03	3.08E-03	2.03E-03	1.68E-03	1.69E-03	35	40	TMT6plex
Q9HCE3	ZN532_HUMAN	KRTVTR	Y	18.98	988.635	6	4	495.3	2	94	F2:12988	1.07E-04	0.00E+00	0.00E+00	4.75E-05	0.00E+00	0.00E+00	374	379	TMT6plex
Q96C00	ZBTB9_HUMAN	PAPPALPP	Y	16.32	987.596	8	0.1	494.8	2	83	F2:11176	7.04E-05	1.09E-04	2.54E-04	1.53E-04	1.34E-04	2.43E-04	273	280	TMT6plex
P15502	ELN_HUMAN	GPQAAVPGV	Y	16.52	1023.59	9	9	512.8	2	71.9	F1:10014	2.99E-04	1.60E-04	1.53E-04	2.07E-04	1.57E-04	3.60E-04	466	474	TMT6plex
Q8WZ42	TITIN_HUMAN	PIVARHP	Y	19.96	816.461	7	4.2	409.2	2	36.8	F1:4565	2.07E-04	3.48E-04	3.30E-04	5.10E-04	2.30E-04	2.88E-04	21093	21099	Formylation

O95544	NADK_HUMAN	LPSICVR	Y	17.8	1015.61	7	5.6	508.8	2	83	F1:11808	5.03E-04	5.83E-04	8.75E-04	1.10E-03	5.36E-04	6.27E-04	405	411	TMT6plex
P07437	TBB5_HUMAN	NEATGGKYVPR	Y	32.17	1419.77	11	3.2	474.3	3	22.8	F1:2375	1.52E-04	1.59E-04	4.27E-05	1.21E-04	7.54E-05	9.70E-05	52	62	TMT6plex
P06753	TPM3_HUMAN	ALKDEEKMELQEIQ LKE	Y	23.28	2989.72	17	2.9	748.4	4	100	F1:14813	7.94E-05	1.73E-04	0.00E+00	7.06E-05	9.71E-05	0.00E+00	135	151	TMT6plex
Q86YW5	TRML1_HUMAN	LPPLPPK	Y	22.84	1218.81	7	1.3	610.4	2	76.7	F1:10781	2.88E-04	9.71E-04	2.45E-04	3.96E-04	3.36E-04	4.08E-04	265	271	TMT6plex
P20929	NEBU_HUMAN	DVIHAR	Y	16	938.55	6	1.1	470.3	2	79.6	F1:11262	1.20E-04	7.83E-05	8.69E-05	1.09E-04	6.93E-05	8.20E-05	2639	2644	TMT6plex
Q9Y6F6	MRV1_HUMAN	FLTRRG	Y	15.84	977.597	6	2.6	489.8	2	77.1	F2:10206	6.65E-05	0.00E+00	9.10E-05	6.67E-05	4.26E-05	0.00E+00	165	170	TMT6plex
Q96MA6	KAD8_HUMAN	PRHVIV	Y	15.25	948.607	6	1.3	475.3	2	112	F2:16368	2.05E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.46E-04	158	163	TMT6plex
Q9H2Y7	ZN106_HUMAN	IYKGH	N	16.86	1074.66	5	-4.8	538.3	2	79.3	F2:10558	2.58E-04	2.11E-04	1.84E-04	3.76E-04	2.74E-04	1.20E-04	1735	1739	TMT6plex
Q05682	CALD1_HUMAN	DLPVPAEGVRN	Y	35.44	1394.77	11	2.4	698.4	2	58.6	F1:7934	6.46E-04	2.22E-03	4.54E-04	6.57E-04	8.64E-04	9.39E-04	701	711	TMT6plex
P02452	CO1A1_HUMAN	PPGPAGPAGPPGP	Y	17.73	1296.7	13	6.7	649.4	2	32.3	F1:3865	2.31E-04	1.75E-04	0.00E+00	9.04E-05	1.47E-04	5.88E-05	840	852	TMT6plex
O95810	SDPR_HUMAN	EGEIAEEAAEKA	Y	45.82	1703.9	12	2.7	853	2	75	F1:10496	3.78E-03	4.40E-03	7.13E-04	2.73E-03	2.97E-03	1.38E-03	348	359	TMT6plex
P0C0L4	CO4A_HUMAN	RYRVFA	Y	18.3	824.466	6	6.2	413.2	2	34.4	F1:4196	1.73E-03	2.87E-03	4.03E-03	2.41E-03	2.29E-03	5.87E-03	157	162	Methyl ester
P02775	CXCL7_HUMAN	NLAKGKEESLDS DL	Y	29.85	1976.08	14	5.8	659.7	3	63.8	F2:8185	7.30E-05	2.45E-04	7.63E-05	2.12E-04	2.16E-04	7.04E-05	44	57	TMT6plex
P0DJ18	SAA1_HUMAN	NIQRFFGHAEDSLA DQ	Y	30.54	2133.04	17	4.4	712	3	83.2	F1:11844	6.10E-05	3.87E-04	7.55E-05	9.95E-05	1.31E-04	1.33E-04	82	98	TMT6plex
P07437	TBB5_HUMAN	SVVPSPKVSDTVVEP YNATLSVH	Y	58.75	2882.58	23	2.8	961.9	3	93.9	F1:13700	2.66E-04	2.46E-04	0.00E+00	1.36E-04	2.25E-04	0.00E+00	168	190	TMT6plex
P02671	FIBA_HUMAN	ADSGEGDF	Y	29.64	1105.42	8	2.1	553.7	2	74.4	F1:10405	4.51E-04	3.96E-04	4.79E-04	4.09E-04	2.87E-04	9.26E-04	20	27	TMT6plex; Phosphorylation
P01024	CO3_HUMAN	RIHWE	Y	20.37	968.54	5	1.9	485.3	2	32.5	F1:3906	5.73E-04	2.70E-03	1.19E-03	2.22E-03	1.51E-03	1.70E-03	1310	1314	TMT6plex
Q3KRA9	ALKB6_HUMAN	GGLPANHVL	Y	17.83	1105.64	9	3.2	553.8	2	91.1	F1:13217	1.90E-04	1.88E-04	3.04E-04	2.26E-04	2.39E-04	2.77E-04	93	101	TMT6plex
P02671	FIBA_HUMAN	SSYSKQFTSSTS SYNRG DSTFES	Y	57.96	2923.39	22	-5.8	975.5	3	66	F2:8537	1.21E-03	6.67E-04	1.36E-03	1.87E-03	4.98E-04	0.00E+00	577	598	TMT6plex
P02675	FIBB_HUMAN	REEAPSLRPAPP PISG GGY	Y	44.61	2195.15	19	0.7	732.7	3	57	F1:7672	2.15E-04	1.53E-04	7.39E-05	1.85E-04	2.04E-04	1.21E-04	53	71	TMT6plex; Hydroxylation
Q9BZ71	PITM3_HUMAN	SSQDHVP	Y	15.14	997.503	7	-4.6	499.8	2	48.2	F1:6270	7.22E-04	8.78E-04	1.49E-03	1.38E-03	9.44E-04	1.14E-03	209	215	TMT6plex
P07437	TBB5_HUMAN	EEEDFGEEAE EEEE	Y	25.82	1740.71	13	6.2	871.4	2	82	F2:10983	1.82E-04	3.66E-04	1.22E-04	2.58E-04	3.03E-04	2.21E-04	432	444	TMT6plex
P02671	FIBA_HUMAN	GDFLAEGGGV	Y	42.54	1149.59	10	2.5	575.8	2	99.2	F1:14652	1.02E-03	7.16E-04	9.04E-04	1.03E-03	4.28E-04	8.97E-04	25	34	TMT6plex
P60709	ACTB_HUMAN	DGQVITIGNE	N	29.85	1274.66	10	5.2	638.3	2	79.6	F2:10603	2.02E-04	5.08E-04	1.62E-04	3.59E-04	3.37E-04	3.37E-04	244	253	TMT6plex; Deamidation
O95810	SDPR_HUMAN	ERSDGPVQPAVLQ	Y	18.83	1738.91	14	3.6	870.5	2	53.4	F2:6657	1.53E-04	1.93E-04	0.00E+00	1.03E-04	1.85E-04	1.48E-04	407	420	TMT6plex
P29317	EPHA2_HUMAN	GVRLPGH	Y	20.21	963.582	7	-1.3	482.8	2	76.8	F1:10783	1.86E-04	9.59E-05	1.30E-04	1.40E-04	1.15E-04	1.17E-04	948	954	TMT6plex
O75600	KBL_HUMAN	GPHIRV	Y	16.19	906.56	6	-2.1	454.3	2	80.1	F2:10677	9.73E-05	0.00E+00	5.02E-04	5.00E-05	8.41E-05	2.33E-04	55	60	TMT6plex
P09493	TPM1_HUMAN	DEEKMEIQEIQ LKE	N	21.65	2448.34	14	2.2	817.1	3	92.7	F1:13511	7.28E-05	3.23E-04	0.00E+00	1.13E-04	3.61E-04	9.76E-05	137	150	TMT6plex
P06753	TPM3_HUMAN	DEEKMELQEIQ LKE	N	21.65	2448.34	14	2.2	817.1	3	92.7	F1:13511	7.28E-05	3.23E-04	0.00E+00	1.13E-04	3.61E-04	9.76E-05	138	151	TMT6plex
Q8NGS4	O13F1_HUMAN	HLMVVVLF	Y	15.29	1185.71	8	1.8	593.9	2	85.2	F1:12206	2.01E-04	2.61E-04	2.88E-04	2.30E-04	3.32E-04	2.44E-04	244	251	TMT6plex
P05160	F13B_HUMAN	RNRCP PP	Y	17.97	1067.59	7	7.3	534.8	2	67.8	F2:8784	2.26E-04	5.67E-04	2.67E-04	2.93E-04	4.07E-04	5.35E-04	271	277	TMT6plex

P02671	FIBA_HUMAN	SSTSYNRGDSTFES	Y	29.33	1765.8	14	1.7	883.9	2	38.9	F1:4881	7.53E-04	4.14E-04	6.37E-04	9.00E-04	3.75E-04	2.08E-04	585	598	TMT6plex
Q9Y490	TLN1_HUMAN	DDELN	N	15.56	833.397	5	3.9	417.7	2	30.3	F2:3335	1.07E-04	5.07E-04	2.93E-04	3.46E-04	2.04E-04	1.81E-04	168	172	TMT6plex
P0C0L4	CO4A_HUMAN	NGFKS	N	17.51	1009.6	5	8.5	505.8	2	28.6	F2:3107	7.67E-04	1.88E-03	8.69E-04	1.19E-03	7.15E-04	2.46E-03	1337	1341	TMT6plex
P02675	FIBB_HUMAN	VNDNEEGFF	Y	18.77	1298.6	9	3.6	650.3	2	107	F2:15321	1.17E-04	8.92E-05	2.68E-04	2.45E-04	5.94E-05	2.89E-04	33	41	TMT6plex
P01042	KNG1_HUMAN	DDLEHQG	Y	22.18	1156.52	8	3.6	579.3	2	25.6	F1:2808	3.51E-04	4.40E-04	2.68E-04	3.79E-04	4.48E-04	3.17E-04	480	487	TMT6plex
P01009	A1AT_HUMAN	EDPQGDAAQKTD	Y	23.7	1832.92	13	1.1	612	3	36.4	F1:4494	1.76E-04	1.52E-04	6.63E-05	1.24E-04	1.59E-04	1.60E-04	25	37	TMT6plex
P0DJ18	SAA1_HUMAN	AGLPEKY	N	20.28	1234.73	7	2.5	618.4	2	59.4	F1:8073	7.29E-04	2.26E-03	9.06E-04	3.94E-03	8.01E-04	7.44E-04	116	122	TMT6plex
P0DJ19	SAA2_HUMAN	DAAKKGGGAWAAE V	Y	22.66	1913.05	15	-0.2	638.7	3	61.6	F1:8406	1.05E-04	8.42E-04	1.46E-04	3.20E-04	2.50E-04	1.80E-04	61	75	TMT6plex
Q9Y490	TLN1_HUMAN	QKAAAFEEQENETVV VKE	Y	41.52	2489.31	18	2	830.8	3	85.1	F1:12189	4.47E-05	1.48E-04	0.00E+00	4.37E-05	8.21E-05	0.00E+00	2475	2492	Pyro-glu from Q; TMT6plex
P50552	VASP_HUMAN	GGPTAPK	Y	20.87	1084.66	7	4.3	543.3	2	22.9	F1:2400	2.30E-04	1.22E-03	3.10E-04	4.50E-04	5.96E-04	2.55E-04	246	252	TMT6plex
O00151	PDL1_HUMAN	QEKQELNEPPKQST	Y	26.44	2096.12	14	4.8	699.7	3	45.6	F2:5518	5.79E-05	8.28E-05	4.30E-05	7.71E-05	5.19E-05	7.32E-05	201	214	Pyro-glu from Q; TMT6plex
Q9Y2D5	AKAP2_HUMAN	RPPSVGGP	Y	20.39	994.576	8	-0.9	498.3	2	83.6	F1:11909	4.79E-05	6.13E-05	9.75E-05	7.28E-05	8.02E-05	7.46E-05	372	379	TMT6plex
A6NHT5	HMX3_HUMAN	PGPDAAGTASAPQP PPPPPPAP	Y	20	2343.21	23	-4.5	586.8	4	52	F1:6870	2.87E-04	1.94E-04	8.51E-04	4.52E-04	5.34E-04	6.34E-04	4	26	TMT6plex
O00391	QSOX1_HUMAN	EPPEHM	Y	26.03	967.464	6	6.7	484.7	2	25	F2:2634	1.88E-04	6.38E-04	3.53E-04	3.86E-04	3.19E-04	2.90E-04	620	625	TMT6plex
P62328	TYB4_HUMAN	SDKPDMAEIE	Y	31.6	1404.66	10	0.1	703.3	2	80.2	F2:10688	4.45E-04	7.18E-04	1.63E-04	3.67E-04	4.38E-04	2.96E-04	2	11	Acetylation ; TMT6plex
Q562R1	ACTBL_HUMAN	DEHPILLTEAPLNPK	Y	22.31	2144.22	15	4.6	715.8	3	75.3	F2:9937	2.02E-04	7.03E-04	9.26E-05	1.98E-04	4.33E-04	8.45E-05	100	114	TMT6plex
P60709	ACTB_HUMAN	EEHPVLLTEAPLNPK	Y	49.5	2144.22	15	4.6	715.8	3	75.3	F2:9938	2.02E-04	7.03E-04	9.26E-05	1.98E-04	4.33E-04	8.45E-05	99	113	TMT6plex
P02671	FIBA_HUMAN	ESSSHHPGIAEFPSRG	Y	39.19	1922.94	16	2.7	642	3	30.9	F1:3654	1.45E-04	1.24E-04	1.01E-04	1.31E-04	1.34E-04	1.23E-04	559	574	TMT6plex
Q96ER9	CCD51_HUMAN	GVPVHLV	Y	18.52	948.596	7	9.6	475.3	2	107	F1:16074	2.41E-03	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.71E-03	15	21	TMT6plex
P0C0L4	CO4A_HUMAN	SLGSKINV	Y	34.72	1274.8	8	-4.2	638.4	2	68.6	F1:9486	1.64E-03	2.16E-03	2.33E-03	2.99E-03	1.37E-03	8.86E-04	1361	1368	TMT6plex
Q92616	GCN1L_HUMAN	KSSGSAALL	Y	15.73	1061.63	9	-9.8	531.8	2	96.8	F1:14231	1.53E-04	1.10E-04	1.40E-04	1.04E-04	6.59E-05	1.84E-04	107	115	TMT6plex
Q8WZ42	TITIN_HUMAN	WGKPA	N	16.25	1015.62	5	-8.1	508.8	2	79.7	F1:11273	1.31E-04	2.06E-04	1.39E-04	1.68E-04	1.42E-04	2.02E-04	20536	20540	TMT6plex
Q5VYK3	ECM29_HUMAN	VSTLVE	N	17.18	875.517	6	1.2	438.8	2	72.1	F1:10040	1.93E-04	1.34E-04	2.73E-04	1.50E-04	1.50E-04	2.38E-04	1025	1030	TMT6plex
P11831	SRF_HUMAN	GRVPGN	Y	15.08	827.482	6	0.4	414.7	2	71.9	F1:10011	0.00E+00	7.65E-05	1.86E-04	5.57E-05	4.97E-05	2.70E-04	42	47	TMT6plex
P02671	FIBA_HUMAN	TESRGSSESGIFT	Y	17.18	1498.75	12	1.8	750.4	2	47.1	F1:6112	4.84E-04	3.56E-04	2.72E-04	5.04E-04	2.67E-04	2.01E-04	544	555	TMT6plex
P16112	PGCA_HUMAN	VVEHAR	Y	15.03	938.55	6	-2.9	470.3	2	72.2	F1:10054	7.38E-05	6.85E-05	1.29E-04	8.46E-05	1.36E-04	8.36E-05	2337	2342	TMT6plex
P50851	LRBA_HUMAN	SPVTHVA	N	17.12	938.539	7	9.1	470.3	2	72.2	F1:10055	7.38E-05	6.85E-05	1.29E-04	8.46E-05	1.36E-04	8.36E-05	2518	2524	TMT6plex
P60709	ACTB_HUMAN	EEHPVLLTKAPLNPK	Y	20.49	2143.28	15	-2.6	715.4	3	76	F1:10652	1.34E-04	8.31E-05	0.00E+00	7.80E-05	1.32E-04	6.35E-05	99	113	TMT6plex; Mutation
Q8TF44	C2C4C_HUMAN	GLYSN	N	15.44	878.47	6	-2.8	440.2	2	53.2	F2:6611	3.55E-04	3.74E-04	7.70E-04	4.42E-04	2.97E-04	5.63E-04	35	40	TMT6plex
Q9Y490	TLN1_HUMAN	GLEGDEESTM	Y	19.59	1295.58	10	1	648.8	2	63.2	F1:8639	5.76E-04	4.88E-04	2.36E-04	6.40E-04	4.26E-04	3.94E-04	410	419	TMT6plex
P02671	FIBA_HUMAN	DAGEGDFLAEGGGV R	Y	31.61	1490.66	15	1.6	746.3	2	76	F1:10644	2.35E-04	4.47E-04	1.63E-04	2.21E-04	3.20E-04	1.84E-04	21	35	Acetylation ; Mutation

O76081	RGS20_HUMAN	RPPHPV	Y	15.56	930.56	6	1.5	466.3	2	74.5	F2:9807	1.26E-04	7.66E-05	1.60E-04	1.24E-04	1.59E-04	1.14E-04	148	153	TMT6plex
P0DJJ8	SAA1_HUMAN	DAAKRGGVWAAEAI	Y	24.03	2026.14	16	-5	676.4	3	75.5	F1:10576	7.95E-05	4.79E-04	5.01E-05	2.51E-04	6.09E-05	1.09E-04	61	76	TMT6plex
Q5HYW3	RGAG4_HUMAN	KPIPLPGVR	Y	16.6	1204.79	9	8.1	603.4	2	121	F2:18156	0.00E+00	3.87E-05	1.57E-04	0.00E+00	0.00E+00	1.20E-04	315	323	TMT6plex
Q14624	ITIH4_HUMAN	RQLGLPGPPDVPDHAAYHPF	Y	25.14	2412.25	20	0.4	805.1	3	85.5	F1:12260	5.91E-05	1.78E-04	0.00E+00	1.08E-04	2.32E-04	0.00E+00	668	687	TMT6plex
P02671	FIBA_HUMAN	SGEGDFLAEG	Y	32.3	1209.57	10	0.7	605.8	2	80.2	F1:11366	1.34E-04	4.73E-04	3.22E-04	2.72E-04	3.42E-04	4.51E-04	22	31	TMT6plex
P02461	CO3A1_HUMAN	KDGSPEGPGANGLP	Y	15.77	1523.78	14	-1.6	762.9	2	54.2	F2:6767	1.86E-04	3.01E-04	1.38E-04	1.70E-04	1.90E-04	2.03E-04	466	479	TMT6plex
Q13443	ADAM9_HUMAN	PPQPKVSS	Y	17.55	1296.78	8	7.2	649.4	2	86	F1:12329	1.63E-04	2.52E-04	9.82E-05	2.12E-04	1.83E-04	1.75E-04	792	799	TMT6plex
P0C0L4	CO4A_HUMAN	SHALQLNN	Y	43.27	1124.61	8	1.1	563.3	2	30.5	F1:3595	3.72E-04	6.21E-04	6.53E-04	5.84E-04	4.74E-04	7.21E-04	1341	1348	TMT6plex
Q15942	ZYX_HUMAN	TLKEVEELE	Y	33	1546.89	9	-2.5	774.4	2	87.9	F1:12655	1.40E-03	4.08E-03	4.89E-04	1.99E-03	2.19E-03	3.25E-04	352	360	TMT6plex
O00151	PDL1_HUMAN	ANSRPL	Y	16.8	886.508	6	3.9	444.3	2	23.6	F1:2497	6.85E-04	1.56E-03	2.52E-04	1.19E-03	1.51E-03	3.89E-04	174	179	TMT6plex; Deamidation
Q12789	TF3C1_HUMAN	SVDVRIP	Y	18.44	1013.61	7	2.2	507.8	2	54.6	F1:7274	4.87E-04	8.85E-04	3.23E-03	1.16E-03	7.24E-04	1.65E-03	1581	1587	TMT6plex
P39059	COFA1_HUMAN	GPPGPPGQPLP	Y	15.12	1298.72	12	4.9	433.9	3	27.7	F1:3139	1.27E-04	8.89E-05	1.51E-04	1.49E-04	1.33E-04	1.09E-04	1118	1129	TMT6plex
O95721	SNP29_HUMAN	DDTDPVPR	Y	22.82	1142.58	8	1.7	572.3	2	30	F1:3510	3.13E-04	5.67E-04	3.17E-04	4.02E-04	3.60E-04	3.32E-04	171	178	TMT6plex
Q86UP3	ZFH4_HUMAN	HHCPN	N	19.42	835.396	5	8.3	418.7	2	28.2	F2:3064	1.12E-04	1.66E-04	3.04E-04	2.10E-04	1.36E-04	3.25E-04	98	102	TMT6plex
P0DJJ9	SAA2_HUMAN	DAAKRGGGAWAA	Y	16.89	1684.94	13	2.6	562.7	3	43.1	F1:5486	7.61E-05	4.45E-04	0.00E+00	9.55E-05	1.28E-04	1.33E-04	61	73	TMT6plex
P02671	FIBA_HUMAN	YSKQF	N	21.74	1129.65	5	-3.6	565.8	2	52.2	F1:6895	6.47E-03	3.24E-03	1.02E-02	7.94E-03	6.05E-03	3.17E-03	579	583	TMT6plex
Q14624	ITIH4_HUMAN	SRQLGLPGPPDVPDHAAYHP	Y	50.1	2352.22	20	1.4	785.1	3	68.2	F1:9443	0.00E+00	1.07E-04	6.10E-05	4.59E-05	7.93E-05	0.00E+00	667	686	TMT6plex
A8TX70	CO6A5_HUMAN	LVSSVI	N	15.92	845.543	6	2.6	423.8	2	114	F1:17582	8.91E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.06E-05	1985	1990	TMT6plex
O15197	EPHB6_HUMAN	LVSSVL	N	15.92	845.543	6	2.6	423.8	2	114	F1:17582	8.91E-05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	5.06E-05	25	30	TMT6plex
Q6ZT07	TBCD9_HUMAN	KPVCMM	Y	19.87	936.48	6	1.6	469.2	2	33.6	F1:4069	1.68E-04	2.70E-04	3.52E-04	1.89E-04	1.88E-04	3.34E-04	1232	1237	TMT6plex
Q15942	ZYX_HUMAN	KPKVNPFRPGDSEPPPAPGAQ	Y	38.2	2872.62	21	1.7	719.2	4	58.4	F1:7899	0.00E+00	9.91E-05	0.00E+00	0.00E+00	5.66E-05	0.00E+00	33	53	TMT6plex
Q15942	ZYX_HUMAN	HVQPQPQPKPQVQLHVQ	Y	47.35	2445.4	17	0.1	612.4	4	45.6	F1:5861	1.70E-04	9.29E-05	0.00E+00	1.37E-04	2.12E-04	0.00E+00	223	239	TMT6plex
P68363	TBA1B_HUMAN	VEGEGEEEGEEY	Y	25.39	1583.67	12	3.1	792.8	2	59.7	F2:7645	1.71E-04	2.06E-04	5.89E-05	2.20E-04	1.45E-04	1.29E-04	440	451	TMT6plex
P0DJJ8	SAA1_HUMAN	RPAGLPE	N	17.3	967.565	7	4.3	484.8	2	30.3	F2:3338	5.24E-04	1.77E-03	5.52E-04	1.24E-03	6.56E-04	4.18E-04	114	120	TMT6plex
P10124	SRGN_HUMAN	DLNRIFPL	Y	31.23	1215.72	8	1.8	608.9	2	115	F1:17810	6.02E-04	2.41E-04	4.45E-04	5.30E-04	3.50E-04	2.65E-04	82	89	TMT6plex
Q15942	ZYX_HUMAN	TPKFTPVAS	Y	26.31	1404.84	9	1.6	703.4	2	59.3	F1:8051	6.60E-04	1.06E-03	3.75E-04	8.26E-04	9.81E-04	5.50E-04	270	278	TMT6plex
Q9BV73	CP250_HUMAN	VKLSA	N	15.77	974.653	5	-6.6	488.3	2	75.1	F1:10522	1.47E-04	0.00E+00	1.05E-04	9.15E-05	6.57E-05	1.49E-04	599	603	TMT6plex
P29474	NOS3_HUMAN	VKISA	N	15.77	974.653	5	-6.6	488.3	2	75.1	F1:10522	1.47E-04	0.00E+00	1.05E-04	9.15E-05	6.57E-05	1.49E-04	503	507	TMT6plex
P02649	APOE_HUMAN	TVGSLAQPLQ	Y	28.47	1298.74	11	5.2	650.4	2	75.3	F2:9924	3.57E-04	1.83E-04	2.32E-04	2.41E-04	4.01E-04	2.14E-04	212	222	TMT6plex
O95810	SDPR_HUMAN	VEGEIAEEAAE	Y	40.87	1374.67	11	1.5	688.3	2	75.8	F1:10622	4.29E-04	5.22E-04	2.31E-04	3.91E-04	4.51E-04	2.23E-04	347	357	TMT6plex
Q8WZ42	TITIN_HUMAN	LFRVVAVN	Y	17.14	1145.71	8	9.7	573.9	2	96.6	F2:13444	6.99E-05	1.26E-04	1.06E-04	1.14E-04	8.67E-05	7.98E-05	24127	24134	TMT6plex

P0DJJ9	SAA2_HUMAN	TGRGAEDSLADQAA NKWG	Y	35.65	2436.21	18	-0.3	813.1	3	82.3	F2:11036	0.00E+00	3.71E-04	9.42E-05	3.47E-04	1.11E-04	1.50E-04	87	104	TMT6plex; Hydroxyphenylg lyoxal arginine
Q8IUX7	AEBP1_HUMAN	NRPIPH	Y	15.38	961.566	6	8.4	481.8	2	38.7	F1:4853	5.33E-04	3.19E-03	8.43E-04	1.38E-03	7.47E-04	1.48E-03	999	1004	TMT6plex
P0C0L4	CO4A_HUMAN	QPVTPL	N	20.63	882.538	6	3.3	442.3	2	60.5	F1:8242	2.03E-04	2.39E-04	4.91E-04	3.10E-04	2.73E-04	4.66E-04	1436	1441	TMT6plex
P42025	ACTY_HUMAN	QYTLPDGSTLDVGP A R	Y	16.84	1918.98	16	-1.8	640.7	3	29.5	F2:3217	5.78E-05	1.01E-04	0.00E+00	5.54E-05	4.59E-05	9.26E-05	240	255	TMT6plex; Deamidation
P04792	HSPB1_HUMAN	ELTVK	N	15.13	1046.67	5	3.1	524.3	2	47.9	F1:6226	4.05E-04	2.02E-03	4.36E-04	6.24E-04	9.39E-04	6.96E-04	108	112	TMT6plex
P21817	RYR1_HUMAN	LGPGQVGH L	Y	19.32	1105.64	9	0.3	553.8	2	89.3	F2:12193	7.01E-05	1.23E-04	1.41E-04	1.01E-04	1.45E-04	1.14E-04	1193	1201	TMT6plex
P0DJJ9	SAA2_HUMAN	GAEDSLADQAANK W G	Y	36.08	1990.02	15	4.3	664.3	3	93.7	F2:12936	6.56E-05	3.02E-04	7.84E-05	1.76E-04	7.53E-05	1.06E-04	90	104	TMT6plex
Q68CP9	ARID2_HUMAN	DPKII	N	15.17	1042.68	5	-4.8	522.3	2	62.5	F1:8541	2.51E-04	8.59E-04	3.77E-04	6.00E-04	6.36E-04	4.61E-04	196	200	TMT6plex
Q96J17	SPTCS_HUMAN	DPKLI	N	15.17	1042.68	5	-4.8	522.3	2	62.5	F1:8541	2.51E-04	8.59E-04	3.77E-04	6.00E-04	6.36E-04	4.61E-04	1049	1053	TMT6plex
P50851	LRBA_HUMAN	DPKIL	N	15.17	1042.68	5	-4.8	522.3	2	62.5	F1:8541	2.51E-04	8.59E-04	3.77E-04	6.00E-04	6.36E-04	4.61E-04	2119	2123	TMT6plex
P21359	NF1_HUMAN	DPKLL	N	15.17	1042.68	5	-4.8	522.3	2	62.5	F1:8541	2.51E-04	8.59E-04	3.77E-04	6.00E-04	6.36E-04	4.61E-04	503	507	TMT6plex
Q8WZ42	TITIN_HUMAN	QICRAL	N	15.52	931.548	6	9.5	466.8	2	60.7	F2:7735	5.57E-05	9.99E-05	1.70E-04	9.03E-05	3.64E-05	1.51E-04	4081	4086	TMT6plex
P60709	ACTB_HUMAN	HPVLLTEAPLNPK	Y	46.32	1886.14	13	2.1	629.7	3	70.8	F1:9812	5.12E-05	2.72E-04	0.00E+00	9.82E-05	1.27E-04	0.00E+00	101	113	TMT6plex
Q6QHK4	FIGLA_HUMAN	RGFAR	N	17.58	834.503	5	2.3	418.3	2	75.5	F2:9966	5.16E-05	5.13E-05	1.77E-04	0.00E+00	0.00E+00	1.98E-04	83	87	TMT6plex
P78347	GTF2L_HUMAN	AVKVPF	N	16.25	1117.73	6	-9.1	559.9	2	112	F1:17131	1.31E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.87E-05	754	759	TMT6plex
Q16186	ADRM1_HUMAN	TTSSTR	Y	20.25	880.482	6	-1.8	441.2	2	51.5	F2:6384	9.15E-03	9.32E-03	2.04E-02	1.23E-02	8.24E-03	1.41E-02	221	226	TMT6plex
P00734	THRB_HUMAN	TFGSGEADC	Y	15.22	1162.47	9	3.8	582.2	2	65.3	F2:8430	2.30E-04	2.72E-04	2.64E-04	2.26E-04	2.25E-04	3.66E-04	328	336	TMT6plex; Cysteine oxidation to cysteic acid
P02671	FIBA_HUMAN	SETESRGSSESGIFT NT KES	Y	35.24	2503.24	19	3.4	835.4	3	48.1	F2:5904	4.67E-04	2.39E-04	1.22E-04	7.39E-04	2.00E-04	1.15E-04	542	560	TMT6plex
P02671	FIBA_HUMAN	STGKTFPG	Y	20.42	1251.72	8	6.8	626.9	2	44.7	F1:5716	2.04E-03	8.27E-04	7.60E-04	1.59E-03	1.28E-03	1.22E-03	524	531	TMT6plex
O60287	NPA1P_HUMAN	RPAGVSSAVI	Y	15.33	1184.71	10	-7.3	593.4	2	83.7	F2:11298	1.80E-04	2.87E-04	6.91E-04	2.63E-04	2.87E-04	4.35E-04	1286	1295	TMT6plex
Q96DN6	MBD6_HUMAN	EAFPPSP	Y	19.32	1119.58	8	-1.4	560.8	2	33.8	F1:4100	3.35E-04	7.70E-04	5.08E-04	6.69E-04	4.95E-04	5.91E-04	516	523	TMT6plex
Q15942	ZYX_HUMAN	TQPRGPPASSPAP APK F	Y	28.63	2163.22	17	4.5	722.1	3	47.9	F2:5867	3.05E-04	7.32E-05	0.00E+00	1.43E-04	2.83E-04	6.49E-05	250	266	TMT6plex
Q8WXI7	MUC16_HUMAN	PTLGLTLP	Y	15.82	1027.61	8	2.8	514.8	2	74	F2:9722	9.50E-05	8.94E-05	8.19E-05	1.43E-04	7.24E-05	7.58E-05	10503	10510	TMT6plex
O95810	SDPR_HUMAN	EGKEELPDENKS LE	Y	29.48	2303.25	14	8.5	768.8	3	62.2	F1:8485	2.64E-04	7.37E-04	1.04E-04	2.29E-04	6.15E-04	0.00E+00	181	194	TMT6plex
O95810	SDPR_HUMAN	GAVEGKEELPDEN KS LEETLH	Y	36.17	3010.61	21	-3.5	753.7	4	75.3	F1:10554	0.00E+00	1.39E-04	0.00E+00	0.00E+00	2.30E-04	0.00E+00	178	198	TMT6plex
Q9P1Y5	CAMP3_HUMAN	GSSSPVF	Y	15.8	908.481	7	0.8	455.2	2	111	F1:16887	1.49E-04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	9.05E-05	348	354	TMT6plex
Q15942	ZYX_HUMAN	GGSGSQPNQKLGHP E A	Y	49.64	2021.07	16	3.5	674.7	3	27.7	F1:3149	1.63E-04	8.91E-04	1.15E-04	9.72E-05	6.16E-04	1.58E-04	286	301	TMT6plex
P02671	FIBA_HUMAN	HPGIAEFPS	Y	21.52	1198.62	9	3.3	600.3	2	48.8	F2:6041	3.49E-04	4.60E-04	3.23E-04	4.10E-04	1.96E-04	4.38E-04	564	572	TMT6plex; Hydroxylation

P02671	FIBA_HUMAN	QLQKVPP	Y	20.96	1020.62	7	3	511.3	2	64.2	F1:8801	4.05E-04	4.63E-04	7.54E-04	4.54E-04	4.53E-04	8.95E-04	240	246	Pyro-glu from Q; TMT6plex
P01024	CO3_HUMAN	RIHWESASL	Y	33.75	1326.72	9	2.3	664.4	2	62.2	F1:8495	4.92E-04	1.24E-03	6.80E-04	8.67E-04	7.55E-04	1.04E-03	1310	1318	TMT6plex
Q15762	CD226_HUMAN	DDTREDIYVNYPT	Y	37.07	1828.87	13	3.5	915.4	2	76.3	F1:10701	1.59E-04	5.47E-04	1.27E-04	2.25E-04	3.02E-04	1.63E-04	315	327	TMT6plex
Q05682	CALD1_HUMAN	SRPGGRASVDTKEAE GAPQVE	Y	40.33	2598.38	21	3	650.6	4	34.6	F1:4228	0.00E+00	8.53E-05	0.00E+00	3.40E-05	8.88E-05	0.00E+00	511	531	TMT6plex
P67936	TPM4_HUMAN	DEEKMEIQEM	N	32.96	1738.85	10	4.6	580.6	3	78.4	F1:11065	0.00E+00	2.99E-04	1.64E-04	1.49E-04	9.58E-05	1.27E-04	101	110	TMT6plex
P07951	TPM2_HUMAN	DEEKMELQEM	N	32.96	1738.85	10	4.6	580.6	3	78.4	F1:11065	0.00E+00	2.99E-04	1.64E-04	1.49E-04	9.58E-05	1.27E-04	137	146	TMT6plex
Q8IX18	DHX40_HUMAN	RLYPVR	Y	17.44	1031.64	6	1.2	516.8	2	114	F2:16697	0.00E+00	7.84E-05	7.00E-04	6.61E-05	2.92E-04	1.86E-04	233	238	TMT6plex
P09493	TPM1_HUMAN	DEEKMEIQEIQ	N	15.65	1848.95	11	5.1	925.5	2	76.6	F2:10139	1.54E-04	4.52E-04	0.00E+00	1.92E-04	1.82E-04	9.25E-05	137	147	TMT6plex
P06753	TPM3_HUMAN	DEEKMELQEIQ	N	15.65	1848.95	11	5.1	925.5	2	76.6	F2:10139	1.54E-04	4.52E-04	0.00E+00	1.92E-04	1.82E-04	9.25E-05	138	148	TMT6plex
Q8IXK2	GLT12_HUMAN	GLGSVLRA	Y	18.18	1000.62	8	7.8	501.3	2	37.5	F2:4410	7.10E-04	1.37E-03	2.88E-04	9.40E-04	4.22E-04	6.59E-04	32	39	TMT6plex
P02671	FIBA_HUMAN	SGEGDFLAEGGV	Y	52.74	1422.68	13	2.8	712.4	2	96.9	F1:14234	1.10E-03	1.66E-03	3.60E-03	5.84E-03	1.27E-03	9.71E-04	22	34	TMT6plex
P0C0L4	CO4A_HUMAN	LGSKINV	Y	28.58	1187.76	7	-2.6	594.9	2	68.9	F1:9524	2.51E-03	3.66E-03	3.08E-03	3.86E-03	2.43E-03	2.39E-03	1362	1368	TMT6plex
Q9ULM0	PKHH1_HUMAN	VKLMY	N	15.12	1110.69	5	1.3	556.4	2	93.4	F2:12881	4.20E-05	4.83E-05	0.00E+00	0.00E+00	6.49E-05	0.00E+00	1088	1092	TMT6plex
Q5R372	RBG1L_HUMAN	VKIMY	N	15.12	1110.69	5	1.3	556.4	2	93.4	F2:12881	4.20E-05	4.83E-05	0.00E+00	0.00E+00	6.49E-05	0.00E+00	644	648	TMT6plex
Q14624	ITIH4_HUMAN	QLGLPGPPDVPDHAA YHPFR	Y	41.26	2166.06	20	9.7	723	3	98.1	F2:13694	0.00E+00	5.44E-05	0.00E+00	3.39E-05	0.00E+00	0.00E+00	669	688	Pyro-glu from Q
Q9HCU4	CELR2_HUMAN	PRTRF	N	15.87	904.545	5	-0.6	453.3	2	99.5	F1:14704	0.00E+00	2.90E-05	0.00E+00	0.00E+00	4.66E-05	0.00E+00	1987	1991	TMT6plex
Q8NH09	OR8S1_HUMAN	SALRAAP	Y	18.57	913.555	7	3.8	457.8	2	23.3	F1:2454	8.75E-04	1.28E-03	2.43E-03	1.09E-03	1.16E-03	3.10E-03	349	355	TMT6plex
P31327	CPSM_HUMAN	TIGYPVMIR	Y	15.38	1277.74	9	9.6	639.9	2	46.2	F2:5603	1.76E-04	2.12E-04	1.70E-04	2.78E-04	1.62E-04	1.58E-04	579	587	TMT6plex
Q9Y490	TLN1_HUMAN	DGAFTEN	Y	28.95	1110.5	8	6.8	556.3	2	47.1	F2:5722	4.27E-04	7.27E-04	3.65E-04	4.80E-04	6.36E-04	5.20E-04	1547	1554	TMT6plex
Q7Z408	CSMD2_HUMAN	NGLRL	N	16.18	800.507	5	6.4	401.3	2	107	F1:16197	0.00E+00	3.54E-05	0.00E+00	0.00E+00	0.00E+00	5.59E-05	2960	2964	TMT6plex
Q01484	ANK2_HUMAN	NGLRI	N	16.18	800.507	5	6.4	401.3	2	107	F1:16197	0.00E+00	3.54E-05	0.00E+00	0.00E+00	0.00E+00	5.59E-05	987	991	TMT6plex
Q96RW7	HMCN1_HUMAN	NGIRL	N	16.18	800.507	5	6.4	401.3	2	107	F1:16197	0.00E+00	3.54E-05	0.00E+00	0.00E+00	0.00E+00	5.59E-05	3933	3937	TMT6plex
Q9Y330	ZBT12_HUMAN	PKPPPPP	Y	25.17	1283.8	8	2.6	642.9	2	35.8	F2:4130	5.68E-04	1.42E-03	4.96E-04	8.58E-04	6.10E-04	7.22E-04	164	171	TMT6plex
Q5TF21	SOGA3_HUMAN	ASHLGI	N	19.52	825.491	6	3.2	413.8	2	41.4	F1:5210	2.47E-04	2.84E-04	6.36E-04	3.06E-04	1.97E-04	8.96E-04	739	744	TMT6plex
P01024	CO3_HUMAN	ASHLGL	N	19.52	825.491	6	3.2	413.8	2	41.4	F1:5210	2.47E-04	2.84E-04	6.36E-04	3.06E-04	1.97E-04	8.96E-04	741	746	TMT6plex
Q27J81	INF2_HUMAN	PPPPPP	N	18.31	926.543	7	-3.8	464.3	2	45.1	F1:5776	4.05E-04	4.95E-04	4.07E-04	5.88E-04	2.76E-04	5.40E-04	421	427	TMT6plex
P42261	GRIA1_HUMAN	FEEGRDQTT	Y	15.3	1310.63	9	4.3	656.3	2	60.8	F1:8302	4.03E-04	1.28E-03	5.53E-04	5.92E-04	9.67E-04	9.55E-04	570	578	TMT6plex
Q9ULB1	NRX1A_HUMAN	GKPPT	N	15.16	956.606	5	5.1	479.3	2	113	F1:17355	7.72E-05	0.00E+00	0.00E+00	0.00E+00	4.92E-05	0.00E+00	1336	1340	TMT6plex
P01042	KNG1_HUMAN	RLLLSLTQ	Y	17.16	956.602	8	9.4	479.3	2	113	F1:17354	7.72E-05	0.00E+00	0.00E+00	0.00E+00	4.92E-05	0.00E+00	12	19	Methyl ester
P25940	CO5A3_HUMAN	PPGPAGV	Y	15	822.48	7	1.8	412.2	2	74.4	F1:10399	1.02E-04	2.43E-04	1.02E-03	4.85E-04	2.74E-04	9.15E-04	912	918	TMT6plex
Q9Y6R4	M3K4_HUMAN	ATPGTK	Y	21.37	1031.64	6	7.1	516.8	2	111	F2:16106	0.00E+00	4.13E-05	9.90E-05	0.00E+00	0.00E+00	1.00E-04	328	333	TMT6plex
Q9Y490	TLN1_HUMAN	EDSVSPK	Y	32.85	1218.69	7	1.3	610.4	2	30.6	F1:3606	1.59E-03	4.49E-03	7.66E-04	2.18E-03	2.65E-03	8.79E-04	421	427	TMT6plex
P60709	ACTB_HUMAN	TLKYPIEHG	N	20.25	1528.9	9	-0.2	510.6	3	53.9	F1:7143	3.90E-04	1.08E-03	3.25E-04	2.90E-04	8.24E-04	4.25E-04	66	74	TMT6plex; Methyl ester

Q66K64	DCA15_HUMAN	SSGRYV	Y	17	896.492	6	-8.7	449.2	2	74.3	F2:9767	2.22E-04	2.10E-04	3.97E-04	3.12E-04	1.74E-04	4.26E-04	567	572	TMT6plex
P02671	FIBA_HUMAN	TGKEKVTSGSTTTT	Y	32.83	1855.03	14	4.6	619.4	3	20.6	F1:2037	6.43E-05	7.91E-05	0.00E+00	5.48E-05	6.14E-05	0.00E+00	444	457	TMT6plex
P21817	RYR1_HUMAN	ASRRI	N	19.97	830.529	5	1.8	416.3	2	31.8	F1:3787	2.02E-04	3.04E-04	5.30E-04	2.29E-04	2.40E-04	7.40E-04	4185	4189	TMT6plex
Q8NDA2	HMCN2_HUMAN	ASRRL	N	19.97	830.529	5	1.8	416.3	2	31.8	F1:3787	2.02E-04	3.04E-04	5.30E-04	2.29E-04	2.40E-04	7.40E-04	4351	4355	TMT6plex
Q96BY7	ATG2B_HUMAN	LINTFNK	Y	16.22	1306.8	7	4.6	654.4	2	113	F1:17279	5.36E-05	1.64E-04	0.00E+00	3.35E-05	5.25E-05	8.57E-05	994	1000	TMT6plex
Q05682	CALD1_HUMAN	DTKEAEGAPQ	Y	19.72	1502.8	10	4.9	752.4	2	23.3	F2:2365	2.00E-04	7.89E-04	7.59E-05	2.07E-04	5.31E-04	5.45E-04	520	529	TMT6plex
Q9UM47	NOTC3_HUMAN	PPPVRALP	Y	16.16	1074.68	8	3.2	538.3	2	38.2	F2:4489	1.03E-03	1.86E-03	1.53E-03	1.71E-03	1.43E-03	1.01E-03	21	28	TMT6plex
Q13402	MYO7A_HUMAN	SRTLITR	Y	19.92	1074.67	7	6.8	538.3	2	38.2	F2:4490	1.03E-03	1.86E-03	1.53E-03	1.71E-03	1.43E-03	1.01E-03	372	378	TMT6plex
P68363	TBA1B_HUMAN	QLFHPEQLITGKEDANNY	N	20.49	2399.2	19	4.1	1201	2	125	F1:19765	1.46E-03	7.66E-05	0.00E+00	9.39E-04	1.11E-03	0.00E+00	85	103	Pyro-glu from Q; TMT6plex
Q9Y239	NOD1_HUMAN	PRQFL	N	16.37	888.538	5	8.2	445.3	2	87.9	F1:12656	0.00E+00	0.00E+00	4.07E-05	0.00E+00	6.21E-05	0.00E+00	339	343	TMT6plex
Q05682	CALD1_HUMAN	NDDDEEEAARE	Y	23.43	1520.64	11	3.6	761.3	2	21.7	F1:2207	1.23E-04	4.19E-04	7.04E-05	1.74E-04	3.83E-04	1.67E-04	30	40	TMT6plex
Q96JK9	MAML3_HUMAN	HNQAQGPR	Y	19.69	1137.57	8	1.5	569.8	2	50.8	F1:6699	7.26E-04	9.95E-04	4.63E-04	5.78E-04	9.10E-04	5.31E-04	894	901	TMT6plex; Deamidation
O14745	NHRF1_HUMAN	SADAAAGAPLPR	Y	33.49	1137.58	12	-2.7	569.8	2	50.8	F1:6700	7.26E-04	9.95E-04	4.63E-04	5.78E-04	9.10E-04	5.31E-04	2	13	Acetylation
P04004	VTNC_HUMAN	GGPSLTSDLQAQSKGNPEQTPV	Y	30.12	2668.41	22	2.6	890.5	3	81.2	F2:10851	0.00E+00	9.02E-05	0.00E+00	0.00E+00	5.97E-05	0.00E+00	94	115	TMT6plex
P67936	TPM4_HUMAN	AMKDEEKMEIQEMQLKE	N	20.04	3025.63	17	1	757.4	4	89.9	F1:12994	0.00E+00	5.25E-05	0.00E+00	3.48E-05	0.00E+00	0.00E+00	98	114	TMT6plex
P07951	TPM2_HUMAN	AMKDEEKMEIQEMQLKE	N	20.04	3025.63	17	1	757.4	4	89.9	F1:12994	0.00E+00	5.25E-05	0.00E+00	3.48E-05	0.00E+00	0.00E+00	134	150	TMT6plex
P50552	VASP_HUMAN	SVPNGPSPEEVEQQ	Y	28.51	1725.83	14	3.2	863.9	2	65.2	F1:8947	7.38E-05	3.85E-04	1.85E-04	2.33E-04	3.30E-04	1.68E-04	128	141	TMT6plex; Deamidation
P09493	TPM1_HUMAN	HIAEDADRKYEEVA	Y	32.37	2103.1	14	3.6	526.8	4	58.8	F1:7963	0.00E+00	2.69E-05	0.00E+00	0.00E+00	4.03E-05	0.00E+00	153	166	TMT6plex
P00734	THRB_HUMAN	TATSEYQTFNPR	Y	57.49	1789.88	13	1.4	896	2	90.7	F1:13150	1.55E-03	9.16E-04	2.60E-03	1.92E-03	1.18E-03	1.51E-03	315	327	TMT6plex
P04792	HSPB1_HUMAN	LPPGVDP	Y	22.89	922.533	7	3.5	462.3	2	76.9	F1:10804	0.00E+00	1.19E-04	1.53E-04	7.91E-05	7.15E-05	1.67E-04	144	150	TMT6plex
P42658	DPP6_HUMAN	SRVPIM	Y	16.37	930.552	6	7.3	466.3	2	91.6	F1:13305	8.70E-05	4.94E-05	4.84E-05	4.41E-05	3.50E-05	1.34E-04	321	326	TMT6plex
P04004	VTNC_HUMAN	EEEEAPAPEVGGASKPEG	Y	39.82	2054.06	16	0.2	685.7	3	53.9	F1:7139	1.45E-04	4.42E-04	1.59E-04	2.37E-04	1.86E-04	2.41E-04	119	134	TMT6plex
P52566	GDIR2_HUMAN	TEKAPEPH	Y	33.96	1178.61	8	4.2	590.3	2	23.3	F1:2456	5.37E-04	2.31E-03	4.45E-04	7.21E-04	1.11E-03	9.43E-04	2	9	Acetylation; TMT6plex
Q8N4T4	ARG39_HUMAN	PPLHLRL	Y	31.35	1073.69	7	2.3	537.9	2	123	F1:19364	1.80E-04	0.00E+00	5.46E-05	4.67E-05	0.00E+00	1.35E-04	262	268	TMT6plex
P37840	SYUA_HUMAN	TKEGVV	Y	17.34	874.533	6	-1.3	438.3	2	121	F2:18058	7.17E-05	0.00E+00	7.27E-05	0.00E+00	7.28E-05	1.02E-04	44	49	TMT6plex; Methyl ester
P02671	FIBA_HUMAN	SYKMADEAGSEADH EGTHS	Y	41.52	2479.13	19	3.4	620.8	4	39.6	F1:4975	0.00E+00	1.39E-04	0.00E+00	5.36E-05	4.51E-05	0.00E+00	600	618	TMT6plex
O95810	SDPR_HUMAN	ENETKSEDLPSSE	Y	18.62	1921.95	13	2.9	641.7	3	46.2	F1:5961	1.05E-04	2.70E-04	1.45E-04	2.04E-04	1.29E-04	1.42E-04	310	322	TMT6plex
Q17RW2	COOA1_HUMAN	GEPGIPG	N	17.69	854.47	7	4.9	428.2	2	39.1	F1:4909	2.83E-04	2.53E-04	3.09E-04	3.27E-04	1.93E-04	3.72E-04	1164	1170	TMT6plex
Q8NFW1	COMA1_HUMAN	GEPGLPG	N	17.69	854.47	7	4.9	428.2	2	39.1	F1:4909	2.83E-04	2.53E-04	3.09E-04	3.27E-04	1.93E-04	3.72E-04	557	563	TMT6plex



O95810	SDPR_HUMAN	LVEGEIAEEAAEKAT	Y	40.75	2017.1	15	2.5	1010	2	108	F1:16331	1.11E-03	8.14E-04	1.31E-04	6.32E-04	1.01E-03	1.11E-04	346	360	TMT6plex
P60709	ACTB_HUMAN	HPVLL	N	16.28	806.522	5	0.7	404.3	2	46.7	F1:6042	1.23E-04	2.05E-04	3.04E-04	2.30E-04	1.12E-04	3.59E-04	101	105	TMT6plex
Q15942	ZYX_HUMAN	FSPGAPGGSGSQPNQ KLGHPEA	Y	59.28	2577.33	22	3.5	860.1	3	56.6	F1:7600	1.51E-04	4.08E-04	4.24E-05	1.07E-04	5.15E-04	1.13E-04	280	301	TMT6plex
P07951	TPM2_HUMAN	DEEKMELQEMQ	N	37.7	1866.91	11	1.4	934.5	2	74.2	F1:10372	1.46E-03	1.85E-03	2.31E-04	1.38E-03	1.37E-03	3.21E-04	137	147	TMT6plex
P67936	TPM4_HUMAN	DEEKMEIQEMQ	N	37.7	1866.91	11	1.4	934.5	2	74.2	F1:10372	1.46E-03	1.85E-03	2.31E-04	1.38E-03	1.37E-03	3.21E-04	101	111	TMT6plex
O95810	SDPR_HUMAN	EGEIAEEAAEKATS	Y	44.88	1891.98	14	3.6	631.7	3	84.5	F1:12068	1.39E-04	2.14E-04	0.00E+00	1.76E-04	1.15E-04	1.15E-04	348	361	TMT6plex
P02671	FIBA_HUMAN	QKVPPEW	Y	31.88	1094.6	7	4.3	548.3	2	89.1	F1:12874	4.26E-04	2.18E-04	1.14E-04	2.04E-04	2.77E-04	2.00E-04	242	248	Pyro-glu from Q; TMT6plex
Q93008	USP9X_HUMAN	QNVADILFVR	Y	16.43	1402.81	10	-2.1	702.4	2	114	F1:17600	4.69E-05	7.84E-05	6.66E-05	6.22E-05	1.04E-04	0.00E+00	2273	2282	TMT6plex
Q9H4B7	TBB1_HUMAN	EEVTEEAEMEPEDKG H	Y	54.76	2316.08	16	1	773	3	56.9	F1:7655	3.12E-04	7.95E-04	2.02E-04	2.50E-04	8.64E-04	3.95E-04	436	451	TMT6plex
Q969S9	RRF2M_HUMAN	FKGVV	N	15.35	1006.66	5	-8.2	504.3	2	101	F2:14299	5.88E-05	3.67E-05	0.00E+00	4.72E-05	6.85E-05	0.00E+00	232	236	TMT6plex
P02452	CO1A1_HUMAN	DGATGAAGPP	Y	29.95	1057.52	10	1.8	529.8	2	23.7	F1:2507	1.15E-04	1.94E-04	6.80E-05	2.00E-04	1.24E-04	0.00E+00	325	334	TMT6plex; Hydroxylation
Q15678	PTN14_HUMAN	RHPPIVV	Y	28.55	1045.66	7	0.3	523.8	2	103	F1:15395	0.00E+00	3.89E-05	1.54E-04	0.00E+00	3.95E-05	2.15E-04	1113	1119	TMT6plex
Q8TDY2	RBCC1_HUMAN	DMEIK	N	16.94	1092.63	5	2.2	547.3	2	54.3	F1:7218	3.52E-03	2.14E-03	1.01E-03	2.41E-03	2.36E-03	1.28E-03	97	101	TMT6plex
Q9Y490	TLN1_HUMAN	NETVVVKE	Y	17.75	1374.81	8	4.7	688.4	2	43.8	F2:5252	4.37E-04	1.17E-03	2.32E-04	2.74E-04	8.70E-04	4.46E-04	2485	2492	TMT6plex
P02671	FIBA_HUMAN	EFPSRG	Y	19.07	920.492	6	1.3	461.3	2	28.2	F1:3232	1.73E-03	8.22E-04	5.41E-04	4.72E-04	5.26E-04	2.71E-03	569	574	TMT6plex
P01024	CO3_HUMAN	GTQVVEKVVL	Y	16.72	1528.96	10	-7.4	765.5	2	120	F2:17809	0.00E+00	4.62E-05	4.56E-05	7.02E-05	4.01E-05	0.00E+00	113	122	TMT6plex
P21333	FLNA_HUMAN	DVGKDQEFTVKS	Y	17.8	2039.15	12	5.1	680.7	3	58.2	F2:7435	8.19E-05	6.56E-04	9.24E-05	1.04E-04	5.44E-04	0.00E+00	984	995	TMT6plex
Q86UX7	URP2_HUMAN	SQDEAPGDPIQQLNL KGCEVV	Y	39.97	2847.45	21	1.3	950.2	3	93.2	F2:12846	1.67E-04	5.77E-04	1.10E-04	3.60E-04	3.12E-04	5.47E-05	390	410	TMT6plex; S- guanylation-2
Q9GZZ9	UBA5_HUMAN	TIPKKQEDSVTELTVE DSG	Y	37.02	2762.52	19	-0.5	921.8	3	75.1	F1:10516	5.38E-05	1.35E-04	0.00E+00	4.85E-05	1.05E-04	0.00E+00	373	391	TMT6plex
O60241	BAI2_HUMAN	ILPPRPPLA	Y	21.11	1298.83	10	6.7	650.4	2	114	F2:16716	0.00E+00	0.00E+00	2.78E-04	3.94E-04	0.00E+00	0.00E+00	827	836	TMT6plex
P50552	VASP_HUMAN	EKTPKDESANQEEPE A	Y	27.97	2488.29	16	2.7	830.4	3	37.6	F1:4684	6.12E-05	2.22E-04	0.00E+00	5.70E-05	2.24E-04	6.27E-05	282	297	TMT6plex
Q13275	SEM3F_HUMAN	AVYARIGR	Y	17.81	1133.69	8	3.3	567.9	2	69.5	F2:9075	2.06E-03	9.22E-04	4.39E-04	8.43E-04	1.53E-03	6.54E-04	291	298	TMT6plex
Q13395	TARB1_HUMAN	VPLAAGFQW	Y	16.86	1216.68	9	-0.1	609.3	2	64.5	F2:8295	3.86E-04	4.56E-04	3.91E-04	3.13E-04	4.02E-04	5.78E-04	1386	1394	TMT6plex
P01042	KNG1_HUMAN	LEHQGGHVL	Y	15.69	1216.69	9	-6.1	609.3	2	64.5	F2:8296	3.86E-04	4.56E-04	3.91E-04	3.13E-04	4.02E-04	5.78E-04	483	491	TMT6plex; Amidation
Q15942	ZYX_HUMAN	EEIFSPPPPPEE	Y	40.25	1692.84	13	4.2	847.4	2	103	F2:14598	3.60E-04	2.38E-04	1.27E-04	2.25E-04	2.71E-04	1.76E-04	111	123	TMT6plex
Q0VDD8	DYH14_HUMAN	RVPISH	Y	17.65	936.571	6	-4.5	469.3	2	80.1	F1:11335	5.75E-05	7.08E-05	2.23E-04	1.10E-04	8.06E-05	1.22E-04	2036	2041	TMT6plex
Q9UPN6	SCAF8_HUMAN	PPQRGIPPP	Y	22.55	1186.7	9	4	594.4	2	104	F1:15480	6.18E-05	8.16E-05	6.71E-04	9.07E-05	5.10E-05	5.04E-04	947	955	TMT6plex
P68366	TBA4A_HUMAN	YEDEDEGEE	Y	26.84	1342.53	9	3.2	672.3	2	41.9	F1:5297	3.14E-04	5.19E-04	4.13E-04	3.94E-04	3.58E-04	5.51E-04	440	448	TMT6plex
P01024	CO3_HUMAN	ENEGFTVTA	Y	31.39	1195.59	9	2.3	598.8	2	71.1	F1:9868	3.86E-04	3.30E-04	3.51E-04	4.86E-04	3.21E-04	3.02E-04	1326	1334	TMT6plex
P68363	TBA1B_HUMAN	VEGEGEEEGEE	Y	26.21	1420.6	11	4.5	711.3	2	36.9	F2:4313	5.67E-04	5.24E-04	5.65E-04	3.86E-04	5.51E-04	6.63E-04	440	450	TMT6plex

P01024	CO3_HUMAN	SEEIKENEFTIVIAE G	Y	52.15	2185.08	16	2.6	1094	2	64.9	F1:8900	1.76E-03	1.90E-03	1.33E-03	3.04E-03	1.77E-03	6.59E-04	1321	1336	TMT6plex
P02671	FIBA_HUMAN	SYSKQFTSSTSYNRG DSTF	Y	26.86	2620.28	19	3.9	874.4	3	69.1	F1:9570	5.51E-04	1.40E-04	2.99E-04	5.01E-04	2.95E-04	8.65E-05	578	596	TMT6plex
A2VEC9	SSPO_HUMAN	QVHRV	N	15.25	866.529	5	1.2	434.3	2	76.5	F2:10106	2.10E-04	2.35E-04	5.21E-04	3.67E-04	1.79E-04	5.05E-04	1972	1976	TMT6plex
Q14624	ITIH4_HUMAN	VHSGSTF	Y	36.46	962.502	7	3	482.3	2	27.8	F1:3164	2.56E-04	3.78E-04	2.64E-04	2.93E-04	4.10E-04	2.36E-04	618	624	TMT6plex
PODJI8	SAA1_HUMAN	DQAANEWG	Y	37.79	1118.52	8	0.3	560.3	2	56.3	F1:7547	2.42E-04	1.02E-03	3.28E-04	4.37E-04	4.29E-04	5.65E-04	97	104	TMT6plex
Q15942	ZYX_HUMAN	HVQPQPQPKVQLH	Y	53.57	2218.27	15	3.7	740.4	3	36.7	F1:4542	5.54E-04	2.48E-04	6.26E-05	2.35E-04	4.18E-04	1.09E-04	223	237	TMT6plex
P62328	TYB4_HUMAN	TQEKNPLPSKETIEQE	Y	49.15	2557.42	16	2.6	853.5	3	65.9	F1:9050	3.60E-04	9.92E-04	1.33E-04	3.66E-04	9.25E-04	3.83E-04	23	38	TMT6plex
Q05682	CALD1_HUMAN	SSPTAAGTPNKETAG LKVG	Y	51.8	2472.42	19	0.8	825.1	3	56.3	F1:7543	5.12E-04	5.99E-04	1.09E-04	3.33E-04	9.50E-04	1.12E-04	723	741	TMT6plex
Q96AA3	RFT1_HUMAN	LGHAAR	N	15.52	852.513	6	-2.4	427.3	2	66.5	F1:9162	9.46E-05	8.85E-05	1.79E-04	1.55E-04	7.81E-05	1.07E-04	7	12	TMT6plex
P68363	TBA1B_HUMAN	DLEPTVIDEV	Y	30.44	1357.72	10	3.8	679.9	2	114	F1:17524	5.21E-04	1.91E-03	3.14E-04	9.43E-04	1.67E-03	4.82E-04	69	78	TMT6plex
Q9Y490	TLN1_HUMAN	DEESTMLEDSVSPK	Y	25.59	2040	14	4.7	681	3	67.2	F1:9282	0.00E+00	1.41E-04	9.85E-05	8.22E-05	1.05E-04	7.85E-05	414	427	TMT6plex; Oxidation
P02675	FIBB_HUMAN	QGVNDNEEGFF	Y	50.05	1484.66	11	1.8	743.3	2	105	F1:15727	2.29E-04	2.92E-04	5.39E-04	3.43E-04	3.59E-04	3.00E-04	31	41	TMT6plex; Deamidation
P02671	FIBA_HUMAN	EGDFLAEG	Y	29.17	1065.52	8	4.2	533.8	2	82.3	F2:11038	2.02E-04	4.39E-04	2.82E-04	2.85E-04	1.70E-04	4.11E-04	24	31	TMT6plex
O00151	PDLI1_HUMAN	ESEEKGDPNKPSG	Y	15.05	2060.1	13	3.2	687.7	3	29.4	F1:3418	1.03E-04	1.02E-03	1.11E-04	2.21E-04	3.71E-04	4.52E-04	224	236	TMT6plex
P37802	TAGL2_HUMAN	EQILIQ	N	19.12	971.585	6	-0.6	486.8	2	90.6	F1:13132	0.00E+00	8.47E-05	7.10E-05	3.62E-05	4.68E-05	9.06E-05	27	32	TMT6plex
Q9Y2D5	AKAP2_HUMAN	EQLLQ	N	19.12	971.585	6	-0.6	486.8	2	90.6	F1:13132	0.00E+00	8.47E-05	7.10E-05	3.62E-05	4.68E-05	9.06E-05	276	281	TMT6plex
P00488	F13A_HUMAN	VPPNNSNAEDDLPT VE	Y	26.16	2009.97	17	3.1	671	3	85.3	F2:11540	4.82E-05	2.93E-05	0.00E+00	4.76E-05	4.15E-05	0.00E+00	15	31	TMT6plex
P10124	SRGN_HUMAN	SLDRNLPSDSQDLGQ HGLEED	Y	61.31	2553.21	21	2.6	852.1	3	68.7	F2:8937	5.46E-04	9.00E-04	8.37E-04	5.87E-04	1.22E-03	6.11E-04	135	155	TMT6plex
P02671	FIBA_HUMAN	SGEGDFLAEGGG	Y	38.58	1323.61	12	2.1	662.8	2	78.2	F1:11038	2.76E-04	4.74E-04	2.21E-04	3.38E-04	3.11E-04	2.76E-04	22	33	TMT6plex
P52565	GDIR1_HUMAN	ENEDEHSVNYKPPA	Y	27.12	2215.08	15	1.3	739.4	3	43.4	F1:5528	0.00E+00	9.85E-05	0.00E+00	4.08E-05	3.74E-05	0.00E+00	17	31	TMT6plex
P02671	FIBA_HUMAN	ADSGEGDFLAEGGG	Y	36.78	1509.68	14	1.8	755.8	2	83.6	F2:11276	2.35E-04	9.47E-04	3.10E-04	8.86E-04	3.11E-04	4.52E-04	20	33	TMT6plex
Q9H4B7	TBB1_HUMAN	EEHGIDLAGSDRGAS ALQLE	Y	41.19	2296.15	20	3.8	766.4	3	78.7	F2:10472	8.24E-05	1.73E-04	0.00E+00	1.29E-04	9.21E-05	0.00E+00	26	45	TMT6plex
Q9H4B7	TBB1_HUMAN	DTVVEPYN	N	34.53	1164.59	8	3.5	583.3	2	60.3	F1:8211	9.56E-04	6.12E-04	3.66E-04	6.73E-04	6.81E-04	4.77E-04	177	184	TMT6plex
Q13748	TBA3C_HUMAN	DLEPTVVDEV	Y	29.33	1343.7	10	4.1	672.9	2	102	F2:14485	1.96E-04	2.06E-04	1.56E-04	1.69E-04	2.00E-04	1.79E-04	69	78	TMT6plex
P0C0L4	CO4A_HUMAN	QFSLGSKI	Y	34.14	1090.62	8	1.9	546.3	2	116	F1:17877	3.83E-04	1.38E-04	3.34E-04	4.03E-04	2.87E-04	1.01E-04	1359	1366	Pyro-glu from Q; TMT6plex
Q15942	ZYX_HUMAN	EGGPEAPIPPPPQPRE KVS	Y	39.13	2439.35	19	1.3	814.1	3	57.5	F1:7753	8.02E-05	3.09E-04	0.00E+00	8.42E-05	2.30E-04	1.31E-04	124	142	TMT6plex
P0C0L4	CO4A_HUMAN	DDPDAPLQPVTPLQL FEGRRN	Y	47.22	2606.37	21	2.9	869.8	3	119	F1:18533	1.59E-04	3.12E-04	8.21E-04	5.37E-04	2.45E-04	3.89E-04	1429	1449	TMT6plex
PODJI8	SAA1_HUMAN	FGHGAEDSLADQAA NEWGR	Y	55.83	2259.05	19	1.5	754	3	88.8	F1:12820	4.35E-05	1.77E-04	0.00E+00	1.11E-04	1.47E-04	0.00E+00	87	105	TMT6plex

O75369	FLNB_HUMAN	PVSIMVVQ	Y	16.11	1100.65	8	-2.7	551.3	2	86.4	F1:12409	7.78E-05	8.82E-05	8.46E-05	1.35E-04	0.00E+00	9.27E-05	1989	1996	TMT6plex
Q86VQ0	LCA5_HUMAN	DEDEGFF	Y	22.19	1086.47	7	1.7	544.2	2	110	F1:16740	4.70E-05	0.00E+00	1.62E-04	1.37E-04	3.89E-05	0.00E+00	652	658	TMT6plex
O95810	SDPR_HUMAN	I <sup>1</sup> SEEAERKSDGDPVQP <sup>1</sup> A	Y	27.53	1915.9	16	2.9	639.6	3	34.9	F1:4268	2.16E-04	2.53E-04	1.84E-04	2.27E-04	2.80E-04	1.67E-04	402	417	TMT6plex
O00151	PDLI1_HUMAN	QE <sup>1</sup> QELNEPPKQSTS	Y	28.03	2183.15	15	5.4	728.7	3	45	F2:5439	0.00E+00	2.06E-04	0.00E+00	0.00E+00	7.85E-05	8.79E-05	201	215	Pyro-glu from Q; TMT6plex
P10124	SRGN_HUMAN	SLDKNLP <sup>1</sup> SDSQDLGQH	Y	37.46	2010	16	-3.1	671	3	53.2	F1:7035	1.88E-04	4.58E-04	5.26E-04	4.37E-04	3.89E-04	4.02E-04	135	150	TMT6plex
Q8N554	ZN276_HUMAN	GATARRA	Y	15.6	930.556	7	4.3	466.3	2	76.1	F1:10678	1.62E-04	5.91E-05	2.16E-04	2.09E-04	1.20E-04	1.36E-04	44	50	TMT6plex
Q05682	CALD1_HUMAN	SSPTAAGTPNKETAG LKVGV <sup>1</sup> S	Y	33.04	2658.52	21	-1	887.2	3	62.6	F1:8551	3.71E-04	5.21E-04	0.00E+00	3.48E-04	4.39E-04	0.00E+00	723	743	TMT6plex
P02671	FIBA_HUMAN	DTASTGKTFPG	Y	54.3	1538.83	11	3.7	770.4	2	51.7	F1:6828	1.32E-02	4.72E-03	2.22E-03	4.88E-03	4.81E-03	8.55E-03	521	531	TMT6plex
P02671	FIBA_HUMAN	FVSETESRGS <sup>1</sup> ESG	Y	26.75	1599.76	13	2.4	800.9	2	37.3	F2:4386	8.51E-04	4.57E-04	2.41E-04	3.89E-04	5.28E-04	7.37E-04	540	552	TMT6plex
Q2QGD7	ZXDC_HUMAN	GQHGGGPGPL	Y	25.68	1105.57	10	-6.9	553.8	2	26.6	F1:2968	1.93E-04	3.33E-04	2.00E-04	2.67E-04	1.57E-04	2.72E-04	15	24	TMT6plex; Deamidation
P60709	ACTB_HUMAN	TEAPLNPK	N	38.11	1326.79	8	1.6	664.4	2	42.9	F1:5454	1.56E-03	3.23E-03	9.02E-04	1.80E-03	2.58E-03	9.03E-04	106	113	TMT6plex
P22888	LSHR_HUMAN	IPGNAF	Y	15.48	846.48	6	0.4	424.2	2	65.7	F1:9021	2.02E-04	1.07E-04	2.54E-04	1.62E-04	1.59E-04	2.19E-04	164	169	TMT6plex
P00488	F13A_HUMAN	NAAEDDLPTVELQGV VPR	Y	55.25	2151.14	18	1.5	718.1	3	107	F1:16103	5.69E-05	4.07E-05	6.91E-05	8.05E-05	0.00E+00	7.25E-05	21	38	TMT6plex
Q8WZ42	TITIN_HUMAN	PVRHVR	Y	30.62	819.483	6	9.1	410.8	2	71.3	F1:9912	0.00E+00	2.51E-05	5.27E-05	0.00E+00	0.00E+00	9.55E-05	292	297	Carbamidomethylation
O95810	SDPR_HUMAN	SEEAERSDGD <sup>1</sup> PVQPA	Y	32.2	1814.85	15	2.3	908.4	2	32.6	F1:3914	1.26E-04	6.23E-04	0.00E+00	3.04E-04	2.59E-04	2.84E-04	403	417	TMT6plex
Q9Y490	TLN1_HUMAN	FGLEGDEESTMLEDS VSPK	Y	48.82	2543.24	19	1.6	848.8	3	107	F1:16069	0.00E+00	1.64E-04	0.00E+00	6.22E-05	7.18E-05	0.00E+00	409	427	TMT6plex; Oxidation
Q96HC4	PDLI5_HUMAN	GEPKEVVKPVPITSPA VS	Y	27	2520.51	18	0	841.2	3	73.2	F1:10201	8.66E-05	2.00E-04	0.00E+00	7.81E-05	2.55E-04	0.00E+00	98	115	TMT6plex
Q15942	ZYX_HUMAN	VNPF <sup>1</sup> RPGDSEPPAPG A	Y	34.25	1932.99	17	5.2	967.5	2	71.4	F2:9358	4.36E-05	2.55E-04	0.00E+00	6.70E-05	2.88E-04	0.00E+00	36	52	TMT6plex
O95810	SDPR_HUMAN	EGKEELPDENKS	Y	32.41	2061.12	12	2.3	688	3	46.2	F1:5954	2.52E-04	1.10E-03	7.17E-05	2.29E-04	6.11E-04	4.13E-04	181	192	TMT6plex
P07437	TBB5_HUMAN	SVV <sup>1</sup> SPKVS <sup>1</sup> DI <sup>1</sup> VVE <sup>1</sup> V	Y	33.57	2160.21	16	4.4	721.1	3	91.2	F1:13232	7.34E-05	3.49E-04	5.89E-05	1.61E-04	2.19E-04	1.50E-04	168	183	TMT6plex
P35579	MYH9_HUMAN	QLKRQLEEA <sup>1</sup> EEEAQR AN	Y	25.26	2253.16	17	0.3	752.1	3	92.6	F1:13488	1.00E-04	3.01E-04	0.00E+00	1.92E-04	1.58E-04	0.00E+00	1874	1890	Pyro-glu from Q; TMT6plex
Q15942	ZYX_HUMAN	GAPG <sup>1</sup> PLTLKEVEELE	Y	51.14	2039.16	15	2.2	680.7	3	119	F1:18586	3.79E-04	6.32E-04	6.54E-05	2.70E-04	4.98E-04	2.21E-04	346	360	TMT6plex
P37840	SYUA_HUMAN	EGVVAAAEKTKQG	Y	45.57	1974.17	13	5.2	659.1	3	57	F2:7228	1.29E-03	3.32E-03	5.61E-04	1.28E-03	2.89E-03	4.94E-04	13	25	TMT6plex
Q15942	ZYX_HUMAN	GPPASSAPAPK	Y	42.19	1533.89	12	4.6	512.3	3	31.8	F2:3555	1.03E-04	2.59E-04	9.21E-05	1.22E-04	1.48E-04	1.57E-04	254	265	TMT6plex
Q9Y566	SHAN1_HUMAN	FVPPH	Y	15.87	824.475	5	1.7	413.2	2	17.3	F2:1467	2.45E-04	8.77E-05	1.20E-03	3.00E-04	0.00E+00	1.03E-03	2054	2058	TMT6plex
P04632	CPNS1_HUMAN	GGGGGLGGGLG	Y	29.54	986.535	11	2	494.3	2	54.6	F1:7268	3.98E-04	1.57E-03	5.43E-04	6.47E-04	6.05E-04	1.08E-03	16	26	TMT6plex
Q15942	ZYX_HUMAN	VQE <sup>1</sup> KQHPVPPPAQ <sup>1</sup> NQ N	Y	29.67	2268.24	16	4.7	757.1	3	25.2	F2:2667	0.00E+00	3.58E-05	0.00E+00	0.00E+00	4.42E-05	0.00E+00	325	340	TMT6plex
PODJ19	SAA2_HUMAN	SGRDPN <sup>1</sup> HFRPAGLPE KY	Y	23.64	2398.29	17	2.3	600.6	4	48.1	F2:5915	4.52E-05	2.26E-04	1.25E-04	2.43E-04	7.53E-05	1.09E-04	106	122	TMT6plex

Q03001	DYST_HUMAN	DMEKL	N	16.82	1092.63	5	3.8	547.3	2	52.5	F2:6507	1.45E-03	9.19E-04	6.02E-04	1.16E-03	9.62E-04	7.35E-04	6094	6098	TMT6plex
P60709	ACTB_HUMAN	DMEKI	N	16.82	1092.63	5	3.8	547.3	2	52.5	F2:6507	1.45E-03	9.19E-04	6.02E-04	1.16E-03	9.62E-04	7.35E-04	81	85	TMT6plex
Q9NYU2	UGGG1_HUMAN	SVASGHLY	N	15.84	1061.57	8	-1.2	531.8	2	72.5	F1:10092	2.46E-04	3.10E-04	6.90E-04	3.24E-04	2.57E-04	5.92E-04	1260	1267	TMT6plex
Q70CQ2	UBP34_HUMAN	AKELA	N	15.58	988.632	5	2	495.3	2	97.4	F1:14329	0.00E+00	3.90E-05	4.91E-05	3.22E-05	0.00E+00	6.61E-05	362	366	TMT6plex
Q8WZ42	TITIN_HUMAN	AKEIA	N	15.58	988.632	5	2	495.3	2	97.4	F1:14329	0.00E+00	3.90E-05	4.91E-05	3.22E-05	0.00E+00	6.61E-05	1669	1673	TMT6plex
P0DJ18	SAA1_HUMAN	GHGAEDSLADQAAN EWG	Y	46.36	1955.88	17	3.2	979	2	81.2	F1:11512	5.21E-05	3.52E-04	4.72E-05	1.40E-04	2.34E-04	1.23E-04	88	104	TMT6plex
O95810	SDPR_HUMAN	VEGEIAEEAAEKATS	Y	51.35	1991.05	15	1.6	996.5	2	101	F1:15028	5.30E-04	9.41E-04	1.11E-04	6.40E-04	8.66E-04	2.04E-04	347	361	TMT6plex
Q05682	CALD1_HUMAN	QKEFDPT	Y	27.74	1075.54	7	4.2	538.8	2	62.9	F1:8606	3.97E-04	6.48E-04	3.48E-04	5.06E-04	4.56E-04	4.71E-04	118	124	Pyro-glu from Q; TMT6plex
Q8WZ42	TITIN_HUMAN	LKGS DVI	Y	20.68	1187.76	7	5.8	594.9	2	67.6	F2:8754	1.00E-03	1.50E-03	1.37E-03	1.67E-03	1.12E-03	1.17E-03	7397	7403	TMT6plex; Amidation
P68363	TBA1B_HUMAN	NYQPPTVVPGDLAK VQ	N	31.36	2241.24	17	2.7	748.1	3	95.3	F1:13962	8.94E-05	1.12E-04	5.86E-05	1.32E-04	1.48E-04	0.00E+00	356	372	TMT6plex; Deamidation
P00488	F13A_HUMAN	AVPPNNSNA AEDDLP TVE	Y	25.11	2081.01	18	1.7	694.7	3	84.9	F1:12140	4.42E-05	1.05E-04	0.00E+00	7.99E-05	5.42E-05	0.00E+00	14	31	TMT6plex
P02671	FIBA_HUMAN	FDTASTGKTFPG	Y	26.87	1685.9	12	3.8	844	2	81.2	F1:11510	1.52E-03	6.58E-04	2.76E-04	7.16E-04	7.61E-04	8.26E-04	520	531	TMT6plex
Q8WZ42	TITIN_HUMAN	LTEGK	Y	24.11	817.475	5	-7.8	409.7	2	33.3	F1:4026	2.19E-04	5.76E-04	1.20E-03	1.37E-03	2.21E-04	2.20E-04	9073	9077	Acetylation ; TMT6plex
O60493	SNX3_HUMAN	ELERESKVVVPLPG	Y	21.83	2106.25	15	1.9	703.1	3	81.6	F2:10925	7.70E-05	2.01E-04	0.00E+00	1.42E-04	1.64E-04	0.00E+00	80	94	TMT6plex
O14745	NHRF1_HUMAN	EPPAAAEVQG	Y	21.42	1196.62	10	2.1	599.3	2	47.4	F1:6155	3.10E-04	2.19E-04	1.61E-04	2.39E-04	1.89E-04	2.46E-04	121	130	TMT6plex
P42858	HD_HUMAN	KFVVATLEAL	Y	15.71	1318.81	10	2.6	660.4	2	112	F2:16384	5.80E-05	7.69E-05	0.00E+00	6.42E-05	8.28E-05	0.00E+00	2251	2260	TMT6plex
P10124	SRGN_HUMAN	SLDRNLP SDSLQGLGQ HGLEEDFML	Y	34.7	2960.4	24	4.7	987.8	3	113	F2:16507	7.27E-05	0.00E+00	1.39E-04	1.46E-04	8.66E-05	0.00E+00	135	158	TMT6plex; Oxidation
P00488	F13A_HUMAN	AVPPNNSNA AEDDLP TVELQG	Y	20.37	2379.18	21	4.4	794.1	3	104	F2:14723	0.00E+00	6.29E-05	0.00E+00	0.00E+00	0.00E+00	5.32E-05	14	34	TMT6plex
P02671	FIBA_HUMAN	DEAGSEADHEGTHS	Y	52.34	1669.7	14	8.4	835.9	2	11.3	F2:592	9.47E-05	5.92E-04	9.31E-05	2.18E-04	1.13E-04	5.21E-04	605	618	TMT6plex
P01042	KNG1_HUMAN	DLEHQGGHV	Y	30.94	1219.61	9	2.8	407.5	3	20.2	F1:1975	4.58E-05	5.61E-05	0.00E+00	4.75E-05	6.34E-05	0.00E+00	482	490	TMT6plex
P07951	TPM2_HUMAN	DEEKMEL	N	18.39	1350.71	7	4	676.4	2	64.9	F2:8365	1.13E-03	3.35E-03	5.05E-04	1.68E-03	2.15E-03	8.28E-04	137	143	TMT6plex
P67936	TPM4_HUMAN	DEEKMEI	N	18.39	1350.71	7	4	676.4	2	64.9	F2:8365	1.13E-03	3.35E-03	5.05E-04	1.68E-03	2.15E-03	8.28E-04	101	107	TMT6plex
Q9H4B7	TBB1_HUMAN	EDEEVTEEAEMEPED KGH	Y	49.53	2560.15	18	7	854.4	3	62.4	F2:7972	0.00E+00	1.25E-04	0.00E+00	0.00E+00	1.46E-04	0.00E+00	434	451	TMT6plex
P01024	CO3_HUMAN	EGFTVTAEG	Y	24.92	1138.57	9	2.6	570.3	2	69.8	F2:9118	1.78E-04	1.36E-04	3.39E-04	2.96E-04	2.03E-04	1.78E-04	1328	1336	TMT6plex
Q15942	ZYX_HUMAN	DDMTKNDPFKA	Y	15.6	1968.06	11	-2.6	657	3	70.1	F1:9715	4.93E-04	7.75E-04	8.26E-05	2.81E-04	7.36E-04	2.47E-04	156	166	TMT6plex
Q8WZ42	TITIN_HUMAN	LEGMGAVHAL	Y	16.03	1010.52	10	3.4	506.3	2	84.6	F1:12080	1.68E-04	7.43E-05	1.42E-04	1.53E-04	8.83E-05	1.55E-04	31958	31967	Methyl ester
P0C0L4	CO4A_HUMAN	NGFKSHALQLNN	Y	41.38	1800	12	1.4	601	3	53.9	F1:7151	3.23E-04	4.95E-04	6.06E-04	4.64E-04	3.68E-04	6.28E-04	1337	1348	TMT6plex
Q6P158	DHX57_HUMAN	AVFVKP	Y	16.01	1117.73	6	-5.7	559.9	2	113	F2:16467	1.49E-04	0.00E+00	0.00E+00	5.19E-05	0.00E+00	7.93E-05	897	902	TMT6plex
P01024	CO3_HUMAN	SHLGLA	Y	20.22	825.491	6	2.8	413.8	2	33.6	F1:4073	2.65E-04	2.59E-04	3.44E-04	2.56E-04	2.36E-04	3.93E-04	742	747	TMT6plex

Q15942	ZYX_HUMAN	GAPGGSGSQPNQKLG HPEA	Y	50.59	2246.18	19	1.7	749.7	3	34.3	F1:4172	1.88E-04	4.49E-04	4.75E-05	1.55E-04	4.04E-04	7.79E-05	283	301	TMT6plex
Q05682	CALD1_HUMAN	KPTKPAASDLPVPAE GV	Y	31.38	2363.4	17	3.4	788.8	3	73.5	F1:10251	6.38E-05	2.21E-04	0.00E+00	9.87E-05	1.42E-04	6.49E-05	693	709	TMT6plex
P02452	CO1A1_HUMAN	RPGERGGP	Y	23.31	878.472	8	-2.2	440.2	2	55.3	F1:7373	3.06E-04	3.34E-04	6.02E-04	4.29E-04	2.85E-04	4.94E-04	240	247	Methyl ester
P30443	1A01_HUMAN	ITGAVVAA	Y	17	929.575	8	5.2	465.8	2	122	F1:19018	0.00E+00	0.00E+00	5.52E-05	0.00E+00	0.00E+00	6.36E-05	322	329	TMT6plex
O95810	SDPR_HUMAN	EKFQHPG	Y	23.15	1052.56	7	2.4	527.3	2	30.6	F1:3601	2.50E-04	2.54E-04	1.72E-04	2.40E-04	2.20E-04	2.08E-04	9	15	Pyro-glu from E; TMT6plex
P00734	THRB_HUMAN	EYQTFNPR	Y	41.34	1429.72	9	1.3	715.9	2	84	F1:11993	1.01E-03	6.81E-04	1.08E-03	6.74E-04	6.27E-04	1.57E-03	319	327	TMT6plex
P02452	CO1A1_HUMAN	SPGSPGPDGKTGPPGP AGQDGRPGPPGP	Y	24.19	2965.49	28	-3.1	742.4	4	37.1	F1:4614	0.00E+00	2.85E-05	0.00E+00	0.00E+00	3.27E-05	0.00E+00	543	570	TMT6plex; Deamidation ; Hydroxylation
P02671	FIBA_HUMAN	SETESRGSESGIFT	Y	22.73	1714.82	14	3.7	858.4	2	48.5	F2:5993	8.07E-04	3.38E-04	1.64E-04	6.36E-04	3.87E-04	2.20E-04	542	555	TMT6plex
O95810	SDPR_HUMAN	YEGSYALTSEEAERS DGDVPQPA	Y	25.91	2699.24	23	6.1	900.8	3	81.7	F2:10936	0.00E+00	7.99E-05	0.00E+00	6.98E-05	0.00E+00	0.00E+00	395	417	TMT6plex
Q8NCM8	DYHC2_HUMAN	VIRGTT	Y	15.67	874.544	6	-9.5	438.3	2	82.6	F2:11104	7.39E-05	3.94E-05	6.18E-05	7.18E-05	0.00E+00	1.13E-04	4100	4105	TMT6plex
O95810	SDPR_HUMAN	ALTSEEAERSDGDVP QPAVLQVHQ	Y	60.64	2804.41	24	2.1	935.8	3	75	F1:10498	1.28E-04	1.42E-04	0.00E+00	1.17E-04	1.36E-04	0.00E+00	400	423	TMT6plex
P02671	FIBA_HUMAN	TESRGSESGIFTNT	Y	28.82	1713.84	14	1.8	857.9	2	50.4	F1:6621	8.29E-04	3.70E-04	2.53E-04	5.67E-04	5.02E-04	3.32E-04	544	557	TMT6plex
A2RRP1	NBAS_HUMAN	EHYAR	Y	15.61	903.477	5	-0.3	452.7	2	31.8	F1:3783	4.30E-04	5.70E-04	1.44E-03	8.54E-04	7.19E-04	9.56E-04	854	858	TMT6plex
P0C0L4	CO4A_HUMAN	NGFKSHALQLNNRQ	Y	49.33	2085.15	14	-0.1	696.1	3	48.9	F1:6389	3.34E-04	9.54E-04	9.26E-04	5.11E-04	5.35E-04	1.25E-03	1337	1350	TMT6plex; Deamidation
O95810	SDPR_HUMAN	SALVEGEIAEEAAEK AT	Y	42.28	2175.17	17	4.5	726.1	3	114	F2:16648	9.23E-05	8.08E-05	0.00E+00	7.17E-05	9.11E-05	0.00E+00	344	360	TMT6plex
P01009	A1AT_HUMAN	EDPQGDAQAQKTDTS	Y	32.8	1919.95	14	1.1	641	3	35.6	F1:4380	1.26E-04	1.77E-04	1.22E-04	1.53E-04	7.05E-05	2.13E-04	25	38	TMT6plex
PODJ18	SAA1_HUMAN	SGKDPNHFRPAGLPE KY	Y	41.89	2599.45	17	3.8	520.9	5	58.5	F1:7914	0.00E+00	3.56E-04	0.00E+00	2.99E-04	0.00E+00	9.48E-05	106	122	TMT6plex
P01024	CO3_HUMAN	EETKENEGFTVT	Y	30.47	1840.95	12	8	921.5	2	60.4	F1:8221	1.01E-03	2.74E-03	9.39E-04	1.71E-03	1.45E-03	1.36E-03	1322	1333	TMT6plex
P08107	HSP71_HUMAN	LLDVAP	N	15	855.527	6	-2	428.8	2	87.9	F1:12649	4.60E-05	8.07E-05	1.66E-04	8.32E-05	8.24E-05	1.18E-04	393	398	TMT6plex
P02452	CO1A1_HUMAN	IIDVAP	N	15	855.527	6	-2	428.8	2	87.9	F1:12649	4.60E-05	8.07E-05	1.66E-04	8.32E-05	8.24E-05	1.18E-04	1439	1444	TMT6plex
Q8N3C0	ASCC3_HUMAN	NIATVR	Y	15.95	1014.64	7	1.9	508.3	2	59	F1:7997	2.98E-04	5.16E-04	5.57E-04	4.53E-04	4.94E-04	4.46E-04	1598	1604	TMT6plex
O95996	APC2_HUMAN	KQHKT	N	16.09	1098.69	5	-3.2	550.4	2	113	F2:16450	0.00E+00	6.53E-05	0.00E+00	0.00E+00	0.00E+00	5.85E-05	1919	1923	TMT6plex
P02671	FIBA_HUMAN	ETESRGSESGIFT	Y	30.91	1627.79	13	1.7	814.9	2	48.3	F2:5945	1.11E-03	5.76E-04	3.80E-04	1.07E-03	4.96E-04	4.32E-04	543	555	TMT6plex
P67936	TPM4_HUMAN	DEEKMEIQEMQLKE	N	45.45	2466.3	14	2.3	823.1	3	88.3	F1:12724	2.89E-04	1.13E-03	1.24E-04	5.04E-04	8.75E-04	7.29E-05	101	114	TMT6plex
P07951	TPM2_HUMAN	DEEKMELQEMQLKE	N	45.45	2466.3	14	2.3	823.1	3	88.3	F1:12724	2.89E-04	1.13E-03	1.24E-04	5.04E-04	8.75E-04	7.29E-05	137	150	TMT6plex
PODJ18	SAA1_HUMAN	GNYDAAKRGGVW AAEAISDARENIQ	Y	55.56	3273.69	27	2.8	819.4	4	101	F2:14278	0.00E+00	6.48E-04	0.00E+00	0.00E+00	5.81E-04	0.00E+00	58	84	TMT6plex
Q9UBW5	BIN2_HUMAN	AQPSPTTERAKSQEE VLPSS	Y	27.45	2599.39	20	1.3	867.5	3	49	F1:6406	1.02E-04	1.42E-04	5.09E-05	1.08E-04	1.74E-04	0.00E+00	346	365	TMT6plex

O15018	PDZD2_HUMAN	LASHVAA	Y	16.69	896.528	7	4	449.3	2	34.3	F2:3922	4.86E-04	3.80E-04	4.47E-04	4.22E-04	4.47E-04	4.37E-04	2057	2063	TMT6plex
P07437	TBB5_HUMAN	DEHGIDP	Y	26.24	1010.49	7	2.1	506.3	2	25	F2:2629	3.55E-04	4.11E-04	3.61E-04	4.09E-04	3.16E-04	3.96E-04	26	32	TMT6plex
P02671	FIBA_HUMAN	SKQF1SS1SYNRGDS1	Y	39.02	2370.19	17	2.9	791.1	3	56.9	F2:7208	8.03E-04	3.35E-04	4.79E-04	8.08E-04	5.02E-04	2.61E-04	580	596	TMT6plex
P02671	FIBA_HUMAN	FLDSGEGDFLAEGGGV	Y	63.16	1764.85	16	5	883.4	2	71.9	F2:9424	3.96E-03	1.64E-03	1.22E-02	9.37E-03	4.38E-03	3.25E-03	20	35	TMT6plex
P0DJ18	SAA1_HUMAN	GNYDAAKRGPGGAW AAEAISDARENIQ	Y	39.01	3245.66	27	2.8	812.4	4	98.6	F1:14534	0.00E+00	3.03E-04	0.00E+00	0.00E+00	3.33E-04	0.00E+00	58	84	TMT6plex; Mutation
P02671	FIBA_HUMAN	SSYSKQFTSSTSYNRG DSTF	Y	23.66	2707.31	20	1.8	903.4	3	69	F1:9542	4.80E-04	1.16E-04	2.33E-04	4.60E-04	2.88E-04	1.10E-04	577	596	TMT6plex
O60701	UGDH_HUMAN	HIYDPK	Y	18.73	1229.72	6	-0.1	410.9	3	37.4	F1:4655	8.89E-05	1.60E-04	5.70E-05	1.33E-04	8.74E-05	7.86E-05	365	370	TMT6plex
Q6ZS81	WDFY4_HUMAN	NARNFF	Y	15.19	996.534	6	0.5	499.3	2	117	F1:18192	8.69E-04	4.37E-05	0.00E+00	0.00E+00	0.00E+00	8.34E-04	416	421	TMT6plex
Q7Z6E9	RBBP6_HUMAN	PPYRR	N	15.77	916.545	5	-2.9	459.3	2	75.3	F1:10555	5.68E-05	6.03E-05	8.10E-05	3.50E-05	0.00E+00	1.74E-04	761	765	TMT6plex
Q5DID0	UROL1_HUMAN	KRFLQQ	N	16.3	1047.64	6	1.7	524.8	2	86.3	F2:11692	0.00E+00	2.60E-05	7.81E-05	6.39E-05	4.60E-05	0.00E+00	1004	1009	TMT6plex
P98160	PGBM_HUMAN	VVSIHPP	Y	16.68	976.591	7	7.7	489.3	2	73.6	F2:9647	4.60E-05	4.92E-05	1.05E-04	6.42E-05	0.00E+00	1.28E-04	1867	1873	TMT6plex
Q13467	FZD5_HUMAN	GFLVRLVVG	Y	16.3	1187.76	9	8.7	594.9	2	109	F1:16546	4.56E-05	5.54E-05	3.62E-05	6.86E-05	6.40E-05	0.00E+00	284	292	TMT6plex
P67936	TPM4_HUMAN	DEEKMEIQE	N	15.59	1607.81	9	6.1	804.9	2	58	F2:7392	1.09E-03	3.84E-03	9.56E-04	1.51E-03	2.13E-03	2.06E-03	101	109	TMT6plex
P07951	TPM2_HUMAN	DEEKMELQE	N	15.59	1607.81	9	6.1	804.9	2	58	F2:7392	1.09E-03	3.84E-03	9.56E-04	1.51E-03	2.13E-03	2.06E-03	137	145	TMT6plex
Q9Y490	TLN1_HUMAN	GLEGDEEST	Y	22.92	1164.53	9	-2.9	583.3	2	40.7	F1:5104	5.37E-04	8.26E-04	3.67E-04	5.69E-04	7.07E-04	4.82E-04	410	418	TMT6plex
O95810	SDPR_HUMAN	SEEAERSDGDVPQPA VLQVH	Y	49.8	2391.19	20	0.3	798.1	3	59.5	F1:8087	6.03E-05	1.58E-04	5.82E-05	9.15E-05	1.03E-04	7.54E-05	403	422	TMT6plex
P00734	THRB_HUMAN	FEKKSLEDKTERELLE SYIDG	Y	30.33	3444.92	21	4.5	1149	3	114	F1:17513	7.43E-05	3.55E-04	1.05E-04	2.53E-04	1.62E-04	1.00E-04	342	362	TMT6plex
Q15942	ZYX_HUMAN	QKKFGPVVAPKPK	Y	27.87	2322.5	13	4.6	581.6	4	56.9	F2:7204	8.14E-04	5.57E-04	9.57E-05	6.95E-04	7.17E-04	1.05E-04	23	35	Pyro-glu from Q; TMT6plex
P40200	TACT_HUMAN	FTETPENG	Y	17.02	1122.54	8	2.8	562.3	2	84.3	F2:11378	8.31E-05	1.07E-04	1.52E-04	8.19E-05	6.54E-05	2.04E-04	91	98	TMT6plex
P0DJ19	SAA2_HUMAN	DAAKRGGGAWAAE VI	Y	21.4	2026.14	16	3.3	676.4	3	79.6	F1:11259	6.99E-05	4.36E-04	9.37E-05	5.43E-04	8.98E-05	0.00E+00	61	76	TMT6plex
P02675	FIBB_HUMAN	GVNDNEEG	Y	27.74	1061.48	8	2.7	531.8	2	21.5	F1:2181	1.46E-04	3.67E-04	2.30E-04	3.19E-04	2.29E-04	1.84E-04	32	39	TMT6plex
Q9Y490	TLN1_HUMAN	FEEQENETVVVKE	Y	33.2	2037.07	13	1.6	680	3	77	F1:10831	1.35E-04	3.36E-04	9.30E-05	2.10E-04	2.53E-04	1.15E-04	2480	2492	TMT6plex
P01042	KNG1_HUMAN	RPPGFSPF	Y	33.92	1132.62	8	3.5	567.3	2	77.7	F1:10946	6.63E-04	7.17E-04	6.12E-03	3.71E-03	8.83E-04	2.61E-03	381	388	TMT6plex
A6NDA9	LRIT2_HUMAN	VHIGPG	Y	18.46	807.481	6	9.3	404.8	2	68.4	F1:9473	1.11E-04	6.02E-05	1.80E-04	1.48E-04	1.61E-04	4.97E-05	409	414	TMT6plex
P62328	TYB4_HUMAN	QEKNPLPS	Y	30.13	1123.61	8	3.1	562.8	2	54.4	F1:7231	5.21E-04	1.08E-03	1.34E-03	7.19E-04	7.22E-04	1.44E-03	24	31	Pyro-glu from Q; TMT6plex
P02656	APOC3_HUMAN	TAKDALSSVQESQVA QQA	Y	45.33	2318.25	18	1.8	773.8	3	77.5	F2:10268	0.00E+00	7.58E-05	6.17E-05	6.85E-05	7.36E-05	0.00E+00	42	59	TMT6plex
Q8WZ42	TITIN_HUMAN	GIARLM	Y	19.64	888.542	6	9.5	445.3	2	81.2	F1:11515	0.00E+00	5.53E-05	9.89E-05	0.00E+00	1.00E-04	5.98E-05	996	1001	TMT6plex
P02671	FIBA_HUMAN	TGKTFFPG	Y	21.51	1164.69	7	3	583.4	2	43.3	F2:5172	2.00E-03	7.30E-04	4.13E-04	1.17E-03	1.06E-03	9.87E-04	525	531	TMT6plex
Q9Y490	TLN1_HUMAN	DDELNLWDHGR	Y	37.73	1698.82	12	3	567.3	3	80.7	F2:10765	0.00E+00	1.34E-04	4.63E-05	3.74E-05	9.18E-05	5.68E-05	168	179	TMT6plex

P01009	A1AT_HUMAN	EDPQGDAAQKTDTS HDQDH	Y	22.74	2689.24	20	2	897.4	3	21.2	F1:2124	4.26E-05	6.67E-05	0.00E+00	4.11E-05	0.00E+00	6.48E-05	25	44	TMT6plex
P02671	FIBA_HUMAN	DFLAEGGG	Y	34.1	993.497	8	2.6	497.8	2	81.3	F1:11535	3.11E-04	2.67E-04	4.81E-04	4.87E-04	3.73E-04	1.84E-04	26	33	TMT6plex
Q8IZX4	TAFIL_HUMAN	NISGAGQ	Y	17.77	874.471	7	4	438.2	2	20	F1:1932	2.18E-04	1.40E-04	1.88E-04	2.29E-04	1.27E-04	1.86E-04	44	50	TMT6plex
Q9UKV0	HDAC9_HUMAN	NGFAVVR	N	18.55	990.581	7	-0.2	496.3	2	96.5	F1:14168	0.00E+00	4.97E-05	0.00E+00	4.71E-05	0.00E+00	0.00E+00	772	778	TMT6plex
Q05682	CALD1_HUMAN	DDDEEEAARE	Y	21.93	1406.6	10	3.1	704.3	2	22.4	F1:2321	1.92E-04	9.85E-04	1.54E-04	2.98E-04	6.69E-04	3.32E-04	31	40	TMT6plex
P02775	CXCL7_HUMAN	NLAKGKEE	Y	27.09	1345.8	8	2.4	449.6	3	19.8	F1:1893	6.98E-05	2.69E-04	1.11E-04	2.56E-04	8.11E-05	1.20E-04	44	51	TMT6plex
Q27J81	INF2_HUMAN	GPPPPPP	N	30.65	983.564	8	3.8	492.8	2	42.6	F1:5410	4.19E-04	5.30E-04	4.78E-04	5.53E-04	3.42E-04	5.26E-04	513	520	TMT6plex
O95810	SDPR_HUMAN	GEDAAQAEKFQ	Y	42.77	1463.71	11	4.2	732.9	2	64.6	F2:8315	4.48E-04	7.74E-04	1.79E-04	3.69E-04	7.00E-04	3.15E-04	2	12	Acetylation ; TMT6plex
P62328	TYB4_HUMAN	SDKPDMAEIEK	Y	44.7	1761.92	11	1.6	882	2	73.4	F1:10221	7.77E-03	2.00E-02	2.52E-03	6.35E-03	2.14E-02	1.96E-03	2	12	Acetylation ; TMT6plex
P0DJ18	SAA1_HUMAN	GNYDAAKQGGVW AAEAISDARENIQ	Y	15.13	3245.65	27	8.5	812.4	4	99.4	F2:13936	0.00E+00	1.38E-04	0.00E+00	0.00E+00	1.34E-04	0.00E+00	58	84	TMT6plex; Mutation
P49137	MAPK2_HUMAN	PLHTSR	Y	16.65	938.55	6	1.4	470.3	2	76.4	F1:10716	1.22E-04	1.13E-04	1.81E-04	1.08E-04	8.54E-05	2.20E-04	335	340	TMT6plex
O95810	SDPR_HUMAN	ALTSEEAEERSDGPV QPAVLQVH	Y	36.34	2676.36	23	-5.6	893.1	3	73.9	F2:9711	0.00E+00	3.13E-05	0.00E+00	0.00E+00	3.05E-05	0.00E+00	400	422	TMT6plex
A8MYU2	KCNU1_HUMAN	SHNKV	N	15.91	1041.63	5	1.1	521.8	2	89.9	F1:12999	5.25E-05	9.37E-05	6.34E-05	9.10E-05	4.77E-05	7.18E-05	452	456	TMT6plex
Q8WZ42	TITIN_HUMAN	FRLIFT	Y	18.07	1038.64	6	9.7	520.3	2	98.6	F1:14541	8.71E-05	6.39E-05	9.57E-05	5.34E-05	0.00E+00	1.91E-04	32331	32336	TMT6plex; Methyl ester
Q9UMY4	SNX12_HUMAN	ELERDSKIVVPPLPG	Y	22.24	2106.25	15	2.3	703.1	3	83.3	F1:11853	4.24E-04	5.48E-04	7.61E-05	4.06E-04	5.44E-04	9.32E-05	81	95	TMT6plex
P62328	TYB4_HUMAN	QEKNPPLPSKETIEQE	Y	45.34	2210.18	15	5.8	737.7	3	75.8	F2:10011	1.61E-04	5.04E-04	0.00E+00	8.10E-05	4.94E-04	8.49E-05	24	38	Pyro-glu from Q; TMT6plex
Q8WZ42	TITIN_HUMAN	KTSRRME	Y	16.1	1135.63	7	3.4	568.8	2	36	F2:4157	1.03E-03	3.34E-03	6.51E-04	1.10E-03	2.83E-03	1.10E-03	10118	10124	TMT6plex
P02671	FIBA_HUMAN	SSSYSKQFTSSTS YNRGDSTFESKSY	Y	41.45	3388.61	26	2.7	848.2	4	66.3	F2:8577	4.37E-05	0.00E+00	0.00E+00	4.35E-05	0.00E+00	0.00E+00	576	601	TMT6plex
Q96PE2	ARHG_HUMAN	APLRRF	Y	23.33	987.618	6	0.4	494.8	2	110	F1:16752	1.37E-04	3.22E-05	0.00E+00	0.00E+00	0.00E+00	1.69E-04	1283	1288	TMT6plex
P11169	GTR3_HUMAN	ADRSKDGVMEMNS IEPAKETTTNV	Y	51.05	3366.74	25	0.4	842.7	4	74.6	F1:10448	0.00E+00	4.45E-05	0.00E+00	4.45E-05	0.00E+00	0.00E+00	472	496	TMT6plex
P02671	FIBA_HUMAN	SSSYSKQFTSSTS YNRGDSTFES	Y	50.33	2781.26	23	4.1	928.1	3	57.2	F2:7260	5.25E-04	2.88E-04	1.11E-03	1.40E-03	5.24E-04	0.00E+00	576	598	TMT6plex