Targeted Proteomics Analysis of ADNI CSF by Mass Spectrometry

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Introduction

The study describes the analysis of cerebrospinal fluid (CSF) samples from Alzheimer's Disease Neuroimaging Initiative (ADNI) cohort using targeted proteomics by mass spectrometry. We report peptide ratios for 69 peptides related to 48 proteins using methods as previously described by Watson et al., 2023 [1]. APOE, ALB, HBA, and HBB peptides are used to confirm genotype and monitor as background peptides. The other 44 proteins were previously identified by integrative proteomics as brain-based CSF biomarkers and reported to change in patients with Alzheimer’s disease [2-4].

Abstract

Cerebrospinal fluid (CSF) proteins from 833 ADNI samples and 80 quality controls (QC) were reduced, alkylated, denatured, and enzymatically digested with Lys-C and trypsin. The resulting peptides were analyzed as a single replicate using a standard flow Agilent 1290 Infinity II liquid chromatography system coupled with Thermo Fisher Scientific TSQ Altis Triple Quadrupole mass spectrometer as described by Watson et al., 2023 [1]. Isotopically labeled peptide standards were added for relative quantification by reporting the total area ratios for the targeted peptides.

Methodology

Patient Sample Selection. In 2022, we reported 69 peptide ratios for 729 baseline CSF samples. We selected all remaining baseline CSF samples (833) that were not previously reported for this dataset.

Quality Controls. Two disease-related quality controls (QC) were generated in-house by pooling approximately 50 individuals considered CSF biomarker positive (Low Aβ – High total Tau) to create ATpos QC, or CSF biomarker negative (High Aβ – Low total Tau) to create ATneg QC reference pools [1]. A third CSF QC (QCpool) was generated in-house by pooling approximately 20 individuals with no distinct pathophysiology. All QCs were processed and analyzed identically to the CSF clinical samples reported.

CSF samples. Each CSF sample was thawed and aliquoted onto shallow-well plates that also included QCs. Each sample and QC were processed independently in parallel.

CSF protein digestion. The protein digestion protocol was performed as described by Watson et al., 2023 [1]. Crude CSF (50 µL) from each sample and QC was reduced, alkylated, and denatured with tris-2(-carboxyethyl)-phosphine (5 mM; TCEP; Thermo Scientific 77720), chloroacetamide (40 mM: CAA; Sigma 22790), and sodium deoxycholate (1%; Sigma D6750) in triethylammonium bicarbonate buffer (100 mM; Honeywell 17902) while heating at 95°C for 10 min, followed by a 10-min cool down at room temperature. CSF proteins were digested with Lys-C (Wako 125-02543; 0.5 µg; 1:100 enzyme to protein ratio) and trypsin (Thermo Scientific 90058; 5 µg; 1:10 enzyme to protein ratio) overnight at 37°C. After digestion, heavy labeled standards for relative quantification (15 µL per 50 µL CSF) were added to the peptide solutions followed by acidification with a 1% trifluoroacetic acid (TFA; Thermo Scientific 85183) and 10% formic acid (FA; Fisher A117) solution to a final concentration of 0.1% TFA and 1% FA (pH ≤ 2). Sample plates were placed on an orbital shaker at 300 rpm for at least 10 minutes to ensure proper mixing. Plates were centrifuged (4680rpm) to pellet the precipitated surfactant.

Peptides were desalted with 30-mg C18 HLB 96-well plates (Waters Corporation 186008054) using a positive pressure system. Each HLB well was conditioned (500 µL methanol) and equilibrated twice (500 µL 0.1% TFA) before 500 µL 0.1% TFA and supernatant were added. Each well was washed twice (500 µL 0.1% TFA) and eluted twice (100 µL 50% acetonitrile). All samples and QCs were dried using a SpeedVac.

MS analysis of CSF. All samples were reconstituted in 50 µL Promega 6 × 5 LC-MS/MS Peptide Reference Mix (50 fmol/µL; Promega V7491) in mobile phase A (0.1% formic acid in water; Fisher LS118). Peptide eluents were separated on an AdvanceBio Peptide Map Guard column (2.1x5mm, 2.7 µm, Agilent) connected to AdvanceBio Peptide analytical column (2.1x150mm, 2.7 µm, Agilent) by a 1290 Infinity II system (Agilent) and monitored on an TSQ Altis Triple Quadrupole mass spectrometer (Thermo Fisher Scientific). Sample elution was performed over a 14-min gradient using mobile phase A (MPA; 0.1% FA in water) and mobile phase B (MPB; 0.1% FA in acetonitrile; Fisher LS120) with flow rate at 0.4 mL/min. The gradient was from 2% to 24% MPB over 12.1 minutes, then from 24% to 80% over 0.2 min and held at 80% B for 0.7 min. The mass spectrometer was set to acquire data in positive-ion mode using single reaction monitoring acquisition. Three transitions were acquired for each target analyte, cycle time set to 0.8 sec, Q1 resolution 0.7 FWHM, Q2 resolution 1.2 FWHM, and CID gas 1.5 mTorr [1]. Data were uploaded into Skyline for analysis. Total area ratios for each peptide are calculated by summing the area for each light (3) and heavy (3) transition and dividing the light total area by the heavy total area. There were 9 total sample plates. Each plate was queued independently with QCs at the beginning, end, and after every 20 samples per plate. We report the total area ratios (peptide ratios) for each target in each sample and QC analyzed.

Monitoring LC-MS/MS Instrument Performance. The sample reconstitution solution contained Promega 6 × 5 LC-MS/MS Peptide Reference Mix (50 fmole/µL). The 6 × 5 LC-MS/MS Peptide Reference Mix provides a convenient way to assess LC column performance and MS instrument parameters, including sensitivity and dynamic range. The mix consists of 30 peptides; 6 sets of 5 isotopologues of the same peptide sequence, differing only in the number of stable, heavy-labeled amino acids incorporated into the sequence using uniform ^{13}C and ^{15}N atoms. Isotopologues are chromatographically indistinguishable and of each isotopologue represents a series of tenfold dilutions, allowing assessment of instrument dynamic range and sensitivity within each run. The Promega

Peptide Reference mix statistics are listed below. Using the percent CV for the 30 monitored Promega peptides, we estimated the lowest limits of detection (LLOD) to be between 1-10 femtomoles (1 fmole) for each peptide.

Reported Peptide Ratios. We report peptide ratios for 69 peptides related to 48 proteins. For this dataset, we considered coefficient of variation (CV) for at least one QC ≤30% as good and 30-35% as acceptable. The average (median) CVs for the QCpool, ATneg QC, and ATpos QCs were 19% (17%), 31% (30%), and 31% (30%), respectively.

Decoding the data file. The provided csv file named "EMORY_PEPTIDERATIOS_SET2" contains total area ratios for all QCs and ADNI CSF samples provided. Column A – Peptide Sequence. Column B – Modified Peptide Sequence. Column C – Protein Name. Column D – individual data file names. Column E – Peptide Ratio. Example data file names decoded:

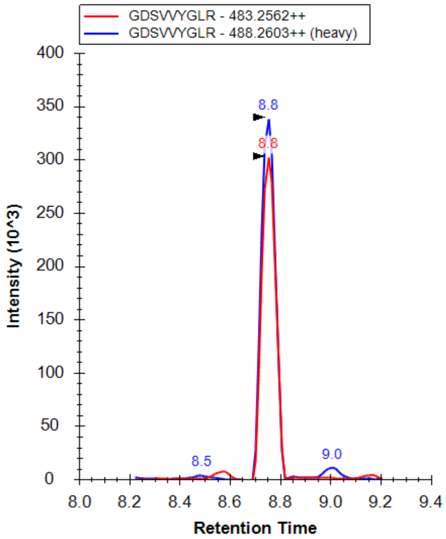
- QCsP1_P01G11_QCpool
    - QCs = quality control
    - P1 = quality control located on plate number 1
    - P01G11 = plate number 1; well position G11
    - QCpool = quality control type
- QCsP1_P01A12_ATpos
    - QCs = quality control
    - P1 = quality control located on plate number 1
    - P01A12 = plate number 1; well position A12
    - ATpos = quality control type; CSF biomarker positive
- QCsP2_P02B12_ATneg
    - QCs = quality control
    - P2 = quality control located on plate number 2
    - P02B12 = plate number 2; well position B12
    - ATneg = quality control type; CSF biomarker negative

Sample Details: Count and description of samples.

Count	Description

833	CSF samples provided
60	QCpool
10	ATpos
10	ATneg

Light and heavy peptide trace example: Light (red) and heavy (blue) chromatographic trace for an SPP1 peptide. Area under the curves used to calculate the reported peptide ratios.



Protein details:

	Protein Name	Protein Gene	Accession Number
1	ALBU	ALB	P02768
2	ALDOA	ALDOA	P04075
3	APOA4	APOA4	P06727
4	APOC1	APOC1	P02654
5	APOC2	APOC2	P02655
6	APOE	APOE	P02649
7	CO9	C9	P02748
8	CALM2	CALM2	P0DP24
9	CD44	CD44	P16070
10	CH3L1	CHI3L1	P36222
11	CERU	CP	P00450
12	DDAH1	DDAH1	O94760
13	DKK3	DKK3	Q9UBP4
14	ENOA	ENO1	P06733
15	THRB	F2	P00734
16	G3P	GAPDH	P04406
17	GUAD	GDA	Q9Y2T3
18	GMFB	GMFB	P60983
19	AATC	GOT1	P17174
20	GELS	GSN	P06396
21	HBA	HBA1	P69905
22	HBB	HBB	P68871
23	KNG1	KNG1	P01042
24	LDHB	LDHB	P07195
25	LDHC	LDHC	P07864
26	MDHC	MDH1	P40925
27	NCAM1	NCAM1	P13591
28	NPTX2	NPTX2	P47972
29	NPTXR	NPTXR	O95502
30	NRX1B	NRXN1	P58400
31	MIME	OGN	P20774
32	OMGP	OMG	P23515
33	PARK7	PARK7	Q99497
34	PEBP1	PEBP1	P30086
35	PGRP2	PGLYRP2	Q96PD5
36	KPYM	PKM	P14618
37	KPYM	PKM	P14618-2
38	PON1	PON1	P27169
39	PPIA	PPIA	P62937
40	PTPRZ	PTPRZ1	P23471
41	SCG2	SCG2	P13521
42	SMOC1	SMOC1	Q9H4F8
43	SODC	SOD1	P00441
44	OSTP	SPP1	P10451
45	TPIS	TPI1	P60174
46	VGF	VGF	O15240
47	1433B	YWHAB	P31946
48	1433Z	YWHAZ	P63104

Quality control statistics: List of peptide targets, protein gene names, and summary QC statistics using total area ratio for each analyte. Intra-assay coefficient of variation (CV) expressed as a percentage.

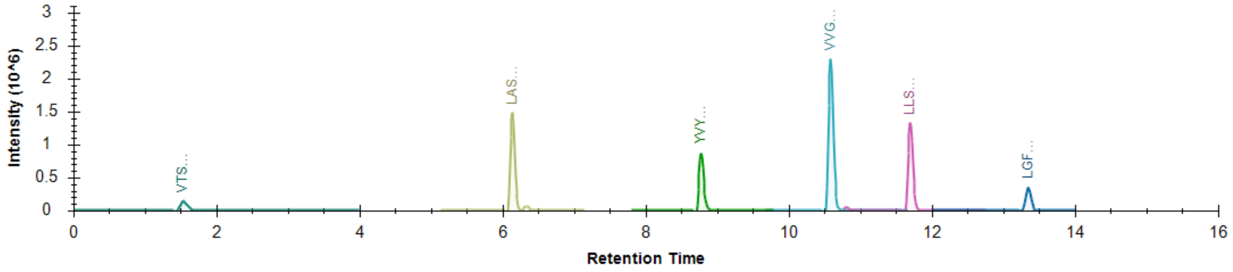
				QC Pool (QCpool)			Biomarker Negative (ATneg)			Biomarker Positive (ATpos)		
Protein Gene	Protein Accession Number	Protein Name	Peptide Sequence	Mean Total Area Ratio	StdDev Total Area	CV Total Area Ratio	Mean Total Area Ratio	StdDev Total Area	CV Total Area Ratio	Mean Total Area Ratio	StdDev Total Area	CV Total Area Ratio
APOE2		APOE2	CLAVYQAGAR	0.037	0.030	82%	4.020	1.355	34%	0.041	0.031	75%
APOE4		APOE4	LGADMEDVR	0.533	0.244	46%	0.457	0.370	81%	1.010	0.717	71%
APOE4		APOE4	LGADM(ox)EDVR	0.049	0.007	14%	0.039	0.011	28%	0.096	0.029	30%
APOE	P02649	APOE2or3	LGADMEDVCGR	0.169	0.037	22%	0.340	0.116	34%	0.242	0.094	39%
APOE	P02649	APOE2or3	LGADM(ox)EDVCGR	0.142	0.025	18%	0.291	0.102	35%	0.210	0.070	33%
APOE	P02649	APOE3or4	LAVYQAGAR	0.593	0.091	15%	0.926	0.270	29%	0.981	0.310	32%
ALB	P02768	ALBU	LVNEVTEFAK	47.404	6.923	15%	50.388	15.372	31%	47.688	14.888	31%
ALB	P02768	ALBU	LVTDLTK	71.066	10.337	15%	76.454	23.534	31%	71.148	21.488	30%
ALDOA	P04075	ALDOA	VLAAVYK	0.011	0.002	16%	0.015	0.004	28%	0.019	0.005	29%
APOA4	P06727	APOA4	SLAPYAQDTQEK	0.101	0.014	14%	0.099	0.027	27%	0.097	0.029	29%
APOC1	P02654	APOC1	QSELSAK	6.977	1.704	24%	8.061	2.448	30%	6.238	1.443	23%
APOC2	P02655	APOC2	TAAQNLYEK	0.013	0.002	14%	0.012	0.004	34%	0.010	0.002	23%
APOE	P02649	APOE	ELQAAQAR	0.336	0.048	14%	0.575	0.171	30%	0.558	0.171	31%
C9	P02748	CO9	TSNFNAAISLK	0.012	0.002	16%	0.009	0.002	27%	0.009	0.003	31%
C9	P02748	CO9	LSPIYNLVPVK	0.017	0.003	16%	0.014	0.004	31%	0.014	0.005	33%
CALM2	P0DP24	CALM2	EAFSLFDK	0.014	0.003	20%	0.018	0.007	37%	0.020	0.004	22%
CD44	P16070	CD44	TEAADLCK	0.017	0.004	25%	0.017	0.009	51%	0.019	0.009	47%
CD44	P16070	CD44	ALSIGFETCR	0.024	0.004	16%	0.023	0.008	32%	0.025	0.009	34%
CHI3L1	P36222	CH3L1	IASNTQSR	0.327	0.047	14%	0.320	0.088	28%	0.472	0.122	26%
CP	P00450	CERU	GEFYIGSK	0.072	0.011	15%	0.066	0.021	32%	0.063	0.019	30%
DDAH1	O94760	DDAH1	EFFVGLSK	0.001	0.000	23%	0.001	0.000	21%	0.001	0.000	24%
DKK3	Q9UBP4	DKK3	DQDGEILLPR	0.151	0.023	15%	0.227	0.073	32%	0.241	0.074	31%
ENO1	P06733	ENOA	IEEELGSK	0.004	0.001	21%	0.005	0.002	36%	0.006	0.003	42%
ENO1	P06733	ENOA	LNVTEQEK	0.003	0.001	18%	0.004	0.001	24%	0.005	0.001	25%
F2	P00734	THRB	YTACETAR	0.013	0.003	26%	0.013	0.007	49%	0.013	0.006	45%
GAPDH	P04406	G3P	AAFNSGK	0.006	0.001	24%	0.009	0.003	32%	0.009	0.002	21%
GAPDH	P04406	G3P	YDNSLK	0.001	0.000	24%	0.001	0.000	39%	0.001	0.000	26%
GDA	Q9Y2T3	GUAD	DHLLGVSDSGK	0.002	0.001	23%	0.003	0.001	29%	0.004	0.001	36%
GMFB	P60983	GMFB	FIVYSYK	0.003	0.001	23%	0.004	0.001	26%	0.004	0.001	29%
GOT1	P17174	AATC	VGNLTVVGK	0.006	0.001	17%	0.010	0.003	30%	0.012	0.004	33%
GOT1	P17174	AATC	IGADFLAR	0.001	0.000	13%	0.002	0.001	30%	0.002	0.001	30%
GSN	P06396	GELS	AGALNSNDAFVLK	0.139	0.021	15%	0.161	0.044	28%	0.167	0.046	27%

HBA1	P69905	HBA	FLASVSTVLTSK	0.116	0.020	17%	0.150	0.046	31%	0.124	0.042	34%
HBB	P68871	HBB	VNVDEVGGEALGR	0.151	0.023	15%	0.192	0.053	28%	0.160	0.049	30%
KNG1	P01042	KNG1	EGDCPVQSGK	0.010	0.002	23%	0.010	0.005	45%	0.010	0.005	49%
KNG1	P01042	KNG1	QVVAGLNFR	4.387	0.766	18%	4.308	1.245	29%	4.108	1.206	29%
KNG1	P01042	KNG1	VQVVAGK	0.044	0.007	16%	0.045	0.014	31%	0.041	0.013	31%
LDHB	P07195	LDHB	FIIPQIVK	0.004	0.001	15%	0.005	0.001	28%	0.006	0.002	31%
LDHC	P07864	LDHC	VIGSGCNLDSAR	0.006	0.001	20%	0.008	0.003	32%	0.010	0.003	28%
MDH1	P40925	MDHC	ENFSCLTR	0.020	0.003	17%	0.026	0.003	12%	0.032	0.008	26%
MDH1	P40925	MDHC	GEFVTTVQQR	0.007	0.001	21%	0.010	0.003	29%	0.012	0.004	34%
NCAM1	P13591	NCAM1	GLGEISAASEFK	0.031	0.005	16%	0.047	0.012	26%	0.048	0.015	31%
NPTX2	P47972	NPTX2	VAELEDEK	0.002	0.000	19%	0.004	0.001	31%	0.003	0.001	17%
NPTXR	O95502	NPTXR	ELDVLQGR	0.305	0.033	11%	0.531	0.155	29%	0.463	0.104	23%
NPTXR	O95502	NPTXR	ADQDTIR	0.002	0.000	22%	0.004	0.001	28%	0.004	0.001	30%
NRXN1	P58400	NRX1B	LAIGFSTVQK	0.012	0.003	24%	0.021	0.005	21%	0.021	0.007	32%
OGN	P20774	MIME	LEGNPIVLGK	0.013	0.002	16%	0.015	0.005	34%	0.015	0.005	30%
OMG	P23515	OMGP	LESLPAHLPR	0.105	0.015	14%	0.142	0.036	26%	0.156	0.040	26%
PARK7	Q99497	PARK7	ALVILAK	0.004	0.001	19%	0.005	0.001	27%	0.007	0.002	29%
PEBP1	P30086	PEBP1	LYEQLSGK	0.010	0.002	18%	0.012	0.004	37%	0.014	0.005	35%
PEBP1	P30086	PEBP1	VLTPTQVK	0.016	0.002	15%	0.021	0.007	33%	0.025	0.007	28%
PGLYRP2	Q96PD5	PGRP2	TFTLLDPK	0.059	0.009	15%	0.059	0.018	31%	0.059	0.015	26%
PKM	P14618	KPYM	VVEVGSK	0.008	0.001	17%	0.012	0.003	26%	0.016	0.005	28%
PKM	P14618	KPYM	GDLGIEIPAEK	0.006	0.001	17%	0.009	0.003	34%	0.011	0.003	25%
PKM	P14618	KPYM	GDYPLEAVR	0.014	0.003	18%	0.021	0.006	27%	0.027	0.007	25%
PKM	P14618-2	KPYM	LFEELVR	0.106	0.015	14%	0.159	0.043	27%	0.192	0.053	28%
PON1	P27169	PON1	LLIGTVFHK	0.005	0.001	18%	0.007	0.002	25%	0.005	0.002	31%
PPIA	P62937	PPIA	VSFELFADK	0.004	0.001	23%	0.005	0.002	38%	0.006	0.002	35%
PTPRZ1	P23471	PTPRZ	AIIDGVESVSR	0.019	0.003	14%	0.025	0.007	29%	0.025	0.007	29%
PTPRZ1	P23471	PTPRZ	DIEEGAIVNPGR	0.010	0.002	16%	0.014	0.004	27%	0.013	0.003	24%
SCG2	P13521	SCG2	IESQTQEEVR	0.009	0.002	18%	0.019	0.006	32%	0.017	0.005	29%
SMOC1	Q9H4F8	SMOC1	AQALEQAK	0.010	0.002	24%	0.011	0.005	42%	0.018	0.006	34%
SOD1	P00441	SODC	HVGDLGNVTADK	0.046	0.014	31%	0.071	0.033	47%	0.073	0.031	42%
SPP1	P10451	OSTP	GDSVVYGLR	0.629	0.053	9%	0.585	0.075	13%	0.784	0.148	19%
SPP1	P10451	OSTP	QETLPSK	3.983	0.618	16%	3.673	0.598	16%	4.048	0.677	17%
TPI1	P60174	TPIS	IAVAAQNCYK	0.003	0.001	24%	0.005	0.001	25%	0.005	0.002	43%
VGF	O15240	VGF	EPVAGDAVPGPK	0.038	0.006	15%	0.105	0.031	30%	0.089	0.025	28%
VGF	O15240	VGF	GLQEAAEER	0.008	0.001	17%	0.022	0.006	28%	0.018	0.006	31%
YWHAB	P31946	1433B	NLLSVAYK	0.014	0.002	15%	0.014	0.003	22%	0.021	0.007	31%
YWHAB	P31946	1433B	VISSIEQK	0.007	0.001	16%	0.007	0.002	24%	0.010	0.003	29%
YWHAZ	P63104	1433Z	VVSSIEQK	0.021	0.005	22%	0.018	0.006	33%	0.031	0.013	41%

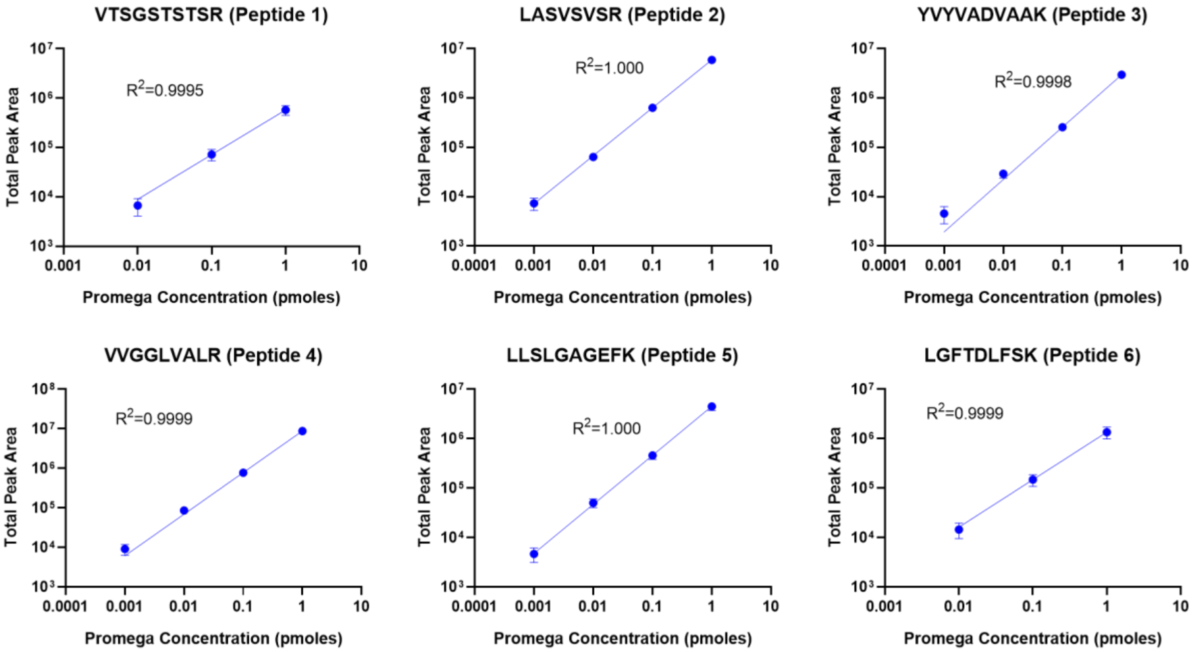
Promega Peptide Reference mix statistics: List of Promega 6 × 5 LC-MS/MS Peptide Reference Mix targets, concentrations, and intra-assay CV (796 individual measurements, 10 days, 9 plates) summary using total area for each isotopologue. Intra-assay coefficient of variation (CV) expressed as a percentage. Peptide concentrations that were not detected (n.d.) are indicated.

Peptide Sequence	Average Retention Time (min)	1 pmole	100 fmole	10 fmole	1 fmole	100 amole
VTSGSTSTSR	1.41	22.2%	25.8%	38.6%	n.d.	n.d.
LASVSVSR	6.21	14.1%	14%	14.5%	27.9%	n.d.
YVYVADVAAK	8.86	15.6%	14.9%	20.5%	38.1%	n.d.
VVGGLVALR	10.67	15.9%	16.1%	15.7%	30%	n.d.
LLSLGAGEFK	11.79	17.3%	16.6%	20%	32.8%	n.d.
LGFTDLFSK	13.34	26.9%	26.7%	34.7%	n.d.	n.d.

Promega peptide chromatogram: Extracted ion chromatogram for the 6 Promega peptides at the 1 pmole level.



Promega peptide linearity: Promega concentration versus average total peak area for each Promega peptide. Error bars represent the standard deviation across 913 injections.



Peptide and transition details: Light (3) and heavy (3) transitions for each peptide.

Protein Gene	Protein Accession	Peptide	Modified Sequence	Isotope Label Type	Precursor m/z	Precursor Charge	Product m/z	Collision Energy	Fragment Ion
ALB	P02768	LVNEVTEFAK	LVNEVTEFAK	light	575.311146	2	937.462538	21.8	y8
ALB	P02768	LVNEVTEFAK	LVNEVTEFAK	light	575.311146	2	595.308603	21.8	y5
ALB	P02768	LVNEVTEFAK	LVNEVTEFAK	light	575.311146	2	213.159754	21.8	b2
ALB	P02768	LVNEVTEFAK	LVNEVTEFAK[+8]	heavy	579.318245	2	945.476737	21.8	y8
ALB	P02768	LVNEVTEFAK	LVNEVTEFAK[+8]	heavy	579.318245	2	603.322802	21.8	y5
ALB	P02768	LVNEVTEFAK	LVNEVTEFAK[+8]	heavy	579.318245	2	213.159754	21.8	b2
ALB	P02768	LVTDLTK	LVTDLTK	light	395.239461	2	676.387582	15.7	y6
ALB	P02768	LVTDLTK	LVTDLTK	light	395.239461	2	577.319168	15.7	y5
ALB	P02768	LVTDLTK	LVTDLTK	light	395.239461	2	248.160482	15.7	y2
ALB	P02768	LVTDLTK	LVTDLTK[+8]	heavy	399.24656	2	684.401781	15.7	y6
ALB	P02768	LVTDLTK	LVTDLTK[+8]	heavy	399.24656	2	585.333367	15.7	y5
ALB	P02768	LVTDLTK	LVTDLTK[+8]	heavy	399.24656	2	256.174681	15.7	y2
ALDOA	P04075	VLAAVYK	VLAAVYK	light	382.239264	2	664.402838	15.3	y6
ALDOA	P04075	VLAAVYK	VLAAVYK	light	382.239264	2	551.318774	15.3	y5
ALDOA	P04075	VLAAVYK	VLAAVYK	light	382.239264	2	310.176132	15.3	y2
ALDOA	P04075	VLAAVYK	VLAAVYK[+8]	heavy	386.246363	2	672.417037	15.3	y6
ALDOA	P04075	VLAAVYK	VLAAVYK[+8]	heavy	386.246363	2	559.332973	15.3	y5
ALDOA	P04075	VLAAVYK	VLAAVYK[+8]	heavy	386.246363	2	318.190331	15.3	y2
APOA4	P06727	SLAPYAQDTQEK	SLAPYAQDTQEK	light	675.830431	2	1079.50038	25.3	y9
APOA4	P06727	SLAPYAQDTQEK	SLAPYAQDTQEK	light	675.830431	2	575.772385	25.3	y10
APOA4	P06727	SLAPYAQDTQEK	SLAPYAQDTQEK	light	675.830431	2	540.253828	25.3	y9
APOA4	P06727	SLAPYAQDTQEK	SLAPYAQDTQEK[+8]	heavy	679.837531	2	1087.514579	25.3	y9
APOA4	P06727	SLAPYAQDTQEK	SLAPYAQDTQEK[+8]	heavy	679.837531	2	579.779484	25.3	y10
APOA4	P06727	SLAPYAQDTQEK	SLAPYAQDTQEK[+8]	heavy	679.837531	2	544.260927	25.3	y9
APOC1	P02654	QSELSAK	QSELSAK	light	381.703243	2	547.308603	15.3	y5
APOC1	P02654	QSELSAK	QSELSAK	light	381.703243	2	418.26601	15.3	y4
APOC1	P02654	QSELSAK	QSELSAK	light	381.703243	2	305.181946	15.3	y3
APOC1	P02654	QSELSAK	QSELSAK[+8]	heavy	385.710342	2	555.322802	15.3	y5
APOC1	P02654	QSELSAK	QSELSAK[+8]	heavy	385.710342	2	426.280209	15.3	y4
APOC1	P02654	QSELSAK	QSELSAK[+8]	heavy	385.710342	2	313.196145	15.3	y3
APOC2	P02655	TAAQNLYEK	TAAQNLYEK	light	519.266738	2	865.441408	19.9	y7
APOC2	P02655	TAAQNLYEK	TAAQNLYEK	light	519.266738	2	794.404294	19.9	y6
APOC2	P02655	TAAQNLYEK	TAAQNLYEK	light	519.266738	2	173.092068	19.9	b2
APOC2	P02655	TAAQNLYEK	TAAQNLYEK[+8]	heavy	523.273838	2	873.455607	19.9	y7
APOC2	P02655	TAAQNLYEK	TAAQNLYEK[+8]	heavy	523.273838	2	802.418493	19.9	y6
APOC2	P02655	TAAQNLYEK	TAAQNLYEK[+8]	heavy	523.273838	2	173.092068	19.9	b2
APOE	P02649	ELQAAQAR	ELQAAQAR	light	443.740691	2	644.347448	17.4	y6
APOE	P02649	ELQAAQAR	ELQAAQAR	light	443.740691	2	516.288871	17.4	y5
APOE	P02649	ELQAAQAR	ELQAAQAR	light	443.740691	2	445.251757	17.4	y4

APOE	P02649	ELQAAQAR	ELQAAQAR[+10]	heavy	448.744825	2	654.355717	17.4	y6
APOE	P02649	ELQAAQAR	ELQAAQAR[+10]	heavy	448.744825	2	526.29714	17.4	y5
APOE	P02649	ELQAAQAR	ELQAAQAR[+10]	heavy	448.744825	2	455.260026	17.4	y4
APOE	P02649	LGADMEDVCGR	LGADMEDVC[+57]GR	light	611.76318	2	981.376442	23.1	y8
APOE	P02649	LGADMEDVCGR	LGADMEDVC[+57]GR	light	611.76318	2	735.309014	23.1	y6
APOE	P02649	LGADMEDVCGR	LGADMEDVC[+57]GR	light	611.76318	2	171.112804	23.1	b2
APOE	P02649	LGADMEDVCGR	LGADMEDVC[+57]GR[+10]	heavy	616.767314	2	991.384711	23.1	y8
APOE	P02649	LGADMEDVCGR	LGADMEDVC[+57]GR[+10]	heavy	616.767314	2	745.317283	23.1	y6
APOE	P02649	LGADMEDVCGR	LGADMEDVC[+57]GR[+10]	heavy	616.767314	2	171.112804	23.1	b2
APOE	P02649	LAVYQAGAR	LAVYQAGAR	light	474.766708	2	764.404963	18.4	y7
APOE	P02649	LAVYQAGAR	LAVYQAGAR	light	474.766708	2	665.336549	18.4	y6
APOE	P02649	LAVYQAGAR	LAVYQAGAR	light	474.766708	2	185.128454	18.4	b2
APOE	P02649	LAVYQAGAR	LAVYQAGAR[+10]	heavy	479.770843	2	774.413232	18.4	y7
APOE	P02649	LAVYQAGAR	LAVYQAGAR[+10]	heavy	479.770843	2	675.344818	18.4	y6
APOE	P02649	LAVYQAGAR	LAVYQAGAR[+10]	heavy	479.770843	2	185.128454	18.4	b2
APOE2		CLAVYQAGAR	C[+57]LAVYQAGAR	light	554.782033	2	835.442077	21.1	y8
APOE2		CLAVYQAGAR	C[+57]LAVYQAGAR	light	554.782033	2	665.336549	21.1	y6
APOE2		CLAVYQAGAR	C[+57]LAVYQAGAR	light	554.782033	2	345.159102	21.1	b3
APOE2		CLAVYQAGAR	C[+57]LAVYQAGAR[+10]	heavy	559.786167	2	845.450346	21.1	y8
APOE2		CLAVYQAGAR	C[+57]LAVYQAGAR[+10]	heavy	559.786167	2	675.344818	21.1	y6
APOE2		CLAVYQAGAR	C[+57]LAVYQAGAR[+10]	heavy	559.786167	2	345.159102	21.1	b3
APOE4		LGADMEDVR	LGADMEDVR	light	503.237124	2	892.382907	19.4	y8
APOE4		LGADMEDVR	LGADMEDVR	light	503.237124	2	274.187366	19.4	y2
APOE4		LGADMEDVR	LGADMEDVR	light	503.237124	2	171.112804	19.4	b2
APOE4		LGADMEDVR	LGADMEDVR[+10]	heavy	508.241258	2	902.391176	19.4	y8
APOE4		LGADMEDVR	LGADMEDVR[+10]	heavy	508.241258	2	284.195635	19.4	y2
APOE4		LGADMEDVR	LGADMEDVR[+10]	heavy	508.241258	2	171.112804	19.4	b2
C9	P02748	TSNFNAAISLK	TSNFNAAISLK	light	583.31422	2	977.541457	22.1	y9
C9	P02748	TSNFNAAISLK	TSNFNAAISLK	light	583.31422	2	716.430115	22.1	y7
C9	P02748	TSNFNAAISLK	TSNFNAAISLK	light	583.31422	2	347.228896	22.1	y3
C9	P02748	TSNFNAAISLK	TSNFNAAISLK[+8]	heavy	587.321319	2	985.555656	22.1	y9
C9	P02748	TSNFNAAISLK	TSNFNAAISLK[+8]	heavy	587.321319	2	724.444314	22.1	y7
C9	P02748	TSNFNAAISLK	TSNFNAAISLK[+8]	heavy	587.321319	2	355.243095	22.1	y3
C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK	light	621.876456	2	1042.629543	23.4	y9
C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK	light	621.876456	2	832.492716	23.4	y7
C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK	light	621.876456	2	343.233982	23.4	y3
C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK[+8]	heavy	625.883555	2	1050.643742	23.4	y9
C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK[+8]	heavy	625.883555	2	840.506915	23.4	y7
C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK[+8]	heavy	625.883555	2	351.248181	23.4	y3
CALM2	P0DP24	EAFSLFDK	EAFSLFDK	light	478.739825	2	609.324253	18.6	y5
CALM2	P0DP24	EAFSLFDK	EAFSLFDK	light	478.739825	2	409.208161	18.6	y3

CALM2	P0DP24	EAFSLFDK	EAFSLFDK	light	478.739825	2	262.139747	18.6	y2
CALM2	P0DP24	EAFSLFDK	EAFSLFDK[+8]	heavy	482.746925	2	617.338452	18.6	y5
CALM2	P0DP24	EAFSLFDK	EAFSLFDK[+8]	heavy	482.746925	2	417.22236	18.6	y3
CALM2	P0DP24	EAFSLFDK	EAFSLFDK[+8]	heavy	482.746925	2	270.153946	18.6	y2
CD44	P16070	TEAADLCK	TEAADLC[+57]K	light	454.213117	2	677.328687	17.7	y6
CD44	P16070	TEAADLCK	TEAADLC[+57]K	light	454.213117	2	606.291573	17.7	y5
CD44	P16070	TEAADLCK	TEAADLC[+57]K	light	454.213117	2	231.097548	17.7	b2
CD44	P16070	TEAADLCK	TEAADLC[+57]K[+8]	heavy	458.220217	2	685.342886	17.7	y6
CD44	P16070	TEAADLCK	TEAADLC[+57]K[+8]	heavy	458.220217	2	614.305772	17.7	y5
CD44	P16070	TEAADLCK	TEAADLC[+57]K[+8]	heavy	458.220217	2	231.097548	17.7	b2
CD44	P16070	ALSIGFETCR	ALSIGFETC[+57]R	light	577.287148	2	969.445842	21.9	y8
CD44	P16070	ALSIGFETCR	ALSIGFETC[+57]R	light	577.287148	2	769.32975	21.9	y6
CD44	P16070	ALSIGFETCR	ALSIGFETC[+57]R	light	577.287148	2	185.128454	21.9	b2
CD44	P16070	ALSIGFETCR	ALSIGFETC[+57]R[+10]	heavy	582.291282	2	979.454111	21.9	y8
CD44	P16070	ALSIGFETCR	ALSIGFETC[+57]R[+10]	heavy	582.291282	2	779.338019	21.9	y6
CD44	P16070	ALSIGFETCR	ALSIGFETC[+57]R[+10]	heavy	582.291282	2	185.128454	21.9	b2
CHI3L1	P36222	IASNTQSR	IASNTQSR	light	438.730323	2	692.332192	17.2	y6
CHI3L1	P36222	IASNTQSR	IASNTQSR	light	438.730323	2	605.300164	17.2	y5
CHI3L1	P36222	IASNTQSR	IASNTQSR	light	438.730323	2	185.128454	17.2	b2
CHI3L1	P36222	IASNTQSR	IASNTQSR[+10]	heavy	443.734457	2	702.340461	17.2	y6
CHI3L1	P36222	IASNTQSR	IASNTQSR[+10]	heavy	443.734457	2	615.308433	17.2	y5
CHI3L1	P36222	IASNTQSR	IASNTQSR[+10]	heavy	443.734457	2	185.128454	17.2	b2
CP	P00450	GEFYIGSK	GEFYIGSK	light	450.726718	2	567.313689	17.6	y5
CP	P00450	GEFYIGSK	GEFYIGSK	light	450.726718	2	404.25036	17.6	y4
CP	P00450	GEFYIGSK	GEFYIGSK	light	450.726718	2	187.071333	17.6	b2
CP	P00450	GEFYIGSK	GEFYIGSK[+8]	heavy	454.733817	2	575.327888	17.6	y5
CP	P00450	GEFYIGSK	GEFYIGSK[+8]	heavy	454.733817	2	412.264559	17.6	y4
CP	P00450	GEFYIGSK	GEFYIGSK[+8]	heavy	454.733817	2	187.071333	17.6	b2
DDAH1	O94760	EFFVGLSK	EFFVGLSK	light	463.752735	2	650.387188	18.1	y6
DDAH1	O94760	EFFVGLSK	EFFVGLSK	light	463.752735	2	503.318774	18.1	y5
DDAH1	O94760	EFFVGLSK	EFFVGLSK	light	463.752735	2	404.25036	18.1	y4
DDAH1	O94760	EFFVGLSK	EFFVGLSK[+8]	heavy	467.759835	2	658.401387	18.1	y6
DDAH1	O94760	EFFVGLSK	EFFVGLSK[+8]	heavy	467.759835	2	511.332973	18.1	y5
DDAH1	O94760	EFFVGLSK	EFFVGLSK[+8]	heavy	467.759835	2	412.264559	18.1	y4
DKK3	Q9UBP4	DQDGEILLPR	DQDGEILLPR	light	578.303852	2	912.514908	21.9	y8
DKK3	Q9UBP4	DQDGEILLPR	DQDGEILLPR	light	578.303852	2	272.171716	21.9	y2
DKK3	Q9UBP4	DQDGEILLPR	DQDGEILLPR	light	578.303852	2	244.092797	21.9	b2
DKK3	Q9UBP4	DQDGEILLPR	DQDGEILLPR[+10]	heavy	583.307987	2	922.523177	21.9	y8
DKK3	Q9UBP4	DQDGEILLPR	DQDGEILLPR[+10]	heavy	583.307987	2	282.179985	21.9	y2
DKK3	Q9UBP4	DQDGEILLPR	DQDGEILLPR[+10]	heavy	583.307987	2	244.092797	21.9	b2
ENO1	P06733	LNVTEQEK	LNVTEQEK	light	480.753464	2	733.37266	18.6	y6

ENO1	P06733	LNVTEQEK	LNVTEQEK	light	480.753464	2	533.256568	18.6	y4
ENO1	P06733	LNVTEQEK	LNVTEQEK	light	480.753464	2	228.134267	18.6	b2
ENO1	P06733	LNVTEQEK	LNVTEQEK[+8]	heavy	484.760563	2	741.386859	18.6	y6
ENO1	P06733	LNVTEQEK	LNVTEQEK[+8]	heavy	484.760563	2	541.270767	18.6	y4
ENO1	P06733	LNVTEQEK	LNVTEQEK[+8]	heavy	484.760563	2	228.134267	18.6	b2
ENO1	P06733	IEEELGSK	IEEELGSK	light	452.73474	2	662.335546	17.7	y6
ENO1	P06733	IEEELGSK	IEEELGSK	light	452.73474	2	291.166296	17.7	y3
ENO1	P06733	IEEELGSK	IEEELGSK	light	452.73474	2	243.133933	17.7	b2
ENO1	P06733	IEEELGSK	IEEELGSK[+8]	heavy	456.741839	2	670.349745	17.7	y6
ENO1	P06733	IEEELGSK	IEEELGSK[+8]	heavy	456.741839	2	299.180495	17.7	y3
ENO1	P06733	IEEELGSK	IEEELGSK[+8]	heavy	456.741839	2	243.133933	17.7	b2
F2	P00734	YTACETAR	YTAC[+57]ETAR	light	486.216191	2	808.361778	18.8	y7
F2	P00734	YTACETAR	YTAC[+57]ETAR	light	486.216191	2	707.3141	18.8	y6
F2	P00734	YTACETAR	YTAC[+57]ETAR	light	486.216191	2	636.276986	18.8	y5
F2	P00734	YTACETAR	YTAC[+57]ETAR[+10]	heavy	491.220326	2	818.370047	18.8	y7
F2	P00734	YTACETAR	YTAC[+57]ETAR[+10]	heavy	491.220326	2	717.322369	18.8	y6
F2	P00734	YTACETAR	YTAC[+57]ETAR[+10]	heavy	491.220326	2	646.285255	18.8	y5
GAPDH	P04406	AAFNSGK	AAFNSGK	light	347.67957	2	623.314751	14.1	y6
GAPDH	P04406	AAFNSGK	AAFNSGK	light	347.67957	2	552.277637	14.1	y5
GAPDH	P04406	AAFNSGK	AAFNSGK	light	347.67957	2	143.081504	14.1	b2
GAPDH	P04406	AAFNSGK	AAFNSGK[+8]	heavy	351.68667	2	631.32895	14.1	y6
GAPDH	P04406	AAFNSGK	AAFNSGK[+8]	heavy	351.68667	2	560.291836	14.1	y5
GAPDH	P04406	AAFNSGK	AAFNSGK[+8]	heavy	351.68667	2	143.081504	14.1	b2
GAPDH	P04406	YDNSLK	YDNSLK	light	370.184686	2	576.298767	14.9	y5
GAPDH	P04406	YDNSLK	YDNSLK	light	370.184686	2	461.271824	14.9	y4
GAPDH	P04406	YDNSLK	YDNSLK	light	370.184686	2	260.196868	14.9	y2
GAPDH	P04406	YDNSLK	YDNSLK[+8]	heavy	374.191785	2	584.312966	14.9	y5
GAPDH	P04406	YDNSLK	YDNSLK[+8]	heavy	374.191785	2	469.286023	14.9	y4
GAPDH	P04406	YDNSLK	YDNSLK[+8]	heavy	374.191785	2	268.211067	14.9	y2
GDA	Q9Y2T3	DHLLGVSDSGK	DHLLGVSDSGK	light	564.288202	2	762.399209	21.5	y8
GDA	Q9Y2T3	DHLLGVSDSGK	DHLLGVSDSGK	light	564.288202	2	253.093131	21.5	b2
GDA	Q9Y2T3	DHLLGVSDSGK	DHLLGVSDSGK	light	564.288202	2	366.177195	21.5	b3
GDA	Q9Y2T3	DHLLGVSDSGK	DHLLGVSDSGK[+8]	heavy	568.295302	2	770.413408	21.5	y8
GDA	Q9Y2T3	DHLLGVSDSGK	DHLLGVSDSGK[+8]	heavy	568.295302	2	253.093131	21.5	b2
GDA	Q9Y2T3	DHLLGVSDSGK	DHLLGVSDSGK[+8]	heavy	568.295302	2	366.177195	21.5	b3
GMFB	P60983	FIVYSYK	FIVYSYK	light	460.249829	2	659.339903	17.9	y5
GMFB	P60983	FIVYSYK	FIVYSYK	light	460.249829	2	560.271489	17.9	y4
GMFB	P60983	FIVYSYK	FIVYSYK	light	460.249829	2	261.159754	17.9	b2
GMFB	P60983	FIVYSYK	FIVYSYK[+8]	heavy	464.256928	2	667.354102	17.9	y5
GMFB	P60983	FIVYSYK	FIVYSYK[+8]	heavy	464.256928	2	568.285688	17.9	y4
GMFB	P60983	FIVYSYK	FIVYSYK[+8]	heavy	464.256928	2	261.159754	17.9	b2

GOT1	P17174	IGADFLAR	IGADFLAR	light	431.742702	2	749.394064	17	y7
GOT1	P17174	IGADFLAR	IGADFLAR	light	431.742702	2	692.3726	17	y6
GOT1	P17174	IGADFLAR	IGADFLAR	light	431.742702	2	171.112804	17	b2
GOT1	P17174	IGADFLAR	IGADFLAR[+10]	heavy	436.746837	2	759.402333	17	y7
GOT1	P17174	IGADFLAR	IGADFLAR[+10]	heavy	436.746837	2	702.380869	17	y6
GOT1	P17174	IGADFLAR	IGADFLAR[+10]	heavy	436.746837	2	171.112804	17	b2
GOT1	P17174	VGNLTVVGK	VGNLTVVGK	light	443.77146	2	787.467229	17.4	y8
GOT1	P17174	VGNLTVVGK	VGNLTVVGK	light	443.77146	2	730.445765	17.4	y7
GOT1	P17174	VGNLTVVGK	VGNLTVVGK	light	443.77146	2	503.318774	17.4	y5
GOT1	P17174	VGNLTVVGK	VGNLTVVGK[+8]	heavy	447.778559	2	795.481428	17.4	y8
GOT1	P17174	VGNLTVVGK	VGNLTVVGK[+8]	heavy	447.778559	2	738.459964	17.4	y7
GOT1	P17174	VGNLTVVGK	VGNLTVVGK[+8]	heavy	447.778559	2	511.332973	17.4	y5
GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	light	660.351334	2	1007.515636	24.7	y9
GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	light	660.351334	2	893.472708	24.7	y8
GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	light	660.351334	2	200.102967	24.7	b3
GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8]	heavy	664.358433	2	1015.529835	24.7	y9
GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8]	heavy	664.358433	2	901.486907	24.7	y8
GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8]	heavy	664.358433	2	200.102967	24.7	b3
HBA1	P69905	FLASVSTVLTSK	FLASVSTVLTSK	light	626.861003	2	992.562252	23.6	y10
HBA1	P69905	FLASVSTVLTSK	FLASVSTVLTSK	light	626.861003	2	735.424696	23.6	y7
HBA1	P69905	FLASVSTVLTSK	FLASVSTVLTSK	light	626.861003	2	261.159754	23.6	b2
HBA1	P69905	FLASVSTVLTSK	FLASVSTVLTSK[+8]	heavy	630.868102	2	1000.576451	23.6	y10
HBA1	P69905	FLASVSTVLTSK	FLASVSTVLTSK[+8]	heavy	630.868102	2	743.438895	23.6	y7
HBA1	P69905	FLASVSTVLTSK	FLASVSTVLTSK[+8]	heavy	630.868102	2	261.159754	23.6	b2
HBB	P68871	VNVDEVGGEALGR	VNVDEVGGEALGR	light	657.836048	2	1002.485064	24.6	y10
HBB	P68871	VNVDEVGGEALGR	VNVDEVGGEALGR	light	657.836048	2	659.347114	24.6	y7
HBB	P68871	VNVDEVGGEALGR	VNVDEVGGEALGR	light	657.836048	2	214.118617	24.6	b2
HBB	P68871	VNVDEVGGEALGR	VNVDEVGGEALGR[+10]	heavy	662.840182	2	1012.493333	24.6	y10
HBB	P68871	VNVDEVGGEALGR	VNVDEVGGEALGR[+10]	heavy	662.840182	2	669.355383	24.6	y7
HBB	P68871	VNVDEVGGEALGR	VNVDEVGGEALGR[+10]	heavy	662.840182	2	214.118617	24.6	b2
KNG1	P01042	EGDCPVQSGK	EGDC[+57]PVQSGK	light	538.737488	2	615.346051	20.6	y6
KNG1	P01042	EGDCPVQSGK	EGDC[+57]PVQSGK	light	538.737488	2	419.224873	20.6	y4
KNG1	P01042	EGDCPVQSGK	EGDC[+57]PVQSGK	light	538.737488	2	291.166296	20.6	y3
KNG1	P01042	EGDCPVQSGK	EGDC[+57]PVQSGK[+8]	heavy	542.744587	2	623.36025	20.6	y6
KNG1	P01042	EGDCPVQSGK	EGDC[+57]PVQSGK[+8]	heavy	542.744587	2	427.239072	20.6	y4
KNG1	P01042	EGDCPVQSGK	EGDC[+57]PVQSGK[+8]	heavy	542.744587	2	299.180495	20.6	y3
KNG1	P01042	QVVAGLNFR	QVVAGLNFR	light	502.287808	2	776.441349	19.4	y7
KNG1	P01042	QVVAGLNFR	QVVAGLNFR	light	502.287808	2	677.372935	19.4	y6
KNG1	P01042	QVVAGLNFR	QVVAGLNFR	light	502.287808	2	606.335821	19.4	y5
KNG1	P01042	QVVAGLNFR	QVVAGLNFR[+10]	heavy	507.291943	2	786.449618	19.4	y7
KNG1	P01042	QVVAGLNFR	QVVAGLNFR[+10]	heavy	507.291943	2	687.381204	19.4	y6

KNG1	P01042	QVVAGLNFR	QVVAGLNFR[+10]	heavy	507.291943	2	616.34409	19.4	y5
KNG1	P01042	VQVVAGK	VQVVAGK	light	350.721238	2	473.308209	14.2	y5
KNG1	P01042	VQVVAGK	VQVVAGK	light	350.721238	2	275.171381	14.2	y3
KNG1	P01042	VQVVAGK	VQVVAGK	light	350.721238	2	228.134267	14.2	b2
KNG1	P01042	VQVVAGK	VQVVAGK[+8]	heavy	354.728338	2	481.322408	14.2	y5
KNG1	P01042	VQVVAGK	VQVVAGK[+8]	heavy	354.728338	2	283.18558	14.2	y3
KNG1	P01042	VQVVAGK	VQVVAGK[+8]	heavy	354.728338	2	228.134267	14.2	b2
LDHB	P07195	FIIPQIVK	FIIPQIVK	light	479.310221	2	697.460687	18.6	y6
LDHB	P07195	FIIPQIVK	FIIPQIVK	light	479.310221	2	584.376623	18.6	y5
LDHB	P07195	FIIPQIVK	FIIPQIVK	light	479.310221	2	261.159754	18.6	b2
LDHB	P07195	FIIPQIVK	FIIPQIVK[+8]	heavy	483.31732	2	705.474886	18.6	y6
LDHB	P07195	FIIPQIVK	FIIPQIVK[+8]	heavy	483.31732	2	592.390822	18.6	y5
LDHB	P07195	FIIPQIVK	FIIPQIVK[+8]	heavy	483.31732	2	261.159754	18.6	b2
LDHC	P07864	VIGSGCNLDSAR	VIGSGC[+57]NLDSAR	light	624.803693	2	1036.447633	23.5	y10
LDHC	P07864	VIGSGCNLDSAR	VIGSGC[+57]NLDSAR	light	624.803693	2	892.394141	23.5	y8
LDHC	P07864	VIGSGCNLDSAR	VIGSGC[+57]NLDSAR	light	624.803693	2	213.159754	23.5	b2
LDHC	P07864	VIGSGCNLDSAR	VIGSGC[+57]NLDSAR[+10]	heavy	629.807828	2	1046.455902	23.5	y10
LDHC	P07864	VIGSGCNLDSAR	VIGSGC[+57]NLDSAR[+10]	heavy	629.807828	2	902.40241	23.5	y8
LDHC	P07864	VIGSGCNLDSAR	VIGSGC[+57]NLDSAR[+10]	heavy	629.807828	2	213.159754	23.5	b2
MDH1	P40925	ENFSCLTR	ENFSC[+57]LTR	light	513.737291	2	783.381785	19.8	y6
MDH1	P40925	ENFSCLTR	ENFSC[+57]LTR	light	513.737291	2	636.313371	19.8	y5
MDH1	P40925	ENFSCLTR	ENFSC[+57]LTR	light	513.737291	2	549.281343	19.8	y4
MDH1	P40925	ENFSCLTR	ENFSC[+57]LTR[+10]	heavy	518.741425	2	793.390054	19.8	y6
MDH1	P40925	ENFSCLTR	ENFSC[+57]LTR[+10]	heavy	518.741425	2	646.32164	19.8	y5
MDH1	P40925	ENFSCLTR	ENFSC[+57]LTR[+10]	heavy	518.741425	2	559.289612	19.8	y4
MDH1	P40925	GEFVTTVQQR	GEFVTTVQQR	light	582.804019	2	732.399878	22.1	y6
MDH1	P40925	GEFVTTVQQR	GEFVTTVQQR	light	582.804019	2	631.352199	22.1	y5
MDH1	P40925	GEFVTTVQQR	GEFVTTVQQR	light	582.804019	2	334.139747	22.1	b3
MDH1	P40925	GEFVTTVQQR	GEFVTTVQQR[+10]	heavy	587.808154	2	742.408147	22.1	y6
MDH1	P40925	GEFVTTVQQR	GEFVTTVQQR[+10]	heavy	587.808154	2	641.360468	22.1	y5
MDH1	P40925	GEFVTTVQQR	GEFVTTVQQR[+10]	heavy	587.808154	2	334.139747	22.1	b3
NCAM1	P13591	GLGEISAASEFK	GLGEISAASEFK	light	604.81151	2	852.446159	22.8	y8
NCAM1	P13591	GLGEISAASEFK	GLGEISAASEFK	light	604.81151	2	739.362095	22.8	y7
NCAM1	P13591	GLGEISAASEFK	GLGEISAASEFK	light	604.81151	2	171.112804	22.8	b2
NCAM1	P13591	GLGEISAASEFK	GLGEISAASEFK[+8]	heavy	608.818609	2	860.460358	22.8	y8
NCAM1	P13591	GLGEISAASEFK	GLGEISAASEFK[+8]	heavy	608.818609	2	747.376294	22.8	y7
NCAM1	P13591	GLGEISAASEFK	GLGEISAASEFK[+8]	heavy	608.818609	2	171.112804	22.8	b2
NPTX2	P47972	VAELEDEK	VAELEDEK	light	466.732197	2	833.388704	18.2	y7
NPTX2	P47972	VAELEDEK	VAELEDEK	light	466.732197	2	762.35159	18.2	y6
NPTX2	P47972	VAELEDEK	VAELEDEK	light	466.732197	2	171.112804	18.2	b2
NPTX2	P47972	VAELEDEK	VAELEDEK[+8]	heavy	470.739296	2	841.402903	18.2	y7

NPTX2	P47972	VAELEDEK	VAELEDEK[+8]	heavy	470.739296	2	770.365789	18.2	y6
NPTX2	P47972	VAELEDEK	VAELEDEK[+8]	heavy	470.739296	2	171.112804	18.2	b2
NPTXR	O95502	ADQDTIR	ADQDTIR	light	409.703774	2	632.336215	16.2	y5
NPTXR	O95502	ADQDTIR	ADQDTIR	light	409.703774	2	504.277637	16.2	y4
NPTXR	O95502	ADQDTIR	ADQDTIR	light	409.703774	2	187.071333	16.2	b2
NPTXR	O95502	ADQDTIR	ADQDTIR[+10]	heavy	414.707908	2	642.344484	16.2	y5
NPTXR	O95502	ADQDTIR	ADQDTIR[+10]	heavy	414.707908	2	514.285906	16.2	y4
NPTXR	O95502	ADQDTIR	ADQDTIR[+10]	heavy	414.707908	2	187.071333	16.2	b2
NPTXR	O95502	ELDVLQGR	ELDVLQGR	light	465.256174	2	687.378414	18.1	y6
NPTXR	O95502	ELDVLQGR	ELDVLQGR	light	465.256174	2	473.283057	18.1	y4
NPTXR	O95502	ELDVLQGR	ELDVLQGR	light	465.256174	2	360.198993	18.1	y3
NPTXR	O95502	ELDVLQGR	ELDVLQGR[+10]	heavy	470.260308	2	697.386683	18.1	y6
NPTXR	O95502	ELDVLQGR	ELDVLQGR[+10]	heavy	470.260308	2	483.291326	18.1	y4
NPTXR	O95502	ELDVLQGR	ELDVLQGR[+10]	heavy	470.260308	2	370.207262	18.1	y3
NRXN1	P58400	LAIGFSTVQK	LAIGFSTVQK	light	532.310949	2	879.493444	20.4	y8
NRXN1	P58400	LAIGFSTVQK	LAIGFSTVQK	light	532.310949	2	766.40938	20.4	y7
NRXN1	P58400	LAIGFSTVQK	LAIGFSTVQK	light	532.310949	2	709.387916	20.4	y6
NRXN1	P58400	LAIGFSTVQK	LAIGFSTVQK[+8]	heavy	536.318048	2	887.507643	20.4	y8
NRXN1	P58400	LAIGFSTVQK	LAIGFSTVQK[+8]	heavy	536.318048	2	774.423579	20.4	y7
NRXN1	P58400	LAIGFSTVQK	LAIGFSTVQK[+8]	heavy	536.318048	2	717.402115	20.4	y6
OGN	P20774	LEGNPIVLGK	LEGNPIVLGK	light	520.310949	2	797.487965	20	y8
OGN	P20774	LEGNPIVLGK	LEGNPIVLGK	light	520.310949	2	626.423573	20	y6
OGN	P20774	LEGNPIVLGK	LEGNPIVLGK	light	520.310949	2	243.133933	20	b2
OGN	P20774	LEGNPIVLGK	LEGNPIVLGK[+8]	heavy	524.318048	2	805.502164	20	y8
OGN	P20774	LEGNPIVLGK	LEGNPIVLGK[+8]	heavy	524.318048	2	634.437772	20	y6
OGN	P20774	LEGNPIVLGK	LEGNPIVLGK[+8]	heavy	524.318048	2	243.133933	20	b2
OMG	P23515	LESLPAHLPR	LESLPAHLPR	light	566.827297	2	890.520662	21.6	y8
OMG	P23515	LESLPAHLPR	LESLPAHLPR	light	566.827297	2	690.404569	21.6	y6
OMG	P23515	LESLPAHLPR	LESLPAHLPR	light	566.827297	2	345.705923	21.6	y6
OMG	P23515	LESLPAHLPR	LESLPAHLPR[+10]	heavy	571.831432	2	900.528931	21.6	y8
OMG	P23515	LESLPAHLPR	LESLPAHLPR[+10]	heavy	571.831432	2	700.412838	21.6	y6
OMG	P23515	LESLPAHLPR	LESLPAHLPR[+10]	heavy	571.831432	2	350.710057	21.6	y6
PARK7	Q99497	ALVILAK	ALVILAK	light	364.257457	2	543.38646	14.7	y5
PARK7	Q99497	ALVILAK	ALVILAK	light	364.257457	2	444.318046	14.7	y4
PARK7	Q99497	ALVILAK	ALVILAK	light	364.257457	2	185.128454	14.7	b2
PARK7	Q99497	ALVILAK	ALVILAK[+8]	heavy	368.264556	2	551.400659	14.7	y5
PARK7	Q99497	ALVILAK	ALVILAK[+8]	heavy	368.264556	2	452.332245	14.7	y4
PARK7	Q99497	ALVILAK	ALVILAK[+8]	heavy	368.264556	2	185.128454	14.7	b2
PEBP1	P30086	VLTPTQVK	VLTPTQVK	light	443.273835	2	673.387916	17.4	y6
PEBP1	P30086	VLTPTQVK	VLTPTQVK	light	443.273835	2	572.340238	17.4	y5
PEBP1	P30086	VLTPTQVK	VLTPTQVK	light	443.273835	2	213.159754	17.4	b2

PEBP1	P30086	VLTPTQVK	VLTPTQVK[+8]	heavy	447.280935	2	681.402115	17.4	y6
PEBP1	P30086	VLTPTQVK	VLTPTQVK[+8]	heavy	447.280935	2	580.354437	17.4	y5
PEBP1	P30086	VLTPTQVK	VLTPTQVK[+8]	heavy	447.280935	2	213.159754	17.4	b2
PEBP1	P30086	LYEQLSGK	LYEQLSGK	light	469.2531	2	661.351531	18.2	y6
PEBP1	P30086	LYEQLSGK	LYEQLSGK	light	469.2531	2	291.166296	18.2	y3
PEBP1	P30086	LYEQLSGK	LYEQLSGK	light	469.2531	2	277.154669	18.2	b2
PEBP1	P30086	LYEQLSGK	LYEQLSGK[+8]	heavy	473.260199	2	669.36573	18.2	y6
PEBP1	P30086	LYEQLSGK	LYEQLSGK[+8]	heavy	473.260199	2	299.180495	18.2	y3
PEBP1	P30086	LYEQLSGK	LYEQLSGK[+8]	heavy	473.260199	2	277.154669	18.2	b2
PGLYRP2	Q96PD5	TFTLLDPK	TFTLLDPK	light	467.765843	2	686.408317	18.2	y6
PGLYRP2	Q96PD5	TFTLLDPK	TFTLLDPK	light	467.765843	2	585.360639	18.2	y5
PGLYRP2	Q96PD5	TFTLLDPK	TFTLLDPK	light	467.765843	2	244.165568	18.2	y2
PGLYRP2	Q96PD5	TFTLLDPK	TFTLLDPK[+8]	heavy	471.772942	2	694.422516	18.2	y6
PGLYRP2	Q96PD5	TFTLLDPK	TFTLLDPK[+8]	heavy	471.772942	2	593.374838	18.2	y5
PGLYRP2	Q96PD5	TFTLLDPK	TFTLLDPK[+8]	heavy	471.772942	2	252.179767	18.2	y2
PKM	P14618	VVEVGSK	VVEVGSK	light	359.210703	2	618.345717	14.5	y6
PKM	P14618	VVEVGSK	VVEVGSK	light	359.210703	2	519.277303	14.5	y5
PKM	P14618	VVEVGSK	VVEVGSK	light	359.210703	2	390.23471	14.5	y4
PKM	P14618	VVEVGSK	VVEVGSK[+8]	heavy	363.217803	2	626.359916	14.5	y6
PKM	P14618	VVEVGSK	VVEVGSK[+8]	heavy	363.217803	2	527.291502	14.5	y5
PKM	P14618	VVEVGSK	VVEVGSK[+8]	heavy	363.217803	2	398.248909	14.5	y4
PKM	P14618	GDLGIEIPAEK	GDLGIEIPAEK	light	571.308603	2	856.477459	21.7	y8
PKM	P14618	GDLGIEIPAEK	GDLGIEIPAEK	light	571.308603	2	686.371932	21.7	y6
PKM	P14618	GDLGIEIPAEK	GDLGIEIPAEK	light	571.308603	2	444.245275	21.7	y4
PKM	P14618	GDLGIEIPAEK	GDLGIEIPAEK[+8]	heavy	575.315703	2	864.491658	21.7	y8
PKM	P14618	GDLGIEIPAEK	GDLGIEIPAEK[+8]	heavy	575.315703	2	694.386131	21.7	y6
PKM	P14618	GDLGIEIPAEK	GDLGIEIPAEK[+8]	heavy	575.315703	2	452.259474	21.7	y4
PKM	P14618	GDYPLEAVR	GDYPLEAVR	light	510.261456	2	684.403901	19.6	y6
PKM	P14618	GDYPLEAVR	GDYPLEAVR	light	510.261456	2	587.351137	19.6	y5
PKM	P14618	GDYPLEAVR	GDYPLEAVR	light	510.261456	2	342.705588	19.6	y6
PKM	P14618	GDYPLEAVR	GDYPLEAVR[+10]	heavy	515.26559	2	694.41217	19.6	y6
PKM	P14618	GDYPLEAVR	GDYPLEAVR[+10]	heavy	515.26559	2	597.359406	19.6	y5
PKM	P14618	GDYPLEAVR	GDYPLEAVR[+10]	heavy	515.26559	2	347.709723	19.6	y6
PKM2		LFEELVR	LFEELVR	light	453.258185	2	792.42503	17.7	y6
PKM2		LFEELVR	LFEELVR	light	453.258185	2	645.356616	17.7	y5
PKM2		LFEELVR	LFEELVR	light	453.258185	2	261.159754	17.7	b2
PKM2		LFEELVR	LFEELVR[+10]	heavy	458.262319	2	802.433299	17.7	y6
PKM2		LFEELVR	LFEELVR[+10]	heavy	458.262319	2	655.364885	17.7	y5
PKM2		LFEELVR	LFEELVR[+10]	heavy	458.262319	2	261.159754	17.7	b2
PON1	P27169	LLIGTVFHK	LLIGTVFHK	light	514.318577	2	801.46175	19.8	y7
PON1	P27169	LLIGTVFHK	LLIGTVFHK	light	514.318577	2	227.175404	19.8	b2

PON1	P27169	LLIGTVFHK	LLIGTVFHK	light	514.318577	2	199.144104	19.8	b4
PON1	P27169	LLIGTVFHK	LLIGTVFHK[+8]	heavy	518.325676	2	809.475949	19.8	y7
PON1	P27169	LLIGTVFHK	LLIGTVFHK[+8]	heavy	518.325676	2	227.175404	19.8	b2
PON1	P27169	LLIGTVFHK	LLIGTVFHK[+8]	heavy	518.325676	2	199.144104	19.8	b4
PPIA	P62937	VSFELFADK	VSFELFADK	light	528.274032	2	956.472374	20.2	y8
PPIA	P62937	VSFELFADK	VSFELFADK	light	528.274032	2	869.440346	20.2	y7
PPIA	P62937	VSFELFADK	VSFELFADK	light	528.274032	2	187.107718	20.2	b2
PPIA	P62937	VSFELFADK	VSFELFADK[+8]	heavy	532.281132	2	964.486573	20.2	y8
PPIA	P62937	VSFELFADK	VSFELFADK[+8]	heavy	532.281132	2	877.454545	20.2	y7
PPIA	P62937	VSFELFADK	VSFELFADK[+8]	heavy	532.281132	2	187.107718	20.2	b2
PTPRZ1	P23471	AIIDGVESVSR	AIIDGVESVSR	light	573.311677	2	961.4949	21.8	y9
PTPRZ1	P23471	AIIDGVESVSR	AIIDGVESVSR	light	573.311677	2	848.410836	21.8	y8
PTPRZ1	P23471	AIIDGVESVSR	AIIDGVESVSR	light	573.311677	2	185.128454	21.8	b2
PTPRZ1	P23471	AIIDGVESVSR	AIIDGVESVSR[+10]	heavy	578.315812	2	971.503169	21.8	y9
PTPRZ1	P23471	AIIDGVESVSR	AIIDGVESVSR[+10]	heavy	578.315812	2	858.419105	21.8	y8
PTPRZ1	P23471	AIIDGVESVSR	AIIDGVESVSR[+10]	heavy	578.315812	2	185.128454	21.8	b2
PTPRZ1	P23471	DIEEGAIVNPGR	DIEEGAIVNPGR	light	635.325316	2	783.447162	23.9	y8
PTPRZ1	P23471	DIEEGAIVNPGR	DIEEGAIVNPGR	light	635.325316	2	655.388585	23.9	y6
PTPRZ1	P23471	DIEEGAIVNPGR	DIEEGAIVNPGR	light	635.325316	2	443.236107	23.9	y4
PTPRZ1	P23471	DIEEGAIVNPGR	DIEEGAIVNPGR[+10]	heavy	640.32945	2	793.455431	23.9	y8
PTPRZ1	P23471	DIEEGAIVNPGR	DIEEGAIVNPGR[+10]	heavy	640.32945	2	665.396854	23.9	y6
PTPRZ1	P23471	DIEEGAIVNPGR	DIEEGAIVNPGR[+10]	heavy	640.32945	2	453.244376	23.9	y4
SCG2	P13521	IESQTQEEVR	IESQTQEEVR	light	609.801674	2	976.469414	23	y8
SCG2	P13521	IESQTQEEVR	IESQTQEEVR	light	609.801674	2	761.378808	23	y6
SCG2	P13521	IESQTQEEVR	IESQTQEEVR	light	609.801674	2	243.133933	23	b2
SCG2	P13521	IESQTQEEVR	IESQTQEEVR[+10]	heavy	614.805808	2	986.477683	23	y8
SCG2	P13521	IESQTQEEVR	IESQTQEEVR[+10]	heavy	614.805808	2	771.387077	23	y6
SCG2	P13521	IESQTQEEVR	IESQTQEEVR[+10]	heavy	614.805808	2	243.133933	23	b2
SMOC1	Q9H4F8	AQALEQAK	AQALEQAK	light	429.737617	2	659.372266	16.9	y6
SMOC1	Q9H4F8	AQALEQAK	AQALEQAK	light	429.737617	2	588.335152	16.9	y5
SMOC1	Q9H4F8	AQALEQAK	AQALEQAK	light	429.737617	2	200.102967	16.9	b2
SMOC1	Q9H4F8	AQALEQAK	AQALEQAK[+8]	heavy	433.744716	2	667.386465	16.9	y6
SMOC1	Q9H4F8	AQALEQAK	AQALEQAK[+8]	heavy	433.744716	2	596.349351	16.9	y5
SMOC1	Q9H4F8	AQALEQAK	AQALEQAK[+8]	heavy	433.744716	2	200.102967	16.9	b2
SOD1	P00441	HVGDLGNVTADK	HVGDLGNVTADK	light	613.312208	2	1088.558229	23.1	y11
SOD1	P00441	HVGDLGNVTADK	HVGDLGNVTADK	light	613.312208	2	989.489815	23.1	y10
SOD1	P00441	HVGDLGNVTADK	HVGDLGNVTADK	light	613.312208	2	237.134602	23.1	b2
SOD1	P00441	HVGDLGNVTADK	HVGDLGNVTADK[+8]	heavy	617.319308	2	1096.572428	23.1	y11
SOD1	P00441	HVGDLGNVTADK	HVGDLGNVTADK[+8]	heavy	617.319308	2	997.504014	23.1	y10
SOD1	P00441	HVGDLGNVTADK	HVGDLGNVTADK[+8]	heavy	617.319308	2	237.134602	23.1	b2
SPP1	P10451	QETLPSK	QETLPSK	light	401.718893	2	545.329339	16	y5

SPP1	P10451	QETLPSK	QETLPSK	light	401.718893	2	331.197596	16	y3
SPP1	P10451	QETLPSK	QETLPSK	light	401.718893	2	234.144832	16	y2
SPP1	P10451	QETLPSK	QETLPSK[+8]	heavy	405.725992	2	553.343538	16	y5
SPP1	P10451	QETLPSK	QETLPSK[+8]	heavy	405.725992	2	339.211795	16	y3
SPP1	P10451	QETLPSK	QETLPSK[+8]	heavy	405.725992	2	242.159031	16	y2
SPP1	P10451	GDSVVYGLR	GDSVVYGLR	light	483.256174	2	607.356222	18.7	y5
SPP1	P10451	GDSVVYGLR	GDSVVYGLR	light	483.256174	2	508.287808	18.7	y4
SPP1	P10451	GDSVVYGLR	GDSVVYGLR	light	483.256174	2	345.22448	18.7	y3
SPP1	P10451	GDSVVYGLR	GDSVVYGLR[+10]	heavy	488.260308	2	617.364491	18.7	y5
SPP1	P10451	GDSVVYGLR	GDSVVYGLR[+10]	heavy	488.260308	2	518.296077	18.7	y4
SPP1	P10451	GDSVVYGLR	GDSVVYGLR[+10]	heavy	488.260308	2	355.232748	18.7	y3
TPI1	P60174	IAVAAQNCYK	IAVAAQNC[+57]YK	light	569.289691	2	953.450927	21.6	y8
TPI1	P60174	IAVAAQNCYK	IAVAAQNC[+57]YK	light	569.289691	2	854.382513	21.6	y7
TPI1	P60174	IAVAAQNCYK	IAVAAQNC[+57]YK	light	569.289691	2	783.3454	21.6	y6
TPI1	P60174	IAVAAQNCYK	IAVAAQNC[+57]YK[+8]	heavy	573.29679	2	961.465126	21.6	y8
TPI1	P60174	IAVAAQNCYK	IAVAAQNC[+57]YK[+8]	heavy	573.29679	2	862.396712	21.6	y7
TPI1	P60174	IAVAAQNCYK	IAVAAQNC[+57]YK[+8]	heavy	573.29679	2	791.359599	21.6	y6
VGF	O15240	EPVAGDAVPGPK	EPVAGDAVPGPK	light	568.800945	2	811.430844	21.6	y9
VGF	O15240	EPVAGDAVPGPK	EPVAGDAVPGPK	light	568.800945	2	740.39373	21.6	y8
VGF	O15240	EPVAGDAVPGPK	EPVAGDAVPGPK	light	568.800945	2	398.239795	21.6	y4
VGF	O15240	EPVAGDAVPGPK	EPVAGDAVPGPK[+8]	heavy	572.808045	2	819.445043	21.6	y9
VGF	O15240	EPVAGDAVPGPK	EPVAGDAVPGPK[+8]	heavy	572.808045	2	748.407929	21.6	y8
VGF	O15240	EPVAGDAVPGPK	EPVAGDAVPGPK[+8]	heavy	572.808045	2	406.253994	21.6	y4
VGF	O15240	GLQEAAEER	GLQEAAEER	light	501.74617	2	832.379536	19.3	y7
VGF	O15240	GLQEAAEER	GLQEAAEER	light	501.74617	2	704.320959	19.3	y6
VGF	O15240	GLQEAAEER	GLQEAAEER	light	501.74617	2	575.278366	19.3	y5
VGF	O15240	GLQEAAEER	GLQEAAEER[+10]	heavy	506.750305	2	842.387805	19.3	y7
VGF	O15240	GLQEAAEER	GLQEAAEER[+10]	heavy	506.750305	2	714.329228	19.3	y6
VGF	O15240	GLQEAAEER	GLQEAAEER[+10]	heavy	506.750305	2	585.286635	19.3	y5
YWHAB	P31946	NLLSVAYK	NLLSVAYK	light	454.26601	2	680.397753	17.7	y6
YWHAB	P31946	NLLSVAYK	NLLSVAYK	light	454.26601	2	567.313689	17.7	y5
YWHAB	P31946	NLLSVAYK	NLLSVAYK	light	454.26601	2	228.134267	17.7	b2
YWHAB	P31946	NLLSVAYK	NLLSVAYK[+8]	heavy	458.27311	2	688.411952	17.7	y6
YWHAB	P31946	NLLSVAYK	NLLSVAYK[+8]	heavy	458.27311	2	575.327888	17.7	y5
YWHAB	P31946	NLLSVAYK	NLLSVAYK[+8]	heavy	458.27311	2	228.134267	17.7	b2
YWHAB	P31946	VISSIEQK	VISSIEQK	light	452.260925	2	691.362095	17.7	y6
YWHAB	P31946	VISSIEQK	VISSIEQK	light	452.260925	2	604.330067	17.7	y5
YWHAB	P31946	VISSIEQK	VISSIEQK	light	452.260925	2	213.159754	17.7	b2
YWHAB	P31946	VISSIEQK	VISSIEQK[+8]	heavy	456.268024	2	699.376294	17.7	y6
YWHAB	P31946	VISSIEQK	VISSIEQK[+8]	heavy	456.268024	2	612.344266	17.7	y5
YWHAB	P31946	VISSIEQK	VISSIEQK[+8]	heavy	456.268024	2	213.159754	17.7	b2

YWHAZ	P63104	VVSSIEQK	VVSSIEQK	light	445.2531	2	691.362095	17.4	y6
YWHAZ	P63104	VVSSIEQK	VVSSIEQK	light	445.2531	2	604.330067	17.4	y5
YWHAZ	P63104	VVSSIEQK	VVSSIEQK	light	445.2531	2	199.144104	17.4	b2
YWHAZ	P63104	VVSSIEQK	VVSSIEQK[+8]	heavy	449.260199	2	699.376294	17.4	y6
YWHAZ	P63104	VVSSIEQK	VVSSIEQK[+8]	heavy	449.260199	2	612.344266	17.4	y5
YWHAZ	P63104	VVSSIEQK	VVSSIEQK[+8]	heavy	449.260199	2	199.144104	17.4	b2

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