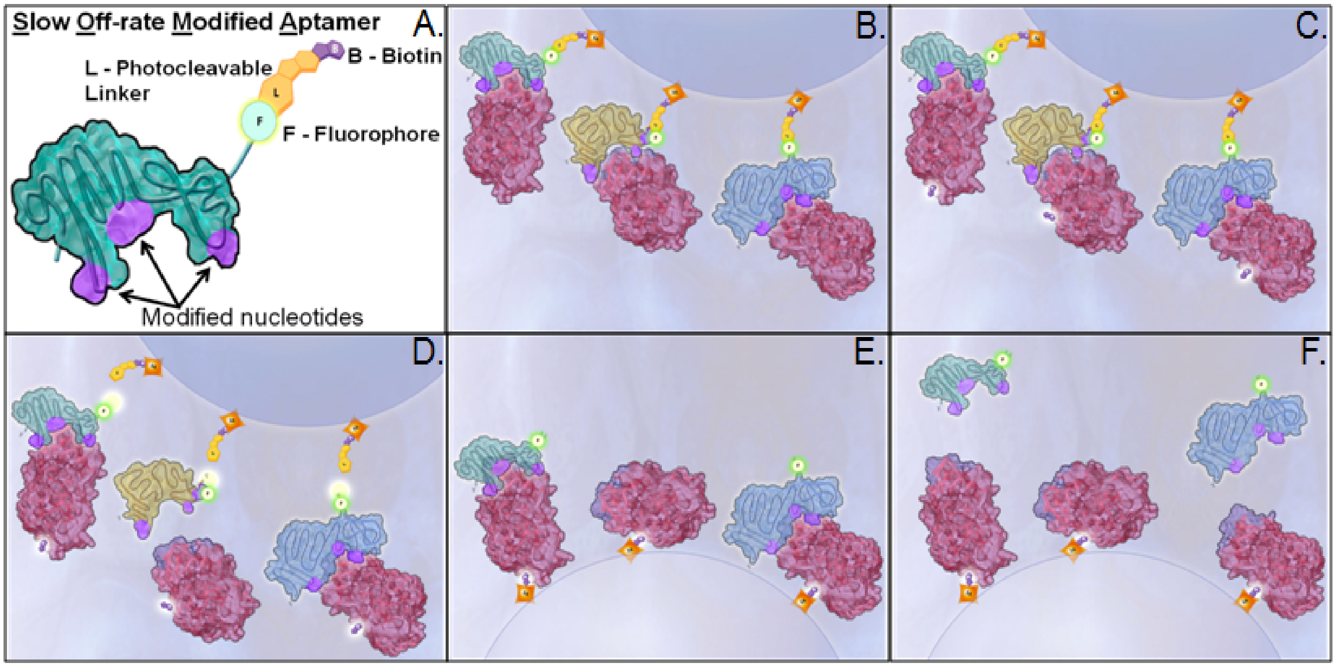
Supplemental Material

Supplemental Methods and Figures

SOMAscan™ Proteomics Assay



Supplemental Figure 1. SOMAscan™ Overview

A SOMAmer reagent is a single-stranded DNA-based aptamer that is chemically modified to enhance binding to conformational protein epitopes with high affinity and specificity. Its flourophore tag allows for detection by standard oligo-array readers. (**Supplemental Figure 1A** demonstrates details of SOMAmer® structure). The assay measures proteins directly from plasma using a multi-step capture, release, and re-capture enrichment process. First, plasma proteins (purple) bind to the bead-immobilized SOMAmers® (**Supplemental Figure 1B**). SOMAmer®-bound proteins are biotinylated (**Supplemental Figure 1C**). SOMAmer®-protein complexes are then released by a photocleavage process and non-specific pairs are disrupted (**Supplemental Figure 1D**). Next, the biotinylated proteins are bound to a second streptavidin bead (**Supplemental Figure 1E**). Following a washing step, SOMAmers® are released from the protein targets and collected (**Supplemental Figure 1F**). The fluorophore-tagged modified nucleotides are quantitated using an oligo-array plate reader (Agilent Technologies).

SOMAscan™ Standardization

To correct for systematic effects on data introduced during the hybridization process, 12 hybridization control sequences were introduced into each clinical sample. There was a predetermined global reference RFU for each hybridization control based on independently run assays. A ratio is determined by this global RFU for each control/measured RFU of each hybridizaton control. The median of the ratios determines the sample based hybridization scale factor. Each sample was multiplied by its own scale factor.

Median normalization was performed to remove sample or assay biases that may be due to differences between samples in overall protein concentration, pipetting variation, variation in reagent concentrations, assay timing, and any other source of systematic variability within a single plate run. Each sample was diluted either to 40%, 1% or 0.05%. A scale factor was derived for each dilution set and all the SOMAmers in each dilution set are scaled together. Median RFU for a SOMAmer within the sample group was the reference SOMAmer RFU. A ratio was determined by the reference SOMAmer RFU/measured RFU of the SOMAmer in the sample. Within each dilution set, the median SOMAmer ratio was the scale factor for all the SOMAmers in that dilution in that sample. The acceptance criteria for these values are 0.4 to 2.5, based on historic trends in these values.

The global reference RFU for each SOMAmer was defined as the median signal measured on a set of samples spanning a number of independent assay runs. There were 5 calibrator samples which comprise of human pooled plasma on each plate. A local median reference value was derived for each SOMAmer by computing the median RFU for that SOMAmer from the 5 calibrator samples within a single plate. A scale factor was determined by the ratio of the global reference calibrator for the SOMAmer/ local median reference value of the SOMAmer. Each SOMAmer on each plate has a unique scale factor. The acceptance criterion for calibrator scale factors is that 95% of SOMAmers must have a calibration scale factor within 60.4 of the median. These calibrator samples were also used to calculate intra-assay CV.

Additionally, the plasma from one individual was run as 2 QC samples on each plate. The QC samples were normalized as above. Hybridization normalized, median normalized and calibrated QC samples were used to calculate inter-assay CV for each SOMAmer because calibration by definition will minimize the plate-to-plate variance of the calibrator samples.

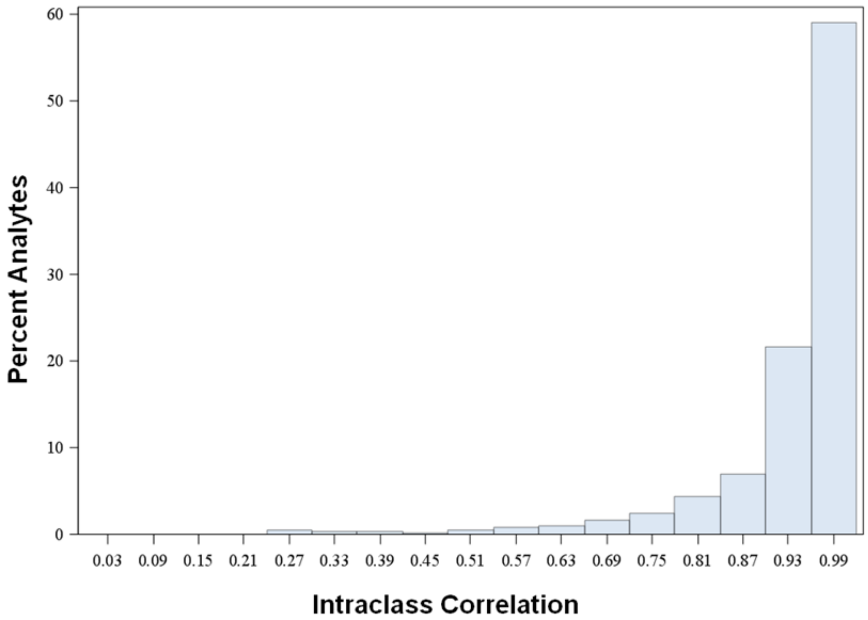
Reproducibility

Coefficient of variation studies

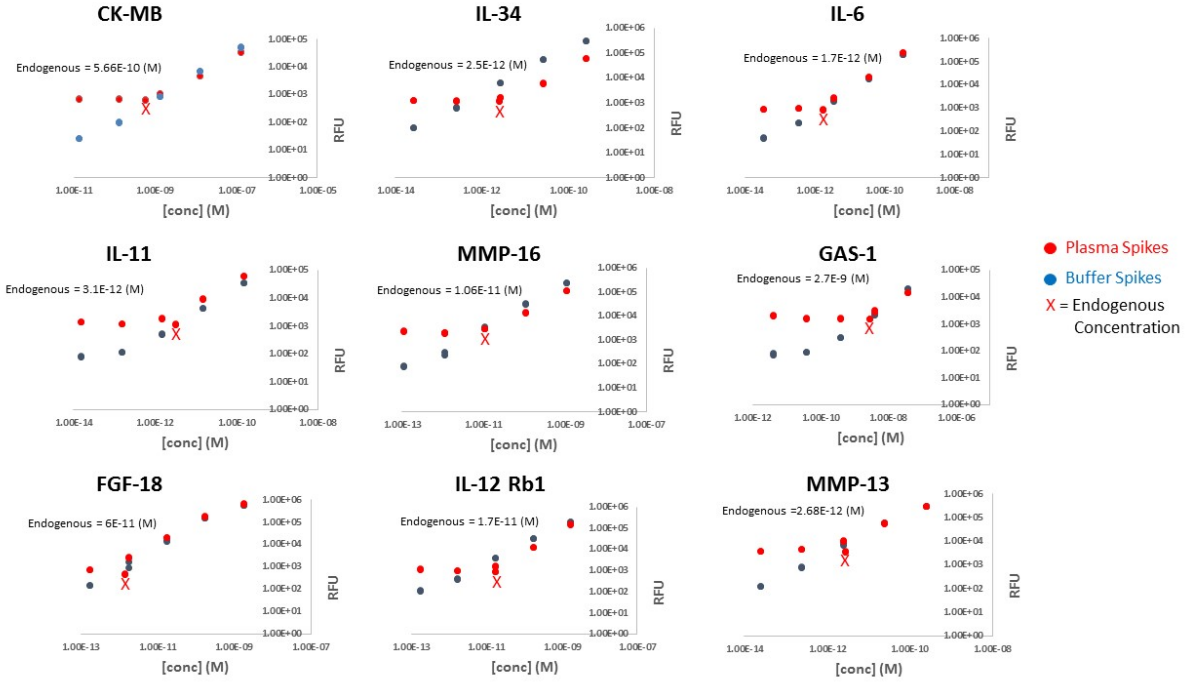
Assay plates contained 24 clinical samples, 5 pooled plasma calibrators, 2 quality control samples and 1 negative control buffer sample. We assayed 5 replicate pooled plasma samples (calibrators) across 43 plates. For each of the 43 plates, median intra-assay CV ≤ 8.2%. We assayed 2 replicate plasma samples across the 43 plates to determine median inter-assay CV of 7.8%.

Intraclass correlation (ICC) studies of blinded duplicate samples.

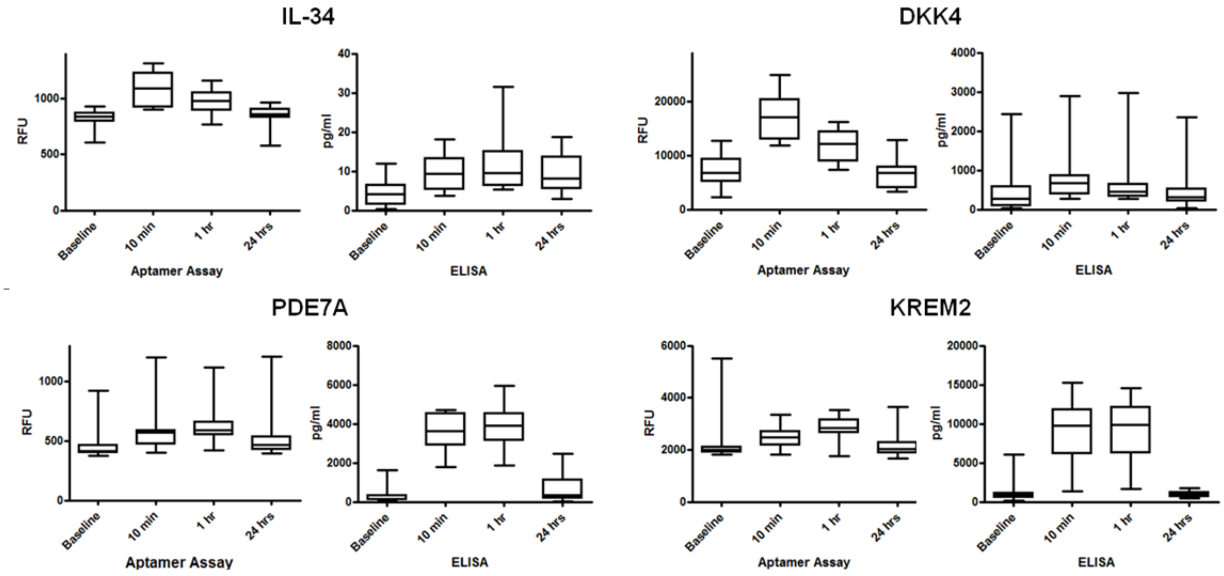
In addition to performing CV studies using pooled plasma samples, we also evaluated reproducibility by analyzing blinded duplicate samples from 94 FHS Offspring participants (N=188 total samples) collected between 1991-1995. ICCs for 1129 proteins assayed demonstrated median ICC >0.95. The entire distribution is plotted in **Supplemental Figure 2**. Taken together, the QC studies using both the pooled plasma samples and the blinded split samples from FHS confirm the reproducibility of the platform established in our laboratory.



Supplemental Figure 2. Distribution of intraclass correlation for duplicate samples

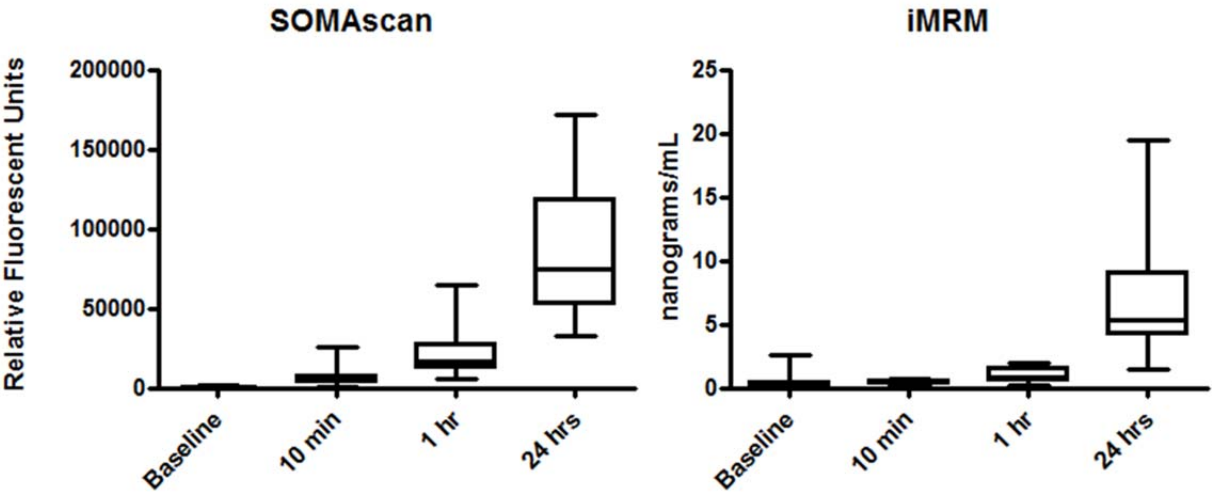


Supplemental Figure 3. SOMAscan™ calibration curves for spiked in protein standards Standards corresponding to proteins associated with PMI were spiked into human pooled plasma or assay buffer (as indicated) to achieve a range of concentrations across 5 orders of magnitude. Samples were run on the aptamer platform. Calibration curves were generated from the concentration versus RFU data. Linear regression analysis was performed to calculate endogenous human pooled plasma protein concentrations.

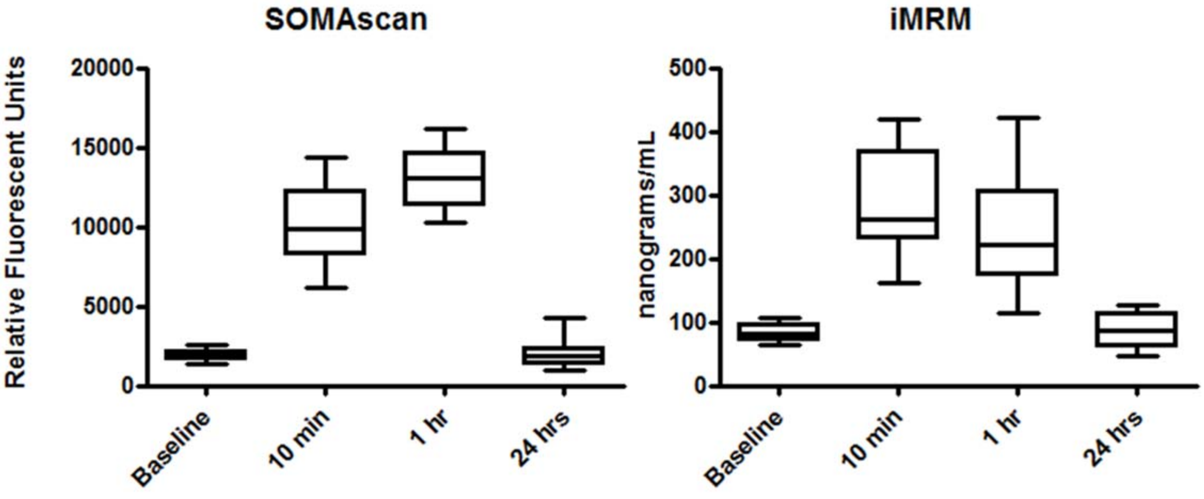


Supplemental Figure 4. Immunoassay validation for selected PMI findings

For each protein, aptamer-based data are presented in the left of each panel (*P* < 2.30E-4 for all proteins by ANOVA) and corresponding immunoassay data in the right of each panel (IL-34: *P* = 8.61E-4; PDE7A: *P* = 3.80E-08; DKK-4: *P* = 8.48E-03; KREM2: *P* = 1.0E-09 by one-way ANOVA). Data are from n ≥ 10 individuals for each biomarker. Edges of boxes denote 25th and 75th percentiles, lines denote median, whiskers denote minimum and maximum values. Due to sample availability, corresponding aptamer and immunoassay were not performed on the identical individuals.



Troponin I



Spondin 1

Supplemental Figure 5. Comparison of protein measurements by SOMAscan aptamer-based assay versus immunoaffinity MRM in PMI patients

SOMAscan data represents protein levels in validation cohort (n=15) and iMRM data represents protein levels in an independent PMI cohort (n=12 for Spondin 1 and n=11 for Troponin I). Edges of boxes denote 25th and 75th percentiles, lines denote median, whiskers denote minimum and maximum values.

Supplemental Methods for Aptamer Affinity Evaluation using targeted LC-MRM-MS and untargeted LC-MS/MS

Aptamer affinity enrichment

Two picomoles of protein for each of the 29 proteins were added to 40 uL of patient plasma (1 hour timepoint) in duplicate. Two additional equivalent volumes of plasma were prepared without proteins added. Samples were brought to 100 uL total by the addition of 60 uL of HEPES buffer (40 mM HEPES, 102 mM NaCl, 1 mM EDTA, 5 mM MgCl2, 5 mM KCl, 0.05% Tween-20, pH 7.5). Ten picomoles each of 29 SOMAmers®, aptamers containing photocleavable linkers and biotin (SOMAlogic, Boulder, CO), generated specifically against these 29 proteins were combined for each affinity enrichment, heated to 95C for 10min, then cooled to room temperature prior to use. For each enrichment, 100 uL of streptavidin (SA) C1 magnetic beads (Dynal, Invitrogen, Thermo) were washed 2 times with 500 uL HEPES buffer. After a brief vortex mix, a magnet was used to pull the beads to the side of the tube and the supernatant was removed. Beads were resuspended in 100 uL HEPES, added to the SOMAmer mixture (290 pmol total/capture) and tumble mixed 20 min at room temperature. After incubation, beads were washed 2 times with 500uL CAPS buffer (50 mM CAPS, 1 mM EDTA, 0.05% Tween-20, pH 11.0). Beads were resuspended in an equivalent starting volume of HEPES buffer (100 uL/capture) and added to one replicate of plasma containing added proteins and one replicate of plasma without additional proteins. As controls, 100 uL of SA beads were washed with HEPES buffer and added to one of each type of plasma sample (with and without added proteins). Samples were tumble mixed overnight at room temperature. After mixing, beads were washed twice with HEPES buffer without Tween-20 and bound material was eluted with 2 volumes of 50 uL of 20 mM NaOH. Eluates were pooled and dried under vacuum prior to digestion.

Preparation of protein response curves

Plasma was obtained from a pool of healthy donors (BioreclamationIVT, Westbury, NY). Fifteen picomoles for each of the 29 proteins were added to 300 uL of 40% plasma (120 uL into 180 uL of HEPES buffer (40 mM HEPES, 102 mM NaCl, 1 mM EDTA, 5 mM MgCl2, 5 mM KCl, 0.05% Tween-20, pH 7.5) and serially diluted in 4-fold increments over 8 concentrations as previously described.[1] A blank plasma sample without added proteins was also prepared. One hundred ul of each curve sample was affinity enriched using a 29-plex of aptamers as described in the section "Aptamer affinity enrichment" in triplicate. After digestion and prior to desalt, 50 fmol of 19 stable isotope standard peptides were added (see **Supplemental Table 21** for sequences and masses).

Trypsin digestion of aptamer-enriched samples

Samples of aptamer enriched plasma were resuspended in 40 uL of 7 M Urea, 2 M thiourea, 5 uL 1 M Tris pH 8.0, and 4 uL 0.5 M tris(2-chloroethyl) phosphate and incubated at 37 °C 850 RPM for 30 min. After reduction and denaturation, samples were cooled to room temperature and 10 uL of 0.5 M iodoacetamide were added. After mixing briefly, the samples were incubated in the dark at room temperature for 30 min. After alkylation, 250 uL of 0.2 M Tris pH 8.1 and 2 ug of porcine trypsin (Promega) were added and samples were incubated at 37 °C 850 RPM overnight. After digestion, 15 uL trifluoroacetic acid (TFA) were added to quench the reaction and samples were desalted using StageTips[2] by centrifugation (Eppendorf) at 2000 RCF for 2 min after each solvent was added. StageTips were washed and equilibrated with 50 uL of 90% acetonitrile/0.1% TFA and 0.1% TFA prior to use. Samples were added to StageTips in 50 uL increments, centrifuging after each load until the entire digestion volume was loaded. After sample loading, StageTips were washed with 75 uL 0.1% TFA and then eluted with 75 uL

40 % acetonitrile/0.1%TFA. Eluates were dried under vacuum and stored at -80 °C until analysis.

Nano-LC-MRM-MS analysis of digested aptamer enriched samples

Samples were resuspended in 10 uL 3% acetonitrile/5% acetic acid, mixed and centrifuged briefly and transferred to HPLC vials and analyzed on a Quantiva triple quadrupole mass spectrometer equipped with a Proxeon Easy-nLC 1000 and Nanospray Flex source (Thermo, San Jose, CA). Samples were injected (20% of sample) on a 75 um ID PicoFrit column (New Objective, Woburn, MA) manually packed to 15 cm with Reprosil-Pur C18 AQ 1.9 um media (Dr. Maisch, Entringen, Germany) and heated to 50 °C. MS source conditions were setas follows: spray voltage 2000, ion transfer tube temperature 300, sweep gas 0, CID gas 1.5 and source fragmentation voltage 10.

Two to nine peptides were monitored per protein, scanning for 3 to 5 transitions per peptide with 0.2 Q1 resolution and 0.7 Q3 resolution scheduled within 8 minute windows using a cycle time of 1.5 s. Where possible, two charge states and transitions were monitored to increase confidence in peptide detection in absence of heavy labeled standards. Collision energies were set for each peptide based on its precursor m/z using collision energy equation calibrated for our Quantiva QQQ-MS (see **Supplemental Table 21** for list of transitions, scheduled retention times and collision energies for all peptides monitored by MRM-MS).   Mobile phases consisted of 3% acetonitrile/0.1% formic acid as solvent A, 90% acetonitrile/0.1% formic acid as solvent B. Flow rate was set to 200 nL/min throughout the gradient, 0% - 6% B in 6 min, 6% - 33% B in 59 min, 33% - 90%B in 4 min with a hold at 90%B for 10 min.

Extracted Ion chromatograms (XIC) of all transition ions were integrated using a Skyline document (Skyline daily version 3.5.0.9319 https://brendanx-uw1.gs.washington.edu/labkey/project/home/software/Skyline/begin.view).[3] Peptides with the correct sequences were identified within Skyline and by manual inspection as those having nearly identical fragment-ion (transition) intensities as the authentic peptides derived by digestion of the protein standards alone or the heavy peptides when present. Integrated peaks were further processed using QuaSAR,[4] (available as an external tool in Skyline or at: http://genepattern.broadinstitute.org/) to perform regression analysis[5] on the curves and calculate the limits of detection (LOD) and quantification (LOQ) of each peptide for each protein. See **Supplemental Table 19 and 20** for a summary of aptamer performance

LC-MS/MS analysis of digested aptamer enriched samples

Samples were resuspended in 10 uL 3% acetonitrile/5% acetic acid, mixed and centrifuged briefly and transferred to HPLC vials and analyzed on a QExactive mass spectrometer (Thermo, San Jose, CA) equipped with a Proxeon Easy-nLC 1000 and a custom built nanospray source (James A. Hill Instrument Services, Arlington, MA). Samples were injected (20% of sample) on a 75 um ID PicoFrit column (New Objective, Woburn, MA) manually packed to 20 cm with Reprosil-Pur C18 AQ 1.9 um media (Dr. Maisch, Entringen, Germany) and heated to 50 °C. MS source conditions were set as follows: spray voltage 2000, capillary temperature 250, S-lens RF level 50. A single Orbitrap MS scan from 300 to 1800 m/z at a resolution of 70,000 with AGC set at 3e6 was followed by up to 12 MS/MS scans at a resolution of 17,500 with AGC set at 5e4. MS/MS spectra were collected with normalized collision energy of 25 and isolation width of 2.5 amu. Dynamic exclusion was set to 20s and peptide match was set to preferred. Mobile phases consisted of 3% acetonitrile/0.1% formic acid as solvent A, 90% acetonitrile/0.1% formic acid as solvent B. Flow rate was set to 200 nL/min throughout the gradient, 2% - 6% B in 1 min, 6% - 30% B in 84 min, 30% - 60%B, 60%-90%B in 1 min with a hold at 90%B for 5 min.

MS data were analyzed using Spectrum Mill MS Proteomics Workbench software Rev B.04.01.142 (Agilent Technologies, Santa Clara, CA). Similar MS/MS spectra acquired on the same precursor m/z within +/- 60 sec were merged. MS/MS spectra were excluded from searching if they failed the quality filter by not having a sequence tag length > 0 (i.e., minimum of two masses separated by the in-chain mass of an amino acid) or did not have a precursor MH+ in the range of 600-6000. All extracted spectra were searched against a UniProt database containing human reference proteome sequences downloaded from the UniProt web site on October 17, 2014 with redundant sequences removed and a set of common laboratory contaminant proteins (150 sequences) added. Search parameters included: ESI-QEXACTIVE-HCD-v2 scoring, parent and fragment mass tolerance of 20 ppm, 40% minimum matched peak intensity and 'trypsin allow P' enzyme specificity up to 4 missed cleavages. Fixed modification was carbamidomethylation at cysteine and variable modifications were acetylation of protein N-termini, oxidized methionine, deamidation of asparagine and pyro-glutamic acid. Database matches were autovalidated at the peptide and protein level in a two-step process with identification FDR estimated by target-decoy-based searches using reversed sequences. Protein-peptide comparison report comprised of all validated peptides was exported to generate a summary of identified peptides for each sample ranked from highest scoring protein to lowest. For the subset of peptides unique to the added proteins standards, peptides with the highest number of spectra were preferentially selected for MRM method generation.

Supplemental references for aptamer-MS studies

1. Kuhn E, Whiteaker JR, Mani DR, Jackson AM, Zhao L, Pope ME, Smith D, Rivera KD, Anderson NL, Skates SJ, Pearson TW, Paulovich AG, Carr SA. Interlaboratory evaluation of automated, multiplexed peptide immunoaffinity enrichment coupled to multiple reaction monitoring mass spectrometry for quantifying proteins in plasma. *Mol Cell Proteomics*. 2012;11:M111.013854.

2. Rappsilber J, Ishihama Y, Mann M. Stop and go extraction tips for matrix-assisted laser desorption/ionization, nanoelectrospray, and LC/MS sample pretreatment in proteomics. *Anal Chem.* 2003;75:663-70.

3. MacLean B, Tomazela DM, Shulman N, Chambers M, Finney GL, Frewen B, Kern R, Tabb, DL, Liebler DC, MacCoss MJ. Skyline: an open source document editor for creating and analyzing targeted proteomics experiments. *Bioinformatics.* 2010;26:966-8.

4. Broudy D, Killeen T, Choi M, Shulman N, Mani DR, Abbatiello SE, Mani D, Ahmad R, Sahu AK, Schilling B, Tamura K, Boss Y, Sharma V, Gibson BW, Carr SA, Vitek O, MacCoss MJ, MacLean B. *Bioinforma. Oxf. Engl.* 2014;30:2521–2523.

5. Mani DR, Abbatiello SE, Carr SA. *BMC Bioinformatics.* 2012;13(Suppl16):S9.

Supplemental Tables

Supplemental Table 1. List of proteins assayed on SOMAscan™ platform

Protein	Protein Full Name	EntrezGene Symbol	EntrezGene ID	UniProt ID
41	Protein 4.1	EPB41	2035	P11171
14-3-3	14-3-3 protein family	YWHAB,YWHAE,YWHAG, YWHAH,YWHAQ, YWHAZ,SFN	7529, 7531, 7532, 7533, 10971, 7534, 2810	P31946, P62258, P61981, Q04917, P27348, P63104, P31947
17-beta-HSD 1	Estradiol 17-beta-dehydrogenase 1	HSD17B1	3292	P14061
3HIDH	3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH	11112	P31937
40S ribosomal protein SA	40S ribosomal protein SA	RPSA	3921	P08865
4-1BB	Tumor necrosis factor receptor superfamily member 9	TNFRSF9	3604	Q07011
4-1BB ligand	Tumor necrosis factor ligand superfamily member 9	TNFSF9	8744	P41273
4EBP2	Eukaryotic translation initiation factor 4E-binding protein 2	EIF4EBP2	1979	Q13542
6Ckine	C-C motif chemokine 21	CCL21	6366	O00585
6-Phosphogluconate dehydrogenase	6-phosphogluconate dehydrogenase, decarboxylating	PGD	5226	P52209
a1-Antichymotrypsin	Alpha-1-antichymotrypsin	SERPINA3	12	P01011
a1-Antitrypsin	Alpha-1-antitrypsin	SERPINA1	5265	P01009
a2-Antiplasmin	Alpha-2-antiplasmin	SERPINF2	5345	P08697
a2-HS-Glycoprotein	Alpha-2-HS-glycoprotein	AHSG	197	P02765
a2-Macroglobulin	Alpha-2-macroglobulin	A2M	2	P01023
ABL1	Tyrosine-protein kinase ABL1	ABL1	25	P00519
ABL2	Abelson tyrosine-protein kinase 2	ABL2	27	P42684
ACE2	Angiotensin-converting enzyme 2	ACE2	59272	Q9BYF1
ACTH	Corticotropin	POMC	5443	P01189
Activated Protein C	Activated Protein C	PROC	5624	P04070
Activin A	Inhibin beta A chain	INHBA	3624	P08476
Activin AB	Inhibin beta A chain:Inhibin beta B chain heterodimer	INHBA INHBB	3624 3625	P08476, P09529
Activin RIB	Activin receptor type-1B	ACVR1B	91	P36896
ADAM 9	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9	8754	Q13443
ADAM12	Disintegrin and metalloproteinase	ADAM12	8038	O43184

	domain-containing protein 12			
ADAMTS-4	A disintegrin and metalloproteinase with thrombospondin motifs 4	ADAMTS4	9507	O75173
ADAMTS-5	A disintegrin and metalloproteinase with thrombospondin motifs 5	ADAMTS5	11096	Q9UNA0
Adiponectin	Adiponectin	ADIPOQ	9370	Q15848
Afamin	Afamin	AFM	173	P43652
Aflatoxin B1 aldehyde reductase	Aflatoxin B1 aldehyde reductase member 2	AKR7A2	8574	O43488
Aggrecan	Aggrecan core protein	ACAN	176	P16112
AGR2	Anterior gradient protein 2 homolog	AGR2	10551	O95994
AIF1	Allograft inflammatory factor 1	AIF1	199	P55008
AIP	AH receptor-interacting protein	AIP	9049	O00170
AK1A1	Alcohol dehydrogenase [NADP(+)]	AKR1A1	10327	P14550
Albumin	Serum albumin	ALB	213	P02768
ALCAM	CD166 antigen	ALCAM	214	Q13740
ALK-1	Serine/threonine-protein kinase receptor R3	ACVRL1	94	P37023
Alkaline phosphatase, bone	Alkaline phosphatase, tissue-nonspecific isozyme	ALPL	249	P05186
alpha-1-antichymotrypsin complex	alpha-1-antichymotrypsin complex	SERPINA3		P07288, P01011
ALT	Alanine aminotransferase 1	GPT	2875	P24298
AMHR2	Anti-Muellerian hormone type-2 receptor	AMHR2	269	Q16671
Aminoacylase-1	Aminoacylase-1	ACY1	95	Q03154
AMNLS	Protein amnionless	AMN	81693	Q9BXJ7
AMPK a1b1g1	AMP Kinase (alpha1beta1gamma1)	PRKAA1 PRKAB1 PRKAG1	5562 5564 5571	Q13131, Q9Y478, P54619
AMPK a2b2g1	AMP Kinase (alpha2beta2gamma1)	PRKAA2 PRKAB2 PRKAG1	5563 5565 5571	P54646, O43741, P54619
AMPM2	Methionine aminopeptidase 2	METAP2	10988	P50579
amyloid precursor protein	Amyloid beta A4 protein	APP	351	P05067
AN32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	10541	Q92688
Angiogenin	Angiogenin	ANG	283	P03950
Angiopoietin-1	Angiopoietin-1	ANGPT1	284	Q15389
Angiopoietin-2	Angiopoietin-2	ANGPT2	285	O15123

Angiopoietin-4	Angiopoietin-4	ANGPT4	51378	Q9Y264
Angiostatin	Angiostatin	PLG	5340	P00747
Angiotensinogen	Angiotensinogen	AGT	183	P01019
ANGL3	Angiopoietin-related protein 3	ANGPTL3	27329	Q9Y5C1
ANGL4	Angiopoietin-related protein 4	ANGPTL4	51129	Q9BY76
Annexin I	Annexin A1	ANXA1	301	P04083
Annexin II	Annexin A2	ANXA2	302	P07355
Annexin VI	Annexin A6	ANXA6	309	P08133
ANP	Atrial natriuretic factor	NPPA	4878	P01160
Antithrombin III	Antithrombin-III	SERPINC1	462	P01008
Apo A-I	Apolipoprotein A-I	APOA1	335	P02647
Apo B	Apolipoprotein B	APOB	338	P04114
Apo D	Apolipoprotein D	APOD	347	P05090
Apo E	Apolipoprotein E	APOE	348	P02649
Apo E2	Apolipoprotein E (isoform E2)	APOE	348	P02649
Apo E3	Apolipoprotein E (isoform E3)	APOE	348	P02649
Apo E4	Apolipoprotein E (isoform E4)	APOE	348	P02649
AREG	Amphiregulin	AREG	374	P15514
ARGI1	Arginase-1	ARG1	383	P05089
ARI3A	AT-rich interactive domain-containing protein 3A	ARID3A	1820	Q99856
ARMEL	Cerebral dopamine neurotrophic factor	CDNF	441549	Q49AH0
ARP19	cAMP-regulated phosphoprotein 19	ARPP19	10776	P56211
ARSB	Arylsulfatase B	ARSB	411	P15848
ART	Agouti-related protein	AGRP	181	O00253
Artemin	Artemin	ARTN	9048	Q5T4W7
ARTS1	Endoplasmic reticulum aminopeptidase 1	ERAP1	51752	Q9NZ08
Arylsulfatase A	Arylsulfatase A	ARSA	410	P15289
ASAH2	Neutral ceramidase	ASAH2	56624	Q9NR71
ASAHL	N-acylethanolamine-hydrolyzing acid amidase	NAAA	27163	Q02083
ASGR1	Asialoglycoprotein receptor 1	ASGR1	432	P07306
ASM3A	Acid sphingomyelinase-like phosphodiesterase 3a	SMPDL3A	10924	Q92484
ATP synthase beta chain	ATP synthase subunit beta,	ATP5B	506	P06576

	mitochondrial			
ATS1	A disintegrin and metalloproteinase with thrombospondin motifs 1	ADAMTS1	9510	Q9UHI8
ATS13	A disintegrin and metalloproteinase with thrombospondin motifs 13	ADAMTS13	11093	Q76LX8
ATS15	A disintegrin and metalloproteinase with thrombospondin motifs 15	ADAMTS15	170689	Q8TE58
AURKB	Aurora kinase B	AURKB	9212	Q96GD4
Aurora kinase A	Aurora kinase A	AURKA	6790	O14965
Azurocidin	Azurocidin	AZU1	566	P20160
b2-Microglobulin	Beta-2-microglobulin	B2M	567	P61769
B7	T-lymphocyte activation antigen CD80	CD80	941	P33681
B7-2	T-lymphocyte activation antigen CD86	CD86	942	P42081
B7-H1	Programmed cell death 1 ligand 1	CD274	29126	Q9NZQ7
B7-H2	ICOS ligand	ICOSLG	23308	O75144
BAFF	Tumor necrosis factor ligand superfamily member 13B	TNFSF13B	10673	Q9Y275
BAFF Receptor	Tumor necrosis factor receptor superfamily member 13C	TNFRSF13C	115650	Q96RJ3
BARK1	beta-adrenergic receptor kinase 1	ADRBK1	156	P25098
BASI	Basigin	BSG	682	P35613
BCAM	Basal Cell Adhesion Molecule	BCAM	4059	P50895
BCAR3	Breast cancer anti-estrogen resistance protein 3	BCAR3	8412	O75815
Bcl-2	Apoptosis regulator Bcl-2	BCL2	596	P10415
BCL2-like 1 protein	Bcl-2-like protein 1	BCL2L1	598	Q07817
BCMA	Tumor necrosis factor receptor superfamily member 17	TNFRSF17	608	Q02223
BDNF	Brain-derived neurotrophic factor	BDNF	627	P23560
b-ECGF	Fibroblast growth factor 1	FGF1	2246	P05230
b-Endorphin	Beta-endorphin	POMC	5443	P01189
bFGF	Fibroblast growth factor 2	FGF2	2247	P09038
bFGF-R	Fibroblast growth factor receptor 1	FGFR1	2260	P11362
BFL1	Bcl-2-related protein A1	BCL2A1	597	Q16548
BGH3	Transforming growth factor-beta-induced protein ig-h3	TGFBI	7045	Q15582

BGN	Biglycan	BGN	633	P21810
BLC	C-X-C motif chemokine 13	CXCL13	10563	O43927
BMP RII	Bone morphogenetic protein receptor type-2	BMPR2	659	Q13873
BMP-1	Bone morphogenetic protein 1	BMP1	649	P13497
BMP10	Bone morphogenetic protein 10	BMP10	27302	O95393
BMP-14	Growth/differentiation factor 5	GDF5	8200	P43026
BMP-6	Bone morphogenetic protein 6	BMP6	654	P22004
BMP-7	Bone morphogenetic protein 7	BMP7	655	P18075
BMPER	BMP-binding endothelial regulator protein	BMPER	168667	Q8N8U9
BMPR1A	Bone morphogenetic protein receptor type-1A	BMPR1A	657	P36894
BMX	Cytoplasmic tyrosine-protein kinase BMX	BMX	660	P51813
b-NGF	beta-nerve growth factor	NGF	4803	P01138
BNP-32	Brain natriuretic peptide 32	NPPB	4879	P16860
BOC	Brother of CDO	BOC	91653	Q9BWV1
Bone proteoglycan II	Decorin	DCN	1634	P07585
BPI	Bactericidal permeability-increasing protein	BPI	671	P17213
BRF-1	Transcription factor IIIB 90 kDa subunit	BRF1	2972	Q92994
BSP	Bone sialoprotein 2	IBSP	3381	P21815
BSSP4	Brain-specific serine protease 4	PRSS22	64063	Q9GZN4
BST1	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 2	BST1	683	Q10588
BTK	Tyrosine-protein kinase BTK	BTK	695	Q06187
C1-Esterase Inhibitor	Plasma protease C1 inhibitor	SERPING1	710	P05155
C1q	Complement C1q subcomponent	C1QA C1QB C1QC	712 713 714	P02745, P02746, P02747
C1QBP	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	708	Q07021
C1r	Complement C1r subcomponent	C1R	715	P00736
C1s	Complement C1s subcomponent	C1S	716	P09871
C2	Complement C2	C2	717	P06681
C3	Complement C3	C3	718	P01024
C34 gp41 HIV Fragment	gp41 C34 peptide, HIV	Human-virus		Q70626

C3a	C3a anaphylatoxin	C3	718	P01024
C3adesArg	C3a anaphylatoxin des Arginine	C3	718	P01024
C3b	Complement C3b	C3	718	P01024
C3d	Complement C3d fragment	C3	718	P01024
C4	Complement C4	C4A C4B	720 721	P0C0L4, P0C0L5
C4b	Complement C4b	C4A C4B	720 721	P0C0L4 P0C0L5
C5	Complement C5	C5	727	P01031
C5a	C5a anaphylatoxin	C5	727	P01031
C5b, 6 Complex	Complement C5b-C6 complex	C5 C6	727 729	P01031,P13671
C6	Complement component C6	C6	729	P13671
C7	Complement component C7	C7	730	P10643
C8	Complement component C8	C8A C8B C8G	731 732 733	P07357, P07358, P07360
C9	Complement component C9	C9	735	P02748
CAD15	Cadherin-15	CDH15	1013	P55291
Cadherin E	Cadherin-1	CDH1	999	P12830
Cadherin-12	Cadherin-12	CDH12	1010	P55289
Cadherin-2	Cadherin-2	CDH2	1000	P19022
Cadherin-5	Cadherin-5	CDH5	1003	P33151
Cadherin-6	Cadherin-6	CDH6	1004	P55285
Calcineurin	Calcineurin	PPP3CA PPP3R1	5530 5534	Q08209, P63098
Calcineurin B a	Calcineurin subunit B type 1	PPP3R1	5534	P63098
calgranulin B	Protein S100-A9	S100A9	6280	P06702
Calpain I	Calpain I	CAPN1 CAPNS1	823 826	P07384, P04632
Calpastatin	Calpastatin	CAST	831	P20810
calreticulin	Calreticulin	CALR	811	P27797
CAMK1	Calcium/calmodulin-dependent protein kinase type 1	CAMK1	8536	Q14012
CAMK1D	Calcium/calmodulin-dependent protein kinase type 1D	CAMK1D	57118	Q8IU85
CAMK2A	Calcium/calmodulin-dependent protein kinase type II subunit alpha	CAMK2A	815	Q9UQM7
CAMK2B	Calcium/calmodulin-dependent protein kinase type II subunit beta	CAMK2B	816	Q13554
CAMK2D	Calcium/calmodulin-dependent protein kinase type II subunit delta	CAMK2D	817	Q13557
CaMKK alpha	Calcium/calmodulin-dependent protein kinase kinase 1	CAMKK1	84254	Q8N5S9

CAPG	Macrophage-capping protein	CAPG	822	P40121
Carbonic anhydrase 6	Carbonic anhydrase 6	CA6	765	P23280
Carbonic anhydrase 9	Carbonic anhydrase 9	CA9	768	Q16790
Carbonic anhydrase I	Carbonic anhydrase 1	CA1	759	P00915
Carbonic anhydrase II	Carbonic anhydrase 2	CA2	760	P00918
Carbonic anhydrase III	Carbonic anhydrase 3	CA3	761	P07451
Carbonic Anhydrase IV	Carbonic anhydrase 4	CA4	762	P22748
Carbonic anhydrase VII	Carbonic anhydrase 7	CA7	766	P43166
Carbonic Anhydrase X	Carbonic anhydrase-related protein 10	CA10	56934	Q9NS85
Carbonic anhydrase XIII	Carbonic anhydrase 13	CA13	377677	Q8N1Q1
Cardiotrophin-1	Cardiotrophin-1	CTF1	1489	Q16619
Caspase-10	Caspase-10	CASP10	843	Q92851
Caspase-2	Caspase-2	CASP2	835	P42575
Caspase-3	Caspase-3	CASP3	836	P42574
Catalase	Catalase	CAT	847	P04040
CATC	Dipeptidyl peptidase 1	CTSC	1075	P53634
CATE	Cathepsin E	CTSE	1510	P14091
Cathepsin A	Lysosomal protective protein	CTSA	5476	P10619
Cathepsin B	Cathepsin B	CTSB	1508	P07858
Cathepsin D	Cathepsin D	CTSD	1509	P07339
Cathepsin G	Cathepsin G	CTSG	1511	P08311
Cathepsin H	Cathepsin H	CTSH	1512	P09668
Cathepsin S	Cathepsin S	CTSS	1520	P25774
Cathepsin V	Cathepsin L2	CTSV	1515	O60911
CATZ	Cathepsin Z	CTSZ	1522	Q9UBR2
CBG	Corticosteroid-binding globulin	SERPINA6	866	P08185
CBPE	Carboxypeptidase E	CPE	1363	P16870
CBX5	Chromobox protein homolog 5	CBX5	23468	P45973
CCL28	C-C motif chemokine 28	CCL28	56477	Q9NRJ3
CD109	CD109 antigen	CD109	135228	Q6YHK3
CD22	B-cell receptor CD22	CD22	933	P20273
CD226	CD226 antigen	CD226	10666	Q15762
CD23	Low affinity immunoglobulin epsilon Fc receptor	FCER2	2208	P06734
CD27	CD27 antigen	CD27	939	P26842
CD30	Tumor necrosis factor receptor	TNFRSF8	943	P28908

	superfamily member 8			
CD30 Ligand	Tumor necrosis factor ligand superfamily member 8	TNFSF8	944	P32971
CD36 ANTIGEN	Platelet glycoprotein 4	CD36	948	P16671
CD39	Ectonucleoside triphosphate diphosphohydrolase 1	ENTPD1	953	P49961
CD40 ligand, soluble	CD40 ligand	CD40LG	959	P29965
CD48	CD48 antigen	CD48	962	P09326
CD5L	CD5 antigen-like	CD5L	922	O43866
CD70	CD70 antigen	CD70	970	P32970
CD97	CD97 antigen	CD97	976	P48960
CDC37	Hsp90 co-chaperone Cdc37	CDC37	11140	Q16543
CDK1/cyclin B	Cyclin-dependent kinase 1:G2/mitotic-specific cyclin-B1 complex	CDC2 CCNB1	983 891	P06493, P14635
CDK2/cyclin A	Cyclin-dependent kinase 2:Cyclin-A2 complex	CDK2 CCNA2	1017 890	P24941, P20248
CDK5/p35	Cyclin-dependent kinase 5:Cyclin-dependent kinase 5 activator 1 complex	CDK5 CDK5R1	1020 8851	Q00535, Q15078
CDK8/cyclin C	Cyclin-dependent kinase 8:Cyclin-C complex	CDK8 CCNC	1024 892	P49336, P24863
CDON	Cell adhesion molecule-related/down-regulated by oncogenes	CDON	50937	Q4KMG0
CFC1	Cryptic protein	CFC1	55997	P0CG37
cGMP-stimulated PDE	cGMP-dependent 3',5'-cyclic phosphodiesterase	PDE2A	5138	O00408
Chitotriosidase-1	Chitotriosidase-1	CHIT1	1118	Q13231
CHK1	Serine/threonine-protein kinase Chk1	CHEK1	1111	O14757
Chk2	Serine/threonine-protein kinase Chk2	CHEK2	11200	O96017
CHL1	Neural cell adhesion molecule L1-like protein	CHL1	10752	O00533
CHST2	Carbohydrate sulfotransferase 2	CHST2	9435	Q9Y4C5
CHST6	Carbohydrate sulfotransferase 6	CHST6	4166	Q9GZX3
Chymase	Chymase	CMA1	1215	P23946
CIAP-2	Baculoviral IAP repeat-containing	BIRC3	330	Q13489

	protein 3			
CK2-A1:B	Casein kinase II 2-alpha:2-beta heterotetramer	CSNK2A1 CSNK2B	1457 1460	P68400, P67870
CK2-A2:B	Casein kinase II 2-alpha':2-beta heterotetramer	CSNK2A2 CSNK2B	1459 1460	P19784, P67870
CKAP2	Cytoskeleton-associated protein 2	CKAP2	26586	Q8WWK9
Ck-b-8-1	Ck-beta-8-1	CCL23	6368	P55773
CK-BB	Creatine kinase B-type	CKB	1152	P12277
CK-MB	Creatine kinase M-type:Creatine kinase B-type heterodimer	CKB CKM	1152 1158	P12277, P06732
CK-MM	Creatine kinase M-type	CKM	1158	P06732
CLC1B	C-type lectin domain family 1 member B	CLEC1B	51266	Q9P126
CLC4K	C-type lectin domain family 4 member K	CD207	50489	Q9UJ71
CLC7A	C-type lectin domain family 7 member A	CLEC7A	64581	Q9BXN2
CLF-1/CLC Complex	Cytokine receptor-like factor 1:Cardiotrophin-like cytokine factor 1 Complex	CRLF1 CLCF1	9244 23529	O75462, Q9UBD9
CLM6	CMRF35-like molecule 6	CD300C	10871	Q08708
Clusterin	Clusterin	CLU	1191	P10909
CNDP1	Beta-Ala-His dipeptidase	CNDP1	84735	Q96KN2
CNTF	Ciliary Neurotrophic Factor	CNTF	1270	P26441
CNTFR alpha	Ciliary neurotrophic factor receptor subunit alpha	CNTFR	1271	P26992
CNTN2	Contactin-2	CNTN2	6900	Q02246
CO8A1	Collagen alpha-1(VIII) chain	COL8A1	1295	P27658
Coactosin-like protein	Coactosin-like protein	COTL1	23406	Q14019
Coagulation Factor IX	Coagulation factor IX	F9	2158	P00740
Coagulation Factor IXab	Coagulation factor IXab	F9	2158	P00740
Coagulation Factor V	Coagulation Factor V	F5	2153	P12259
Coagulation Factor VII	Coagulation Factor VII	F7	2155	P08709
Coagulation Factor X	Coagulation Factor X	F10	2159	P00742
Coagulation Factor Xa	Coagulation factor Xa	F10	2159	P00742
Coagulation Factor XI	Coagulation Factor XI	F11	2160	P03951
Cofilin-1	Cofilin-1	CFL1	1072	P23528
COLEC12	Collectin-12	COLEC12	81035	Q5KU26

Collectin Kidney 1	Collectin-11	COLEC11	78989	Q9BWP8
COMMD7	COMM domain-containing protein 7	COMMD7	149951	Q86VX2
complement factor H-related 5	Complement factor H-related protein 5	CFHR5	81494	Q9BXR6
CONA1	Collagen alpha-1(XXIII) chain	COL23A1	91522	Q86Y22
Contactin-1	Contactin-1	CNTN1	1272	Q12860
Contactin-4	Contactin-4	CNTN4	152330	Q8IWV2
Contactin-5	Contactin-5	CNTN5	53942	O94779
COX-2	Prostaglandin G/H synthase 2	PTGS2	5743	P35354
CPNE1	Copine-1	CPNE1	8904	Q99829
CRDL1	Chordin-like protein 1	CHRDL1	91851	Q9BU40
Cripto	Teratocarcinoma-derived growth factor 1	TDGF1	6997	P13385
CRIS3	Cysteine-rich secretory protein 3	CRISP3	10321	P54108
CRK	Adapter molecule crk	CRK	1398	P46108
CRP	C-reactive protein	CRP	1401	P02741
CRTAM	Cytotoxic and regulatory T-cell molecule	CRTAM	56253	O95727
CSF-1	Macrophage colony-stimulating factor 1	CSF1	1435	P09603
CSK	Tyrosine-protein kinase CSK	CSK	1445	P41240
CSK21	Casein kinase II subunit alpha	CSNK2A1	1457	P68400
CTACK	C-C motif chemokine 27	CCL27	10850	Q9Y4X3
CTAP-III	Connective tissue-activating peptide III	PPBP	5473	P02775
CTGF	Connective tissue growth factor	CTGF	1490	P29279
CTLA-4	Cytotoxic T-lymphocyte protein 4	CTLA4	1493	P16410
CXCL16, soluble	C-X-C motif chemokine 16	CXCL16	58191	Q9H2A7
Cyclin B1	G2/mitotic-specific cyclin-B1	CCNB1	891	P14635
Cyclophilin A	Peptidyl-prolyl cis-trans isomerase A	PPIA	5478	P62937
Cyclophilin F	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	PPIF	10105	P30405
Cystatin C	Cystatin-C	CST3	1471	P01034
Cystatin M	Cystatin-M	CST6	1474	Q15828
Cystatin-S	Cystatin-S	CST4	1472	P01036
CYTD	Cystatin-D	CST5	1473	P28325
CYTF	Cystatin-F	CST7	8530	O76096

Cytidylate kinase	UMP-CMP kinase	CMPK1	51727	P30085
CYTN	Cystatin-SN	CST1	1469	P01037
Cytochrome c	Cytochrome c	CYCS	54205	P99999
Cytochrome P450 3A4	Cytochrome P450 3A4	CYP3A4	1576	P08684
CYTT	Cystatin-SA	CST2	1470	P09228
DAF	Complement decay-accelerating factor	CD55	1604	P08174
DAN	Neuroblastoma suppressor of tumorigenicity 1	NBL1	4681	P41271
DAPK2	Death-associated protein kinase 2	DAPK2	23604	Q9UIK4
DBNL	Drebrin-like protein	DBNL	28988	Q9UJU6
DcR3	Tumor necrosis factor receptor superfamily member 6B	TNFRSF6B	8771	O95407
DC-SIGN	CD209 antigen	CD209	30835	Q9NNX6
DC-SIGNR	C-type lectin domain family 4 member M	CLEC4M	10332	Q9H2X3
D-dimer	D-dimer	FGA FGB FGG	2243 2244 2266	P02671, P02675, P02679
DEAD-box protein 19B	ATP-dependent RNA helicase DDX19B	DDX19B	11269	Q9UMR2
DERM	Dermatopontin	DPT	1805	Q07507
Desmoglein-1	Desmoglein-1	DSG1	1828	Q02413
Desmoglein-2	Desmoglein-2	DSG2	1829	Q14126
DHH	Desert hedgehog protein N-product	DHH	50846	O43323
Discoidin domain receptor 1	Epithelial discoidin domain-containing receptor 1	DDR1	780	Q08345
Discoidin domain receptor 2	Discoidin domain-containing receptor 2	DDR2	4921	Q16832
DKK1	Dickkopf-related protein 1	DKK1	22943	O94907
DKK3	Dickkopf-related protein 3	DKK3	27122	Q9UBP4
Dkk-4	Dickkopf-related protein 4	DKK4	27121	Q9UBT3
DLC8	Dynein light chain 1, cytoplasmic	DYNLL1	8655	P63167
DLL1	Delta-like protein 1	DLL1	28514	O00548
DLL4	Delta-like protein 4	DLL4	54567	Q9NR61
DLRB1	Dynein light chain roadblock-type 1	DYNLRB1	83658	Q9NP97
DMP1	Dentin matrix acidic phosphoprotein 1	DMP1	1758	Q13316
DnaJ homolog	Mitochondrial import inner membrane translocase subunit	DNAJC19	131118	Q96DA6

	TIM14			
Dopa decarboxylase	Aromatic-L-amino-acid decarboxylase	DDC	1644	P20711
DPP2	Dipeptidyl peptidase 2	DPP7	29952	Q9UHL4
DR3	Tumor necrosis factor receptor superfamily member 25	TNFRSF25	8718	Q93038
DR6	Tumor necrosis factor receptor superfamily member 21	TNFRSF21	27242	O75509
DRAK2	Serine/threonine-protein kinase 17B	STK17B	9262	O94768
DRG-1	Vacuolar protein sorting-associated protein VTA1 homolog	VTA1	51534	Q9NP79
DRR1	Protein FAM107A	FAM107A	11170	O95990
DSC3	Desmocollin-3	DSC3	1825	Q14574
Dtk	Tyrosine-protein kinase receptor TYRO3	TYRO3	7301	Q06418
DUS3	Dual specificity protein phosphatase 3	DUSP3	1845	P51452
Dynactin subunit 2	Dynactin subunit 2	DCTN2	10540	Q13561
DYRK3	Dual specificity tyrosine-phosphorylation-regulated kinase 3	DYRK3	8444	O43781
ECM1	Extracellular matrix protein 1	ECM1	1893	Q16610
EDA	Ectodysplasin-A, secreted form	EDA	1896	Q92838
EDAR	Tumor necrosis factor receptor superfamily member EDAR	EDAR	10913	Q9UNE0
EF-1-beta	Elongation factor 1-beta	EEF1B2	1933	P24534
EG-VEGF	Prokineticin-1	PROK1	84432	P58294
eIF-5	Eukaryotic translation initiation factor 5	EIF5	1983	P55010
eIF-5A-1	Eukaryotic translation initiation factor 5A-1	EIF5A	1984	P63241
Elafin	Elafin	PI3	5266	P19957
Elastase	Neutrophil elastase	ELANE	1991	P08246
EMAP-2	Endothelial monocyte-activating polypeptide 2	AIMP1	9255	Q12904
EMR2	EGF-like module-containing mucin-like hormone receptor-like 2	EMR2	30817	Q9UHX3
ENA-78	C-X-C motif chemokine 5	CXCL5	6374	P42830
Endocan	Endothelial cell-specific molecule 1	ESM1	11082	Q9NQ30
Endoglin	Endoglin	ENG	2022	P17813

Endostatin	Endostatin	COL18A1	80781	P39060
Endothelin-converting enzyme 1	Endothelin-converting enzyme 1	ECE1	1889	P42892
ENPP7	Ectonucleotide pyrophosphatase/phosphodiesterase family member 7	ENPP7	339221	Q6UWV6
Enterokinase	Enteropeptidase	TMPRSS15	5651	P98073
ENTP3	Ectonucleoside triphosphate diphosphohydrolase 3	ENTPD3	956	O75355
ENTP5	Ectonucleoside triphosphate diphosphohydrolase 5	ENTPD5	957	O75356
Eotaxin	Eotaxin	CCL11	6356	P51671
Eotaxin-2	C-C motif chemokine 24	CCL24	6369	O00175
EP15R	Epidermal growth factor receptor substrate 15-like 1	EPS15L1	58513	Q9UBC2
EphA1	Ephrin type-A receptor 1	EPHA1	2041	P21709
EPHA3	Ephrin type-A receptor 3	EPHA3	2042	P29320
EphA5	Ephrin type-A receptor 5	EPHA5	2044	P54756
EPHAA	Ephrin type-A receptor 10	EPHA10	284656	Q5JZY3
EPHB2	Ephrin type-B receptor 2	EPHB2	2048	P29323
EphB4	Ephrin type-B receptor 4	EPHB4	2050	P54760
EphB6	Ephrin type-B receptor 6	EPHB6	2051	O15197
Ephrin-A4	Ephrin-A4	EFNA4	1945	P52798
Ephrin-A5	Ephrin-A5	EFNA5	1946	P52803
Ephrin-B3	Ephrin-B3	EFNB3	1949	Q15768
EPI	Epiregulin	EREG	2069	O14944
Epithelial cell kinase	Ephrin type-A receptor 2	EPHA2	1969	P29317
Epo	Erythropoietin	EPO	2056	P01588
EPO-R	Erythropoietin receptor	EPOR	2057	P19235
ER	Estrogen receptor	ESR1	2099	P03372
ERAB	3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	3028	Q99714
ERBB1	Epidermal growth factor receptor	EGFR	1956	P00533
ERBB2	Receptor tyrosine-protein kinase erbB-2	ERBB2	2064	P04626
ERBB3	Receptor tyrosine-protein kinase erbB-3	ERBB3	2065	P21860
ERBB4	Receptor tyrosine-protein kinase	ERBB4	2066	Q15303

	erbB-4			
ERK-1	Mitogen-activated protein kinase 3	MAPK3	5595	P27361
ERP29	Endoplasmic reticulum resident protein 29	ERP29	10961	P30040
ESAM	Endothelial cell-selective adhesion molecule	ESAM	90952	Q96AP7
Esterase D	S-formylglutathione hydrolase	ESD	2098	P10768
ETHE1	Persulfide dioxygenase ETHE1, mitochondrial	ETHE1	23474	O95571
FABP	Fatty acid-binding protein, heart	FABP3	2170	P05413
FABPE	Fatty acid-binding protein, epidermal	FABP5	2171	Q01469
Factor B	Complement factor B	CFB	629	P00751
Factor D	Complement factor D	CFD	1675	P00746
Factor H	Complement factor H	CFH	3075	P08603
Factor I	Complement factor I	CFI	3426	P05156
FAK1	Focal adhesion kinase 1	PTK2	5747	Q05397
FAM107B	Protein FAM107B	FAM107B	83641	Q9H098
Fas ligand, soluble	Tumor necrosis factor ligand superfamily member 6, soluble form	FASLG	356	P48023
FCAR	Immunoglobulin alpha Fc receptor	FCAR	2204	P24071
FCG2A/B	Low affinity immunoglobulin gamma Fc region receptor II-a/b	FCGR2A FCGR2B		P12318, P31994
FCG3B	Low affinity immunoglobulin gamma Fc region receptor III-B	FCGR3B	2215	O75015
FCGR1	High affinity immunoglobulin gamma Fc receptor I	FCGR1A	2209	P12314
FCN1	Ficolin-1	FCN1	2219	O00602
FCN2	Ficolin-2	FCN2	2220	Q15485
FCRL3	Fc receptor-like protein 3	FCRL3	115352	Q96P31
FER	Tyrosine-protein kinase Fer	FER	2241	P16591
Ferritin	Ferritin	FTH1 FTL	2495 2512	P02794, P02792
FETUB	Fetuin-B	FETUB	26998	Q9UGM5
FGF-10	Fibroblast growth factor 10	FGF10	2255	O15520
FGF-12	Fibroblast growth factor 12	FGF12	2257	P61328
FGF-16	Fibroblast growth factor 16	FGF16	8823	O43320
FGF-17	Fibroblast growth factor 17	FGF17	8822	O60258
FGF-18	Fibroblast growth factor 18	FGF18	8817	O76093
FGF-19	Fibroblast growth factor 19	FGF19	9965	O95750

FGF-20	Fibroblast growth factor 20	FGF20	26281	Q9NP95
FGF23	Fibroblast growth factor 23	FGF23	8074	Q9GZV9
FGF-4	Fibroblast growth factor 4	FGF4	2249	P08620
FGF-5	Fibroblast growth factor 5	FGF5	2250	P12034
FGF-6	Fibroblast growth factor 6	FGF6	2251	P10767
FGF7	Fibroblast growth factor 7	FGF7	2252	P21781
FGF-8A	Fibroblast growth factor 8 isoform A	FGF8	2253	P55075
FGF-8B	Fibroblast growth factor 8 isoform B	FGF8	2253	P55075
FGF9	Fibroblast growth factor 9	FGF9	2254	P31371
FGFR-2	Fibroblast growth factor receptor 2	FGFR2	2263	P21802
FGFR-3	Fibroblast growth factor receptor 3	FGFR3	2261	P22607
FGFR4	Fibroblast growth factor receptor 4	FGFR4	2264	P22455
FGR	Tyrosine-protein kinase Fgr	FGR	2268	P09769
Fibrinogen	Fibrinogen	FGA FGB FGG	2243 2244 2266	P02671, P02675, P02679
Fibrinogen g-chain dimer	Fibrinogen gamma chain	FGG	2266	P02679
Fibronectin	Fibronectin	FN1	2335	P02751
Ficolin-3	Ficolin-3	FCN3	8547	O75636
FLRT1	Leucine-rich repeat transmembrane protein FLRT1	FLRT1	23769	Q9NZU1
Flt-3	Receptor-type tyrosine-protein kinase FLT3	FLT3	2322	P36888
Flt3 ligand	Fms-related tyrosine kinase 3 ligand	FLT3LG	2323	P49771
FN1.3	Fibronectin Fragment 3	FN1	2335	P02751
FN1.4	Fibronectin Fragment 4	FN1	2335	P02751
Fractalkine/CX3CL-1	Fractalkine	CX3CL1	6376	P78423
FSH	Follicle stimulating hormone	CGA FSHB	1081 2488	P01215, P01225
FST	Follistatin	FST	10468	P19883
FSTL3	Follistatin-related protein 3	FSTL3	10272	O95633
Fucosyltransferase 3	Galactoside 3(4)-L-fucosyltransferase	FUT3	2525	P21217
FUT5	Alpha-(1,3)-fucosyltransferase 5	FUT5	2527	Q11128
FYN	Tyrosine-protein kinase Fyn	FYN	2534	P06241
GA733-1 protein	Tumor-associated calcium signal transducer 2	TACSTD2	4070	P09758
Galectin-2	Galectin-2	LGALS2	3957	P05162
Galectin-3	Galectin-3	LGALS3	3958	P17931
Galectin-4	Galectin-4	LGALS4	3960	P56470

Galectin-8	Galectin-8	LGALS8	3964	O00214
GAPDH, liver	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	2597	P04406
GAS1	Growth arrest-specific protein 1	GAS1	2619	P54826
GCKR	Glucokinase regulatory protein	GCKR	2646	Q14397
GCP-2	C-X-C motif chemokine 6	CXCL6	6372	P80162
G-CSF	Granulocyte colony-stimulating factor	CSF3	1440	P09919
G-CSF-R	Granulocyte colony-stimulating factor receptor	CSF3R	1441	Q99062
GDF-11	Growth/differentiation factor 11	GDF11	10220	O95390
GDF2	Growth/differentiation factor 2	GDF2	2658	Q9UK05
GDF-9	Growth/differentiation factor 9	GDF9	2661	O60383
Gelsolin	Gelsolin	GSN	2934	P06396
GFAP	Glial fibrillary acidic protein	GFAP	2670	P14136
GFRa-1	GDNF family receptor alpha-1	GFRA1	2674	P56159
GFRa-2	GDNF family receptor alpha-2	GFRA2	2675	O00451
GFRa-3	GDNF family receptor alpha-3	GFRA3	2676	O60609
GHC2	Mitochondrial glutamate carrier 2	SLC25A18	83733	Q9H1K4
GIB	Phospholipase A2	PLA2G1B	5319	P04054
GIIE	Group IIE secretory phospholipase A2	PLA2G2E	30814	Q9NZK7
GITR	Tumor necrosis factor receptor superfamily member 18	TNFRSF18	8784	Q9Y5U5
Glucagon	Glucagon	GCG	2641	P01275
Glucocorticoid receptor	Glucocorticoid receptor	NR3C1	2908	P04150
Glutamate carboxypeptidase	Cytosolic non-specific dipeptidase	CNDP2	55748	Q96KP4
Glutathione S-transferase Pi	Glutathione S-transferase P	GSTP1	2950	P09211
Glypican 3	Glypican-3	GPC3	2719	P51654
GM-CSF	Granulocyte-macrophage colony-stimulating factor	CSF2	1437	P04141
GNS	N-acetylglucosamine-6-sulfatase	GNS	2799	P15586
GOT1	Aspartate aminotransferase, cytoplasmic	GOT1	2805	P17174
GP114	Probable G-protein coupled receptor 114	GPR114	221188	Q8IZF4
gp130, soluble	Interleukin-6 receptor subunit beta	IL6ST	3572	P40189

GP1BA	Platelet glycoprotein Ib alpha chain	GP1BA	2811	P07359
GPC2	Glypican-2	GPC2	221914	Q8N158
GPC5	Glypican-5	GPC5	2262	P78333
gpIIbIIIa	Integrin alpha-IIb: beta-3 complex	ITGA2B ITGB3	3674 3690	P08514, P05106
GPNMB	Transmembrane glycoprotein NMB	GPNMB	10457	Q14956
GPVI	Platelet glycoprotein VI	GP6	51206	Q9HCN6
Granulysin	Granulysin	GNLY	10578	P22749
Granzyme A	Granzyme A	GZMA	3001	P12544
Granzyme B	Granzyme B	GZMB	3002	P10144
Granzyme H	Granzyme H	GZMH	2999	P20718
GRB2-related adapter protein 2	GRB2-related adapter protein 2	GRAP2	9402	O75791
GREM1	Gremlin-1	GREM1	26585	O60565
GRN	Granulins	GRN	2896	P28799
Gro-a	Growth-regulated alpha protein	CXCL1	2919	P09341
Gro-b/g	Gro-beta/gamma	CXCL3 CXCL2		P19876, P19875
Growth hormone receptor	Growth hormone receptor	GHR	2690	P10912
GSK-3 alpha/beta	Glycogen synthase kinase-3 alpha/beta	GSK3A GSK3B	2931 2932	P49840, P49841
GSTA3	Glutathione S-transferase A3	GSTA3	2940	Q16772
GV	Calcium-dependent phospholipase A2	PLA2G5	5322	P39877
GX	Group 10 secretory phospholipase A2	PLA2G10	8399	O15496
H6ST1	Heparan-sulfate 6-O-sulfotransferase 1	HS6ST1	9394	O60243
HAI-1	Kunitz-type protease inhibitor 1	SPINT1	6692	O43278
Haptoglobin, Mixed Type	Haptoglobin	HP	3240	P00738
Hat1	Histone acetyltransferase type B catalytic subunit	HAT1	8520	O14929
HB-EGF	Heparin-binding EGF-like growth factor	HBEGF	1839	Q99075
HCC-1	C-C motif chemokine 14	CCL14	6358	Q16627
HCC-4	C-C motif chemokine 16	CCL16	6360	O15467
HCG	Human Chorionic Gonadotropin	CGA CGB	1081 1082	P01215, P01233
HCK	Tyrosine-protein kinase HCK	HCK	3055	P08631
HDAC8	Histone deacetylase 8	HDAC8	55869	Q9BY41
HDGR2	Hepatoma-derived growth factor-	HDGFRP2	84717	Q7Z4V5

	related protein 2			
Hemoglobin	Hemoglobin	HBA1 HBB	3039 3043	P69905, P68871
Hemopexin	Hemopexin	HPX	3263	P02790
Heparin cofactor II	Heparin cofactor 2	SERPIND1	3053	P05546
HGF	Hepatocyte growth factor	HGF	3082	P14210
HGFA	Hepatocyte growth factor activator	HGFAC	3083	Q04756
HINT1	Histidine triad nucleotide-binding protein 1	HINT1	3094	P49773
HIPK3	Homeodomain-interacting protein kinase 3	HIPK3	10114	Q9H422
Histone H1.2	Histone H1.2	HIST1H1C	3006	P16403
Histone H2A.z	Histone H2A.z	H2AFZ	3015	P0C0S5
HIV-2 Rev	Protein Rev_HV2BE	Human-virus	1724716	P18093
HMG-1	High mobility group protein B1	HMGB1	3146	P09429
HMGR	3-hydroxy-3-methylglutaryl-coenzyme A reductase	HMGCR	3156	P04035
HNRNP A/B	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	3182	Q99729
HNRNP A2/B1	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	3181	P22626
HNRNP K	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	3190	P61978
HNRPQ	Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	10492	O60506
HO-2	Heme oxygenase 2	HMOX2	3163	P30519
HPG	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	HPGD	3248	P15428
HPLN1	Hyaluronan and proteoglycan link protein 1	HAPLN1	1404	P10915
HPV E7 Type 16	Protein E7_HPV16	Human-virus	1489079	P03129
HPV E7 Type18	Protein E7_HPV18	Human-virus	1489089	P06788
HRG	Histidine-rich glycoprotein	HRG	3273	P04196
HSP 40	DnaJ homolog subfamily B member 1	DNAJB1	3337	P25685
HSP 60	60 kDa heat shock protein, mitochondrial	HSPD1	3329	P10809
HSP 70	Heat shock 70 kDa protein 1A/1B	HSPA1A	3303	P08107
HSP 90a/b	Heat shock protein HSP 90-alpha/beta	HSP90AA1 HSP90AB1		P07900, P08238

HSP70 protein 8	Heat shock cognate 71 kDa protein	HSPA8	3312	P11142
HTRA2	Serine protease HTRA2, mitochondrial	HTRA2	27429	O43464
HVEM	Tumor necrosis factor receptor superfamily member 14	TNFRSF14	8764	Q92956
I-309	C-C motif chemokine 1	CCL1	6346	P22362
iC3b	Complement C3b, inactivated	C3	718	P01024
ICOS	Inducible T-cell costimulator	ICOS	29851	Q9Y6W8
IDE	Insulin-degrading enzyme	IDE	3416	P14735
IDS	Iduronate 2-sulfatase	IDS	3423	P22304
IDUA	alpha-L-iduronidase	IDUA	3425	P35475
IF4A3	Eukaryotic initiation factor 4A-III	EIF4A3	9775	P38919
IF4G2	Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	1982	P78344
IFN-aA	Interferon alpha-2	IFNA2	3440	P01563
IFN-g	Interferon gamma	IFNG	3458	P01579
IFN-g R1	Interferon gamma receptor 1	IFNGR1	3459	P15260
IFN-lambda 1	Interferon lambda-1	IFNL1	282618	Q8IU54
IFN-lambda 2	Interferon lambda-2	IFNL2	282616	Q8IZJ0
IgD	Immunoglobulin D	IGHD IGK@ IGL@	3495 50802 3535	P01880
IgE	Immunoglobulin E	IGHE IGK@ IGL@	3497 50802 3535	P01854
IGFBP-1	Insulin-like growth factor-binding protein 1	IGFBP1	3484	P08833
IGFBP-2	Insulin-like growth factor-binding protein 2	IGFBP2	3485	P18065
IGFBP-3	Insulin-like growth factor-binding protein 3	IGFBP3	3486	P17936
IGFBP-4	Insulin-like growth factor-binding protein 4	IGFBP4	3487	P22692
IGFBP-5	Insulin-like growth factor-binding protein 5	IGFBP5	3488	P24593
IGFBP-6	Insulin-like growth factor-binding protein 6	IGFBP6	3489	P24592
IGFBP-7	Insulin-like growth factor-binding protein 7	IGFBP7	3490	Q16270
IGF-I	Insulin-like growth factor I	IGF1	3479	P05019
IGF-I sR	Insulin-like growth factor 1 receptor	IGF1R	3480	P08069
IGF-II receptor	Cation-independent mannose-6-	IGF2R	3482	P11717

	phosphate receptor			
IgG	Immunoglobulin G	IGHG1 IGHG2 IGHG3 IGHG4 IGK@ IGL@	3500 3501 3502 3503 50802 3535	P01857
IgM	Immunoglobulin M	IGHM IGJ IGK@ IGL@	3507 3512 50802 3535	P01871
IL-1 R AcP	Interleukin-1 Receptor accessory protein	IL1RAP	3556	Q9NPH3
IL-1 R1	Interleukin-1 receptor-like 1	IL1RL1	9173	Q01638
IL-1 sR9	X-linked interleukin-1 receptor accessory protein-like 2	IL1RAPL2	26280	Q9NP60
IL-1 sRI	Interleukin-1 receptor type 1	IL1R1	3554	P14778
IL-10	Interleukin-10	IL10	3586	P22301
IL-10 Rb	Interleukin-10 receptor subunit beta	IL10RB	3588	Q08334
IL-11	Interleukin-11	IL11	3589	P20809
IL-11 RA	Interleukin-11 receptor subunit alpha	IL11RA	3590	Q14626
IL-12	Interleukin-12	IL12A IL12B	3592 3593	P29459, P29460
IL-12 Rb1	Interleukin-12 receptor subunit beta-1	IL12RB1	3594	P42701
IL-12 RB2	Interleukin-12 receptor subunit beta-2	IL12RB2	3595	Q99665
IL-13	Interleukin-13	IL13	3596	P35225
IL-13 Ra1	Interleukin-13 receptor subunit alpha-1	IL13RA1	3597	P78552
IL-15 Ra	Interleukin-15 receptor subunit alpha	IL15RA	3601	Q13261
IL-16	Interleukin-16	IL16	3603	Q14005
IL-17	Interleukin-17A	IL17A	3605	Q16552
IL-17 RC	Interleukin-17 receptor C	IL17RC	84818	Q8NAC3
IL-17 RD	Interleukin-17 receptor D	IL17RD	54756	Q8NFM7
IL-17 sR	Interleukin-17 receptor A	IL17RA	23765	Q96F46
IL-17B	Interleukin-17B	IL17B	27190	Q9UHF5
IL-17B R	interleukin-17 receptor B	IL17RB	55540	Q9NRM6
IL-17D	Interleukin-17D	IL17D	53342	Q8TAD2
IL-17E	Interleukin-25	IL25	64806	Q9H293
IL-17F	Interleukin-17F	IL17F	112744	Q96PD4
IL-18 BPa	Interleukin-18-binding protein	IL18BP	10068	O95998
IL-18 Ra	Interleukin-18 receptor 1	IL18R1	8809	Q13478
IL-18 Rb	Interleukin-18 receptor accessory protein	IL18RAP	8807	O95256

IL-19	Interleukin-19	IL19	29949	Q9UHD0
IL-1a	Interleukin-1 alpha	IL1A	3552	P01583
IL-1b	Interleukin-1 beta	IL1B	3553	P01584
IL-1F7	Interleukin-37	IL37	27178	Q9NZH6
IL-1Rrp2	Interleukin-1 receptor-like 2	IL1RL2	8808	Q9HB29
IL-2	Interleukin-2	IL2	3558	P60568
IL-2 sRa	Interleukin-2 receptor subunit alpha	IL2RA	3559	P01589
IL-2 sRg	Cytokine receptor common subunit gamma	IL2RG	3561	P31785
IL-20	Interleukin-20	IL20	50604	Q9NYY1
IL-20 Ra	Interleukin-20 receptor subunit alpha	IL20RA	53832	Q9UHF4
IL-22	Interleukin-22	IL22	50616	Q9GZX6
IL-22BP	Interleukin-22 receptor subunit alpha-2	IL22RA2	116379	Q969J5
IL-22RA1	Interleukin-22 receptor subunit alpha-1	IL22RA1	58985	Q8N6P7
IL-23	Interleukin-23	IL12B IL23A	3593 51561	P29460, Q9NPF7
IL-23 R	Interleukin-23 receptor	IL23R	149233	Q5VWK5
IL-24	Interleukin-24	IL24	11009	Q13007
IL-27	Interleukin-27	IL27 EBI3	246778 10148	Q8NEV9, Q14213
IL-3	Interleukin-3	IL3	3562	P08700
IL-3 Ra	Interleukin-3 receptor subunit alpha	IL3RA	3563	P26951
IL-34	Interleukin-34	IL34	146433	Q6ZMJ4
IL-4	Interleukin-4	IL4	3565	P05112
IL-4 sR	Interleukin-4 receptor subunit alpha	IL4R	3566	P24394
IL-5	Interleukin-5	IL5	3567	P05113
IL-5 Ra	Interleukin-5 receptor subunit alpha	IL5RA	3568	Q01344
IL-6	Interleukin-6	IL6	3569	P05231
IL-6 sRa	Interleukin-6 receptor subunit alpha	IL6R	3570	P08887
IL-7	Interleukin-7	IL7	3574	P13232
IL-7 Ra	Interleukin-7 receptor subunit alpha	IL7R	3575	P16871
IL-8	Interleukin-8	CXCL8	3576	P10145
ILT-2	Leukocyte immunoglobulin-like receptor subfamily B member 1	LILRB1	10859	Q8NHL6
ILT-4	Leukocyte immunoglobulin-like receptor subfamily B member 2	LILRB2	10288	Q8N423
IMB1	Importin subunit beta-1	KPNB1	3837	Q14974

IMDH1	Inosine-5'-monophosphate dehydrogenase 1	IMPDH1	3614	P20839
IMDH2	Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	3615	P12268
ING1	Inhibitor of growth protein 1	ING1	3621	Q9UK53
Insulin	Insulin	INS	3630	P01308
Integrin a1b1	Integrin alpha-I: beta-1 complex	ITGA1 ITGB1	3672 3688	P56199, P05556
Integrin aVb5	Integrin alpha-V: beta-5 complex	ITGAV ITGB5	3685 3693	P06756, P18084
IP-10	C-X-C motif chemokine 10	CXCL10	3627	P02778
IR	Insulin receptor	INSR	3643	P06213
I-TAC	C-X-C motif chemokine 11	CXCL11	6373	O14625
ITI heavy chain H4	Inter-alpha-trypsin inhibitor heavy chain H4	ITIH4	3700	Q14624
JAG1	Protein jagged-1	JAG1	182	P78504
JAG2	Protein jagged-2	JAG2	3714	Q9Y219
JAK2	Tyrosine-protein kinase JAK2	JAK2	3717	O60674
JAM-B	Junctional adhesion molecule B	JAM2	58494	P57087
JAM-C	Junctional adhesion molecule C	JAM3	83700	Q9BX67
JAML1	Junctional adhesion molecule-like	AMICA1	120425	Q86YT9
JNK2	Mitogen-activated protein kinase 9	MAPK9	5601	P45984
Kallikrein 11	Kallikrein-11	KLK11	11012	Q9UBX7
Kallikrein 12	Kallikrein-12	KLK12	43849	Q9UKR0
Kallikrein 13	Kallikrein-13	KLK13	26085	Q9UKR3
Kallikrein 14	Kallikrein-14	KLK14	43847	Q9P0G3
Kallikrein 4	Kallikrein-4	KLK4	9622	Q9Y5K2
Kallikrein 5	Kallikrein-5	KLK5	25818	Q9Y337
Kallikrein 6	Kallikrein-6	KLK6	5653	Q92876
Kallikrein 7	Kallikrein-7	KLK7	5650	P49862
Kallikrein 8	Kallikrein-8	KLK8	11202	O60259
Kallistatin	Kallistatin	SERPINA4	5267	P29622
Karyopherin-a2	Importin subunit alpha-1	KPNA2	3838	P52292
Keratin 18	Keratin, type I cytoskeletal 18	KRT18	3875	P05783
KI2L4	Killer cell immunoglobulin-like receptor 2DL4	KIR2DL4	3805	Q99706
KI3L2	Killer cell immunoglobulin-like receptor 3DL2	KIR3DL2	3812	P43630
KI3S1	Killer cell immunoglobulin-like	KIR3DS1	3813	Q14943

	receptor 3DS1			
KIF23	Kinesin-like protein KIF23	KIF23	9493	Q02241
Kininogen, HMW	Kininogen-1	KNG1	3827	P01042
KIRR3	Kin of IRRE-like protein 3	KIRREL3	84623	Q8IZU9
KLRF1	Killer cell lectin-like receptor subfamily F member 1	KLRF1	51348	Q9NZS2
KPCI	Protein kinase C iota type	PRKCI	5584	P41743
KPCT	Protein kinase C theta type	PRKCQ	5588	Q04759
K-ras	GTPase KRas	KRAS	3845	P01116
KREM2	Kremen protein 2	KREMEN2	79412	Q8NCW0
Ku70	X-ray repair cross-complementing protein 6	XRCC6	2547	P12956
KYNU	Kynureninase	KYNU	8942	Q16719
Lactoferrin	Lactotransferrin	LTF	4057	P02788
LAG-1	C-C motif chemokine 4-like	CCL4L1	388372	Q8NHW4
LAG-3	Lymphocyte activation gene 3 protein	LAG3	3902	P18627
Lamin-B1	Lamin-B1	LMNB1	4001	P20700
Laminin	Laminin	LAMA1 LAMB1 LAMC1	284217 3912 3915	P25391, P07942, P11047
Layilin	Layilin	LAYN	143903	Q6UX15
LBP	Lipopolysaccharide-binding protein	LBP	3929	P18428
LCK	Tyrosine-protein kinase Lck	LCK	3932	P06239
LCMT1	Leucine carboxyl methyltransferase 1	LCMT1	51451	Q9UIC8
LD78-beta	C-C motif chemokine 3-like 1	CCL3L1	414062	P16619
LDH-H 1	L-lactate dehydrogenase B chain	LDHB	3945	P07195
LEAP-1	Hepcidin	HAMP	57817	P81172
Leptin	Leptin	LEP	3952	P41159
LG3BP	Galectin-3-binding protein	LGALS3BP	3959	Q08380
LGMN	Legumain	LGMN	5641	Q99538
LIF sR	Leukemia inhibitory factor receptor	LIFR	3977	P42702
LIGHT	Tumor necrosis factor ligand superfamily member 14	TNFSF14	8740	O43557
LIMP II	Lysosome membrane protein 2	SCARB2	950	Q14108
LIN7B	Protein lin-7 homolog B	LIN7B	64130	Q9HAP6
Lipocalin 2	Neutrophil gelatinase-associated lipocalin	LCN2	3934	P80188

Livin B	Baculoviral IAP repeat-containing protein 7 Isoform beta	BIRC7	79444	Q96CA5
LKHA4	Leukotriene A-4 hydrolase	LTA4H	4048	P09960
LRIG3	Leucine-rich repeats and immunoglobulin-like domains protein 3	LRIG3	121227	Q6UXM1
LRP8	Low-density lipoprotein receptor-related protein 8	LRP8	7804	Q14114
LRRT1	Leucine-rich repeat transmembrane neuronal protein 1	LRRTM1	347730	Q86UE6
LRRT3	Leucine-rich repeat transmembrane neuronal protein 3	LRRTM3	347731	Q86VH5
LSAMP	Limbic system-associated membrane protein	LSAMP	4045	Q13449
Luteinizing hormone	Luteinizing hormone	CGA LHB	1081 3972	P01215, P01229
LY86	Lymphocyte antigen 86	LY86	9450	O95711
LY9	T-lymphocyte surface antigen Ly-9	LY9	4063	Q9HBG7
Lymphotactin	Lymphotactin	XCL1	6375	P47992
Lymphotoxin a1/b2	Lymphotoxin alpha1:beta2	LTA LTB	4049 4050	P01374, Q06643
Lymphotoxin a2/b1	Lymphotoxin alpha2:beta1	LTA LTB	4049 4050	P01374, Q06643
Lymphotoxin b R	Tumor necrosis factor receptor superfamily member 3	LTBR	4055	P36941
LYN	Tyrosine-protein kinase Lyn	LYN	4067	P07948
LYNB	Tyrosine-protein kinase Lyn, isoform B	LYN	4067	P07948
Lysozyme	Lysozyme C	LYZ	4069	P61626
LYVE1	Lymphatic vessel endothelial hyaluronic acid receptor 1	LYVE1	10894	Q9Y5Y7
M2-PK	Pyruvate kinase PKM	PKM2	5315	P14618
Macrophage mannose receptor	Macrophage mannose receptor 1	MRC1	4360	P22897
Macrophage scavenger receptor	Macrophage scavenger receptor types I and II	MSR1	4481	P21757
Mammaglobin 2	Mammaglobin-B	SCGB2A1	4246	O75556
MAPK14	Mitogen-activated protein kinase 14	MAPK14	1432	Q16539
MAPK2	MAP kinase-activated protein kinase 2	MAPKAPK2	9261	P49137
MAPK5	MAP kinase-activated protein kinase 5	MAPKAPK5	8550	Q8IW41

MAPKAPK3	MAP kinase-activated protein kinase 3	MAPKAPK3	7867	Q16644
Marapsin	Serine protease 27	PRSS27	83886	Q9BQR3
MASP3	Mannan-binding lectin serine protease 1	MASP1	5648	P48740
MATK	Megakaryocyte-associated tyrosine-protein kinase	MATK	4145	P42679
MATN2	Matrilin-2	MATN2	4147	O00339
MATN3	Matrilin-3	MATN3	4148	O15232
MBD4	Methyl-CpG-binding domain protein 4	MBD4	8930	O95243
MBL	Mannose-binding protein C	MBL2	4153	P11226
MCP-1	C-C motif chemokine 2	CCL2	6347	P13500
MCP-2	C-C motif chemokine 8	CCL8	6355	P80075
MCP-3	C-C motif chemokine 7	CCL7	6354	P80098
MCP-4	C-C motif chemokine 13	CCL13	6357	Q99616
M-CSF R	Macrophage colony-stimulating factor 1 receptor	CSF1R	1436	P07333
MDC	C-C motif chemokine 22	CCL22	6367	O00626
MDHC	Malate dehydrogenase, cytoplasmic	MDH1	4190	P40925
MDM2	E3 ubiquitin-protein ligase Mdm2	MDM2	4193	Q00987
MED-1	Mediator of RNA polymerase II transcription subunit 1	MED1	5469	Q15648
MEK1	Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	5604	Q02750
MEPE	Matrix extracellular phosphoglycoprotein	MEPE	56955	Q9NQ76
Mesothelin	Mesothelin	MSLN	10232	Q13421
Met	Hepatocyte growth factor receptor	MET	4233	P08581
METAP1	Methionine aminopeptidase 1	METAP1	23173	P53582
MFGM	Lactadherin	MFGE8	4240	Q08431
MFRP	Membrane frizzled-related protein	MFRP	83552	Q9BY79
MIA	Melanoma-derived growth regulatory protein	MIA	8190	Q16674
MICA	MHC class I polypeptide-related sequence A	MICA	4276	Q29983
MICB	MHC class I polypeptide-related sequence B	MICB	4277	Q29980

Midkine	Midkine	MDK	4192	P21741
MIF	Macrophage migration inhibitory factor	MIF	4282	P14174
MIP-1a	C-C motif chemokine 3	CCL3	6348	P10147
MIP-3a	C-C motif chemokine 20	CCL20	6364	P78556
MIP-3b	C-C motif chemokine 19	CCL19	6363	Q99731
MIP-5	C-C motif chemokine 15	CCL15	6359	Q16663
MIS	Muellerian-inhibiting factor	AMH	268	P03971
MK01	Mitogen-activated protein kinase 1	MAPK1	5594	P28482
MK08	Mitogen-activated protein kinase 8	MAPK8	5599	P45983
MK11	Mitogen-activated protein kinase 11	MAPK11	5600	Q15759
MK12	Mitogen-activated protein kinase 12	MAPK12	6300	P53778
MK13	Mitogen-activated protein kinase 13	MAPK13	5603	O15264
MMEL2	Membrane metallo-endopeptidase-like 1	MMEL1	79258	Q495T6
MMP-1	Interstitial collagenase	MMP1	4312	P03956
MMP-10	Stromelysin-2	MMP10	4319	P09238
MMP-12	Macrophage metalloelastase	MMP12	4321	P39900
MMP-13	Collagenase 3	MMP13	4322	P45452
MMP-14	Matrix metalloproteinase-14	MMP14	4323	P50281
MMP-16	Matrix metalloproteinase-16	MMP16	4325	P51512
MMP-17	Matrix metalloproteinase-17	MMP17	4326	Q9ULZ9
MMP-2	72 kDa type IV collagenase	MMP2	4313	P08253
MMP-3	Stromelysin-1	MMP3	4314	P08254
MMP-7	Matrilysin	MMP7	4316	P09237
MMP-8	Neutrophil collagenase	MMP8	4317	P22894
MMP-9	Matrix metalloproteinase-9	MMP9	4318	P14780
Mn SOD	Superoxide dismutase [Mn], mitochondrial	SOD2	6648	P04179
MO2R1	Cell surface glycoprotein CD200 receptor 1	CD200R1	131450	Q8TD46
Moesin	Moesin	MSN	4478	P26038
MOZ	Histone acetyltransferase KAT6A	KAT6A	7994	Q92794
MP2K2	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	5605	P36507
MP2K4	Dual specificity mitogen-activated protein kinase kinase 4	MAP2K4	6416	P45985

MPIF-1	C-C motif chemokine 23	CCL23	6368	P55773
MRC2	C-type mannose receptor 2	MRC2	9902	Q9UBG0
MRCKB	Serine/threonine-protein kinase MRCK beta	CDC42BPB	9578	Q9Y5S2
MSP	Hepatocyte growth factor-like protein	MST1	4485	P26927
MSP R	Macrophage-stimulating protein receptor	MST1R	4486	Q04912
Myeloperoxidase	Myeloperoxidase	MPO	4353	P05164
Myoglobin	Myoglobin	MB	4151	P02144
Myokinase, human	Adenylate kinase isoenzyme 1	AK1	203	P00568
NACA	Nascent polypeptide-associated complex subunit alpha	NACA	4666	Q13765
NADPH-P450 Oxidoreductase	NADPH--cytochrome P450 reductase	POR	5447	P16435
NAGK	N-acetyl-D-glucosamine kinase	NAGK	55577	Q9UJ70
NANOG	Homeobox protein NANOG	NANOG	79923	Q9H9S0
NAP-2	Neutrophil-activating peptide 2	PPBP	5473	P02775
NCAM-120	Neural cell adhesion molecule 1, 120 kDa isoform	NCAM1	4684	P13591
NCAM-L1	Neural cell adhesion molecule L1	L1CAM	3897	P32004
NCC27	Chloride intracellular channel protein 1	CLIC1	1192	O00299
NCK1	Cytoplasmic protein NCK1	NCK1	4690	P16333
NDP kinase B	Nucleoside diphosphate kinase B	NME2	4831	P22392
Nectin-like protein 1	Cell adhesion molecule 3	CADM3	57863	Q8N126
Nectin-like protein 2	Cell adhesion molecule 1	CADM1	23705	Q9BY67
NET4	Netrin-4	NTN4	59277	Q9HB63
Neurotrophin-3	Neurotrophin-3	NTF3	4908	P20783
Neurotrophin-5	Neurotrophin-4	NTF4	4909	P34130
NG36	Histone-lysine N-methyltransferase EHMT2	EHMT2	10919	Q96KQ7
NID2	Nidogen-2	NID2	22795	Q14112
Nidogen	Nidogen-1	NID1	4811	P14543
NKG2D	NKG2-D type II integral membrane protein	KLRK1	22914	P26718
NKp30	Natural cytotoxicity triggering receptor 3	NCR3	259197	O14931
NKp44	Natural cytotoxicity triggering	NCR2	9436	O95944

	receptor 2			
NKp46	Natural cytotoxicity triggering receptor 1	NCR1	9437	O76036
NLGNX	Neuroligin-4, X-linked	NLGN4X	57502	Q8N0W4
NMT1	Glycylpeptide N-tetradecanoyltransferase 1	NMT1	4836	P30419
Noggin	Noggin	NOG	9241	Q13253
Nogo Receptor	Reticulon-4 receptor	RTN4R	65078	Q9BZR6
NOTC2	Neurogenic locus notch homolog protein 2	NOTCH2	4853	Q04721
Notch 1	Neurogenic locus notch homolog protein 1	NOTCH1	4851	P46531
Notch-3	Neurogenic locus notch homolog protein 3	NOTCH3	4854	Q9UM47
NovH	Protein NOV homolog	NOV	4856	P48745
NPS-PLA2	Phospholipase A2, membrane associated	PLA2G2A	5320	P14555
NR1D1	Nuclear receptor subfamily 1 group D member 1	NR1D1	9572	P20393
Nr-CAM	Neuronal cell adhesion molecule	NRCAM	4897	Q92823
NRP1	Neuropilin-1	NRP1	8829	O14786
NRX1B	Neurexin-1-beta	NRXN1	9378	P58400
NRX3B	Neurexin-3-beta	NRXN3	9369	Q9HDB5
NSF1C	NSFL1 cofactor p47	NSFL1C	55968	Q9UNZ2
Nucleoside diphosphate kinase A	Nucleoside diphosphate kinase A	NME1	4830	P15531
NUDC3	NudC domain-containing protein 3	NUDCD3	23386	Q8IVD9
NXPH1	Neurexophilin-1	NXPH1	30010	P58417
OBCAM	Opioid-binding protein/cell adhesion molecule	OPCML	4978	Q14982
OCAD1	OCIA domain-containing protein 1	OCIAD1	54940	Q9NX40
Olfactomedin-4	Olfactomedin-4	OLFM4	10562	Q6UX06
OLR1	Oxidized low-density lipoprotein receptor 1	OLR1	4973	P78380
OMD	Osteomodulin	OMD	4958	Q99983
ON	SPARC	SPARC	6678	P09486
OPG	Tumor necrosis factor receptor superfamily member 11B	TNFRSF11B	4982	O00300

OSM	Oncostatin-M	OSM	5008	P13725
OX2G	OX-2 membrane glycoprotein	CD200	4345	P41217
OX40 Ligand	Tumor necrosis factor ligand superfamily member 4	TNFSF4	7292	P23510
p27Kip1	Cyclin-dependent kinase inhibitor 1B	CDKN1B	1027	P46527
PA2G4	Proliferation-associated protein 2G4	PA2G4	5036	Q9UQ80
PACAP-27	Pituitary adenylate cyclase-activating polypeptide 27	ADCYAP1	116	P18509
PACAP-38	Pituitary adenylate cyclase-activating polypeptide 38	ADCYAP1	116	P18509
PAFAH	Platelet-activating factor acetylhydrolase	PLA2G7	7941	Q13093
PAFAH beta subunit	Platelet-activating factor acetylhydrolase IB subunit beta	PAFAH1B2	5049	P68402
PAI-1	Plasminogen activator inhibitor 1	SERPINE1	5054	P05121
PAK3	Serine/threonine-protein kinase PAK 3	PAK3	5063	O75914
PAK6	Serine/threonine-protein kinase PAK 6	PAK6	56924	Q9NQU5
PAK7	Serine/threonine-protein kinase PAK 7	PAK7	57144	Q9P286
PAPP-A	Pappalysin-1	PAPPA	5069	Q13219
Paraoxonase 1	Serum paraoxonase/arylesterase 1	PON1	5444	P27169
PARC	C-C motif chemokine 18	CCL18	6362	P55774
PARK7	Protein DJ-1	PARK7	11315	Q99497
PBEF	Nicotinamide phosphoribosyltransferase	NAMPT	10135	P43490
P-Cadherin	Cadherin-3	CDH3	1001	P22223
PCI	Plasma serine protease inhibitor	SERPINA5	5104	P05154
PCNA	Proliferating cell nuclear antigen	PCNA	5111	P12004
PCSK7	Proprotein convertase subtilisin/kexin type 7	PCSK7	9159	Q16549
PCSK9	Proprotein convertase subtilisin/kexin type 9	PCSK9	255738	Q8NBP7
PDE11	Dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11A	PDE11A	50940	Q9HCR9
PDE3A	cGMP-inhibited 3',5'-cyclic phosphodiesterase A	PDE3A	5139	Q14432
PDE4D	cAMP-specific 3',5'-cyclic	PDE4D	5144	Q08499

	phosphodiesterase 4D			
PDE5A	cGMP-specific 3',5'-cyclic phosphodiesterase	PDE5A	8654	O76074
PDE7A	High affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A	PDE7A	5150	Q13946
PDE9A	High affinity cGMP-specific 3',5'-cyclic phosphodiesterase 9A	PDE9A	5152	O76083
PDGF Rb	Platelet-derived growth factor receptor beta	PDGFRB	5159	P09619
PDGF-AA	Platelet-derived growth factor subunit A	PDGFA	5154	P04085
PDGF-BB	Platelet-derived growth factor subunit B	PDGFB	5155	P01127
PDGF-CC	Platelet-derived growth factor C	PDGFC	56034	Q9NRA1
PDK1	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	5163	Q15118
PD-L2	Programmed cell death 1 ligand 2	PDCD1LG2	80380	Q9BQ51
PDPK1	3-phosphoinositide-dependent protein kinase 1	PDPK1	5170	O15530
PECAM-1	Platelet endothelial cell adhesion molecule	PECAM1	5175	P16284
Periostin	Periostin	POSTN	10631	Q15063
PERL	Lactoperoxidase	LPO	4025	P22079
Peroxiredoxin-1	Peroxiredoxin-1	PRDX1	5052	Q06830
Peroxiredoxin-5	Peroxiredoxin-5, mitochondrial	PRDX5	25824	P30044
Peroxiredoxin-6	Peroxiredoxin-6	PRDX6	9588	P30041
Persephin	Persephin	PSPN	5623	O60542
PESC	Pescadillo homolog	PES1	23481	O00541
PF-4	Platelet factor 4	PF4	5196	P02776
PFD5	Prefoldin subunit 5	PFDN5	5204	Q99471
PGCB	Brevican core protein	BCAN	63827	Q96GW7
PGP9.5	Ubiquitin carboxyl-terminal hydrolase isozyme L1	UCHL1	7345	P09936
PGRP-S	Peptidoglycan recognition protein 1	PGLYRP1	8993	O75594
PH	Pancreatic hormone	PPY	5539	P01298
PHI	Glucose-6-phosphate isomerase	GPI	2821	P06744
Phosphoglycerate kinase	Phosphoglycerate kinase 1	PGK1	5230	P00558

1				
Phosphoglycerate mutase 1	Phosphoglycerate mutase 1	PGAM1	5223	P18669
PIGR	Polymeric immunoglobulin receptor	PIGR	5284	P01833
PIK3CA/PIK3R1	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform:Phosphatidylinositol 3-kinase regulatory subunit alpha complex	PIK3CA PIK3R1	5290 5295	P42336, P27986
PIM1	Serine/threonine-protein kinase pim-1	PIM1	5292	P11309
PK3CG	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform	PIK3CG	5294	P48736
PKB a/b/g	Protein kinase B alpha/beta/gamma		8413	Family
PKC-A	Protein kinase C alpha type	PRKCA	5578	P17252
PKC-B-II	Protein kinase C beta type (splice variant beta-II)	PRKCB	5579	P05771
PKC-D	Protein kinase C delta type	PRKCD	5580	Q05655
PKC-G	Protein kinase C gamma type	PRKCG	5582	P05129
PKC-Z	Protein kinase C zeta type	PRKCZ	5590	Q05513
Plasmin	Plasmin	PLG	5340	P00747
Plasminogen	Plasminogen	PLG	5340	P00747
PLCG1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	PLCG1	5335	P19174
PlGF	Placenta growth factor	PGF	5228	P49763
PLK-1	Serine/threonine-protein kinase PLK1	PLK1	5347	P53350
PLPP	Pyridoxal phosphate phosphatase	PDXP	57026	Q96GD0
PLXC1	Plexin-C1	PLXNC1	10154	O60486
PPAC	Low molecular weight phosphotyrosine protein phosphatase	ACP1	52	P24666
PPase	Inorganic pyrophosphatase	PPA1	5464	Q15181
PPIB	Peptidyl-prolyl cis-trans isomerase B	PPIB	5479	P23284
PPID	Peptidyl-prolyl cis-trans isomerase D	PPID	5481	Q08752
PPIE	Peptidyl-prolyl cis-trans isomerase E	PPIE	10450	Q9UNP9

Prekallikrein	Plasma kallikrein	KLKB1	3818	P03952
PRKACA	cAMP-dependent protein kinase catalytic subunit alpha	PRKACA	5566	P17612
PRL	Prolactin	PRL	5617	P01236
Prolactin Receptor	Prolactin receptor	PRLR	5618	P16471
Properdin	Properdin	CFP	5199	P27918
Prostatic binding protein	Phosphatidylethanolamine-binding protein 1	PEBP1	5037	P30086
Protease nexin I	Glia-derived nexin	SERPINE2	5270	P07093
Protein C	Vitamin K-dependent protein C	PROC	5624	P04070
Protein disulfide isomerase A3	Protein disulfide-isomerase A3	PDIA3	2923	P30101
Protein disulfide-isomerase	Protein disulfide-isomerase	P4HB	5034	P07237
Protein S	Vitamin K-dependent protein S	PROS1	5627	P07225
Proteinase-3	Myeloblastin	PRTN3	5657	P24158
Prothrombin	Prothrombin	F2	2147	P00734
PSA	Prostate-specific antigen	KLK3	354	P07288
PSA1	Proteasome subunit alpha type-1	PSMA1	5682	P25786
PSA2	Proteasome subunit alpha type-2	PSMA2	5683	P25787
PSA6	Proteasome subunit alpha type-6	PSMA6	5687	P60900
PSD7	26S proteasome non-ATPase regulatory subunit 7	PSMD7	5713	P51665
P-Selectin	P-Selectin	SELP	6403	P16109
PSMA	Glutamate carboxypeptidase 2	FOLH1	2346	Q04609
PSME1	Proteasome activator complex subunit 1	PSME1	5720	Q06323
PSME3	Proteasome activator complex subunit 3	PSME3	10197	P61289
PTEN	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN	PTEN	5728	P60484
PTH	Parathyroid hormone	PTH	5741	P01270
PTHrP	Parathyroid hormone-related protein	PTHLH	5744	P12272
PTK6	Protein-tyrosine kinase 6	PTK6	5753	Q13882
PTN	Pleiotrophin	PTN	5764	P21246
PTP-1B	Tyrosine-protein phosphatase non-	PTPN1	5770	P18031

	receptor type 1			
PTP-1C	Tyrosine-protein phosphatase non-receptor type 6	PTPN6	5777	P29350
PUR8	Adenylosuccinate lyase	ADSL	158	P30566
PYY	Peptide YY	PYY	5697	P10082
Rab GDP dissociation inhibitor, beta	Rab GDP dissociation inhibitor beta	GDI2	2665	P50395
RAC1	Ras-related C3 botulinum toxin substrate 1	RAC1	5879	P63000
RAD51	DNA repair protein RAD51 homolog 1	RAD51	5888	Q06609
RAN	GTP-binding nuclear protein Ran	RAN	5901	P62826
RANK	Tumor necrosis factor receptor superfamily member 11A	TNFRSF11A	8792	Q9Y6Q6
RANTES	C-C motif chemokine 5	CCL5	6352	P13501
RAP	alpha-2-macroglobulin receptor-associated protein	LRPAP1	4043	P30533
RASA1	Ras GTPase-activating protein 1	RASA1	5921	P20936
Rb	Retinoblastoma-associated protein	RB1	5925	P06400
RBM39	RNA-binding protein 39	RBM39	9584	Q14498
RBP	Retinol-binding protein 4	RBP4	5950	P02753
RELT	Tumor necrosis factor receptor superfamily member 19L	RELT	84957	Q969Z4
Renin	Renin	REN	5972	P00797
Resistin	Resistin	RETN	56729	Q9HD89
RET	Proto-oncogene tyrosine-protein kinase receptor Ret	RET	5979	P07949
RGMA	Repulsive guidance molecule A	RGMA	56963	Q96B86
RGMB	RGM domain family member B	RGMB	285704	Q6NW40
RGM-C	Hemojuvelin	HFE2	148738	Q6ZVN8
ROBO2	Roundabout homolog 2	ROBO2	6092	Q9HCK4
ROBO3	Roundabout homolog 3	ROBO3	64221	Q96MS0
ROR1	Tyrosine-protein kinase transmembrane receptor ROR1	ROR1	4919	Q01973
RPS6KA3	Ribosomal protein S6 kinase alpha-3	RPS6KA3	6197	P51812
RS3	40S ribosomal protein S3	RPS3	6188	P23396
RS7	40S ribosomal protein S7	RPS7	6201	P62081
RSK-like protein kinase	Ribosomal protein S6 kinase alpha-5	RPS6KA5	9252	O75582

RSPO2	R-spondin-2	RSPO2	340419	Q6UXX9
RTN4	Reticulon-4	RTN4	57142	Q9NQC3
RUXF	Small nuclear ribonucleoprotein F	SNRPF	6636	P62306
SAA	Serum amyloid A-1 protein	SAA1	6288	P0DJI8
SAP	Serum amyloid P-component	APCS	325	P02743
SARP-2	Secreted frizzled-related protein 1	SFRP1	6422	Q8N474
SBDS	Ribosome maturation protein SBDS	SBDS	51119	Q9Y3A5
SCD163	Scavenger receptor cysteine-rich type 1 protein M130	CD163	9332	Q86VB7
sCD4	T-cell surface glycoprotein CD4	CD4	920	P01730
SCF sR	Mast/stem cell growth factor receptor Kit	KIT	3815	P10721
SCGF-alpha	Stem Cell Growth Factor-alpha	CLEC11A	6320	Q9Y240
SCGF-beta	Stem Cell Growth Factor-beta	CLEC11A	6320	Q9Y240
SDF-1	Stromal cell-derived factor 1	CXCL12	6387	P48061
SE6L2	Seizure 6-like protein 2	SEZ6L2	26470	Q6UXD5
Secretin	Secretin	SCT	6343	P09683
Semaphorin 3A	Semaphorin-3A	SEMA3A	10371	Q14563
Semaphorin 3E	Semaphorin-3E	SEMA3E	9723	O15041
Semaphorin-6A	Semaphorin-6A	SEMA6A	57556	Q9H2E6
SEPR	Seprase	FAP	2191	Q12884
sE-Selectin	E-Selectin	SELE	6401	P16581
SET	Protein SET	SET	6418	Q01105
sFRP-3	Secreted frizzled-related protein 3	FRZB	2487	Q92765
SGTA	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	6449	O43765
SH21A	SH2 domain-containing protein 1A	SH2D1A	4068	O60880
SHBG	Sex hormone-binding globulin	SHBG	6462	P04278
SHC1	SHC-transforming protein 1	SHC1	6464	P29353
SHP-2	Tyrosine-protein phosphatase non-receptor type 11	PTPN11	5781	Q06124
Sialoadhesin	Sialoadhesin	SIGLEC1	6614	Q9BZZ2
sICAM-1	Intercellular adhesion molecule 1	ICAM1	3383	P05362
sICAM-2	Intercellular adhesion molecule 2	ICAM2	3384	P13598
sICAM-3	Intercellular adhesion molecule 3	ICAM3	3385	P32942
sICAM-5	Intercellular adhesion molecule 5	ICAM5	7087	Q9UMF0

SIG14	Sialic acid-binding Ig-like lectin 14	SIGLEC14	100049587	Q08ET2
Siglec-3	Myeloid cell surface antigen CD33	CD33	945	P20138
Siglec-6	Sialic acid-binding Ig-like lectin 6	SIGLEC6	946	O43699
Siglec-7	Sialic acid-binding Ig-like lectin 7	SIGLEC7	27036	Q9Y286
Siglec-9	Sialic acid-binding Ig-like lectin 9	SIGLEC9	27180	Q9Y336
SIRT2	NAD-dependent protein deacetylase sirtuin-2	SIRT2	22933	Q8IXJ6
SKP1	S-phase kinase-associated protein 1	SKP1	6500	P63208
SLAF5	SLAM family member 5	CD84	8832	Q9UIB8
SLAF6	SLAM family member 6	SLAMF6	114836	Q96DU3
SLAF7	SLAM family member 7	SLAMF7	57823	Q9NQ25
sLeptin R	Leptin receptor	LEPR	3953	P48357
SLIK5	SLIT and NTRK-like protein 5	SLITRK5	26050	O94991
SLPI	Antileukoproteinase	SLPI	6590	P03973
sL-Selectin	L-Selectin	SELL	6402	P14151
SMAC	Diablo homolog, mitochondrial	DIABLO	56616	Q9NR28
SNAA	Alpha-soluble NSF attachment protein	NAPA	8775	P54920
SOD	Superoxide dismutase [Cu-Zn]	SOD1	6647	P00441
Soggy-1	Dickkopf-like protein 1	DKKL1	27120	Q9UK85
Somatostatin-28	Somatostatin-28	SST	6750	P61278
Sonic Hedgehog	Sonic hedgehog protein	SHH	6469	Q15465
SORC2	VPS10 domain-containing receptor SorCS2	SORCS2	57537	Q96PQ0
Sorting nexin 4	Sorting nexin-4	SNX4	8723	O95219
SPARCL1	SPARC-like protein 1	SPARCL1	8404	Q14515
SP-D	Pulmonary surfactant-associated protein D	SFTPD	6441	P35247
Sphingosine kinase 1	Sphingosine kinase 1	SPHK1	8877	Q9NYA1
SPHK2	Sphingosine kinase 2	SPHK2	56848	Q9NRA0
SPINT2	Kunitz-type protease inhibitor 2	SPINT2	10653	O43291
Spondin-1	Spondin-1	SPON1	10418	Q9HCB6
SPTA2	Spectrin alpha chain, non-erythrocytic 1	SPTAN1	6709	Q13813
sRAGE	Advanced glycosylation end product-specific receptor, soluble	AGER	177	Q15109
sRANKL	Tumor necrosis factor ligand superfamily member 11	TNFSF11	8600	O14788

SRCN1	Proto-oncogene tyrosine-protein kinase Src	SRC	6714	P12931
SREC-I	Scavenger receptor class F member 1	SCARF1	8578	Q14162
SREC-II	Scavenger receptor class F member 2	SCARF2	91179	Q96GP6
SSRP1	FACT complex subunit SSRP1	SSRP1	6749	Q08945
ST4S6	Carbohydrate sulfotransferase 15	CHST15	51363	Q7LFX5
STAB2	Stabilin-2	STAB2	55576	Q8WWQ8
STC1	Stanniocalcin-1	STC1	6781	P52823
sTie-1	Tyrosine-protein kinase receptor Tie-1, soluble	TIE1	7075	P35590
sTie-2	Angiopoietin-1 receptor, soluble	TEK	7010	Q02763
STK16	Serine/threonine-protein kinase 16	STK16	8576	O75716
STRATIFIN	14-3-3 protein sigma	SFN	2810	P31947
Stress-induced-phosphoprotein 1	Stress-induced-phosphoprotein 1	STIP1	10963	P31948
STX1a	Syntaxin-1A	STX1A	6804	Q16623
SUPAR	Urokinase plasminogen activator surface receptor	PLAUR	5329	Q03405
Survivin	Baculoviral IAP repeat-containing protein 5	BIRC5	332	O15392
TACI	Tumor necrosis factor receptor superfamily member 13B	TNFRSF13B	23495	O14836
TAFI	Carboxypeptidase B2	CPB2	1361	Q96IY4
TAJ	Tumor necrosis factor receptor superfamily member 19	TNFRSF19	55504	Q9NS68
TAK1-TAB1	Mitogen-activated protein kinase kinase kinase 7:TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 fusion	MAP3K7 TAB1	6885 10454	O43318, Q15750
TARC	C-C motif chemokine 17	CCL17	6361	Q92583
Tau	Microtubule-associated protein tau	MAPT	4137	P10636
TBK1	Serine/threonine-protein kinase TBK1	TBK1	29110	Q9UHD2
TBP	TATA-box-binding protein	TBP	6908	P20226
TCCR	Interleukin-27 receptor subunit alpha	IL27RA	9466	Q6UWB1
TCPTP	Tyrosine-protein phosphatase non-receptor type 2	PTPN2	5771	P17706

TCTP	Translationally-controlled tumor protein	TPT1	7178	P13693
TEC	Tyrosine-protein kinase Tec	TEC	7006	P42680
TECK	C-C motif chemokine 25	CCL25	6370	O15444
Tenascin	Tenascin	TNC	3371	P24821
Testican-1	Testican-1	SPOCK1	6695	Q08629
Testican-2	Testican-2	SPOCK2	9806	Q92563
TF	Tissue Factor	F3	2152	P13726
TFF3	Trefoil factor 3	TFF3	7033	Q07654
TFPI	Tissue factor pathway inhibitor	TFPI	7035	P10646
TGF-b R II	TGF-beta receptor type-2	TGFBR2	7048	P37173
TGF-b R III	Transforming growth factor beta receptor type 3	TGFBR3	7049	Q03167
TGF-b1	Transforming growth factor beta-1	TGFB1	7040	P01137
TGF-b2	Transforming growth factor beta-2	TGFB2	7042	P61812
TGF-b3	Transforming growth factor beta-3	TGFB3	7043	P10600
TGM3	Protein-glutamine gamma-glutamyltransferase E	TGM3	7053	Q08188
Thrombin	Thrombin	F2	2147	P00734
Thrombopoietin Receptor	Thrombopoietin Receptor	MPL	4352	P40238
Thrombospondin-1	Thrombospondin-1	THBS1	7057	P07996
Thymidine kinase	Thymidine kinase, cytosolic	TK1	7083	P04183
Thyroglobulin	Thyroglobulin	TG	7038	P01266
Thyroxine-Binding Globulin	Thyroxine-Binding Globulin	SERPINA7	6906	P05543
TIG2	Retinoic acid receptor responder protein 2	RARRES2	5919	Q99969
TIMD3	Hepatitis A virus cellular receptor 2	HAVCR2	84868	Q8TDQ0
TIMP-1	Metalloproteinase inhibitor 1	TIMP1	7076	P01033
TIMP-2	Metalloproteinase inhibitor 2	TIMP2	7077	P16035
TIMP-3	Metalloproteinase inhibitor 3	TIMP3	7078	P35625
TLR2	Toll-like receptor 2	TLR2	7097	O60603
TLR4:MD-2 complex	Toll-like receptor 4:Lymphocyte antigen 96 complex	TLR4 LY96	7099 23643	O00206, Q9Y6Y9
TMA	Thyroid peroxidase	TPO	7173	P07202
TNF sR-I	Tumor necrosis factor receptor superfamily member 1A	TNFRSF1A	7132	P19438
TNF sR-II	Tumor necrosis factor receptor	TNFRSF1B	7133	P20333

	superfamily member 1B			
TNF-a	Tumor necrosis factor	TNF	7124	P01375
TNF-b	Lymphotoxin-alpha	LTA	4049	P01374
TNFSF15	Tumor necrosis factor ligand superfamily member 15	TNFSF15	9966	O95150
TNFSF18	Tumor necrosis factor ligand superfamily member 18	TNFSF18	8995	Q9UNG2
TNR4	Tumor necrosis factor receptor superfamily member 4	TNFRSF4	7293	P43489
Topoisomerase I	DNA topoisomerase 1	TOP1	7150	P11387
tPA	Tissue-type plasminogen activator	PLAT	5327	P00750
TPSB2	Tryptase beta-2	TPSB2	64499	P20231
TPSG1	Tryptase gamma	TPSG1	25823	Q9NRR2
TRAIL R1	Tumor necrosis factor receptor superfamily member 10A	TNFRSF10A	8797	O00220
Transcription factor MLR1, isoform CRA_b	Ligand-dependent nuclear receptor corepressor-like protein	LCORL	254251	Q8N3X6
Transferrin	Serotransferrin	TF	7018	P02787
Transketolase	Transketolase	TKT	7086	P29401
TrATPase	Tartrate-resistant acid phosphatase type 5	ACP5	54	P13686
Triosephosphate isomerase	Triosephosphate isomerase	TPI1	7167	P60174
TrkA	High affinity nerve growth factor receptor	NTRK1	4914	P04629
TrkB	BDNF/NT-3 growth factors receptor	NTRK2	4915	Q16620
TrkC	NT-3 growth factor receptor	NTRK3	4916	Q16288
Tropomyosin 1 alpha chain	Tropomyosin alpha-1 chain	TPM1	7168	P09493
Tropomyosin 2	Tropomyosin beta chain	TPM2	7169	P07951
Troponin I	Troponin I, cardiac muscle	TNNI3	7137	P19429
Troponin I, skeletal, fast twitch	Troponin I, fast skeletal muscle	TNNI2	7136	P48788
TRY3	Trypsin-3	PRSS3	5646	P35030
Trypsin	Trypsin-1	PRSS1	5644	P07477
Trypsin 2	Trypsin-2	PRSS2	5645	P07478
TS	Thymidylate synthase	TYMS	7298	P04818
TSG-6	Tumor necrosis factor-inducible gene	TNFAIP6	7130	P98066

	6 protein			
TSH	Thyroid Stimulating Hormone	CGA TSHB	1081 12372	P01215, P01222
TSLP	Thymic stromal lymphopoietin	TSLP	85480	Q969D9
TSLP R	Cytokine receptor-like factor 2	CRLF2	64109	Q9HC73
TSP2	Thrombospondin-2	THBS2	7058	P35442
TSP4	Thrombospondin-4	THBS4	7060	P35443
TWEAK	Tumor necrosis factor ligand superfamily member 12	TNFSF12	8742	O43508
TWEAKR	Tumor necrosis factor receptor superfamily member 12A	TNFRSF12A	51330	Q9NP84
TXD12	Thioredoxin domain-containing protein 12	TXNDC12	51060	O95881
TYK2	Non-receptor tyrosine-protein kinase TYK2	TYK2	7297	P29597
UB2L3	Ubiquitin-conjugating enzyme E2 L3	UBE2L3	7332	P68036
UBC9	SUMO-conjugating enzyme UBC9	UBE2I	7329	P63279
UBE2N	Ubiquitin-conjugating enzyme E2 N	UBE2N	7334	P61088
Ubiquitin	Ubiquitin	RPS27A	6233	P62979
Ubiquitin+1	Ubiquitin+1, truncated mutation for UbB	RPS27A	6233	P62979
UFC1	Ubiquitin-fold modifier-conjugating enzyme 1	UFC1	51506	Q9Y3C8
UFM1	Ubiquitin-fold modifier 1	UFM1	51569	P61960
ULBP-1	NKG2D ligand 1	ULBP1	80329	Q9BZM6
ULBP-2	NKG2D ligand 2	ULBP2	80328	Q9BZM5
ULBP-3	NKG2D ligand 3	ULBP3	79465	Q9BZM4
UNC5H3	Netrin receptor UNC5C	UNC5C	8633	O95185
UNC5H4	Netrin receptor UNC5D	UNC5D	137970	Q6UXZ4
uPA	Urokinase-type plasminogen activator	PLAU	5328	P00749
URB	Coiled-coil domain-containing protein 80	CCDC80	151887	Q76M96
Vasoactive Intestinal Peptide	Vasoactive Intestinal Peptide	VIP	7432	P01282
VCAM-1	Vascular cell adhesion protein 1	VCAM1	7412	P19320
VEGF	Vascular endothelial growth factor A	VEGFA	7422	P15692
VEGF sR2	Vascular endothelial growth factor receptor 2	KDR	3791	P35968

VEGF sR3	Vascular endothelial growth factor receptor 3	FLT4	2324	P35916
VEGF121	Vascular endothelial growth factor A, isoform 121	VEGFA	7422	P15692
VEGF-C	Vascular endothelial growth factor C	VEGFC	7424	P49767
vWF	von Willebrand factor	VWF	7450	P04275
WFKN1	WAP, kazal, immunoglobulin, kunitz and NTR domain-containing protein 1	WFIKKN1	117166	Q96NZ8
WFKN2	WAP, Kazal, immunoglobulin, Kunitz and NTR domain-containing protein 2	WFIKKN2	124857	Q8TEU8
WIF-1	Wnt inhibitory factor 1	WIF1	11197	Q9Y5W5
WISP-1	WNT1-inducible-signaling pathway protein 1	WISP1	8840	O95388
WNT7A	Protein Wnt-7a	WNT7A	7476	O00755
XEDAR	Tumor necrosis factor receptor superfamily member 27	EDA2R	60401	Q9HAV5
XPNPEP1	Xaa-Pro aminopeptidase 1	XPNPEP1	7511	Q9NQW7
XTP3A	dCTP pyrophosphatase 1	DCTPP1	79077	Q9H773
YES	Tyrosine-protein kinase Yes	YES1	7525	P07947
ZAP70	Tyrosine-protein kinase ZAP-70	ZAP70	7535	P43403

Supplemental Table 2. Baseline clinical characteristics of PMI study cohorts

	PMI Derivation N=15	PMI Validation N=15	SMI Cases N= 23	SMI Control N=23
Age (yr)	65 ± 10	62 ± 10	60 ± 12	60 ± 12
Female (%)	53	27	22	26
White (%)	93	93	87	94
Creatinine baseline (mg/dl)	0.96 ± 0.22	1.13 ± 0.36	1.00 ± 0.45	0.97 ± 0.16
Peak troponin T (ng/ml)	2.4 ± 1.3	3.4 ± 1.7	6.0 ± 6.2	NA
Peak CK-MB (ng/ml)	120 ± 79	145 ± 68	151 ± 116	NA
Peak CK (U/l)	1126 ± 611	997 ± 351	1476 ± 1213	NA
Total cholesterol (mg/dl)	188 ± 46	142 ± 14*	NA	186 ± 36
Aspirin exposure (%)	46	83	100	48***
Beta-blocker exposure (%)	87	93	97	26
Calcium channel blocker exposure (%)	53	58	4.3	35
Statin exposure (%)	60	86	96	43

Continuous variable are mean ± SD; categorical variables are shown as percentages. * *P* < 0.05 PMI derivation vs. validation or SMI cases vs. controls. *** *P* < 0.0001 versus PMI derivation vs. validation or SMI cases vs. controls. *P* calculated by Student’s t-test for continuous variables and Fisher’s Exact test for categorical values.

Supplemental Table 3. Proteins changed after heparin administration during cardiac catheterization

Protein	*P*
40S ribosomal protein SA	4.93E-03
6Ckine	9.18E-03
a2-Macroglobulin	6.93E-03
ABL2	2.88E-02
Activin A	4.12E-02
Alkaline phosphatase, bone	9.59E-03
Aminoacylase-1	8.59E-03
ANP	1.83E-02
ANGL3	2.93E-02
ANGL4	5.82E-04
Apo A-I	3.13E-03
Apo B	1.08E-06
Apo E	8.87E-07
Apo E2	2.57E-02
Apo E3	5.54E-04
Apo E4	1.97E-04
ARMEL	3.53E-02
ART	5.73E-05
ARTS1	2.51E-02
ASAH2	2.21E-02
ASAHL	2.89E-02
ATP synthase beta chain	2.18E-02
b-NGF	3.92E-02
BAFF	3.50E-02
BCAR3	2.16E-02
BDNF	4.34E-02
bFGF	8.10E-03
BFL1	4.13E-03
BGN	7.54E-04
BMP-14	3.11E-02
BMP-6	3.06E-02
BMP-7	2.65E-02
BMPR2	2.67E-02
BMP-10	1.28E-03
Bone proteoglycan II	1.33E-03
BSP	2.48E-03
C1QBP	2.11E-02

C3a	3.00E-02
C3b	4.97E-02
C4	2.92E-02
C5a	2.67E-03
CAD15	1.26E-04
Calreticulin	1.94E-02
CAMK1D	7.20E-03
Carbonic anhydrase III	4.85E-02
Caspase-2	3.06E-02
Catalase	3.53E-02
Cathepsin B	1.59E-02
CCL28	1.74E-04
CD226	3.49E-02
CD30	6.59E-03
CD36 ANTIGEN	2.03E-02
CFC1	3.14E-02
CK2-A1:B	4.32E-02
CKAP2	1.23E-02
CLC7A	4.70E-04
Coactosin-like protein	4.04E-02
Coagulation Factor IXab	2.43E-02
Coagulation Factor V	8.72E-03
COLEC12	4.17E-03
CTGF	1.72E-02
CTLA-4	1.69E-02
Cystatin M	6.08E-03
CYTD	1.71E-02
Cytochrome c	3.97E-02
Cytochrome P450 3A4	5.19E-04
DAN	1.99E-02
DC-SIGN	1.69E-02
DC-SIGNR	6.69E-03
Discoidin domain receptor 1	4.80E-02
Discoidin domain receptor 2	3.85E-03
DKK3	1.58E-02
DnaJ homolog	9.99E-03
DPP2	2.67E-02
DR6	4.90E-02
DSC3	2.42E-02
Dynactin subunit 2	3.79E-03
EDA	7.95E-04
Elafin	4.15E-02
Elastase	3.03E-02

EMR2	4.64E-02
Endocan	3.66E-03
ENTP5	1.67E-02
Eotaxin	3.33E-02
EP15R	4.63E-03
Ephrin-A4	4.43E-02
Ephrin-B3	2.83E-02
ER	2.21E-02
FAM107B	1.29E-02
Fas ligand, soluble	1.08E-02
FCGR1	4.54E-04
FCN1	4.96E-03
FCN2	6.87E-06
FGF-17	3.03E-03
FGF7	8.36E-04
FGFR-3	2.51E-02
Ficolin-3	6.09E-03
Flt3 ligand	4.61E-02
FST	7.20E-03
G-CSF	4.24E-02
G-CSF-R	3.48E-02
GCKR	1.67E-02
GCP-2	1.59E-02
GFAP	2.93E-02
GFRa-1	6.22E-04
GHC2	3.84E-02
GITR	4.39E-02
Glucagon	1.32E-03
Glypican 3	1.31E-03
GM-CSF	2.72E-02
GOT1	5.12E-03
Granulysin	1.85E-02
GRB2-related adapter protein 2	2.81E-03
HAI-1	1.13E-02
HAT1	2.22E-02
HCG	3.28E-02
HGF	7.55E-04
HPG	3.45E-04
HSP 70	6.02E-05
iC3b	2.72E-02
IDUA	3.06E-02
IF4A3	1.49E-02
IFN-aA	4.43E-02

IL-1 sR9	4.18E-02
IL-12	4.88E-03
IL-13 Ra1	1.22E-02
IL-17B	8.27E-04
IL-17F	2.95E-02
IL-19	2.89E-02
IL-2	2.75E-04
IL-20	3.82E-02
IL-3	1.00E-02
IL-4 sR	3.55E-02
IL-5 Ra	3.20E-02
IL-6 sRa	7.82E-03
IL-7 Ra	3.24E-02
IL-22 Ra1	6.26E-03
ILT-4	2.53E-02
Insulin	2.70E-02
Integrin aVb5	8.72E-04
kallikrein 5	4.45E-03
Karyopherin-a2	1.63E-02
KLRF1	2.90E-02
KYNU	2.94E-02
Lactoferrin	7.89E-03
LAG-3	4.91E-03
LCMT1	1.22E-02
LD78-beta	1.16E-03
Leptin	3.63E-02
LG3BP	2.42E-02
LKHA4	2.17E-02
LRP8	2.34E-02
LSAMP	3.49E-02
LY86	2.46E-03
LY9	4.33E-02
Macrophage scavenger receptor	4.61E-02
MFGM	9.16E-04
Midkine	4.96E-04
MIP-1a	9.09E-03
MIP-3b	2.05E-02
MK11	4.38E-02
MK12	1.61E-02
MMEL2	3.88E-03
MMP-17	2.58E-02
MMP-9	1.41E-02
MO2R1	3.43E-02

Moesin	3.64E-02
MOZ	4.65E-03
MP2K2	1.05E-02
MRCKB	6.89E-03
Myeloperoxidase	3.72E-02
NADPH-P450 Oxidoreductase	2.29E-04
NCK1	1.79E-02
Nectin-like protein 1	4.59E-02
Nectin-like protein 2	1.93E-02
NG36	4.79E-03
NID2	3.13E-02
NOTC2	1.68E-02
NovH	4.69E-02
NRX1B	9.95E-03
NUDC3	3.40E-03
OCAD1	2.69E-03
OX2G	5.38E-03
PBEF	3.44E-02
PCSK7	8.12E-03
PDE11	2.76E-02
PDE4D	4.57E-02
PECAM-1	2.18E-02
PERL	3.30E-02
Peroxiredoxin-5	3.22E-02
PF-4	2.80E-03
PGP9.5	8.25E-03
PGRP-S	2.65E-02
PIK3CA/PIK3R1	2.98E-02
PKC-D	3.34E-02
PKC-G	1.38E-02
PKC-Z	2.55E-02
PIGF	2.45E-03
Properdin	9.97E-03
Protein disulfide-isomerase	2.90E-03
Protease nexin 1	2.15E-03
PSA1	1.45E-02
PSA2	1.87E-02
PSME1	3.60E-02
PTN	9.98E-04
PUR8	2.38E-03
PYY	5.39E-04
RELT	2.52E-02
RET	2.82E-02

RGMB	4.22E-02
RS3	2.22E-02
RS7	1.01E-02
RSPO2	1.92E-02
RUXF	2.95E-04
SAA	1.11E-02
SARP-2	1.15E-02
SEPR	4.97E-02
sFRP-3	1.41E-04
SH21A	2.83E-02
SIRT2	6.14E-04
SLAF5	5.00E-03
SLIK5	1.67E-02
SOD	7.84E-03
SPARCL1	4.58E-02
SPINT2	1.35E-02
Spondin-1	3.24E-03
sRAGE	1.76E-02
sRANKL	2.30E-02
SREC-I	1.38E-02
STRATIFIN	5.80E-04
suPAR	1.97E-02
TARC	7.69E-03
TAU	1.46E-02
TEC	3.82E-02
Testican-2	7.82E-03
TFPI	7.08E-05
TGF-b1	2.86E-02
TGF-b3	6.83E-03
TIG2	2.48E-02
TLR2	1.98E-02
TNFSF18	4.05E-02
TRAIL R1	2.78E-02
Transferrin	1.92E-02
TrkA	1.56E-02
TrkB	1.99E-02
Tropomyosin 1 alpha chain	2.13E-02
Trypsin 2	4.02E-02
TSH	1.21E-02
TWEAK	2.08E-03
TYK2	3.36E-02
UNC5H3	2.61E-03
VEGF	2.34E-03

VEGF121	3.96E-02
WFKN2	3.50E-02

Proteins with *P* < 0.05 (one-way ANOVA repeated measures, n=4) were excluded from PMI analyses, listed in alphabetical order. See **Supplemental Table 1** for full protein names, Entrez Gene symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 4. Proteins changed in the peripheral blood after myocardial injury

Protein	%Change (IQR) 10 min vs. Baseline	%Change (IQR) 1 hr vs. Baseline	%Change (IQR) 24 hr vs. Baseline	*P*
Angiogenin	34.1 (29.3 to 61.8)	24.5 (19.9 to 38.1)	-1.6 (-6.5 to 15.3)	2.63E-06
annexin VI	-46.0 (-75.6 to -32.3)	-34.9 (-76.9 to -30.7)	33.9 (21.5 to 193.1)	3.58E-06
b-ECGF	72.7 (32.3 to 102.4)	103 (82.0 to 158.9)	-3.4 (-7.2 to 6.5)	1.34E-10
C3d	-20.0 (-23.5 to -13.0)	-20.9 (-24.2 to -17.7)	0.2 (-7.2 to 6.3)	7.57E-06
Cadherin-12	101 (34.9 to 168.7)	213 (84.2 to 239.0)	15.4 (-17.6 to 42.5)	1.02E-04
Cardiotrophin-1	-15.3 (-18.3 to -9.5)	-17.3 (-21.3 to -13.4)	1.5 (-5.6 to 4.6)	4.52E-05
CATC	-16.1 (-21.7 to - 10.1)	-20.2 (-22.7 to -16.8)	3.6 (-6.9 to 9.4)	5.59E-09
CDC37	45.0 (2.1 to 69.2)	64.3 (22.6 to 81.9)	7.4 (-6.5 to 18.3)	2.67E-07
CDK8/cyclin C	-13.3 (-17.4 to -10.1)	-12.2 (-17.8 to -7.9)	-5.0 (-7.9 to 1.3)	1.96E-04
Chymase	41.3 (22.3 to 52.6)	43.3 (30.5 to 67.5)	19.1 (-1.7 to 28.9)	1.91E-04
CK-b-8-1	-7.6 (-15.0 to -4.5)	-21.1 (-26.3 to -17.2)	22.4 (13.9 to 49.8)	2.27E-05
CK-MB	144 (46.6 to 305.1)	506 (374.5 to 690.6)	346 (138.7 to 1053.3)	9.60E-08
CK-MM	42.0 (13.7 to 81.4)	233 (146.1 to 287.7)	234 (108.1 to 484.9)	7.28E-07
Cripto	45.5 (14.0 to 66.1)	63.6 (24.4 to 80.7)	4.9 (-7.3 to 16.4)	1.74E-04
Dkk-4	124 (101.9 to 157.4)	56.7 (39.6 to 100.1)	-11.2 (-24.1 to 12.5)	1.29E-15
Dopa decarboxylase	-20.8 (-26.7 to -11.9)	-22.1 (-25.5 to -14.7)	8.8 (-9.5 to 19.4)	2.48E-08
EPO-R	-12.2 (-17.1 to 0.2)	-18.4 (-19.6 to -16.2)	3.1 (-2.5 to 8.4)	5.54E-06
FABP	178 (105.3 to 399.1)	742 (551.8 to 1354.9)	69.3 (5.3 to 235.0)	1.28E-15
FAK1	-13.4 (-17.4 to -9.9)	-16.8 (-21.0 to -11.3)	-3.2 (-8.7 to 4.4)	6.35E-06
FCG2A/B	-9.5 (-12.9 to -3.5)	-9.2 (-15.3 to -4.5)	-7.4 (-11.2 to -1.9)	1.93E-05
FGF-18	134 (83.6 to 173.0)	272 (189.9 to 359.2)	-8.4 (-27.3 to 98.2)	6.31E-08

FGF-8B	29.4 (15.7 to 38.9)	39.1 (26.1 to 56.9)	-0.1 (-10.1 to 8.8)	1.54E-04
Galectin-8	-17.6 (-20.3 to -12.2)	-23.1 (-25.8 to -17.9)	-8.2 (-15.9 to 0.1)	1.77E-04
GAS1	38.3 (18.8 to 51.7)	65.3 (35.7 to 79.5)	10.2 (1.0 to 15.1)	4.73E-05
GREM1	131 (62.2 to 154.3)	176 (101.4 to 230.9)	2.2 (-5.6 to 20.6)	2.78E-07
HDGR2	6.1 (-8.0 to 14.2)	19.9 (8.3 to 27.7)	6.7 (-5.7 to 13.9)	1.79E-05
Histone H2A.z	-61.0 (-73.0 to -48.7)	-38.3 (-52.6 to -23.5)	84.1 (31.4 to 257.0)	5.41E-10
HNRPQ	-7.6 (-16.4 to -2.1)	-13.6 (-19.1 to -0.5)	2.5 (-0.9 to 11.7)	9.21E-05
IL-11	32.6 (15.8 to 48.0)	44.4 (19.2 to 63.4)	5.3 (-1.3 to 14.4)	3.65E-08
IL-12 Rb1	11.5 (-0.3 to 16.0)	13.9 (4.8 to 27.1)	-2.0 (-6.7 to 3.3)	2.17E-04
IL-13	-11.4 (-16.9 to -8.9)	-15.3 (-19.0 to -14.2)	-1.0 (-5.4 to 3.5)	1.14E-04
IL-17D	18.6 (7.6 to 23.9)	27.3 (18.6 to 37.3)	2.2 (-3.3 to 9.6)	7.55E-05
IL-1a	-18.7 (-24.1 to -14.4)	-23.8 (-31.1 to -20.8)	-3.7 (-4.9 to -0.3)	3.12E-05
IL-20 Ra	-12.0 (-16.9 to -8.1)	-17.3 (-22.0 to -11.0)	-4.4 (-12.6 to 6.8)	2.75E-05
IL-34	28.6 (18.9 to 51.0)	24.4 (11.2 to 27.0)	3.1 (-1.3 to 11.2)	8.71E-09
IL-5	31.2 (17.7 to 59.0)	48.9 (30.5 to 71.8)	23.8 (-5.3 to 50.8)	3.98E-05
IL-6	-6.0 (-20.2 to 3.9)	7.0 (-11.6 to 13.2)	113 (35.9 to 173.7)	1.20E-04
JAML1	-13.6 (-16.3 to -8.9)	-17.2 (-21.6 to -15.0)	-3.3 (-8.3 to 3.6)	2.29E-04
KIRR3	-13.6 (-19.7 to 0.5)	-20.3 (-24.9 to -12.5)	-1.8 (-9.2 to 5.4)	1.40E-06
KREM2	11.9 (4.6 to 27.8)	36.1 (24.9 to 39.7)	-1.9 (-10.1 to 6.4)	1.08E-04
LBP	-28.9 (-40.5 to -26.6)	-30.5 (-36.9 to -23.1)	78.5 (59.6 to 92.3)	1.03E-07
LDH-H 1	6.7 (0.8 to 18.8)	8.7 (1.7 to 20.3)	73.4 (52.4 to 144.2)	8.76E-14
LIF sR	196 (126.8 to 247.0)	175 (114.2 to 217.0)	19.2 (-3.4 to 27.7)	2.68E-07
LIN7B	-17.3 (-20.4 to -1.6)	-21.9 (-25.7 to -10.7)	-2.6 (-9.0 to 1.7)	1.58E-04
MDHC	50.3 (14.6 to 67.0)	221 (149.3 to 279.4)	144 (45.4 to 232.4)	1.48E-08
MK13	-17.8 (-22.7 to -13.7)	-25.9 (-28.5 to -17.0)	-2.2 (-15.0 to 5.4)	5.77E-07

MMP-13	141 (102.7 to 237.8)	64.8 (36.1 to 170.4)	3.6 (-3.8 to 17.1)	1.65E-14
MMP-16	50.7 (20.9 to 68.5)	62.2 (27.0 to 75.0)	7.1 (4.2 to 36.9)	7.33E-10
Myoglobin	88.3 (59.5 to 161.1)	152 (105.7 to 231.0)	16.6 (-2.2 to 32.3)	8.53E-11
NACA	49.7 (16.6 to 70.4)	43.3 (26.6 to 65.8)	25.8 (11.2 to 46.6)	4.72E-05
NET4	115 (61.0 to 152.3)	63.3 (20.1 to 82.5)	1.7 (-9.9 to 23.4)	1.11E-04
NKp30	-14.8 (-18.9 to -5.7)	-20.4 (-25.7 to -17.7)	-5.9 (-11.1 to 1.9)	1.16E-04
NMT1	-14.8 (-22.0 to -12.2)	-20.0 (-25.7 to -12.6)	-4.6 (-14.9 to 2.8)	1.93E-04
PDE7A	27.9 (14.4 to 38.7)	30.5 (22.3 to 47.3)	6.0 (2.8 to 17.7)	2.45E-10
PDGF-CC	-20.5 (-22.6 to -9.8)	-22.1 (-25.6 to -16.8)	-5.0 (-9.3 to3.1)	1.98E-04
PDK1	-20.2 (-25.6 to -14.8)	-26.0 (-29.8 to -18.6)	-4.6 (-9.5 to 3.5)	5.15E-05
PLXC1	-9.9 (-15.1 to -8.0)	-11.6 (-16.0 to -6.1)	-9.3 (-12.5 to -3.8)	2.01E-07
PPIB	42.7 (17.8 to 78.4)	61.5 (38.3 to 95.5)	22.9 (10.6 to 59.0)	3.87E-05
PTP-1B	-11.2 (-15.8 to-7.0)	-7.7 (-16.4 to -3.6)	4.9 (-6.1 to 12.9)	6.80E-05
RTN4	-4.2 (-10.8 to 0.9)	-0.2 (-3.7 to 9.1)	-7.2 (-10.1 to -2.3)	2.01E-04
SCGF-alpha	31.4 (19.0 to 55.7)	48.0 (32.4 to 70.2)	13.7 (2.3 to 34.2)	5.89E-07
SDF-1	120 (78.8 to 193.9)	82.8 (45.3 to 119.4)	-6.7 (-17.3 to 3.5)	4.41E-06
Secretin	-16.5 (-18.9 to -12.5)	-17.8 (-21.6 to -12.2)	-1.1 (-8.2 to 1.2)	1.52E-12
SIG14	-7.6 (-12.1 to -3.5)	-11.3 (-14.1 to -4.5)	0.3 (-2.8 to 19.5)	4.44E-06
Somatostatin-28	7.3 (-2.9 to 14.6)	25.8 (7.4 to 36.9)	0.9 (-3.3 to 6.4)	1.99E-04
SPHK2	-14.0 (-16.0 to -10.2)	-16.4 (-19.0 to -14.2)	-4.2 (-9.9 to 0.6)	6.33E-12
ST4S6	43.6 (33.1 to 58.8)	20.7 (12.9 to 34.5)	7.2 (-5.4 to 33.3)	9.94E-07
sTie-2	-16.1 (-20.9 to -10.3)	-21.9 (-27.1 to -17.4)	-3.2 (-9.3 to -0.3)	4.54E-05
TCPTP	-7.3 (-9.8 to -4.8)	-7.4 (-9.8 to -3.8)	-3.8 (-6.0 to 1.6)	7.96E-08
TECK	530 (264.8 to 634.9)	213 (80.5 to 251.4)	-20.1 (-33.3 to 9.7)	5.53E-18
Thrombopoietin	-12.0 (-17.1 to -7.1)	-15.1 (-20.1 to -11.0)	-1.3 (-4.7 to 1.1)	8.73E-06

Receptor				
Transketolase	32.1 (7.7 to 72.9)	85.3 (53.4 to 151.3)	2.7 (-9.8 to 40.1)	4.24E-08
TPI	45.1 (8.1 to 58.2)	89.1 (59.3 to 145.7)	2.4 (-9.1 to 37.5)	4.21E-08
Troponin I	836 (452 to 1241)	2692 (1756 to 5241)	11400 (8435 to 20459)	1.34E-26
TRY3	-14.3 (-20.5 to -11.8)	-18.0 (-20.7 to -15.9)	5.6 (-4.2 to 11.9)	1.13E-04
TWEAKR	-16.1 (-19.9 to 3.1)	-24.2 (-26.1 to -5.9)	-9.3 (-13.4 to 7.9)	1.31E-04
URB	39.1 (23.7 to 51.9)	18.9 (12.1 to 25.8)	-17.6 (-26.4 to -4.5)	1.76E-04
WNT7A	-16.7 (-19.4 to -13.0)	-21.4 (-22.6 to -17.8)	-2.2 (-9.5 to 3.2)	1.15E-04

All proteins in validation cohort with *P* < 2.30 x 10E-04 (one-way ANOVA on log transformed RFU values), listed in alphabetical order. All proteins listed were significant in derivation cohort with *P* < 5.70E-05 (one-way ANOVA on log transformed RFU values). Change values denote median percent change (first and third quartiles). See **Supplemental Table 1** for full protein names, Entrez Gene symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 5. Novel proteins that increased in coronary sinus versus periphery after PMI

Protein	**Fold Change at 10 min (CS vs. Peripheral)**	**Fold Change at 1hr (CS vs. Peripheral)**	***P***
GREM1	1.9	1.4	1.17E-04
IL-11	1.6	1.2	4.96E-04
Cripto	2.3	1.6	1.00E-03
Cadherin-12	2.1	1.8	1.36E-03
GAS1	2.4	1.9	1.85E-03
CDC37	1.6	1.3	3.43E-03
IL-12 Rb1	5.3	2.2	9.46E-03
MMP-16	1.6	1.4	1.77E-02
KREM2	3.7	2.2	2.78E-02

Shown are proteins that increased at 10 min and/or 1 hr in the coronary sinus compared to peripheral blood with $P < 0.05$, listed in ascending *P* (2-way ANOVA on log transformed RFU values). See **Supplemental Table 1** for full protein names, Entrez Gene Symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 6. Clinical characteristics of the FHS participants (n=899)

Age (yrs)	56 ± 10
Female (%)	52
Framingham Risk Score†	3.34 ± 4.03
Total Cholesterol (mg/dl)	207 ± 37
HDL (mg/dl)‡	49 ± 15
Systolic blood pressure (mmHg)	129 ± 20
Diabetes (%)	9
Smoking (%)	20

† n=893, ‡ n=897

Supplemental Table 7. Top FHS protein associations with age (sex-adjusted)

	Age		
Protein	**Estimated β**	**S.E.**	***P***
PTN	0.5036	0.0281	1.02E-61
FSH	0.3719	0.0215	7.05E-58
MMP 12	0.4406	0.0295	3.01E-45
HCG	0.3279	0.0253	2.27E-35
Cathepsin V	-0.3948	0.0309	1.71E-34
ERBB1	-0.3773	0.0295	1.81E-34
URB	0.3750	0.0311	3.51E-31
DKK4	0.3716	0.0308	3.86E-31
FSTL3	0.3568	0.0300	2.16E-30
Luteinizing hormone	0.2672	0.0230	2.94E-29
Chitotriosidase 1	0.3644	0.0315	7.16E-29
DERM	0.3593	0.0314	2.33E-28
b2 Microglobulin	0.3365	0.0310	7.68E-26
a2 Antiplasmin	-0.3365	0.0320	1.78E-24
Cystatin C	0.3149	0.0304	8.93E-24
Carbonic anhydrase III	0.3151	0.0310	4.23E-23
PH	0.3209	0.0318	1.00E-22
CYTD	0.3161	0.0314	1.18E-22
UNC5H3	0.3118	0.0313	2.84E-22
TNF sR I	0.2901	0.0294	7.50E-22
CRDL1	0.3003	0.0306	1.14E-21
CDON	-0.3018	0.0309	1.91E-21

SCF sR	-0.2958	0.0316	6.16E-20
ATS13	-0.2953	0.0316	7.40E-20
ADAMTS 5	0.3004	0.0327	2.54E-19
DKK3	0.2865	0.0317	8.78E-19
Cathepsin H	0.2781	0.0310	1.50E-18
MMP 7	0.2712	0.0302	1.61E-18
sL Selectin	-0.2848	0.0318	2.11E-18
PARC	0.2761	0.0316	1.14E-17
Antithrombin III	-0.2769	0.0319	1.82E-17
Epithelial cell kinase	0.2752	0.0322	5.02E-17
HAI 1	-0.2686	0.0316	7.14E-17
Layilin	0.2763	0.0326	9.47E-17
XEDAR	0.2806	0.0332	1.24E-16
tPA	0.2706	0.0323	1.85E-16
IL 16	0.2716	0.0324	1.98E-16
MP2K2	0.2709	0.0325	3.19E-16
Prothrombin	-0.2613	0.0316	4.61E-16
Spondin 1	0.2674	0.0324	5.74E-16

Shown are the top 40 proteins listed by ascending *P*. See **Supplemental Table 1** for full protein names, Entrez Gene symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 8. Top FHS protein associations with female sex (age-adjusted)

	Female		
Protein	**Estimated β**	**S.E.**	***P***
FSH	1.3625	0.0431	4.13E-148
Luteinizing hormone	1.3865	0.0459	8.36E-139
Leptin	1.2592	0.0538	7.76E-95
HCG	1.1301	0.0506	2.52E-88
PSA	-0.9177	0.0546	2.87E-55
SAP	-0.9763	0.0606	1.57E-51
LSAMP	0.7875	0.0556	3.14E-41
Nidogen	-0.8601	0.0613	1.55E-40
IGFBP 3	0.7983	0.0569	1.62E-40
Albumin	-0.8251	0.0599	2.37E-39
Myoglobin	-0.8159	0.0615	7.79E-37
ALCAM	0.7991	0.0606	2.12E-36
Persephin	-0.7880	0.0605	1.20E-35
IGFBP 6	-0.7319	0.0597	4.96E-32
BGH3	-0.7619	0.0623	6.89E-32
MMP 3	-0.7704	0.0637	2.71E-31
IL 1 R4	-0.7657	0.0637	6.40E-31
SHBG	0.7651	0.0638	8.30E-31
Angiogenin	-0.7344	0.0642	2.29E-28
RELT	-0.7017	0.0624	1.55E-27
GDF 11	-0.6491	0.0597	5.70E-26

WFKN1	-0.6485	0.0615	1.47E-24
Carbonic anhydrase 6	-0.6489	0.0621	3.20E-24
FETUB	0.6637	0.0642	9.60E-24
Troponin I skel fast twitch	-0.6530	0.0635	1.50E-23
Angiotensinogen	0.6549	0.0648	8.58E-23
CK MM	-0.6248	0.0623	1.71E-22
Thyroxine Binding Globulin	0.6378	0.0637	1.81E-22
Galectin 3	0.6146	0.0617	3.17E-22
NPS PLA2	0.6149	0.0623	6.71E-22
NID2	-0.6218	0.0649	9.46E-21
Adiponectin	0.6042	0.0639	2.71E-20
a2 Macroglobulin	0.6077	0.0658	1.76E-19
LEAP 1	-0.6020	0.0652	1.83E-19
IGF I	0.5873	0.0638	2.23E-19
Cystatin M	-0.5559	0.0605	2.56E-19
ROBO2	0.5775	0.0635	6.08E-19
HCC 4	-0.5869	0.0650	1.10E-18
ERBB3	0.5452	0.0605	1.15E-18
Lymphotoxin a1 b2	0.5502	0.0625	6.70E-18

Shown are the top 40 proteins listed by ascending *P*. See **Supplemental Table 1** for full protein names, Entrez Gene symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 9. Top FHS protein associations with total cholesterol (age- and sex-adjusted)

Total Cholesterol

Protein	Estimated β	S.E.	*P*
Apo E4	0.5428	0.0297	1.22E-63
Apo E	0.5265	0.0297	1.45E-60
Apo E3	0.5148	0.0309	1.88E-54
Apo E2	0.4603	0.0323	1.31E-41
Apo B	0.3918	0.0314	4.60E-33
TFPI	0.3837	0.0313	5.32E-32
BMP 1	0.3476	0.0310	1.83E-27
Protein C	0.3143	0.0320	9.44E-22
TSG 6	-0.3152	0.0335	4.02E-20
Cadherin E	0.3066	0.0331	1.61E-19
NRP1	-0.2977	0.0325	3.23E-19
TIMP 2	-0.2932	0.0333	6.49E-18
Prekallikrein	0.2577	0.0317	1.32E-15
ERBB3	0.2430	0.0300	1.72E-15
AMHR2	-0.2634	0.0328	2.80E-15
IgG	-0.2584	0.0328	1.00E-14
Desmoglein 2	-0.2519	0.0323	1.80E-14
Endocan	-0.2585	0.0337	4.21E-14
PCSK9	0.2538	0.0332	5.71E-14
Ficolin 3	0.2521	0.0333	8.68E-14

PAFAH	0.2449	0.0336	6.75E-13
Notch 3	-0.2435	0.0339	1.48E-12
RTN4	-0.2370	0.0331	1.75E-12
SAP	0.2160	0.0303	2.00E-12
PAPP A	-0.2271	0.0329	1.01E-11
TECK	0.2308	0.0335	1.09E-11
Angiostatin	0.2203	0.0327	2.89E-11
Growth hormone receptor	0.2238	0.0337	5.18E-11
Protein S	0.2191	0.0330	5.25E-11
Laminin	0.2100	0.0320	8.71E-11
a1 Antitrypsin	-0.2193	0.0335	9.92E-11
IGFBP 2	-0.2130	0.0328	1.44E-10
Proteinase 3	-0.2119	0.0334	3.60E-10
Coagulation Factor Xa	0.2028	0.0321	4.10E-10
SHBG	-0.2027	0.0321	4.24E-10
resistin	-0.2071	0.0329	4.85E-10
Apo A I	0.2223	0.0356	6.26E-10
PAI 1	0.2134	0.0342	6.45E-10
tPA	0.2010	0.0324	8.83E-10
Aminoacylase 1	0.2046	0.0334	1.42E-09

Shown are the top 40 proteins listed by ascending *P*. See **Supplemental Table 1** for full protein names, Entrez Gene symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 10. Top FHS protein associations with HDL cholesterol (age- and sex-adjusted)

HDL Cholesterol

Protein	Estimated β	S.E.	*P*
Adiponectin	0.4779	0.0298	4.73E-51
SHBG	0.4216	0.0307	3.48E-39
Nogo Receptor	-0.3737	0.0339	1.24E-26
PAI 1	-0.3661	0.0339	1.14E-25
Carbonic anhydrase 6	0.3275	0.0311	1.56E-24
IGFBP 2	0.3317	0.0327	6.21E-23
IGFBP 1	0.3156	0.0329	8.26E-21
Factor H	-0.3040	0.0342	3.65E-18
Antithrombin III	0.2789	0.0325	4.42E-17
CRP	-0.2947	0.0348	9.74E-17
BFL1	0.2859	0.0339	1.32E-16
Leptin	-0.2313	0.0275	1.70E-16
MnSOD	0.2707	0.0327	4.28E-16
MMP 2	0.2784	0.0340	9.00E-16
Sonic Hedgehog	0.2785	0.0343	1.49E-15
tPA	-0.2656	0.0330	2.82E-15
TrkC	0.2682	0.0338	5.87E-15
sCD163	-0.2645	0.0334	7.03E-15
WFKN2	0.2598	0.0330	1.02E-14
CD23	-0.2551	0.0339	1.24E-13

Met	0.2625	0.0351	1.75E-13
AK1A1	-0.2496	0.0337	2.81E-13
Cathepsin S	-0.2507	0.0341	4.50E-13
NCAM 120	0.2470	0.0338	6.31E-13
GFRa 1	-0.2504	0.0348	1.27E-12
ERBB1	0.2193	0.0305	1.32E-12
C1s	-0.2462	0.0345	1.86E-12
PARC	-0.2318	0.0326	2.52E-12
DKK3	0.2314	0.0326	2.69E-12
TSP2	-0.2389	0.0338	3.24E-12
Mammaglobin 2	0.2399	0.0351	1.56E-11
Growth hormone receptor	-0.2346	0.0347	2.59E-11
Cathepsin V	0.2141	0.0320	3.87E-11
IL 1 R AcP	0.2240	0.0335	3.95E-11
Apo E4	-0.2332	0.0349	4.03E-11
Notch 3	0.2337	0.0351	4.75E-11
MDC	-0.2200	0.0331	5.10E-11
C1QBP	0.2284	0.0346	7.02E-11
CCL28	0.2320	0.0358	1.48E-10
TGF b R III	0.2231	0.0345	1.59E-10

Shown are the top 40 proteins listed by ascending *P*. See **Supplemental Table 1** for full protein names, Entrez Gene symbol, Entrez Gene ID and Uniprot ID.

Supplemental Table 11. Top FHS protein associations with SBP (age- and sex-adjusted)

Systolic Blood Pressure

Protein	Estimated β	S.E.	*P*
IGFBP 2	-0.3153	0.0340	1.46E-19
PAI 1	0.3227	0.0354	5.10E-19
Growth hormone receptor	0.3078	0.0351	9.22E-18
Coagulation Factor IXab	0.3004	0.0349	3.51E-17
Coagulation Factor IX	0.3002	0.0351	4.73E-17
tPA	0.2887	0.0338	5.47E-17
SHBG	-0.2833	0.0335	1.06E-16
CRP	0.2822	0.0359	1.08E-14
IGFBP 1	-0.2665	0.0344	2.48E-14
Leptin	0.2187	0.0284	3.72E-14
Aminoacylase 1	0.2603	0.0352	3.02E-13
DKK3	-0.2466	0.0335	4.10E-13
Factor I	0.2539	0.0347	5.82E-13
SAP	0.2322	0.0321	9.80E-13
TFPI	0.2510	0.0349	1.38E-12
Adiponectin	-0.2364	0.0339	6.07E-12
PHI	0.2465	0.0356	8.65E-12
BMP 1	0.2329	0.0342	1.77E-11
Endocan	-0.2427	0.0360	2.69E-11
sE Selectin	0.2258	0.0345	1.02E-10
LG3BP	0.2268	0.0350	1.46E-10

CHL1	-0.2257	0.0355	3.11E-10
LSAMP	-0.1877	0.0297	3.84E-10
Antithrombin III	-0.2138	0.0340	5.09E-10
Renin	-0.2081	0.0334	6.88E-10
NCAM 120	-0.2095	0.0351	3.37E-09
Laminin	0.2018	0.0341	4.56E-09
Factor H	0.2123	0.0360	5.19E-09
Afamin	0.2100	0.0363	1.03E-08
sRAGE	-0.2016	0.0351	1.23E-08
RET	0.1990	0.0346	1.24E-08
Notch 1	-0.1992	0.0348	1.44E-08
IGFBP 4	0.2086	0.0369	2.08E-08
ESAM	-0.1899	0.0336	2.16E-08
bFGF R	-0.1949	0.0355	5.28E-08
HDGR2	0.1937	0.0355	6.39E-08
OMD	-0.1893	0.0349	7.58E-08
SDF 1	-0.1996	0.0369	8.02E-08
TIMP 2	-0.1943	0.0362	1.05E-07

Shown are the top 40 proteins listed by ascending *P*. See **Supplemental Table 1** for full protein names, Entrez Gene symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 12. Top FHS protein associations with diabetes (age- and sex-adjusted)

	Diabetes		
Protein	**Estimated β**	**S.E.**	***P***
Gelsolin	-1.3026	0.1329	1.28E-21
IL 18 Ra	1.0707	0.1358	8.97E-15
Adiponectin	-1.0259	0.1307	1.21E-14
Collectin Kidney 1	0.9927	0.1333	2.24E-13
IGFBP 2	-0.9678	0.1345	1.31E-12
PGCB	-0.9643	0.1344	1.50E-12
LG3BP	0.9228	0.1354	1.71E-11
SHBG	-0.8852	0.1318	3.26E-11
Trypsin	-0.8259	0.1245	5.68E-11
PAI 1	0.9228	0.1403	8.14E-11
Angiopoietin 2	0.8664	0.1339	1.60E-10
C2	0.8504	0.1327	2.38E-10
Galectin 4	0.8415	0.1363	9.94E-10
PERL	0.8067	0.1318	1.40E-09
TGF b R III	-0.8363	0.1387	2.43E-09
Siglec 7	0.8101	0.1372	5.04E-09
Transferrin	-0.7706	0.1337	1.12E-08
TSP2	0.7738	0.1359	1.70E-08
UNC5H4	-0.7650	0.1359	2.44E-08
a1 Antichymotrypsin	-0.7827	0.1399	2.97E-08
tPA	0.7481	0.1341	3.19E-08

Apo B	-0.7648	0.1377	3.69E-08
PLXC1	0.7507	0.1353	3.76E-08
Prothrombin	-0.7237	0.1313	4.66E-08
MIA	-0.7771	0.1423	6.20E-08
Antithrombin III	-0.7130	0.1327	9.97E-08
NCAM 120	-0.7175	0.1368	1.93E-07
Laminin	0.6939	0.1328	2.18E-07
Semaphorin 6A	0.7195	0.1393	2.96E-07
IL 23 R	0.6968	0.1350	2.99E-07
IL 1 R AcP	-0.6935	0.1348	3.27E-07
Renin	0.6666	0.1304	3.92E-07
IGFBP 6	-0.6349	0.1245	4.19E-07
ENPP7	0.7092	0.1397	4.71E-07
OMD	-0.6823	0.1358	6.08E-07
Apo E	0.7003	0.1401	6.99E-07
Nogo Receptorz	0.6929	0.1419	1.23E-06
Aminoacylase 1	0.6766	0.1387	1.27E-06
Cathepsin D	0.6929	0.1428	1.44E-06
RSPO2	0.7015	0.1453	1.61E-06

Shown are the top 40 proteins listed by ascending *P*. See **Supplemental Table 1** for full protein names, Entrez Gene symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 13. Top FHS protein associations with smoking (age- and sex-adjusted)

	Smoking		
Protein	**Estimated β**	**S.E.**	***P***
PIGR	1.1623	0.0769	3.75E-46
MMP 12	0.7673	0.0702	3.70E-26
OMD	-0.8299	0.0778	4.25E-25
SLIK5	-0.7043	0.0783	1.37E-18
SLPI	0.7155	0.0825	1.98E-17
sICAM 5	0.7032	0.0812	2.26E-17
EMR2	-0.6363	0.0794	3.48E-15
WFKN1	-0.5728	0.0757	9.46E-14
Heparin cofactor II	0.5983	0.0835	1.63E-12
NCAM 120	-0.5709	0.0811	3.76E-12
MDC	0.5466	0.0789	8.42E-12
Cathepsin H	0.5234	0.0765	1.47E-11
bFGF R	-0.5580	0.0820	1.82E-11
RGM C	-0.5577	0.0823	2.20E-11
MMP 7	0.5059	0.0747	2.34E-11
Carbonic anhydrase 6	-0.5112	0.0769	5.08E-11
Angiopoietin 2	0.5268	0.0803	8.87E-11
Siglec 7	0.5280	0.0820	1.97E-10
FUT5	0.4993	0.0809	1.02E-09
Laminin	0.4886	0.0792	1.04E-09
MMP 1	0.5141	0.0842	1.52E-09

M CSF R	-0.4886	0.0811	2.48E-09
DERM	-0.4698	0.0781	2.64E-09
Eotaxin	0.4848	0.0807	2.69E-09
P Selectin	0.4817	0.0814	4.66E-09
Haptoglobin Mixed Type	0.4885	0.0836	7.20E-09
Nogo Receptorz	-0.4944	0.0846	7.21E-09
ATS13	-0.4590	0.0787	7.65E-09
LAG 3	-0.4830	0.0829	8.04E-09
Semaphorin 3E	-0.4806	0.0829	9.32E-09
MMP 9	0.4612	0.0824	2.94E-08
Trypsin 2	0.4504	0.0812	3.81E-08
Desmoglein 2	-0.4487	0.0811	4.16E-08
PGCB	-0.4485	0.0815	4.89E-08
Ephrin A5	-0.4529	0.0825	5.19E-08
SEPR	-0.4599	0.0838	5.24E-08
suPAR	0.4517	0.0829	6.53E-08
Cadherin E	0.4591	0.0843	6.64E-08
RGMB	-0.4350	0.0803	7.82E-08
OLR1	0.4595	0.0848	7.84E-08

Shown are the top 40 proteins listed by ascending *P*. See **Supplemental Table 1** for full protein names, Entrez Gene symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 14. Proteins associated with Framingham CHD Risk Score (age- and sex- adjusted)

	FRS		
Protein	**Estimated β**	**S.E.**	***P***
PAI 1	0.4840	0.0327	1.63E-44
SHBG	-0.4315	0.0311	7.18E-40
tPA	0.4360	0.0315	1.10E-39
Adiponectin	-0.4180	0.0313	3.74E-37
TFPI	0.4022	0.0329	6.40E-32
Endocan	-0.4084	0.0336	1.46E-31
BMP 1	0.3826	0.0322	2.91E-30
IGFBP 2	-0.3853	0.0326	4.96E-30
Apo E	0.3900	0.0333	1.65E-29
OMD	-0.3754	0.0325	7.55E-29
Apo E4	0.3852	0.0339	4.73E-28
SAP	0.3467	0.0305	4.84E-28
Gelsolin	-0.3738	0.0332	1.34E-27
TIMP 2	-0.3813	0.0340	2.01E-27
CRP	0.3824	0.0344	5.18E-27
NCAM 120	-0.3665	0.0331	8.94E-27
Notch 3	-0.3678	0.0343	2.61E-25
IGFBP 1	-0.3509	0.0330	6.39E-25
bFGF R	-0.3567	0.0336	7.51E-25
DKK3	-0.3361	0.0321	2.94E-24
Coagulation Factor IX	0.3546	0.0340	4.79E-24

Coagulation Factor IXab	0.3517	0.0339	7.74E-24
Growth hormone receptor	0.3502	0.0341	2.12E-23
Laminin	0.3272	0.0325	1.07E-22
PGCB	-0.3347	0.0333	1.36E-22
MMP 2	-0.3398	0.0339	1.87E-22
Aminoacylase 1	0.3386	0.0339	2.54E-22
Factor I	0.3307	0.0335	7.53E-22
Apo E3	0.3353	0.0352	1.37E-20
LG3BP	0.3167	0.0336	4.04E-20
Siglec 7	0.3072	0.0341	1.28E-18
UNC5H4	-0.3027	0.0336	1.34E-18
Antithrombin III	-0.2945	0.0329	2.02E-18
sE Selectin	0.2984	0.0334	2.44E-18
TSG 6	-0.3123	0.0352	3.72E-18
Factor H	0.3048	0.0348	9.90E-18
IGFBP 4	0.3101	0.0356	1.60E-17
ESAM	-0.2793	0.0322	2.12E-17
Carbonic anhydrase 6	-0.2767	0.0321	3.08E-17
RGMB	-0.2858	0.0332	3.42E-17
WFKN2	-0.2845	0.0332	4.66E-17
TIG2	0.2846	0.0333	5.71E-17
Heparin cofactor II	0.2989	0.0351	6.61E-17
IDS	-0.2895	0.0342	9.73E-17
Galectin 4	0.2876	0.0340	1.20E-16
MMP 12	0.2537	0.0306	3.93E-16

Leptin	0.2303	0.0280	6.46E-16
Notch 1	-0.2765	0.0336	7.00E-16
EphB6	-0.2702	0.0331	1.15E-15
CHL1	-0.2791	0.0345	2.00E-15
C5a	0.2846	0.0353	2.43E-15
SLIK5	-0.2687	0.0335	3.49E-15
TGF b R III	-0.2764	0.0346	4.17E-15
KYNU	0.2666	0.0336	6.09E-15
C1s	0.2738	0.0347	8.47E-15
Ficolin 3	0.2727	0.0347	1.18E-14
Protein S	0.2635	0.0343	3.82E-14
PIGR	0.2712	0.0354	4.66E-14
BSP	-0.2704	0.0360	1.50E-13
RGM C	-0.2571	0.0345	2.09E-13
ROR1	-0.2534	0.0341	2.52E-13
Afamin	0.2629	0.0355	3.06E-13
NRP1	-0.2530	0.0345	4.74E-13
EMAP 2	0.2425	0.0335	9.52E-13
sL Selectin	-0.2385	0.0334	1.86E-12
Calpastatin	-0.2480	0.0350	2.86E-12
Apo E2	0.2571	0.0365	3.66E-12
MIA	-0.2464	0.0355	7.85E-12
IL 1 R AcP	-0.2346	0.0339	9.14E-12
Factor B	0.2414	0.0350	9.54E-12
ENPP7	0.2403	0.0352	1.56E-11

TrkC	-0.2323	0.0345	3.10E-11
TSP2	0.2307	0.0344	3.57E-11
Transferrin	-0.2265	0.0338	3.70E-11
MDC	0.2245	0.0336	4.01E-11
IL 18 Ra	0.2313	0.0349	6.01E-11
WISP 1	0.2288	0.0350	1.04E-10
Cystatin M	-0.2068	0.0318	1.22E-10
SDF 1	-0.2347	0.0361	1.33E-10
sRAGE	-0.2237	0.0345	1.45E-10
AK1A1	0.2168	0.0345	4.88E-10
Cadherin E	0.2235	0.0356	5.60E-10
Cadherin 5	-0.2199	0.0351	5.85E-10
BOC	-0.2146	0.0343	6.02E-10
Periostin	-0.2148	0.0343	6.27E-10
Sonic Hedgehog	-0.2185	0.0350	6.38E-10
NADPH P450 Oxidoreductase	0.2190	0.0351	6.50E-10
contactin 1	-0.2361	0.0378	6.59E-10
NET4	0.2123	0.0347	1.36E-09
AMPM2	0.2175	0.0358	1.83E-09
HDGR2	0.2111	0.0350	2.44E-09
WIF 1	-0.2113	0.0351	2.67E-09
IGFBP 6	-0.1894	0.0316	2.84E-09
6Ckine	0.2046	0.0341	2.86E-09
CYTT	-0.2045	0.0343	3.72E-09

IL 1 sRI	-0.2094	0.0352	3.82E-09
LSAMP	-0.1739	0.0294	4.53E-09
PHI	0.2079	0.0355	6.66E-09
Glypican 3	-0.2021	0.0347	7.73E-09
Met	-0.2099	0.0360	8.06E-09
NRX3B	-0.2025	0.0349	9.46E-09
CYTN	-0.2025	0.0351	1.11E-08
RET	0.1955	0.0343	1.59E-08
Ephrin A5	-0.1987	0.0350	1.81E-08
FCN2	0.2010	0.0354	1.91E-08
a1 Antitrypsin	-0.1998	0.0353	1.98E-08
HSP 90a b	0.2015	0.0356	1.99E-08
MDHC	0.1912	0.0338	2.05E-08
Cathepsin S	0.1973	0.0350	2.37E-08
C3b	0.1990	0.0355	2.85E-08
Nogo Receptorz	0.2017	0.0360	2.89E-08
Rab GDP dissoc inhib b	0.1953	0.0351	3.56E-08
Angiopoietin 2	0.1893	0.0343	4.33E-08
HCC 4	0.1899	0.0345	4.80E-08
GNS	0.1949	0.0357	6.42E-08
MMP 7	0.1735	0.0320	7.41E-08
LYVE1	-0.1906	0.0355	1.03E-07
Cathepsin D	0.1944	0.0363	1.06E-07
ARMEL	-0.1828	0.0341	1.07E-07
RTN4	-0.1871	0.0351	1.25E-07

SLPI	0.1905	0.0359	1.39E-07
a1 Antichymotrypsin	-0.1881	0.0357	1.74E-07
LY86	-0.1816	0.0345	1.76E-07
UNC5H3	-0.1728	0.0331	2.25E-07
HSP 70	0.1832	0.0353	2.52E-07
Apo D	0.1872	0.0361	2.70E-07
CATZ	0.1801	0.0347	2.70E-07
PARC	0.1735	0.0335	2.82E-07
TECK	0.1839	0.0356	2.85E-07
IL 17B R	-0.1791	0.0347	3.14E-07
C2	0.1754	0.0341	3.29E-07
IgG	-0.1801	0.0351	3.49E-07
Coagulation Factor X	0.1723	0.0344	6.45E-07
CNTFR alpha	-0.1736	0.0347	6.87E-07
hnRNP A2 B1	0.1735	0.0351	9.43E-07
sCD163	0.1696	0.0346	1.10E-06
ECM1	-0.1722	0.0351	1.13E-06
C3	0.1750	0.0358	1.20E-06
Soggy 1	0.1737	0.0356	1.28E-06
BMPR1A	-0.1767	0.0363	1.34E-06
GFRa 1	0.1729	0.0359	1.67E-06
AIP	0.1679	0.0352	2.15E-06
TrATPase	0.1653	0.0350	2.63E-06
ERBB1	-0.1483	0.0314	2.69E-06
Coagulation Factor Xa	0.1605	0.0340	2.70E-06

Desmoglein 2	-0.1630	0.0346	2.82E-06
CRDL1	-0.1530	0.0325	2.97E-06
BCMA	-0.1604	0.0341	3.03E-06
AMHR2	-0.1647	0.0351	3.23E-06
IGFBP 5	-0.1567	0.0335	3.31E-06
Contactin 5	-0.1650	0.0354	3.72E-06
Amyloid Precursor Protein	-0.1645	0.0356	4.34E-06
Dkk 4	-0.1517	0.0328	4.34E-06
RSPO2	0.1706	0.0371	4.83E-06
Semaphorin 3E	-0.1626	0.0354	5.07E-06
PDGF Rb	-0.1635	0.0357	5.46E-06

Shown are all proteins with *P* < 5.54E-06, listed by ascending *P*. See **Supplemental Table 1** for full protein names, Entrez Gene Symbol, Entrez Gene ID and UniProt ID.

Supplemental Table 15. Proteins associated with incident CVD (age- and sex-adjusted, *P* < 0.05)

Protein	**HR per s.d.**	**CI**	***P***
tPA	1.65	(1.31- 2.07)	2.13E-05
Cathepsin H	1.47	(1.21-1.79)	1.27E-04
NCAM 120	0.68	(0.55-0.83)	2.46E-04
IDS	0.69	(0.56-0.85)	3.94E-04
C1s	1.42	(1.17-1.73)	5.08E-04
IGFBP 4	1.48	(1.18-1.86)	7.79E-04
Coagulation Factor IX	1.45	(1.15-1.82)	1.38E-03
MMP 7	1.35	(1.11-1.63)	2.07E-03
ERBB1	0.71	(0.56-0.89)	2.82E-03
Angiopoietin 2	1.36	(1.11-1.65)	2.87E-03
NPS PLA2	1.37	(1.11-1.70)	3.17E-03
TNF sR I	1.33	(1.10-1.61)	3.41E-03
Gelsolin	0.76	(0.63-0.91)	3.47E-03
CRP	1.41	(1.12-1.79)	3.60E-03
Transferrin	0.74	(0.60-0.91)	3.81E-03
TSP2	1.32	(1.09-1.60)	4.27E-03
sRAGE	0.73	(0.58-0.90)	4.30E-03
MMP 12	1.38	(1.11-1.73)	4.30E-03
Galectin 4	1.23	(1.07-1.42)	4.39E-03
sE Selectin	1.37	(1.10-1.69)	4.39E-03
TrkC	0.73	(0.59-0.91)	5.07E-03

prostatic binding protein	1.40	(1.10-1.78)	5.89E-03
Cathepsin S	1.28	(1.07-1.53)	6.27E-03
MMP 2	0.76	(0.63-0.93)	6.43E-03
SPARCL1	0.74	(0.60-0.92)	6.46E-03
UNC5H4	0.74	(0.60-0.92)	6.48E-03
Siglec 7	1.31	(1.08-1.59)	7.10E-03
OMD	0.76	(0.62-0.93)	7.41E-03
LRP8	0.69	(0.53-0.91)	8.20E-03
Mn SOD	0.75	(0.61-0.93)	8.81E-03
ERP29	1.32	(1.07-1.63)	9.39E-03
IGFBP 7	1.32	(1.07-1.62)	9.57E-03
MDC	1.26	(1.06-1.50)	9.65E-03
WFKN2	0.76	(0.61-0.94)	1.10E-02
PERL	1.26	(1.05-1.51)	1.11E-02
Ubiquitin 1	1.30	(1.06-1.59)	1.16E-02
C2	1.35	(1.06-1.71)	1.38E-02
AK1A1	1.30	(1.05-1.60)	1.44E-02
IL 18 Ra	1.29	(1.05-1.58)	1.48E-02
KYNU	1.28	(1.05-1.57)	1.50E-02
b2 Microglobulin	1.25	(1.04-1.49)	1.55E-02
TSG 6	0.78	(0.63-0.95)	1.60E-02
PAI 1	1.27	(1.04-1.55)	1.70E-02
LG3BP	1.26	(1.04-1.53)	1.80E-02
Laminin	1.29	(1.04-1.60)	1.84E-02
RGM C	0.78	(0.63-0.96)	1.93E-02
SLIK5	0.76	(0.61-0.96)	2.06E-02

Aminoacylase 1	1.27	(1.04-1.56)	2.10E-02
bFGF R	0.79	(0.65-0.97)	2.11E-02
Peroxiredoxin 1	1.23	(1.03-1.48)	2.21E-02
Rab GDP dissoc inhib b	1.27	(1.03-1.55)	2.27E-02
Met	0.84	(0.72-0.98)	2.28E-02
Factor H	1.28	(1.03-1.59)	2.58E-02
UBE2N	1.25	(1.03-1.53)	2.70E-02
CLM6	1.26	(1.03-1.54)	2.75E-02
Cystatin C	1.28	(1.03-1.59)	2.82E-02
FSTL3	1.28	(1.03-1.59)	2.92E-02
PGCB	0.78	(0.63-0.98)	3.05E-02
Ephrin A4	1.22	(1.02-1.46)	3.11E-02
Myokinase human	1.27	(1.02-1.59)	3.22E-02
TYK2	1.23	(1.02-1.48)	3.38E-02
Antithrombin III	0.80	(0.66-0.98)	3.39E-02
Phosphoglycerate mutase 1	0.79	(0.63-0.98)	3.45E-02
EMAP 2	1.24	(1.02-1.51)	3.52E-02
Myoglobin	0.76	(0.59-0.99)	3.79E-02
eIF 5	1.18	(1.01-1.39)	3.87E-02
TNF sR II	1.23	(1.01-1.49)	4.08E-02
Prothrombin	0.80	(0.65-0.99)	4.16E-02
AREG	1.23	(1.01-1.50)	4.26E-02
Kallikrein 11	0.78	(0.61-0.99)	4.27E-02
TIMD3	1.23	(1.01-1.51)	4.31E-02
Cadherin E	1.23	(1.01-1.51)	4.34E-02

CK2 A1 B	1.23	(1.00-1.50)	4.74E-02
TIMP 2	0.81	(0.65-1.00)	4.78E-02
TIG2	1.19	(1.00-1.41)	4.94E-02
Ubiquitin	1.20	(1.00-1.43)	4.96E-02
CTGF	1.22	(1.00-1.49)	4.97E-02

Shown are proteins with $P < 0.05$, listed by ascending *P*. Values are hazard ratios per standard deviation (95% confidence intervals) for incident CVD from proportional hazards regression models. See Supplemental Table 1 for full protein names, Entrez Gene symbol/ID and UniProt ID.

Supplemental Table 16. Peptides from the 29 target proteins detected by LC-MS/MS after aptamer affinity enrichment

No	Uniprot	Protein Name	Sequence
1	Q9UQ80	Proliferation-associated protein 2G4	KADVIK
2	Q9UQ80	Proliferation-associated protein 2G4	DAGQRTTIYK
3	Q9UQ80	Proliferation-associated protein 2G4	YKMGGDIANR
4	Q9UQ80	Proliferation-associated protein 2G4	EGDLVK
5	Q9UQ80	Proliferation-associated protein 2G4	MGGDIANRVLR
6	Q9UQ80	Proliferation-associated protein 2G4	AFFSEVERR
7	Q9UQ80	Proliferation-associated protein 2G4	TSRAFFSEVER
8	Q9UQ80	Proliferation-associated protein 2G4	KGIAFPTSISVNNCVCHFSPLKSDQDYILK
9	Q9UQ80	Proliferation-associated protein 2G4	SDQDYILK
10	Q9UQ80	Proliferation-associated protein 2G4	RFDAMPFTLR
11	Q9UQ80	Proliferation-associated protein 2G4	MGGDIANR
12	Q9UQ80	Proliferation-associated protein 2G4	AFFSEVER
13	Q9UQ80	Proliferation-associated protein 2G4	ALLQSSASRK
14	Q9UQ80	Proliferation-associated protein 2G4	FDAMPFTLR
15	Q9UQ80	Proliferation-associated protein 2G4	GDAMIMEETGK
16	Q9UQ80	Proliferation-associated protein 2G4	EGEFVAQFK
17	Q9UQ80	Proliferation-associated protein 2G4	ALLQSSASR
18	Q9UQ80	Proliferation-associated protein 2G4	FTVLLMPNGPMR
19	Q9UQ80	Proliferation-associated protein 2G4	DPSKQYGLK
20	Q9UQ80	Proliferation-associated protein 2G4	TIIQNPTDQQKK
21	Q9UQ80	Proliferation-associated protein 2G4	SEMEVQDAELK
22	Q9UQ80	Proliferation-associated protein 2G4	TIIQNPTDQQK
23	Q9UQ80	Proliferation-associated protein 2G4	MGVVECAK
24	Q9UQ80	Proliferation-associated protein 2G4	HELLQPFNVLYEKEGEFVAQFK
25	Q9UQ80	Proliferation-associated protein 2G4	VAHSFNCTPIEGMLSHQLK
26	Q9UQ80	Proliferation-associated protein 2G4	GIAFPTSISVNNCVCHFSPLKSDQDYILK
27	Q9UQ80	Proliferation-associated protein 2G4	ITSGPFEPDLYK
28	Q9UQ80	Proliferation-associated protein 2G4	AAHLCAEAALR
29	Q9UQ80	Proliferation-associated protein 2G4	GIAFPTSISVNNCVCHFSPLK
30	Q9UQ80	Proliferation-associated protein 2G4	LVKPGNQNTQVTEAWNK
31	Q9UQ80	Proliferation-associated protein 2G4	SLVEASSSGVSVLSLCEK
32	Q9UQ80	Proliferation-associated protein 2G4	MSGEDEQQEQTIAEDLVVTK
33	Q9UQ80	Proliferation-associated protein 2G4	HELLQPFNVLYEK
34	Q9UQ80	Proliferation-associated protein 2G4	AEFEVHEVYAVDVLVSSGEGK
35	Q9UQ80	Proliferation-associated protein 2G4	ITSGPFEPDLYKSEMEVQDAELK
36	Q9UQ80	Proliferation-associated protein 2G4	KGIAFPTSISVNNCVCHFSPLK
37	Q9UQ80	Proliferation-associated protein 2G4	IDLGVHVDGFIANVAHTFVVDVAQGTQVTGR
38	P00533	Epidermal growth factor receptor	TCPAGVMGENNTLVWK
39	P00533	Epidermal growth factor receptor	NYDLSFLK
40	P00533	Epidermal growth factor receptor	TGLKELPMR
41	P00533	Epidermal growth factor receptor	LFGTSGQK
42	P00533	Epidermal growth factor receptor	KVCNGIGIGEFK
43	P00533	Epidermal growth factor receptor	ESDCLVCR
44	P00533	Epidermal growth factor receptor	KLFGTSGQK
45	P00533	Epidermal growth factor receptor	GKSPSDCCHNQCAAGCTGPR
46	P00533	Epidermal growth factor receptor	GDSFTHTPPLDPQELDILKTVK
47	P00533	Epidermal growth factor receptor	YSFGATCVK

48	P00533	Epidermal growth factor receptor	EISDGDVIISGNK
49	P00533	Epidermal growth factor receptor	SLKEISDGDVIISGNK
50	P00533	Epidermal growth factor receptor	VCNGIGIGEFK
51	P00533	Epidermal growth factor receptor	NLQEILHGAVR
52	P00533	Epidermal growth factor receptor	NLCYANTINWK
53	P00533	Epidermal growth factor receptor	ELPMRNLQEILHGAVR
54	P00533	Epidermal growth factor receptor	IPLENLQIIR
55	P00533	Epidermal growth factor receptor	GNMYYENSYALAVLSNYDANK
56	P00533	Epidermal growth factor receptor	IICAQQCSGR
57	P00533	Epidermal growth factor receptor	ACGADSYEMEEDGVR
58	P00533	Epidermal growth factor receptor	FSNNPALCNVESIQWR
59	P00533	Epidermal growth factor receptor	NYVVTDHGSCVR
60	P00533	Epidermal growth factor receptor	GDSFTHTPPLDPQELDILK
61	P00533	Epidermal growth factor receptor	ACGADSYEMEEDGVRK
62	P00533	Epidermal growth factor receptor	TDLHAFENLEIIR
63	P00533	Epidermal growth factor receptor	SPSDCCHNQCAAGCTGPR
64	P00533	Epidermal growth factor receptor	DTCPPLMLYNPTTYQMDVNPEGK
65	P00533	Epidermal growth factor receptor	LTQLGTFEDHFLSLQR
66	P00533	Epidermal growth factor receptor	CDPSCPNGSCWGAGEENCQK
67	P00533	Epidermal growth factor receptor	TIQEVAGYVLIALNTVER
68	P00533	Epidermal growth factor receptor	GPDNCIQCAHYIDGPHCVK
69	P00533	Epidermal growth factor receptor	ATGQVCHALCSPEGCWGPEPR
70	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	YEEEIK
71	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	LATALQKLEEAEK
72	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	KMQMLK
73	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	LVIIESDLER
74	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	GTEDELDKYSEALKDAQEK
75	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	AEERAELSEGQVR
76	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	HIAEDADRK
77	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	IMDQTLK
78	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	AEFAER
79	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	HIAEDADR
80	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	QLEEQLR
81	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	AELSEGQVR
82	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	ATDAEADVASLNRR
83	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	EDRYEEEIK
84	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	AAEDRSKQLEDELVSLQK
85	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	LDKENALDR
86	P09493-4	Isoform 4 of Tropomyosin alpha-1	KATDAEADVASLNRR

		chain	
87	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	ALMAAEDK
88	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	AQKDEEKMEIQEIQLK
89	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	LATALQK
90	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	IQLVEEELDRAQER
91	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	LKGTEDELDKYSEALK
92	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	EAETRAEFAER
93	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	YSEALKDAQEK
94	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	ALMAAEDKYSQKEDR
95	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	QLEDELVSLQK
96	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	IQLVEEELDR
97	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	ALMAAEDKYSQK
98	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	KATDAEADVASLNR
99	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	AISEELDHALNDMTSI
100	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	KLVIIESDLER
101	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	ATDAEADVASLNR
102	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	LEKSIDDLEDELYAQK
103	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	DAQEKLELAEK
104	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	SIDDLEDELYAQK
105	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	SKQLEDELVSLQK
106	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	YSQKEDRYEEEIK
107	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	RIQLVEEELDR
108	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	GTEDELDKYSEALK
109	P09493-4	Isoform 4 of Tropomyosin alpha-1 chain	LEEAEKAADESER
110	P67936	Tropomyosin alpha-4 chain	YSEKEDKYEEEIK
111	P67936	Tropomyosin alpha-4 chain	EKAEGDVAALNR
112	P67936	Tropomyosin alpha-4 chain	IQALQQQADEAEDR
113	P06753-6	Isoform 6 of Tropomyosin alpha-3 chain	IQVLQQQADDAEER
114	Q5TCU8	Tropomyosin beta chain	LDKENAIDR
115	Q5TCU8	Tropomyosin beta chain	KLVILEGELER
116	P14618	Pyruvate kinase PKM	SGMNVAR
117	P14618	Pyruvate kinase PKM	VNFAMNVGK

118	P14618	Pyruvate kinase PKM	VFLAQK
119	P14618	Pyruvate kinase PKM	DIQDLK
120	P14618	Pyruvate kinase PKM	MQHLIAR
121	P14618	Pyruvate kinase PKM	SVETLK
122	P14618	Pyruvate kinase PKM	GSGTAEVELK
123	P14618	Pyruvate kinase PKM	GIFPVLCK
124	P14618	Pyruvate kinase PKM	GDYPLEAVR
125	P14618	Pyruvate kinase PKM	GVNLPGAAVDLPAVSEKDIQDLK
126	P14618	Pyruvate kinase PKM	LDIDSPPITAR
127	P14618	Pyruvate kinase PKM	APIIAVTR
128	P14618	Pyruvate kinase PKM	IYVDDGLISLQVK
129	P14618	Pyruvate kinase PKM	CDENILWLDYK
130	P14618	Pyruvate kinase PKM	ITLDNAYMEK
131	P14618	Pyruvate kinase PKM	GSGTAEVELKK
132	P14618	Pyruvate kinase PKM	CCSGAIIVLTK
133	P14618	Pyruvate kinase PKM	KGVNLPGAAVDLPAVSEK
134	P14618	Pyruvate kinase PKM	KASDVHEVR
135	P14618	Pyruvate kinase PKM	NTGIICTIGPASR
136	P14618	Pyruvate kinase PKM	GDLGIEIPAEK
137	P14618	Pyruvate kinase PKM	KGVNLPGAAVDLPAVSEKDIQDLK
138	P14618	Pyruvate kinase PKM	GVNLPGAAVDLPAVSEK
139	P14618	Pyruvate kinase PKM	TATESFASDPILYRPVAVALDTK
140	P14618	Pyruvate kinase PKM	LAPITSDPTEATAVGAVEASFK
141	P14618	Pyruvate kinase PKM	LNFSHGTHEYHAETIK
142	P14618	Pyruvate kinase PKM	KGDVVIVLTGWRPGSGFTNTMR
143	P14618	Pyruvate kinase PKM	GADFLVTEVENGGSLGSK
144	P14618	Pyruvate kinase PKM	AEGSDVANAVLDGADCIMLSGETAK
145	P14618	Pyruvate kinase PKM	FGVEQDVDMVFASFIR
146	P14618	Pyruvate kinase PKM	AGKPVICATQMLESMIK
147	P14618	Pyruvate kinase PKM	EAEAAIYHLQLFEELRR
148	P14618	Pyruvate kinase PKM	GIFPVLCKDPVQEAWAEDVDLR
149	P14618	Pyruvate kinase PKM	RFDEILEASDGIMVAR
150	P14618	Pyruvate kinase PKM	EAEAAIYHLQLFEELR
151	P06576	ATP synthase subunit beta, mitochondrial	ILQDYK
152	P06576	ATP synthase subunit beta, mitochondrial	LVPLKETIK
153	P06576	ATP synthase subunit beta, mitochondrial	TIAMDGTEGLVR
154	P06576	ATP synthase subunit beta, mitochondrial	VLDSGAPIK
155	P06576	ATP synthase subunit beta, mitochondrial	IMNVIGEPIDER
156	P06576	ATP synthase subunit beta, mitochondrial	VVDLLAPYAK
157	P06576	ATP synthase subunit beta, mitochondrial	IGLFGGAGVGK
158	P06576	ATP synthase subunit beta, mitochondrial	AHGGYSVFAGVGER
159	P06576	ATP synthase subunit beta, mitochondrial	TVLIMELINNVAK
160	P06576	ATP synthase subunit beta, mitochondrial	FLSQPFQVAEVFTGHMGK
161	P06576	ATP synthase subunit beta,	VALVYGQMNEPPGAR

		mitochondrial	
162	P06576	ATP synthase subunit beta, mitochondrial	IPVGPETLGR
163	P06576	ATP synthase subunit beta, mitochondrial	VALTGLTVAEYFR
164	P06576	ATP synthase subunit beta, mitochondrial	FTQAGSEVSALLGR
165	P06576	ATP synthase subunit beta, mitochondrial	AIAELGIYPAVDPLDSTSR
166	P06576	ATP synthase subunit beta, mitochondrial	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR
167	P06576	ATP synthase subunit beta, mitochondrial	TREGNDLYHEMIESGVINLK
168	P06576	ATP synthase subunit beta, mitochondrial	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK
169	P06576	ATP synthase subunit beta, mitochondrial	IPSAVGYQPTLATDMGTMQER
170	P06576	ATP synthase subunit beta, mitochondrial	EGNDLYHEMIESGVINLK
171	P06576	ATP synthase subunit beta, mitochondrial	DQEGQDVLLFIDNIFR
172	P06576	ATP synthase subunit beta, mitochondrial	IMDPNIVGSEHYDVAR
173	P06576	ATP synthase subunit beta, mitochondrial	QFAPIHAEAPEFMEMSVEQEILVTGIK
174	P06576	ATP synthase subunit beta, mitochondrial	VLDSGAPIKIPVGPETLGR
175	P06576	ATP synthase subunit beta, mitochondrial	LVLEVAQHLGESTVR
176	P06576	ATP synthase subunit beta, mitochondrial	SLQDIIAILGMDELSEEDKLTVSR
177	P06576	ATP synthase subunit beta, mitochondrial	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR
178	O15530	3-phosphoinositide-dependent protein kinase 1	VLSPESK
179	O15530	3-phosphoinositide-dependent protein kinase 1	ELATSREYAIK
180	O15530	3-phosphoinositide-dependent protein kinase 1	ENKVPYVTR
181	O15530	3-phosphoinositide-dependent protein kinase 1	LEYDFPEK
182	O15530	3-phosphoinositide-dependent protein kinase 1	TTSQLYDAVPIQSSVVLCSCPSPSMVR
183	O15530	3-phosphoinositide-dependent protein kinase 1	LDHPFFVK
184	O15530	3-phosphoinositide-dependent protein kinase 1	VPYVTR
185	O15530	3-phosphoinositide-dependent protein kinase 1	VLKGEIPWSQELRPEAK
186	O15530	3-phosphoinositide-dependent protein kinase 1	VLSPESKQAR
187	O15530	3-phosphoinositide-dependent protein kinase 1	HIIKENKVPYVTR
188	O15530	3-phosphoinositide-dependent protein kinase 1	QAGGNPWHQFVENNLILK
189	O15530	3-phosphoinositide-dependent	LLVLDATK

		protein kinase 1	
190	O15530	3-phosphoinositide-dependent protein kinase 1	TFFVHTPNR
191	O15530	3-phosphoinositide-dependent protein kinase 1	IIKLEYDFPEK
192	O15530	3-phosphoinositide-dependent protein kinase 1	LGCEEMEGYGPLK
193	O15530	3-phosphoinositide-dependent protein kinase 1	TYYLMDPSGNAHK
194	O15530	3-phosphoinositide-dependent protein kinase 1	QLLLTEGPHLYYVDPVNK
195	O15530	3-phosphoinositide-dependent protein kinase 1	LYFGLSYAK
196	O15530	3-phosphoinositide-dependent protein kinase 1	KKRPEDFK
197	O15530	3-phosphoinositide-dependent protein kinase 1	LLVLDATKR
198	O15530	3-phosphoinositide-dependent protein kinase 1	IGSFDETCTR
199	O15530	3-phosphoinositide-dependent protein kinase 1	DVMSRLDHPFFVK
200	O15530	3-phosphoinositide-dependent protein kinase 1	QGPAMDGTAAEPRPGAGSLQHAQPPPQPR
201	O15530	3-phosphoinositide-dependent protein kinase 1	YQSHPDAAVQ
202	O15530	3-phosphoinositide-dependent protein kinase 1	TQTESSTPPGIPGGSR
203	O15530	3-phosphoinositide-dependent protein kinase 1	RQLLLTEGPHLYYVDPVNK
204	O15530	3-phosphoinositide-dependent protein kinase 1	GEIPWSQELRPEAK
205	O15530	3-phosphoinositide-dependent protein kinase 1	FYTAEIVSALEYLHGK
206	O15530	3-phosphoinositide-dependent protein kinase 1	ILGEGSFSTVVLAR
207	O15530	3-phosphoinositide-dependent protein kinase 1	DLKPENILLNEDMHIQITDFGTAK
208	O15530	3-phosphoinositide-dependent protein kinase 1	AHPFFESVTWENLHQQTPPK
209	O15530	3-phosphoinositide-dependent protein kinase 1	SGSNIEQYIHDLDSNSFELDLQFSEDEKR
210	P04083	Annexin A1	AAYLQETGKPLDETLK
211	P04083	Annexin A1	SYPQLR
212	P04083	Annexin A1	TPAQFDADELR
213	P04083	Annexin A1	NALLSLAK
214	P04083	Annexin A1	ALYEAGER
215	P04083	Annexin A1	MYGISLCQAILDETK
216	P04083	Annexin A1	DITSDTSGDFR
217	P04083	Annexin A1	CLTAIVK
218	P04083	Annexin A1	SEIDMNDIK
219	P04083	Annexin A1	CATSKPAFFAEK
220	P04083	Annexin A1	ILVALCGGN
221	P04083	Annexin A1	KGTDVNVFNTILTTR
222	P04083	Annexin A1	GLGTDEDTLIEILASRTNK
223	P04083	Annexin A1	GTDVNVFNTILTTR

224	P04083	Annexin A1	DITSDTSGDFRNALLSLAK
225	P04083	Annexin A1	QAWFIENEEQEYVQTVK
226	P04083	Annexin A1	GVDEATIIDILTK
227	P04083	Annexin A1	GGPGSAVSPYPTFNPSSDVAALHK
228	P04083	Annexin A1	GDRSEDFGVNEDLADSDAR
229	P04083	Annexin A1	GLGTDEDTLIEILASR
230	P04083	Annexin A1	AAYLQETGKPLDETLKK
231	P04083	Annexin A1	GVDEATIIDILTKR
232	P04083	Annexin A1	SEDFGVNEDLADSDAR
233	P04083	Annexin A1	KALTGHLEEVVLALLK
234	P04083	Annexin A1	ALTGHLEEVVLALLK
235	P48357	Leptin receptor	NLNEDGEIK
236	P48357	Leptin receptor	ISWSSPPLVPFPLQYQVK
237	P48357	Leptin receptor	KYYIHDHFIPIEK
238	P48357	Leptin receptor	YYIHDHFIPIEK
239	P48357	Leptin receptor	WSTSTIQSLAESTLQLR
240	P48357	Leptin receptor	LFICYVESLFK
241	P48357	Leptin receptor	GPEFWR
242	P48357	Leptin receptor	TTFHCCFR
243	P48357	Leptin receptor	IINSFTQDDIEK
244	P48357	Leptin receptor	EIVWWMNLAEK
245	P48357	Leptin receptor	AEITINIGLLK
246	P48357	Leptin receptor	MYEVYDAK
247	P48357	Leptin receptor	VFTTQDVIYFPPK
248	P48357	Leptin receptor	SSLYCSDIPSIHPISEPK
249	P48357	Leptin receptor	ISWEKPVFPENNLQFQIR
250	P48357	Leptin receptor	YQFSLYPIFMEGVGKPK
251	P48357	Leptin receptor	SVSLPVPDLCAVYAVQVR
252	P48357	Leptin receptor	RLDGPGIWSDWSTPR
253	P48357	Leptin receptor	EADKIVSATSLLVDSILPGSSYEVQVR
254	P48357	Leptin receptor	IPQSQYDVVSDHVSK
255	P48357	Leptin receptor	FTYDAVYCCNEHECHHR
256	P48357	Leptin receptor	VHLLYVLPEVLEDSPLVPQK
257	P21860	Receptor tyrosine-protein kinase erbB-3	GTQVYDGK
258	P21860	Receptor tyrosine-protein kinase erbB-3	DAEIVVK
259	P21860	Receptor tyrosine-protein kinase erbB-3	CPQPLVYNK
260	P21860	Receptor tyrosine-protein kinase erbB-3	HFNDSGACVPR
261	P21860	Receptor tyrosine-protein kinase erbB-3	IYISANR
262	P21860	Receptor tyrosine-protein kinase erbB-3	DRDAEIVVK
263	P21860	Receptor tyrosine-protein kinase erbB-3	ACPPDKMEVDK
264	P21860	Receptor tyrosine-protein kinase erbB-3	GFSLLIMK
265	P21860	Receptor tyrosine-protein kinase erbB-3	IPALDPEK
266	P21860	Receptor tyrosine-protein kinase erbB-3	LTFQLEPNPHTK
267	P21860	Receptor tyrosine-protein kinase	LTQLTEILSGGVYIEK

		erbB-3	
268	P21860	Receptor tyrosine-protein kinase erbB-3	SCPPCHEVCK
269	P21860	Receptor tyrosine-protein kinase erbB-3	LCHMDTIDWR
270	P21860	Receptor tyrosine-protein kinase erbB-3	NDKLCHMDTIDWR
271	P21860	Receptor tyrosine-protein kinase erbB-3	CWGPGSEDCQTLTK
272	P21860	Receptor tyrosine-protein kinase erbB-3	DGPHCVSSCPHGVLGAK
273	P21860	Receptor tyrosine-protein kinase erbB-3	ILGNLDFLITGLNGDPWHK
274	P21860	Receptor tyrosine-protein kinase erbB-3	GPELQDCLGQTLVLIGK
275	P21860	Receptor tyrosine-protein kinase erbB-3	YQYGGVCVASCPHNFVVDQTSCVR
276	P21860	Receptor tyrosine-protein kinase erbB-3	GGVCVTHCNFLNGEPR
277	P21860	Receptor tyrosine-protein kinase erbB-3	IPALDPEKLNVFR
278	P04626	Receptor tyrosine-protein kinase erbB-2	VLQGLPR
279	P04626	Receptor tyrosine-protein kinase erbB-2	GQECVEECR
280	P04626	Receptor tyrosine-protein kinase erbB-2	SLTEILK
281	P04626	Receptor tyrosine-protein kinase erbB-2	GPLPTDCCHEQCAAGCTGPK
282	P04626	Receptor tyrosine-protein kinase erbB-2	CWGESSEDCQSLTR
283	P04626	Receptor tyrosine-protein kinase erbB-2	GGVLIQR
284	P04626	Receptor tyrosine-protein kinase erbB-2	GHCWGPGPTQCVNCSQFLR
285	P04626	Receptor tyrosine-protein kinase erbB-2	VCYGLGMEHLR
286	P04626	Receptor tyrosine-protein kinase erbB-2	NNQLALTLIDTNR
287	P04626	Receptor tyrosine-protein kinase erbB-2	ACHPCSPMCK
288	P04626	Receptor tyrosine-protein kinase erbB-2	AVTSANIQEFAGCKK
289	P04626	Receptor tyrosine-protein kinase erbB-2	NPHQALLHTANRPEDECVGEGLACHQLCAR
290	P04626	Receptor tyrosine-protein kinase erbB-2	AVTSANIQEFAGCK
291	P04626	Receptor tyrosine-protein kinase erbB-2	ELGSGLALIHHNTHLCFVHTVPWDQLFR
292	P04626	Receptor tyrosine-protein kinase erbB-2	NPQLCYQDTILWK
293	P04626	Receptor tyrosine-protein kinase erbB-2	LRLPASPETHLDMLR
294	P04626	Receptor tyrosine-protein kinase erbB-2	CPSGVKPDLSYMPIWK
295	P04626	Receptor tyrosine-protein kinase	LPASPETHLDMLR

		erbB-2	
296	P04626	Receptor tyrosine-protein kinase erbB-2	YTFGASCVTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQR
297	P04626	Receptor tyrosine-protein kinase erbB-2	CKGPLPTDCCHEQCAAGCTGPK
298	Q05513	Protein kinase C zeta type	GFLNKDPK
299	Q05513	Protein kinase C zeta type	HDSIKDDSEDLKPVIDGMDGIK
300	Q05513	Protein kinase C zeta type	DEGLIIHVFPSTPEQPGLPCPGEDK
301	Q05513	Protein kinase C zeta type	SIDWDLLEKK
302	Q05513	Protein kinase C zeta type	SHAFFR
303	Q05513	Protein kinase C zeta type	LTDYGMCK
304	Q05513	Protein kinase C zeta type	ANGHLFQAK
305	Q05513	Protein kinase C zeta type	LHQQHPLTLK
306	Q05513	Protein kinase C zeta type	CHGLVPLTCR
307	Q05513	Protein kinase C zeta type	WVDSEGDPCTVSSQMELEEAFR
308	Q05513	Protein kinase C zeta type	DLKLDNVLLDADGHIK
309	Q05513	Protein kinase C zeta type	LDNVLLDADGHIK
310	Q05513	Protein kinase C zeta type	LGCRPQTGFSDIK
311	Q05513	Protein kinase C zeta type	ISQGLGLQDFDLIR
312	Q05513	Protein kinase C zeta type	SIDWDLLEK
313	Q05513	Protein kinase C zeta type	ELVHDDEDIDWVQTEK
314	Q05513	Protein kinase C zeta type	KHDSIKDDSEDLKPVIDGMDGIK
315	Q05513	Protein kinase C zeta type	HVFEQASSNPFLVGLHSCFQTTSR
316	Q05513	Protein kinase C zeta type	AHYGGDIFITSVDAATTFEELCEEVR
317	Q05513	Protein kinase C zeta type	SPFDIITDNPDMNTEDYLFQVILEKPIR
318	P38919	Eukaryotic initiation factor 4A-III	ELAVQIQK
319	P38919	Eukaryotic initiation factor 4A-III	DELTLEGIK
320	P38919	Eukaryotic initiation factor 4A-III	FMTDPIR
321	P38919	Eukaryotic initiation factor 4A-III	QFFVAVER
322	P38919	Eukaryotic initiation factor 4A-III	RKVDWLTEK
323	P38919	Eukaryotic initiation factor 4A-III	KVDWLTEK
324	P38919	Eukaryotic initiation factor 4A-III	ELYIHR
325	P38919	Eukaryotic initiation factor 4A-III	KGVAINFVKNDDIR
326	P38919	Eukaryotic initiation factor 4A-III	ETQALILAPTR
327	P38919	Eukaryotic initiation factor 4A-III	VDWLTEK
328	P38919	Eukaryotic initiation factor 4A-III	VLISTDVWAR
329	P38919	Eukaryotic initiation factor 4A-III	YLPPATQVVLISATLPHEILEMTNK
330	P38919	Eukaryotic initiation factor 4A-III	KGVAINFVK
331	P38919	Eukaryotic initiation factor 4A-III	LDYGQHVVAGTPGR
332	P38919	Eukaryotic initiation factor 4A-III	LLKEEDMTK
333	P38919	Eukaryotic initiation factor 4A-III	GLDVPQVSLIINYDLPNNR
334	P38919	Eukaryotic initiation factor 4A-III	MLVLDEADEMLNK
335	P38919	Eukaryotic initiation factor 4A-III	EANFTVSSMHGDMPQK
336	P38919	Eukaryotic initiation factor 4A-III	GIYAYGFEKPSAIQQR
337	P38919	Eukaryotic initiation factor 4A-III	GRDVIAQSQSGTGK
338	P38919	Eukaryotic initiation factor 4A-III	KLDYGQHVVAGTPGR
339	P27361	Mitogen-activated protein kinase 3	EIQILLR
340	P27361	Mitogen-activated protein kinase 3	YIHSANVLHR
341	P27361	Mitogen-activated protein kinase 3	ALDLLDR
342	P27361	Mitogen-activated protein kinase 3	ICDFGLAR
343	P27361	Mitogen-activated protein kinase 3	NYLQSLPSK
344	P27361	Mitogen-activated protein kinase 3	MLTFNPNKR
345	P27361	Mitogen-activated protein kinase 3	GQPFDVGPR
346	P27361	Mitogen-activated protein kinase 3	FQPGVLEAP

347	P27361	Mitogen-activated protein kinase 3	RTEGVGPGVPGEVEMVK
348	P27361	Mitogen-activated protein kinase 3	APEIMLNSK
349	P27361	Mitogen-activated protein kinase 3	ELIFQETAR
350	P27361	Mitogen-activated protein kinase 3	LKELIFQETAR
351	P27361	Mitogen-activated protein kinase 3	DLKPSNLLINTTCDLK
352	P27361	Mitogen-activated protein kinase 3	TEGVGPGVPGEVEMVK
353	P27361	Mitogen-activated protein kinase 3	SQQLSNDHICYFLYQILR
354	P27361	Mitogen-activated protein kinase 3	ISPFEHQTYCQR
355	P27361	Mitogen-activated protein kinase 3	FRHENVIGIR
356	P27361	Mitogen-activated protein kinase 3	YTQLQYIGEGAYGMVSSAYDHVR
357	P27361	Mitogen-activated protein kinase 3	IADPEHDHTGFLTEYVATR
358	P28482	Mitogen-activated protein kinase 1	LKELIFEETAR
359	P28482	Mitogen-activated protein kinase 1	DLKPSNLLLNTTCDLK
360	P08069	Insulin-like growth factor 1 receptor	DKIPIR
361	P08069	Insulin-like growth factor 1 receptor	GAKSEILYIR
362	P08069	Insulin-like growth factor 1 receptor	VAGLESLGDLFPNLTVIR
363	P08069	Insulin-like growth factor 1 receptor	NDYQQLK
364	P08069	Insulin-like growth factor 1 receptor	YRPPDYR
365	P08069	Insulin-like growth factor 1 receptor	QPQDGYLYR
366	P08069	Insulin-like growth factor 1 receptor	LCVSEIYR
367	P08069	Insulin-like growth factor 1 receptor	TIDSVTSAQMLQGCTIFK
368	P08069	Insulin-like growth factor 1 receptor	DLISFTVYYK
369	P08069	Insulin-like growth factor 1 receptor	MYFAFNPK
370	P08069	Insulin-like growth factor 1 receptor	IIITWHR
371	P08069	Insulin-like growth factor 1 receptor	ECGDLCPGTMEEKPMCEK
372	P08069	Insulin-like growth factor 1 receptor	TVISNLRPFTLYR
373	P08069	Insulin-like growth factor 1 receptor	HSHALVSLSFLK
374	P08069	Insulin-like growth factor 1 receptor	LGCSASNFVFAR
375	P08069	Insulin-like growth factor 1 receptor	VFENFLHNSIFVPRPER
376	P08069	Insulin-like growth factor 1 receptor	AVTLTMVENDHIR
377	P08069	Insulin-like growth factor 1 receptor	TMPAEGADDIPGPVTWEPRPENSIFLK
378	P08069	Insulin-like growth factor 1 receptor	KVFENFLHNSIFVPRPER
379	P08069	Insulin-like growth factor 1 receptor	HYYYAGVCVPACPPNTYR
380	P08069	Insulin-like growth factor 1 receptor	IDIHSCNHEAEK
381	P61981	14-3-3 protein gamma	YLAEVATGEKR
382	Q04917	14-3-3 protein eta	EAFEISK
383	P61981	14-3-3 protein gamma	MVDREQLVQK
384	P61981	14-3-3 protein gamma	KIEMVR
385	P61981	14-3-3 protein gamma	MKGDYYR
386	P61981	14-3-3 protein gamma	NLLSVAYK
387	P61981	14-3-3 protein gamma	ATVVESSEK
388	P61981	14-3-3 protein gamma	DSTLIMQLLR
389	P61981	14-3-3 protein gamma	RATVVESSEK
390	P61981	14-3-3 protein gamma	VISSIEQK
391	P61981	14-3-3 protein gamma	EHMQPTHPIR
392	P61981	14-3-3 protein gamma	YDDMAAAMK
393	P61981	14-3-3 protein gamma	YLAEVATGEK
394	P61981	14-3-3 protein gamma	NCSETQYESK
395	P61981	14-3-3 protein gamma	AYSEAHEISK
396	P61981	14-3-3 protein gamma	LGLALNYSVFYYEIQNAPEQACHLAK
397	P61981	14-3-3 protein gamma	NVTELNEPLSNEER
398	P61981	14-3-3 protein gamma	TAFDDAIAELDTLNEDSYK
399	P61981	14-3-3 protein gamma	ELEAVCQDVLSLLDNYLIK
400	P31947	14-3-3 protein sigma	GEELSCEER

401	P31947	14-3-3 protein sigma	ASLIQK
402	P31947	14-3-3 protein sigma	SAYQEAMDISKK
403	P31947	14-3-3 protein sigma	VLSSIEQK
404	P31947	14-3-3 protein sigma	YLAEVATGDDK
405	P31947	14-3-3 protein sigma	YEDMAAFMK
406	P31947	14-3-3 protein sigma	NLLSVAYKNVVGGQR
407	P31947	14-3-3 protein sigma	SNEEGSEEKGPEVR
408	P31947	14-3-3 protein sigma	GAVEKGEELSCEER
409	P31947	14-3-3 protein sigma	YLAEVATGDDKKR
410	P31947	14-3-3 protein sigma	VETELQGVCDTVLGLLDSHLIK
411	P63104	14-3-3 protein zeta/delta	YLAEVAAGDDKK
412	P62258	14-3-3 protein epsilon	AAFDDAIAELDTLSEESYKDSTLIMQLLR
413	Q16539	Mitogen-activated protein kinase 14	NYIQSLTQMPK
414	Q16539	Mitogen-activated protein kinase 14	ILDFGLAR
415	Q16539	Mitogen-activated protein kinase 14	TIWEVPER
416	Q16539	Mitogen-activated protein kinase 14	LSRPFQSIIHAK
417	Q16539	Mitogen-activated protein kinase 14	MLVLDSDKR
418	Q16539	Mitogen-activated protein kinase 14	LVGTPGAELLK
419	Q16539	Mitogen-activated protein kinase 14	KLSRPFQSIIHAK
420	Q16539	Mitogen-activated protein kinase 14	LVGTPGAELLKK
421	Q16539	Mitogen-activated protein kinase 14	SLTYDEVISFVPPPLDQEEMES
422	Q16539	Mitogen-activated protein kinase 14	DLLIDEWK
423	Q16539	Mitogen-activated protein kinase 14	YIHSADIIHR
424	Q16539	Mitogen-activated protein kinase 14	DLKPSNLAVNEDCELK
425	Q16539	Mitogen-activated protein kinase 14	TLFPGTDHIDQLK
426	Q16539	Mitogen-activated protein kinase 14	HENVIGLLDVFTPAR
427	Q16539	Mitogen-activated protein kinase 14	LTDDHVQFLIYQILR
428	Q16539	Mitogen-activated protein kinase 14	YQNLSPVGSGAYGSVCAAFDTK
429	P07288	Prostate-specific antigen	SVILLGR
430	P07288	Prostate-specific antigen	IVGGWECEK
431	P07288	Prostate-specific antigen	LQCVDLHVISNDVCAQVHPQK
432	P07288	Prostate-specific antigen	LSEPAELTDAVK
433	P07288	Prostate-specific antigen	HSLFHPEDTGQVFQVSHSFPHPLYDMSLLK
434	P07288	Prostate-specific antigen	STCSGDSGGPLVCNGVLQGITSWGSEPCALPERPSLYTK
435	P07288	Prostate-specific antigen	FLRPGDDSSHDLMLLR
436	P07288	Prostate-specific antigen	HSQPWQVLVASR
437	P07288	Prostate-specific antigen	KLQCVDLHVISNDVCAQVHPQK
438	P07288	Prostate-specific antigen	VMDLPTQEPALGTTCYASGWGSIEPEEFLTPK
439	P07288	Prostate-specific antigen	AVCGGVLVHPQWVLTAAHCIR
440	Q99497	Protein DJ-1 (PARK7)	RALVILAK
441	Q99497	Protein DJ-1 (PARK7)	APLVLK
442	Q99497	Protein DJ-1 (PARK7)	EILKEQENR
443	Q99497	Protein DJ-1 (PARK7)	ALVILAK
444	Q99497	Protein DJ-1 (PARK7)	DGLILTSR
445	Q99497	Protein DJ-1 (PARK7)	KGLIAAICAGPTALLAHEIGFGSK
446	Q99497	Protein DJ-1 (PARK7)	VTVAGLAGKDPVQCSR
447	Q99497	Protein DJ-1 (PARK7)	GAEEMETVIPVDVMR
448	Q99497	Protein DJ-1 (PARK7)	DVVICPDASLEDAK
449	Q99497	Protein DJ-1 (PARK7)	DVVICPDASLEDAKK
450	Q99497	Protein DJ-1 (PARK7)	EGPYDVVVLPGGNLGAQNLSESAAVK
451	Q99497	Protein DJ-1 (PARK7)	GPGTSFEFALAIVEALNGK
452	Q99497	Protein DJ-1 (PARK7)	GLIAAICAGPTALLAHEIGFGSK
453	P04179	Superoxide dismutase [Mn],	DFGSFDKFK

		mitochondrial	
454	P04179	Superoxide dismutase [Mn], mitochondrial	DFGSFDK
455	P04179	Superoxide dismutase [Mn], mitochondrial	YQEALAK
456	P04179	Superoxide dismutase [Mn], mitochondrial	FNGGGHINHSIFWTNLSPNGGGEPK
457	P04179	Superoxide dismutase [Mn], mitochondrial	GELLEAIK
458	P04179	Superoxide dismutase [Mn], mitochondrial	NVRPDYLK
459	P04179	Superoxide dismutase [Mn], mitochondrial	GELLEAIKR
460	P04179	Superoxide dismutase [Mn], mitochondrial	LTAASVGVQGSGWGWLGFNK
461	P04179	Superoxide dismutase [Mn], mitochondrial	GDVTAQIALQPALK
462	P04179	Superoxide dismutase [Mn], mitochondrial	AIWNVINWENVTER
463	P04179	Superoxide dismutase [Mn], mitochondrial	HHAAYVNNLNVTEEK
464	P04179	Superoxide dismutase [Mn], mitochondrial	GHLQIAACPNQDPLQGTTGLIPLLGIDVWEHAYYLQYK
465	D6RFX5	Amphiregulin	THSMIDSSLSK
466	D6RFX5	Amphiregulin	TESENTSDKPK
467	D6RFX5	Amphiregulin	CQQEYFGER
468	D6RFX5	Amphiregulin	VEQVVKPPQNKTESENTSDKPK
469	D6RFX5	Amphiregulin	VEQVVKPPQNK
470	D6RFX5	Amphiregulin	KNPCNAEFQNFCIHGECK
471	D6RFX5	Amphiregulin	NPCNAEFQNFCIHGECK
472	D6RFX5	Amphiregulin	YIEHLEAVTCK
473	D6RFX5	Amphiregulin	KKNPCNAEFQNFCIHGECK
474	P29353-6	Isoform 6 of SHC-transforming protein 1	GEPWFHGK
475	P29353-6	Isoform 6 of SHC-transforming protein 1	HLLLVDPEGVVRTKDHR
476	P29353-6	Isoform 6 of SHC-transforming protein 1	HLLLVDPEGVVRTK
477	P29353-6	Isoform 6 of SHC-transforming protein 1	ESTTTPGQYVLTGLQSGQPK
478	P29353-6	Isoform 6 of SHC-transforming protein 1	HLLLVDPEGVVR
479	P29353-6	Isoform 6 of SHC-transforming protein 1	EAEALLQLNGDFLVR
480	P29353-6	Isoform 6 of SHC-transforming protein 1	REAEALLQLNGDFLVR
481	P29353-6	Isoform 6 of SHC-transforming protein 1	FESVSHLISYHMDNHLPIISAGSELCLQQPVER
482	P15692-11	Isoform L-VEGF165 of Vascular endothelial growth factor A	QLELNER
483	P15692-11	Isoform L-VEGF165 of Vascular endothelial growth factor A	QENPCGPCSER
484	P15692-11	Isoform L-VEGF165 of Vascular endothelial growth factor A	FMDVYQR
485	P15692-11	Isoform L-VEGF165 of Vascular	IKPHQGQHIGEMSFLQHNK

		endothelial growth factor A	
486	P15692-11	Isoform L-VEGF165 of Vascular endothelial growth factor A	ARQENPCGPCSER
487	P15692-11	Isoform L-VEGF165 of Vascular endothelial growth factor A	HLFVQDPQTCK
488	P15692-11	Isoform L-VEGF165 of Vascular endothelial growth factor A	KHLFVQDPQTCK
489	P15692-11	Isoform L-VEGF165 of Vascular endothelial growth factor A	CGGCCNDEGLECVPTEESNITMQIMR
490	P15692-11	Isoform L-VEGF165 of Vascular endothelial growth factor A	SYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMR
491	P52823	Stanniocalcin-1	VFLAIR
492	P52823	Stanniocalcin-1	SFLYSAAK
493	P52823	Stanniocalcin-1	NPEAITEVVQLPNHFSNR
494	P52823	Stanniocalcin-1	CIANGVTSK
495	P52823	Stanniocalcin-1	MIAEVQEECYSK
496	P52823	Stanniocalcin-1	VAAQNSAEVVR
497	P52823	Stanniocalcin-1	SLLECDEDTVSTIR
498	P52823	Stanniocalcin-1	RNPEAITEVVQLPNHFSNR
499	P52823	Stanniocalcin-1	IGPNMASLFHILQTDHCAQTHPR
500	Q9NX40	OCIA domain-containing protein 1	VNKYGDTWDE
501	Q9NX40	OCIA domain-containing protein 1	KLENSPLGEALR
502	Q9NX40	OCIA domain-containing protein 1	TDPSVRPMHER
503	Q9NX40	OCIA domain-containing protein 1	ESYEVSLTQK
504	Q9NX40	OCIA domain-containing protein 1	SVPLAATSMLITQGLISK
505	Q9NX40	OCIA domain-containing protein 1	GILSSHPK
506	Q9NX40	OCIA domain-containing protein 1	LENSPLGEALR
507	Q9NX40	OCIA domain-containing protein 1	VFAECNDESFWFR
508	Q9NX40	OCIA domain-containing protein 1	SSPPGHYYQK
509	Q9NX40	OCIA domain-containing protein 1	ADFREPNAEVPRPIPHIGPDYIPTEEER
510	O15392	Baculoviral IAP repeat-containing protein 5	QFEELTLGEFLK
511	O15392	Baculoviral IAP repeat-containing protein 5	KQFEELTLGEFLK
512	O15392	Baculoviral IAP repeat-containing protein 5	NWPFLEGCACTPER
513	O15392	Baculoviral IAP repeat-containing protein 5	MAEAGFIHCPTENEPDLAQCFFCFK
514	O15392	Baculoviral IAP repeat-containing protein 5	ELEGWEPDDDPIEEHKK
515	P51671	Eotaxin	AVIFKTKLAK
516	P51671	Eotaxin	WVQDSMK
517	P51671	Eotaxin	KIPLQRLESYR
518	P51671	Eotaxin	DICADPKK
519	P51671	Eotaxin	SPTPKP
520	P51671	Eotaxin	DICADPK
521	P51671	Eotaxin	TKLAKDICADPK
522	P51671	Eotaxin	KWVQDSMK
523	P21802-11	Isoform 11 of Fibroblast growth factor receptor 2	MLKDDATEK
524	P21802-11	Isoform 11 of Fibroblast growth factor receptor 2	QLVEDLDR
525	P21802-11	Isoform 11 of Fibroblast growth factor receptor 2	LTLGKPLGEGCFGQVVMAEAVGIDKDKPK
526	P21802-11	Isoform 11 of Fibroblast growth factor	GMEYLASQK

		receptor 2	
527	P21802-11	Isoform 11 of Fibroblast growth factor receptor 2	EAVTVAVK
528	P21802-11	Isoform 11 of Fibroblast growth factor receptor 2	LSSTADTPMLAGVSEYELPEDPKWEFPR
529	P10145-2	Isoform 2 of Interleukin-8	ENWVQR
530	P10145-2	Isoform 2 of Interleukin-8	ELCLDPK
531	P10145-2	Isoform 2 of Interleukin-8	TYSKPFHPK
532	P10145-2	Isoform 2 of Interleukin-8	VIESGPHCANTEIIVK

Supplemental Table 17. Peptides, masses and transition ions selected for aptamer-MRM-MS analyses in representative eight proteins in Figure 6a

Protein	Peptide Sequence	Precursor (z)	Precursor (m/z)	Product (m/z)	Ion type	Collision Energy (V)	Transition color in figures
Annexin A1	GTDVNVFNTILTTR	(+2)	775.912287	1064.6099	[y9]	26.2	blue
Annexin A1	GTDVNVFNTILTTR	(+2)	775.912287	965.54146	[y8]	26.2	purple
Annexin A1	GTDVNVFNTILTTR	(+2)	775.912287	818.47304	[y7]	26.2	red
ERBB1 - peptide 1	NLQEILHGAVR	(+2)	625.354211	894.51558	[y8]	21.7	blue
ERBB1 - peptide 1	NLQEILHGAVR	(+2)	625.354211	765.47298	[y7]	21.7	purple
ERBB1 - peptide 1	NLQEILHGAVR	(+2)	625.354211	652.38892	[y6]	21.7	red
ERBB1 - peptide 2	IPLENLQIIR	(+2)	604.871705	1095.6521	[y9]	21.1	blue
ERBB1 - peptide 2	IPLENLQIIR	(+2)	604.871705	885.51524	[y7]	21.1	purple
ERBB1 - peptide 2	IPLENLQIIR	(+2)	604.871705	756.47265	[y6]	21.1	red
ERBB1 - peptide 2	IPLENLQIIR	(+2)	604.871705	642.42972	[y5]	21.1	orange
ERBB1 - peptide 3	TDLHAFENLEIIR	(+3)	524.278978	757.45666	[y6]	22.2	blue
ERBB1 -	TDLHAFENLEIIR	(+3)	524.278978	643.41374	[y5]	22.2	purple

peptide 3							
ERBB1 - peptide 3	TDLHAFENLEIIR	(+3)	524.278978	530.32967	[y4]	22.2	red
ERBB3	LTFQLEPNPHTK	(+3)	475.589264	693.36785	[y6]	20.4	blue
ERBB3	LTFQLEPNPHTK	(+3)	475.589264	596.31509	[y5]	20.4	purple
ERBB3	LTFQLEPNPHTK	(+3)	475.589264	482.27216	[y4]	20.4	red
IL8	TYSKPFHPK	(+2)	552.795466	840.47265	[y7]	19.5	blue
IL8	TYSKPFHPK	(+2)	552.795466	753.44062	[y6]	19.5	purple
IL8	TYSKPFHPK	(+2)	552.795466	625.34566	[y5]	19.5	red
PSA	LSEPAELTDAVK	(+2)	636.837725	943.50949	[y9]	22	blue
PSA	LSEPAELTDAVK	(+2)	636.837725	846.45672	[y8]	22	purple
PSA	LSEPAELTDAVK	(+2)	636.837725	775.41961	[y7]	22	red
PSA	LSEPAELTDAVK	(+2)	636.837725	646.37702	[y6]	22	orange
MnSOD	GDVTAQIALQPALK	(+2)	712.909016	981.60914	[y9]	24.3	blue
MnSOD	GDVTAQIALQPALK	(+2)	712.909016	853.55057	[y8]	24.3	purple
MnSOD	GDVTAQIALQPALK	(+2)	712.909016	740.4665	[y7]	24.3	red
MnSOD	GDVTAQIALQPALK	(+2)	712.909016	428.28675	[y4]	24.3	orange
STC1	SFLYSAAK	(+2)	443.737085	799.43487	[y7]	16.2	blue
STC1	SFLYSAAK	(+2)	443.737085	652.36645	[y6]	16.2	purple
STC1	SFLYSAAK	(+2)	443.737085	539.28239	[y5]	16.2	red
VEGF	HLFVQDPQTCK	(+2)	686.837536	975.45641	[y8]	23.5	blue
VEGF	HLFVQDPQTCK	(+2)	686.837536	876.38799	[y7]	23.5	purple
VEGF	HLFVQDPQTCK	(+2)	686.837536	748.32942	[y6]	23.5	red
VEGF	HLFVQDPQTCK	(+2)	686.837536	633.30247	[y5]	23.5	orange

Supplemental Table 18. Summary of top 40 most abundant proteins identified by LC-MS/MS in plasma after enrichment with streptavidin beads or aptamer-coated streptavidin beads

Beads				Beads + 29 Aptamers		
No. of Spectra	Total Intensity	Protein Name		No. of Spectra	Total Intensity	Protein Name
222	2.81E+11	Serum albumin		239	2.73E+10	Apolipoprotein B-100
168	5.03E+10	Complement C3		226	1.37E+11	Complement C3
142	1.01E+10	Keratin, type II cytoskeletal 2 epidermal		220	4.16E+11	C4b-binding protein alpha chain
121	1.12E+09	Apolipoprotein B-100		207	3.03E+11	Serum albumin
88	8.84E+09	Serotransferrin		152	4.37E+10	Coagulation factor V
84	3.28E+09	Alpha-2-macroglobulin		139	5.17E+10	Complement C4-B
78	6.01E+11	Streptavidin		133	2.91E+10	von Willebrand factor
74	2.17E+10	Ig gamma-1 chain C region		131	1.81E+10	Fibronectin
72	7.66E+09	Keratin, type I cytoskeletal 10		130	3.99E+10	Complement factor H
68	3.32E+09	Complement C4-B		123	7.58E+11	Streptavidin
66	5.68E+09	Alpha-1-antitrypsin		116	3.00E+11	Ig mu chain C region
61	5.73E+09	Apolipoprotein A-I		101	4.91E+11	Complement C1q subcomponent subunit B
49	2.74E+09	Fibrinogen beta chain		98	7.68E+10	Ig gamma-1 chain C region
47	5.82E+09	Haptoglobin		90	1.67E+11	Complement C1q subcomponent subunit A
47	3.87E+09	Fibrinogen alpha chain		85	2.57E+09	Filamin-A
42	5.00E+08	Complement factor H		84	5.78E+10	Apolipoprotein A-I
41	1.82E+09	Apolipoprotein A-IV		60	9.52E+09	Serotransferrin
39	2.55E+08	Fibronectin		59	1.52E+10	Fibrinogen alpha chain
34	1.21E+09	Isoform C of Proteoglycan 4		56	3.29E+09	Alpha-2-macroglobulin
32	2.06E+09	Fibrinogen gamma chain		51	2.66E+09	Complement C5
31	9.62E+08	Ceruloplasmin		50	1.01E+10	Fibrinogen beta chain
29	1.99E+09	Hemopexin		50	2.77E+10	ITIH4 protein
29	1.10E+09	ITIH4 protein		48	1.09E+10	Isoform C of Proteoglycan 4
29	5.48E+08	Vitamin D-binding protein		46	3.79E+10	Protein AMBP
28	1.65E+08	Complement C5		44	3.22E+09	Lactotransferrin
27	8.05E+09	Ig kappa chain C region		44	5.74E+09	Alpha-1-antitrypsin
27	2.55E+09	Isoform 2 of Clusterin		43	3.31E+11	Complement C1q subcomponent subunit C
27	7.70E+08	Kininogen-1		43	6.36E+10	Ig kappa chain C region
26	8.95E+09	Apolipoprotein C-III		43	8.19E+08	Talin-1
25	1.69E+09	Ig mu chain C region		42	1.15E+10	Fibrinogen gamma chain
23	9.50E+09	Protein APOC4-APOC2		42	1.50E+10	Coagulation factor XII
23	4.76E+09	Apolipoprotein A-II		41	4.02E+09	Apolipoprotein A-IV
23	2.08E+08	C4b-binding protein alpha chain		41	6.60E+09	Haptoglobin
23	1.45E+08	Coagulation factor XI		39	1.04E+10	Apolipoprotein E
22	3.99E+08	Apolipoprotein E		39	5.98E+08	Myosin-9
22	3.23E+08	Antithrombin-III		37	2.34E+09	Catalase
22	2.97E+08	Uncharacterized protein		36	2.85E+09	Apolipoprotein(a)
21	9.13E+10	Trypsin		35	1.64E+10	Kininogen-1
21	1.36E+09	Alpha-1-acid glycoprotein 1		35	2.52E+09	Plasma kallikrein
20	2.90E+09	Ig lambda-2 chain C regions		34	2.87E+10	Ig lambda-2 chain C regions

Supplemental Table 19. Aptamer-enriched MRM assay performance using heavy isotope labeled peptides

Gene	Uniprot	Species	Peptide	Transition.ID	slope	y-intercept	Rsquare	LOD (fmol/uL)	LOQ (fmol/uL)	Comments
ANXA1	P04083	HUMAN	ALYEAGER	2.y6.1.0	0.0369	0.0167	0.9740	0.37	1.11	
ANXA1	P04083	HUMAN	GTDVNVFNTILTTR	2.y8.1.0	0.0363	0.0171	0.9688	0.22	0.65	
ANXA1	P04083	HUMAN	GVDEATIIDILTK	2.y6.1.0	0.0218	0.0114	0.9762	0.65	1.96	
ANXA1	P04083	HUMAN	TPAQFDADELR	2.y6.1.0	0.0383	0.0330	0.9859	0.27	0.82	
EGFR	P00533	HUMAN	NLQEILHGAVR	2.y8.1.0	0.3343	0.3595	0.9144	0.70	2.10	endogenous detected
EGFR	P00533	HUMAN	NYDLSFLK	2.y6.1.0	0.0376	0.0581	0.9403	1.50	4.51	endogenous detected
ERBB2	P04626	HUMAN	AVTSANIQEFAGCK	2.y7.1.0	0.0643	0.0584	0.9368	4.64	13.92	
ERBB2	P04626	HUMAN	NNQLALTLIDTNR	2.y9.1.0	0.0276	-0.0008	0.9662	0.07	0.22	
KLK3	P07288	HUMAN	HSQPWQVLVASR	2.y9.1.0	0.1346	0.0161	0.9869	0.16	0.49	
KLK3	P07288	HUMAN	IVGGWECEK	2.y6.1.0	0.0605	-0.0004	0.9633	0.40	1.19	
KLK3	P07288	HUMAN	LSEPAELTDAVK	2.y9.1.0	0.1406	0.0003	0.9646	0.19	0.56	
MK03	P27361	HUMAN	IADPEHDHTGFLTEYVATR	3.y7.1.0	0.0094	-0.0012	0.9757	9.96	29.87	
MK14	Q16539	HUMAN	HENVIGLLDVFTPAR	3.y5.1.0	0.0238	0.0102	0.9629	0.42	1.25	
PARK7	Q99497	HUMAN	VTVAGLAGK	2.y7.1.0	0.0052	0.0039	0.9329	0.60	1.79	
TPM1	P09493	HUMAN	LVIIESDLER	2.y7.1.0	0.0252	0.0000	0.9954	0.07	0.21	
TPM1	P09493	HUMAN	QLEDELVSLQK	2.y6.1.0	0.1019	-0.0117	0.9893	1.30	3.89	
TPM1	P09493	HUMAN	SIDDLEDELYAQK	2.y8.1.0	0.1595	-0.0041	0.9782	0.40	1.21	
1433S	P31947	HUMAN	NLLSVAYK	2.y6.1.0	0.0502	0.9418	0.9634	16.38	49.14	endogenous detected
1433S	P31947	HUMAN	VLSSIEQK	2.y6.1.0	0.0575	0.0216	0.9635	3.27	9.80	endogenous detected

Supplemental Table 20. Aptamer-enriched MRM assay performance using light peptide peak areas

Gene	UniProt	Species	Peptide	TransitionID	slope	y-intercept	Rsquare	LOD (fmol/uL)	LOQ (fmol/uL)	Comments
ANXA1	P04083	HUMAN	ALYEAGER	2.y6.1.0	49596	22008	0.8981	0.21	0.63	
ANXA1	P04083	HUMAN	GTDVNVFNTILTTR	2.y8.1.0	7990	3308	0.9454	0.33	1.00	
ANXA1	P04083	HUMAN	GVDEATIIDILTK	2.y6.1.0	8509	2860	0.9596	0.26	0.79	
ANXA1	P04083	HUMAN	TPAQFDADELR	2.y7.1.0	19434	6070	0.9700	0.69	2.08	
AREG	P15514	HUMAN	CQQEYFGER	2.y7.1.0	57506	-462	0.9752	0.05	0.16	
AREG	P15514	HUMAN	VEQVVKPPQNK	3.y5.1.0	319364	5062	0.9435	0.06	0.19	
AREG	P15514	HUMAN	YIEHLEAVTCK	2.y6.1.0	43358	-971	0.9002	0.12	0.35	
ATPB	P06576	HUMAN	AIAELGIYPAVDPLDSTSR	2.y12.1.0	14398	3	0.9460	0.35	1.05	
ATPB	P06576	HUMAN	FTQAGSEVSALLGR	2.y10.1.0	31376	-287	0.9523	0.39	1.17	
ATPB	P06576	HUMAN	LVLEVAQHLGESTVR	3.y6.1.0	44816	-396	0.9537	0.21	0.64	
ATPB	P06576	HUMAN	VLDSGAPIK	2.y6.1.0	40579	1419	0.9492	0.03	0.10	
BIRC5	O15392	HUMAN	HSSGCAFLSVK	2.y8.1.0	567	-17	0.9340	6.90	20.69	
BIRC5	O15392	HUMAN	QFEELTLGEFLK	2.y7.1.0	1826	-71	0.9449	0.96	2.87	
CCL11	P51671	HUMAN	DICADPK	2.y5.1.0	37669	1662	0.8131	0.16	0.48	
CCL11	P51671	HUMAN	WVQDSMK	2.y5.1.0	40583	692	0.9182	0.39	1.18	
EGFR	P00533	HUMAN	FSNNPALCNVESIQWR	2.y9.1.0	16593	13493	0.8398	1.11	3.33	endogenous detected
EGFR	P00533	HUMAN	IPLENLQIIR	2.y7.1.0	59914	64945	0.8861	1.00	3.00	endogenous detected
EGFR	P00533	HUMAN	NLQEILHGAVR	2.y8.1.0	46190	50365	0.8863	0.26	0.78	endogenous detected
EGFR	P00533	HUMAN	NYDLSFLK	2.y6.1.0	47916	86708	0.8963	1.61	4.84	endogenous detected
EGFR	P00533	HUMAN	TDLHAFENLEIIR	3.y4.1.0	43818	83158	0.9148	1.29	3.88	endogenous detected
EGFR	P00533	HUMAN	TIQEVAGYVLIALNTVER	2.y9.1.0	2141	2574	0.7949	0.74	2.23	endogenous detected
ERBB2	P04626	HUMAN	AVTSANIQEFAGCK	2.y7.1.0	5871	4134	0.9201	1.17	3.51	
ERBB2	P04626	HUMAN	NNQLALTLIDTNR	2.y9.1.0	5381	-155	0.9148	0.07	0.21	
ERBB2	P04626	HUMAN	VLQGLPR	2.y5.1.0	152912	725	0.9240	0.03	0.08	
ERBB3	P21860	HUMAN	CWGPGSEDCQTLTK	2.y11.1.0	1535	-183	0.9156	0.45	1.35	
ERBB3	P21860	HUMAN	IPALDPEK	2.y3.1.0	37642	4365	0.9441	1.09	3.28	
ERBB3	P21860	HUMAN	IYISANR	2.y5.1.0	158663	22521	0.9877	0.11	0.34	
ERBB3	P21860	HUMAN	LTFQLEPNPHTK	2.y6.1.0	15532	5651	0.9499	0.33	0.99	
FGFR2	P21802	HUMAN	EAVTVAVK	2.y5.1.0	18789	861	0.9585	0.13	0.39	
FGFR2	P21802	HUMAN	IADFGLAR	2.y6.1.0	21518	9918	0.9256	1.81	5.43	
FGFR2	P21802	HUMAN	QLVEDLDR	2.y5.1.0	3838	1069	0.9751	0.51	1.54	

IF4A3	P38919	HUMAN	ELAVQIQK	2.y4.1.0	14510	-1554	0.9678	0.50	1.51	
IF4A3	P38919	HUMAN	EQIYDVYR	2.y5.1.0	6434	500	0.9453	1.42	4.25	
IF4A3	P38919	HUMAN	GVAINFVK	2.y6.1.0	6608	1385	0.9886	0.41	1.23	
IF4A3	P38919	HUMAN	VLISTDVWAR	2.y7.1.0	6936	391	0.9655	0.66	1.98	
IGF1R	P08069	HUMAN	SEILYIR	2.y4.1.0	24086	-201	0.9631	0.20	0.61	
IGF1R	P08069	HUMAN	TVISNLRPFTLYR	3.y6.1.0	1952	-244	0.9220	0.16	0.49	
IGF1R	P08069	HUMAN	YADGTIDIEEVTENPK	2.y8.1.0	918	118	0.9708	1.17	3.51	
IGF1R	P08069	HUMAN	YGSQVEDQR	2.y5.1.0	10302	-4111	0.9091	0.96	2.89	
IL8	P10145	HUMAN	ELCLDPK	2.y4.1.0	82976	-1714	0.9589	0.17	0.50	
IL8	P10145	HUMAN	ENWVQR	2.y3.1.0	312937	287	0.8953	0.02	0.07	
IL8	P10145	HUMAN	TYSKPFHPK	2.y5.1.0	70553	-6	0.8972	0.01	0.04	
IL8	P10145	HUMAN	VIESGPHCANTEIIVK	3.y7.1.0	1814	-201	0.9458	0.72	2.15	
KLK3	P07288	HUMAN	HSQPWQVLVASR	2.y9.1.0	8542	1147	0.8845	0.03	0.10	
KLK3	P07288	HUMAN	IVGGWECEK	2.y6.1.0	1351	-10	0.9205	0.41	1.24	
KLK3	P07288	HUMAN	LSEPAELTDAVK	2.y9.1.0	45342	-545	0.9564	0.17	0.50	
KLK3	P07288	HUMAN	SVILLGR	2.y5.1.0	117336	2799	0.9351	0.03	0.09	
KPCZ	Q05513	HUMAN	ISQGLGLQDFDLIR	2.y9.1.0	24357	-671	0.9347	0.07	0.20	
KPCZ	Q05513	HUMAN	LDNVLLDADGHIK	2.y9.1.0	4056	-121	0.9155	0.29	0.88	
KPCZ	Q05513	HUMAN	LHQQHPLTLK	3.y5.1.0	23147	416	0.9295	0.30	0.91	
KPCZ	Q05513	HUMAN	SIDWDLLEK	2.y7.1.0	13439	-105	0.9555	0.01	0.03	
KPYM	P14618	HUMAN	APIIAVTR	2.y5.1.0	109353	345272	0.9416	1.80	5.40	endogenous detected
KPYM	P14618	HUMAN	CCSGAIIVLTK	2.y4.1.0	1321	5413	0.9849	6.23	18.68	
KPYM	P14618	HUMAN	GDLGIEIPAEK	2.y6.1.0	28175	47204	0.9716	2.59	7.76	endogenous detected
KPYM	P14618	HUMAN	GDYPLEAVR	2.y6.1.0	29585	104351	0.9681	2.72	8.15	endogenous detected
KPYM	P14618	HUMAN	GSGTAEVELK	2.y6.1.0	9422	25998	0.9322	2.65	7.94	endogenous detected
KPYM	P14618	HUMAN	ITLDNAYMEK	2.y7.1.0	2602	5513	0.8601	11.35	34.06	endogenous detected
KPYM	P14618	HUMAN	LDIDSPPITAR	2.y6.1.0	46360	143728	0.9706	2.49	7.46	endogenous detected
LEPR	P48357	HUMAN	IINSFTQDDIEK	2.y7.1.0	3804	1087	0.9625	1.16	3.48	
LEPR	P48357	HUMAN	LDGPGIWSDWSTPR	2.y8.1.0	1320	-11	0.9175	1.20	3.61	
LEPR	P48357	HUMAN	SSLYCSDIPSIHPISEPK	3.y6.1.0	1012	1	0.9620	5.10	15.30	
LEPR	P48357	HUMAN	YYIHDHFIPIEK	3.y4.1.0	2454	395	0.9528	5.10	15.29	
MK03	P27361	HUMAN	ELIFQETAR	2.y6.1.0	16298	170	0.9767	0.52	1.57	
MK03	P27361	HUMAN	IADPEHDHTGFLTEYVATR	3.y7.1.0	423	-55	0.9804	6.88	20.63	
MK03	P27361	HUMAN	ICDFGLAR	2.y6.1.0	34408	11481	0.9188	0.44	1.33	

MK03	P27361	HUMAN	NYLQSLPSK	2.y5.1.0	5124	2537	0.9880	0.54	1.61	
MK14	Q16539	HUMAN	DLKPSNLAVNEDCELK	3.y7.1.0	733	-7	0.9870	0.18	0.53	
MK14	Q16539	HUMAN	HENVIGLLDVFTPAR	3.y5.1.0	5042	1893	0.9652	0.35	1.05	
MK14	Q16539	HUMAN	ILDFGLAR	2.y6.1.0	70912	14077	0.9382	0.74	2.21	
MK14	Q16539	HUMAN	LSRPFQSIIHAK	3.y4.1.0	1769	477	0.8434	4.37	13.11	
MK14	Q16539	HUMAN	LVGTPGAELLK	2.y7.1.0	4273	2829	0.9295	1.82	5.47	
OCAD1	Q9NX40	HUMAN	LENSPLGEALR	2.y7.1.0	5610	27	0.9721	0.98	2.94	
OCAD1	Q9NX40	HUMAN	NITYEELR	2.y6.1.0	8539	437	0.9640	1.85	5.55	
PA2G4	Q9UQ80	HUMAN	AAHLCAEAALR	3.y4.1.0	153776	13926	0.8620	0.23	0.68	
PA2G4	Q9UQ80	HUMAN	ITSGPFEPDLYK	2.y5.1.0	63088	13558	0.9235	1.41	4.23	endogenous detected
PA2G4	Q9UQ80	HUMAN	LVKPGNQNTQVTEAWNK	3.y6.1.0	23015	988	0.9399	0.23	0.70	
PA2G4	Q9UQ80	HUMAN	SDQDYILK	2.y6.1.0	45310	2938	0.9519	0.31	0.93	
PA2G4	Q9UQ80	HUMAN	TIIQNPTDQQK	2.y6.1.0	141126	7772	0.9288	0.22	0.66	
PARK7	Q99497	HUMAN	DGLILTSR	2.y4.1.0	56823	7592	0.9254	0.77	2.30	endogenous detected
PARK7	Q99497	HUMAN	VTTHPLAK	2.y7.1.0	3975	1230	0.7596	0.48	1.43	
PARK7	Q99497	HUMAN	VTVAGLAGK	2.y7.1.0	9695	6691	0.8832	0.59	1.77	
PDPK1	O15530	HUMAN	ILGEGSFSTVVLAR	2.y7.1.0	13552	-59	0.9515	0.18	0.54	
PDPK1	O15530	HUMAN	TFFVHTPNR	3.y3.1.0	26519	-410	0.9016	0.19	0.57	
PDPK1	O15530	HUMAN	TQTESSTPPGIPGGSR	2.y5.1.0	46235	872	0.9106	0.25	0.75	
PDPK1	O15530	HUMAN	VLSPESK	2.y5.1.0	28775	5832	0.8073	1.26	3.77	
SHC1	P29353	HUMAN	EAEALLQLNGDFLVR	2.y8.1.0	39351	1115	0.7030	0.08	0.25	
SHC1	P29353	HUMAN	GEPWFHGK	2.y6.1.0	525143	-426	0.7144	0.01	0.03	
SHC1	P29353	HUMAN	HLLLVDPEGVVR	2.y6.1.0	1040221	6046	0.7993	0.02	0.06	
SODM	P04179	HUMAN	AIWNVINWENVTER	2.y9.1.0	6310	-24	0.9136	0.05	0.14	
SODM	P04179	HUMAN	GDVTAQIALQPALK	2.y4.1.0	50774	2260	0.9278	0.18	0.55	
SODM	P04179	HUMAN	GELLEAIK	2.y5.1.0	6775	-59	0.9780	0.38	1.14	
SODM	P04179	HUMAN	YQEALAK	2.y5.1.0	19411	2135	0.8259	0.36	1.08	
STC1	P52823	HUMAN	SFLYSAAK	2.y6.1.0	20839	5009	0.9343	1.09	3.28	
STC1	P52823	HUMAN	VAAQNSAEVVR	2.y6.1.0	13658	8201	0.9668	0.59	1.77	
TPM1	P09493	HUMAN	LVIIESDLER	2.y7.1.0	18379	7	0.9621	0.07	0.20	
TPM1	P09493	HUMAN	QLEDELVSLQK	2.y6.1.0	9666	-1135	0.9513	1.18	3.53	
TPM1	P09493	HUMAN	SIDDLEDELYAQK	2.y8.1.0	6588	-177	0.9579	0.36	1.09	
VEGFA	P15692	HUMAN	FMDVYQR	2.y5.1.0	245496	1140	0.9211	0.07	0.20	
VEGFA	P15692	HUMAN	HLFVQDPQTCK	2.y5.1.0	170003	360	0.9574	0.07	0.22	

VEGFA	P15692	HUMAN	QLELNER	2.y4.1.0	200646	1728	0.9673	0.03	0.09	
1433G	P61981	HUMAN	NVTELNEPLSNEER	2.y7.1.0	16279	80153	0.7411	2.80	8.41	endogenous detected
1433G	P61981	HUMAN	YLAEVATGEK	2.y8.1.0	51428	166745	0.6797	0.26	0.79	endogenous detected
1433S	P31947	HUMAN	GEELSCEER	2.y5.1.0	9028	4567	0.8669	1.16	3.49	endogenous detected
1433S	P31947	HUMAN	NLLSVAYK	2.y6.1.0	30297	672631	0.9355	2.04	6.13	endogenous detected
1433S	P31947	HUMAN	VLSSIEQK	2.y6.1.0	142575	19204	0.9203	2.82	8.45	endogenous detected
1433S	P31947	HUMAN	YLAEVATGDDK	2.y6.1.0	8704	9831	0.9097	6.10	18.30	endogenous detected

Supplemental Table 21. Peptides, masses and transition ions selected for scheduled MRM analysis for all targeted peptides

Compound	Start Time (min)	End Time (min)	Precursor (m/z)	Product (m/z)	Collision Energy (V)
AAHLC[+57.0]AEAALR(+3)	32.02	40.02	394.8731	630.357	17.3
AAHLC[+57.0]AEAALR(+3)	32.02	40.02	394.8731	559.3198	17.3
AAHLC[+57.0]AEAALR(+3)	32.02	40.02	394.8731	430.2772	17.3
AIAELGIYPAVDPLDSTSR(+2)	52.78	60.78	994.5204	1320.643	32.7
AIAELGIYPAVDPLDSTSR(+2)	52.78	60.78	994.5204	1157.58	32.7
AIAELGIYPAVDPLDSTSR(+2)	52.78	60.78	994.5204	1060.527	32.7
AIAELGIYPAVDPLDSTSR(+2)	52.78	60.78	994.5204	775.3945	32.7
AIWNVINWENVTER(+2)	55.6	63.6	872.4443	1160.569	29.1
AIWNVINWENVTER(+2)	55.6	63.6	872.4443	1047.485	29.1
AIWNVINWENVTER(+2)	55.6	63.6	872.4443	933.4425	29.1
ALYEAGER (heavy)(+2)	29.89	37.89	459.7314	847.4184	16.5
ALYEAGER (heavy)(+2)	29.89	37.89	459.7314	734.3343	16.5
ALYEAGER (heavy)(+2)	29.89	37.89	459.7314	571.271	16.5
ALYEAGER(+2)	29.89	37.89	454.7272	837.4101	16.5
ALYEAGER(+2)	29.89	37.89	454.7272	724.326	16.5
ALYEAGER(+2)	29.89	37.89	454.7272	561.2627	16.5
APIIAVTR(+2)	36.29	44.29	420.7687	769.4931	15.5
APIIAVTR(+2)	36.29	44.29	420.7687	672.4403	15.5
APIIAVTR(+2)	36.29	44.29	420.7687	559.3562	15.5
APIIAVTR(+2)	36.29	44.29	420.7687	446.2722	15.5
AVTSANIQEFAGC[+57.0]K (heavy)(+2)	39.98	47.98	751.3742	1072.519	25.4
AVTSANIQEFAGC[+57.0]K (heavy)(+2)	39.98	47.98	751.3742	958.4758	25.4
AVTSANIQEFAGC[+57.0]K (heavy)(+2)	39.98	47.98	751.3742	845.3917	25.4
AVTSANIQEFAGC[+57.0]K(+2)	39.98	47.98	748.3641	1066.499	25.4
AVTSANIQEFAGC[+57.0]K(+2)	39.98	47.98	748.3641	952.4557	25.4
AVTSANIQEFAGC[+57.0]K(+2)	39.98	47.98	748.3641	839.3716	25.4
C[+57.0]C[+57.0]SGAIIVLTK(+2)	41.14	49.14	611.3201	814.5397	21.2
C[+57.0]C[+57.0]SGAIIVLTK(+2)	41.14	49.14	611.3201	686.4811	21.2
C[+57.0]C[+57.0]SGAIIVLTK(+2)	41.14	49.14	611.3201	573.397	21.2
C[+57.0]C[+57.0]SGAIIVLTK(+2)	41.14	49.14	611.3201	460.313	21.2
C[+57.0]QQEYFGER(+2)	32.94	40.94	608.7562	928.4159	21.2
C[+57.0]QQEYFGER(+2)	32.94	40.94	608.7562	800.3573	21.2
C[+57.0]QQEYFGER(+2)	32.94	40.94	608.7562	671.3148	21.2
C[+57.0]WGPGSEDC[+57.0]QTLTK(+2)	37.33	45.33	819.848	1235.557	27.5
C[+57.0]WGPGSEDC[+57.0]QTLTK(+2)	37.33	45.33	819.848	1081.483	27.5
C[+57.0]WGPGSEDC[+57.0]QTLTK(+2)	37.33	45.33	819.848	994.451	27.5
C[+57.0]WGPGSEDC[+57.0]QTLTK(+2)	37.33	45.33	819.848	865.4084	27.5
DGLILTSR(+2)	39.21	47.21	437.7533	702.4509	16

DGLILTSR(+2)	39.21	47.21	437.7533	589.3668	16
DGLILTSR(+2)	39.21	47.21	437.7533	476.2827	16
DIC[+57.0]ADPK(+2)	25.64	33.64	409.6893	703.3443	15.2
DIC[+57.0]ADPK(+2)	25.64	33.64	409.6893	590.2603	15.2
DIC[+57.0]ADPK(+2)	25.64	33.64	409.6893	430.2296	15.2
DIC[+57.0]ADPK(+2)	25.64	33.64	409.6893	359.1925	15.2
DLKPSNLAVNEDC[+57.0]ELK(+3)	39.63	47.63	615.6401	907.3826	25.7
DLKPSNLAVNEDC[+57.0]ELK(+3)	39.63	47.63	615.6401	793.3396	25.7
DLKPSNLAVNEDC[+57.0]ELK(+3)	39.63	47.63	615.6401	664.2971	25.7
EAEALLQLNGDFLVR(+2)	54.6	62.6	844.4543	1174.658	28.2
EAEALLQLNGDFLVR(+2)	54.6	62.6	844.4543	1061.574	28.2
EAEALLQLNGDFLVR(+2)	54.6	62.6	844.4543	933.5152	28.2
EAVTVAVK(+2)	31.11	39.11	408.7449	616.4028	15.2
EAVTVAVK(+2)	31.11	39.11	408.7449	517.3344	15.2
EAVTVAVK(+2)	31.11	39.11	408.7449	416.2867	15.2
ELAVQIQK(+2)	35.39	43.39	464.7767	686.4196	16.8
ELAVQIQK(+2)	35.39	43.39	464.7767	615.3824	16.8
ELAVQIQK(+2)	35.39	43.39	464.7767	516.314	16.8
ELC[+57.0]LDPK(+2)	35.45	43.45	437.7206	745.3913	16
ELC[+57.0]LDPK(+2)	35.45	43.45	437.7206	632.3072	16
ELC[+57.0]LDPK(+2)	35.45	43.45	437.7206	472.2766	16
ELIFQETAR(+2)	41.24	49.24	553.7957	864.4574	19.5
ELIFQETAR(+2)	41.24	49.24	553.7957	751.3733	19.5
ELIFQETAR(+2)	41.24	49.24	553.7957	604.3049	19.5
ENWVQR(+2)	30.85	38.85	416.209	702.3682	15.4
ENWVQR(+2)	30.85	38.85	416.209	588.3253	15.4
ENWVQR(+2)	30.85	38.85	416.209	402.2459	15.4
ENWVQR(+2)	30.85	38.85	416.209	430.1721	15.4
ENWVQR(+2)	30.85	38.85	416.209	529.2405	15.4
EQIYDVYR(+2)	38.48	46.48	543.2667	828.425	19.2
EQIYDVYR(+2)	38.48	46.48	543.2667	715.341	19.2
EQIYDVYR(+2)	38.48	46.48	543.2667	552.2776	19.2
FMDVYQR(+2)	37.61	45.61	479.7262	811.3767	17.3
FMDVYQR(+2)	37.61	45.61	479.7262	680.3362	17.3
FMDVYQR(+2)	37.61	45.61	479.7262	565.3093	17.3
FSNNPALC[+57.0]NVESIQWR(+2)	47.73	55.73	967.9625	1472.731	31.9
FSNNPALC[+57.0]NVESIQWR(+2)	47.73	55.73	967.9625	1304.642	31.9
FSNNPALC[+57.0]NVESIQWR(+2)	47.73	55.73	967.9625	1191.558	31.9
FSNNPALC[+57.0]NVESIQWR(+2)	47.73	55.73	967.9625	1031.527	31.9
FTQAGSEVSALLGR(+2)	46.46	54.46	718.3806	988.5422	24.5
FTQAGSEVSALLGR(+2)	46.46	54.46	718.3806	931.5207	24.5
FTQAGSEVSALLGR(+2)	46.46	54.46	718.3806	844.4887	24.5
GDLGIEIPAEK(+2)	42.99	50.99	571.3086	856.4775	20

GDLGIEIPAEK(+2)	42.99	50.99	571.3086	799.456	20
GDLGIEIPAEK(+2)	42.99	50.99	571.3086	686.3719	20
GDLGIEIPAEK(+2)	42.99	50.99	571.3086	444.2453	20
GDVTAQIALQPALK(+2)	43.81	51.81	712.909	981.6091	24.3
GDVTAQIALQPALK(+2)	43.81	51.81	712.909	853.5506	24.3
GDVTAQIALQPALK(+2)	43.81	51.81	712.909	740.4665	24.3
GDVTAQIALQPALK(+2)	43.81	51.81	712.909	428.2867	24.3
GDYPLEAVR(+2)	38.82	46.82	510.2615	847.4672	18.2
GDYPLEAVR(+2)	38.82	46.82	510.2615	684.4039	18.2
GDYPLEAVR(+2)	38.82	46.82	510.2615	587.3511	18.2
GEELSC[+57.0]EER(+2)	27.06	35.06	554.7324	793.3509	19.5
GEELSC[+57.0]EER(+2)	27.06	35.06	554.7324	680.2668	19.5
GEELSC[+57.0]EER(+2)	27.06	35.06	554.7324	593.2348	19.5
GELLEAIK(+2)	40.69	48.69	436.758	686.4447	16
GELLEAIK(+2)	40.69	48.69	436.758	573.3606	16
GELLEAIK(+2)	40.69	48.69	436.758	460.2766	16
GEPWFHGK(+2)	33.67	41.67	479.2325	771.3937	17.3
GEPWFHGK(+2)	33.67	41.67	479.2325	674.3409	17.3
GEPWFHGK(+2)	33.67	41.67	479.2325	488.2616	17.3
GSGTAEVELK(+2)	30.85	38.85	495.7587	789.4353	17.8
GSGTAEVELK(+2)	30.85	38.85	495.7587	688.3876	17.8
GSGTAEVELK(+2)	30.85	38.85	495.7587	617.3505	17.8
GTDVNVFNTILTTR (heavy)(+2)	52.05	60.05	780.9164	1074.618	26.2
GTDVNVFNTILTTR (heavy)(+2)	52.05	60.05	780.9164	975.5497	26.2
GTDVNVFNTILTTR (heavy)(+2)	52.05	60.05	780.9164	828.4813	26.2
GTDVNVFNTILTTR(+2)	52.05	60.05	775.9123	1064.61	26.2
GTDVNVFNTILTTR(+2)	52.05	60.05	775.9123	965.5415	26.2
GTDVNVFNTILTTR(+2)	52.05	60.05	775.9123	818.473	26.2
GVAINFVK(+2)	40.62	48.62	424.2554	691.4137	15.6
GVAINFVK(+2)	40.62	48.62	424.2554	620.3766	15.6
GVAINFVK(+2)	40.62	48.62	424.2554	507.2926	15.6
GVDEATIIDILTK (heavy)(+2)	56.82	64.82	698.3947	924.5856	23.7
GVDEATIIDILTK (heavy)(+2)	56.82	64.82	698.3947	823.5379	23.7
GVDEATIIDILTK (heavy)(+2)	56.82	64.82	698.3947	710.4538	23.7
GVDEATIIDILTK(+2)	56.82	64.82	694.3876	916.5714	23.7
GVDEATIIDILTK(+2)	56.82	64.82	694.3876	815.5237	23.7
GVDEATIIDILTK(+2)	56.82	64.82	694.3876	702.4396	23.7
HENVIGLLDVFTPAR (heavy)(+3)	54.46	62.46	564.3099	815.4285	23.6
HENVIGLLDVFTPAR (heavy)(+3)	54.46	62.46	564.3099	700.4016	23.6
HENVIGLLDVFTPAR (heavy)(+3)	54.46	62.46	564.3099	601.3332	23.6
HENVIGLLDVFTPAR (heavy)(+3)	54.46	62.46	564.3099	353.2171	23.6
HENVIGLLDVFTPAR(+3)	54.46	62.46	560.9738	805.4203	23.6
HENVIGLLDVFTPAR(+3)	54.46	62.46	560.9738	690.3933	23.6

HENVIGLLDVFTPAR(+3)	54.46	62.46	560.9738	591.3249	23.6
HENVIGLLDVFTPAR(+3)	54.46	62.46	560.9738	343.2088	23.6
HLFVQDPQTC[+57.0]K(+2)	33.22	41.22	686.8375	975.4564	23.5
HLFVQDPQTC[+57.0]K(+2)	33.22	41.22	686.8375	876.388	23.5
HLFVQDPQTC[+57.0]K(+2)	33.22	41.22	686.8375	748.3294	23.5
HLFVQDPQTC[+57.0]K(+2)	33.22	41.22	686.8375	633.3025	23.5
HLLLVDPEGVVR(+2)	44.61	52.61	673.8932	983.552	23.1
HLLLVDPEGVVR(+2)	44.61	52.61	673.8932	870.468	23.1
HLLLVDPEGVVR(+2)	44.61	52.61	673.8932	771.3995	23.1
HLLLVDPEGVVR(+2)	44.61	52.61	673.8932	656.3726	23.1
HSQPWQVLVASR (heavy)(+2)	42.94	50.94	707.3883	1061.62	24
HSQPWQVLVASR (heavy)(+2)	42.94	50.94	707.3883	964.567	24
HSQPWQVLVASR (heavy)(+2)	42.94	50.94	707.3883	778.4877	24
HSQPWQVLVASR (heavy)(+3)	42.94	50.94	471.9279	1061.62	20.1
HSQPWQVLVASR (heavy)(+3)	42.94	50.94	471.9279	778.4877	20.1
HSQPWQVLVASR (heavy)(+3)	42.94	50.94	471.9279	650.4291	20.1
HSQPWQVLVASR (heavy)(+3)	42.94	50.94	471.9279	551.3607	20.1
HSQPWQVLVASR(+2)	42.94	50.94	704.3782	1055.6	24
HSQPWQVLVASR(+2)	42.94	50.94	704.3782	958.5469	24
HSQPWQVLVASR(+2)	42.94	50.94	704.3782	772.4676	24
HSQPWQVLVASR(+3)	42.94	50.94	469.9212	1055.6	20.1
HSQPWQVLVASR(+3)	42.94	50.94	469.9212	772.4676	20.1
HSQPWQVLVASR(+3)	42.94	50.94	469.9212	644.409	20.1
HSQPWQVLVASR(+3)	42.94	50.94	469.9212	545.3406	20.1
HSSGC[+57.0]AFLSVK(+2)	34.74	42.74	596.7926	881.455	20.8
HSSGC[+57.0]AFLSVK(+2)	34.74	42.74	596.7926	824.4335	20.8
HSSGC[+57.0]AFLSVK(+2)	34.74	42.74	596.7926	664.4028	20.8
HSSGC[+57.0]AFLSVK(+3)	34.74	42.74	398.1975	664.4028	17.4
HSSGC[+57.0]AFLSVK(+3)	34.74	42.74	398.1975	593.3657	17.4
HSSGC[+57.0]AFLSVK(+3)	34.74	42.74	398.1975	446.2973	17.4
IADFGLAR(+2)	40.32	48.32	431.7427	749.3941	15.9
IADFGLAR(+2)	40.32	48.32	431.7427	678.357	15.9
IADFGLAR(+2)	40.32	48.32	431.7427	563.33	15.9
IADPEHDHTGFLTEYVATR (heavy)(+3)	42.71	50.71	728.0195	962.5181	29.8
IADPEHDHTGFLTEYVATR (heavy)(+3)	42.71	50.71	728.0195	849.434	29.8
IADPEHDHTGFLTEYVATR (heavy)(+3)	42.71	50.71	728.0195	748.3863	29.8
IADPEHDHTGFLTEYVATR(+3)	42.71	50.71	724.6834	952.5098	29.8
IADPEHDHTGFLTEYVATR(+3)	42.71	50.71	724.6834	839.4258	29.8
IADPEHDHTGFLTEYVATR(+3)	42.71	50.71	724.6834	738.3781	29.8
IC[+57.0]DFGLAR(+2)	40.13	48.13	476.2395	838.3876	17.2
IC[+57.0]DFGLAR(+2)	40.13	48.13	476.2395	678.357	17.2
IC[+57.0]DFGLAR(+2)	40.13	48.13	476.2395	563.33	17.2
IINSFTQDDIEK(+2)	39.77	47.77	711.8592	995.468	24.3

IINSFTQDDIEK(+2)	39.77	47.77	711.8592	848.3996	24.3
IINSFTQDDIEK(+2)	39.77	47.77	711.8592	747.3519	24.3
ILDFGLAR(+2)	46.29	54.29	452.7662	791.441	16.5
ILDFGLAR(+2)	46.29	54.29	452.7662	678.357	16.5
ILDFGLAR(+2)	46.29	54.29	452.7662	563.33	16.5
ILGEGSFSTVVLAR(+2)	48.51	56.51	724.909	979.5571	24.7
ILGEGSFSTVVLAR(+2)	48.51	56.51	724.909	892.5251	24.7
ILGEGSFSTVVLAR(+2)	48.51	56.51	724.909	745.4567	24.7
IPALDPEK(+2)	35.75	43.75	441.7502	769.409	16.2
IPALDPEK(+2)	35.75	43.75	441.7502	672.3563	16.2
IPALDPEK(+2)	35.75	43.75	441.7502	601.3192	16.2
IPALDPEK(+2)	35.75	43.75	441.7502	488.2351	16.2
IPALDPEK(+2)	35.75	43.75	441.7502	373.2082	16.2
IPLENLQIIR(+2)	48.3	56.3	604.8717	1095.652	21.1
IPLENLQIIR(+2)	48.3	56.3	604.8717	885.5152	21.1
IPLENLQIIR(+2)	48.3	56.3	604.8717	756.4726	21.1
IPLENLQIIR(+2)	48.3	56.3	604.8717	642.4297	21.1
ISQGLGLQDFDLIR(+2)	54.09	62.09	787.9305	1076.573	26.5
ISQGLGLQDFDLIR(+2)	54.09	62.09	787.9305	1019.552	26.5
ISQGLGLQDFDLIR(+2)	54.09	62.09	787.9305	906.468	26.5
ITLDNAYMEK(+2)	39.8	47.8	599.2946	870.3662	20.9
ITLDNAYMEK(+2)	39.8	47.8	599.2946	755.3393	20.9
ITLDNAYMEK(+2)	39.8	47.8	599.2946	641.2963	20.9
ITLDNAYMEK(+2)	39.8	47.8	599.2946	570.2592	20.9
ITSGPFEPDLYK(+2)	43.97	51.97	683.8481	1008.504	23.4
ITSGPFEPDLYK(+2)	43.97	51.97	683.8481	911.4509	23.4
ITSGPFEPDLYK(+2)	43.97	51.97	683.8481	764.3825	23.4
ITSGPFEPDLYK(+2)	43.97	51.97	683.8481	635.3399	23.4
IVGGWEC[+57.0]EK (heavy)(+2)	35.09	43.09	542.2654	814.3495	19.1
IVGGWEC[+57.0]EK (heavy)(+2)	35.09	43.09	542.2654	757.3281	19.1
IVGGWEC[+57.0]EK (heavy)(+2)	35.09	43.09	542.2654	571.2488	19.1
IVGGWEC[+57.0]EK(+2)	35.09	43.09	539.2553	808.3294	19.1
IVGGWEC[+57.0]EK(+2)	35.09	43.09	539.2553	751.308	19.1
IVGGWEC[+57.0]EK(+2)	35.09	43.09	539.2553	565.2286	19.1
IYISANR(+2)	31.55	39.55	418.7349	723.3784	15.5
IYISANR(+2)	31.55	39.55	418.7349	560.3151	15.5
IYISANR(+2)	31.55	39.55	418.7349	447.231	15.5
LDGPGIWSDWSTPR(+2)	50.56	58.56	793.8835	1034.469	26.7
LDGPGIWSDWSTPR(+2)	50.56	58.56	793.8835	848.3897	26.7
LDGPGIWSDWSTPR(+2)	50.56	58.56	793.8835	761.3577	26.7
LDGPGIWSDWSTPR(+2)	50.56	58.56	793.8835	646.3307	26.7
LDIDSPPITAR(+2)	41.38	49.38	599.3273	856.4523	20.9
LDIDSPPITAR(+2)	41.38	49.38	599.3273	741.4254	20.9

LDIDSPPITAR(+2)	41.38	49.38	599.3273	654.3933	20.9
LDIDSPPITAR(+2)	41.38	49.38	599.3273	557.3406	20.9
LDNVLLDADGHIK(+2)	42.88	50.88	711.883	981.5364	24.3
LDNVLLDADGHIK(+2)	42.88	50.88	711.883	868.4523	24.3
LDNVLLDADGHIK(+2)	42.88	50.88	711.883	755.3682	24.3
LDNVLLDADGHIK(+3)	42.88	50.88	474.9244	755.3682	20.3
LDNVLLDADGHIK(+3)	42.88	50.88	474.9244	640.3413	20.3
LDNVLLDADGHIK(+3)	42.88	50.88	474.9244	569.3042	20.3
LENSPLGEALR(+2)	41.24	49.24	599.825	842.473	20.9
LENSPLGEALR(+2)	41.24	49.24	599.825	755.441	20.9
LENSPLGEALR(+2)	41.24	49.24	599.825	658.3883	20.9
LHQQHPLTLK(+3)	27.75	35.75	405.5717	708.4403	17.7
LHQQHPLTLK(+3)	27.75	35.75	405.5717	571.3814	17.7
LHQQHPLTLK(+3)	27.75	35.75	405.5717	474.3286	17.7
LSEPAELTDAVK (heavy)(+2)	40.52	48.52	639.8478	949.5296	22
LSEPAELTDAVK (heavy)(+2)	40.52	48.52	639.8478	852.4769	22
LSEPAELTDAVK (heavy)(+2)	40.52	48.52	639.8478	781.4397	22
LSEPAELTDAVK (heavy)(+2)	40.52	48.52	639.8478	652.3971	22
LSEPAELTDAVK(+2)	40.52	48.52	636.8377	943.5095	22
LSEPAELTDAVK(+2)	40.52	48.52	636.8377	846.4567	22
LSEPAELTDAVK(+2)	40.52	48.52	636.8377	775.4196	22
LSEPAELTDAVK(+2)	40.52	48.52	636.8377	646.377	22
LSRPFQSIIHAK(+3)	38.7	46.7	466.2735	1040.589	20
LSRPFQSIIHAK(+3)	38.7	46.7	466.2735	668.409	20
LSRPFQSIIHAK(+3)	38.7	46.7	466.2735	581.377	20
LSRPFQSIIHAK(+3)	38.7	46.7	466.2735	468.2929	20
LTFQLEPNPHTK(+2)	39.92	47.92	712.8803	1063.553	24.3
LTFQLEPNPHTK(+2)	39.92	47.92	712.8803	935.4945	24.3
LTFQLEPNPHTK(+2)	39.92	47.92	712.8803	822.4104	24.3
LTFQLEPNPHTK(+2)	39.92	47.92	712.8803	693.3678	24.3
LTFQLEPNPHTK(+2)	39.92	47.92	712.8803	482.2722	24.3
LTFQLEPNPHTK(+3)	39.92	47.92	475.5893	693.3678	20.4
LTFQLEPNPHTK(+3)	39.92	47.92	475.5893	596.3151	20.4
LTFQLEPNPHTK(+3)	39.92	47.92	475.5893	482.2722	20.4
LVGTPGAELLK(+2)	42.06	50.06	549.3319	727.4349	19.4
LVGTPGAELLK(+2)	42.06	50.06	549.3319	630.3821	19.4
LVGTPGAELLK(+2)	42.06	50.06	549.3319	573.3606	19.4
LVIIESDLER (heavy)(+2)	43.85	51.85	598.8417	871.4395	20.7
LVIIESDLER (heavy)(+2)	43.85	51.85	598.8417	758.3554	20.7
LVIIESDLER (heavy)(+2)	43.85	51.85	598.8417	629.3128	20.7
LVIIESDLER(+2)	43.85	51.85	593.8375	861.4312	20.7
LVIIESDLER(+2)	43.85	51.85	593.8375	748.3472	20.7
LVIIESDLER(+2)	43.85	51.85	593.8375	619.3046	20.7

LVKPGNQNTQVTEAWNK(+3)	35.3	43.3	643.0059	847.4308	26.7
LVKPGNQNTQVTEAWNK(+3)	35.3	43.3	643.0059	748.3624	26.7
LVKPGNQNTQVTEAWNK(+3)	35.3	43.3	643.0059	647.3148	26.7
LVLEVAQHLGESTVR(+3)	44.09	52.09	550.9773	761.4152	23.2
LVLEVAQHLGESTVR(+3)	44.09	52.09	550.9773	648.3311	23.2
LVLEVAQHLGESTVR(+3)	44.09	52.09	550.9773	591.3097	23.2
NITYEELR(+2)	37.31	45.31	519.2667	810.3992	18.5
NITYEELR(+2)	37.31	45.31	519.2667	709.3515	18.5
NITYEELR(+2)	37.31	45.31	519.2667	546.2882	18.5
NLLSVAYK (heavy)(+2)	41.23	49.23	458.2731	688.412	16.5
NLLSVAYK (heavy)(+2)	41.23	49.23	458.2731	575.3279	16.5
NLLSVAYK (heavy)(+2)	41.23	49.23	458.2731	488.2959	16.5
NLLSVAYK(+2)	41.23	49.23	454.266	680.3978	16.5
NLLSVAYK(+2)	41.23	49.23	454.266	567.3137	16.5
NLLSVAYK(+2)	41.23	49.23	454.266	480.2817	16.5
NLQEILHGAVR (heavy)(+2)	42.47	50.47	628.3643	900.5357	21.7
NLQEILHGAVR (heavy)(+2)	42.47	50.47	628.3643	771.4931	21.7
NLQEILHGAVR (heavy)(+2)	42.47	50.47	628.3643	658.409	21.7
NLQEILHGAVR(+2)	42.47	50.47	625.3542	894.5156	21.7
NLQEILHGAVR(+2)	42.47	50.47	625.3542	765.473	21.7
NLQEILHGAVR(+2)	42.47	50.47	625.3542	652.3889	21.7
NNQLALTLIDTNR (heavy)(+2)	46.85	54.85	746.4147	1022.594	25.2
NNQLALTLIDTNR (heavy)(+2)	46.85	54.85	746.4147	951.5565	25.2
NNQLALTLIDTNR (heavy)(+2)	46.85	54.85	746.4147	838.4724	25.2
NNQLALTLIDTNR(+2)	46.85	54.85	743.4046	1016.573	25.2
NNQLALTLIDTNR(+2)	46.85	54.85	743.4046	945.5364	25.2
NNQLALTLIDTNR(+2)	46.85	54.85	743.4046	832.4523	25.2
NVTELNEPLSNEER(+2)	38.1	46.1	822.3972	1087.501	27.6
NVTELNEPLSNEER(+2)	38.1	46.1	822.3972	973.4585	27.6
NVTELNEPLSNEER(+2)	38.1	46.1	822.3972	844.4159	27.6
NYDLSFLK (heavy)(+2)	46.95	54.95	503.271	891.4918	17.9
NYDLSFLK (heavy)(+2)	46.95	54.95	503.271	728.4284	17.9
NYDLSFLK (heavy)(+2)	46.95	54.95	503.271	613.4015	17.9
NYDLSFLK(+2)	46.95	54.95	500.2609	885.4716	17.9
NYDLSFLK(+2)	46.95	54.95	500.2609	722.4083	17.9
NYDLSFLK(+2)	46.95	54.95	500.2609	607.3814	17.9
NYLQSLPSK(+2)	37.81	45.81	525.2849	772.4563	18.7
NYLQSLPSK(+2)	37.81	45.81	525.2849	659.3723	18.7
NYLQSLPSK(+2)	37.81	45.81	525.2849	531.3137	18.7
NYLQSLPSK(+2)	37.81	45.81	525.2849	331.1976	18.7
QFEELTLGEFLK(+2)	55.57	63.57	727.3823	1049.588	24.7
QFEELTLGEFLK(+2)	55.57	63.57	727.3823	920.5451	24.7
QFEELTLGEFLK(+2)	55.57	63.57	727.3823	807.4611	24.7

QLEDELVSLQK (heavy)(+2)	43.7	51.7	655.3581	939.5237	22.4
QLEDELVSLQK (heavy)(+2)	43.7	51.7	655.3581	824.4967	22.4
QLEDELVSLQK (heavy)(+2)	43.7	51.7	655.3581	695.4542	22.4
QLEDELVSLQK(+2)	43.7	51.7	651.351	931.5095	22.4
QLEDELVSLQK(+2)	43.7	51.7	651.351	816.4825	22.4
QLEDELVSLQK(+2)	43.7	51.7	651.351	687.44	22.4
QLELNER(+2)	31.79	39.79	451.2405	773.4152	16.4
QLELNER(+2)	31.79	39.79	451.2405	660.3311	16.4
QLELNER(+2)	31.79	39.79	451.2405	531.2885	16.4
QLVEDLDR(+2)	36.06	44.06	494.2589	746.3679	17.7
QLVEDLDR(+2)	36.06	44.06	494.2589	647.2995	17.7
QLVEDLDR(+2)	36.06	44.06	494.2589	518.2569	17.7
SDQDYILK(+2)	35.93	43.93	491.248	779.4298	17.6
SDQDYILK(+2)	35.93	43.93	491.248	651.3712	17.6
SDQDYILK(+2)	35.93	43.93	491.248	536.3443	17.6
SEILYIR(+2)	40.66	48.66	447.2582	677.4345	16.3
SEILYIR(+2)	40.66	48.66	447.2582	564.3504	16.3
SEILYIR(+2)	40.66	48.66	447.2582	451.2663	16.3
SFLYSAAK(+2)	36.83	44.83	443.7371	652.3665	16.2
SFLYSAAK(+2)	36.83	44.83	443.7371	539.2824	16.2
SFLYSAAK(+2)	36.83	44.83	443.7371	376.2191	16.2
SIDDLEDELYAQK (heavy)(+2)	46.42	54.42	773.8718	1116.566	26
SIDDLEDELYAQK (heavy)(+2)	46.42	54.42	773.8718	1003.482	26
SIDDLEDELYAQK (heavy)(+2)	46.42	54.42	773.8718	874.4396	26
SIDDLEDELYAQK(+2)	46.42	54.42	769.8647	1108.552	26
SIDDLEDELYAQK(+2)	46.42	54.42	769.8647	995.468	26
SIDDLEDELYAQK(+2)	46.42	54.42	769.8647	866.4254	26
SIDWDLLEK(+2)	49.44	57.44	559.79	918.4567	19.7
SIDWDLLEK(+2)	49.44	57.44	559.79	803.4298	19.7
SIDWDLLEK(+2)	49.44	57.44	559.79	617.3505	19.7
SSLYC[+57.0]SDIPSIHPISEPK(+3)	43.84	51.84	677.3348	1104.605	28
SSLYC[+57.0]SDIPSIHPISEPK(+3)	43.84	51.84	677.3348	1007.552	28
SSLYC[+57.0]SDIPSIHPISEPK(+3)	43.84	51.84	677.3348	807.4359	28
SSLYC[+57.0]SDIPSIHPISEPK(+3)	43.84	51.84	677.3348	670.377	28
SVILLGR(+2)	40.05	48.05	379.2502	571.3926	14.3
SVILLGR(+2)	40.05	48.05	379.2502	458.3085	14.3
SVILLGR(+2)	40.05	48.05	379.2502	345.2245	14.3
TDLHAFENLEIIR(+3)	48.76	56.76	524.279	757.4567	22.2
TDLHAFENLEIIR(+3)	48.76	56.76	524.279	643.4137	22.2
TDLHAFENLEIIR(+3)	48.76	56.76	524.279	530.3297	22.2
TFFVHTPNR(+2)	35.5	43.5	559.7907	870.4581	19.7
TFFVHTPNR(+2)	35.5	43.5	559.7907	723.3896	19.7
TFFVHTPNR(+2)	35.5	43.5	559.7907	624.3212	19.7

TFFVHTPNR(+2)	35.5	43.5	559.7907	386.2146	19.7
TFFVHTPNR(+3)	35.5	43.5	373.5296	624.3212	16.5
TFFVHTPNR(+3)	35.5	43.5	373.5296	487.2623	16.5
TFFVHTPNR(+3)	35.5	43.5	373.5296	386.2146	16.5
TIIQNPTDQQK(+2)	32.31	40.31	643.341	958.4588	22.2
TIIQNPTDQQK(+2)	32.31	40.31	643.341	830.4003	22.2
TIIQNPTDQQK(+2)	32.31	40.31	643.341	716.3573	22.2
TIQEVAGYVLIALNTVER(+2)	67.23	75.23	995.0544	1290.742	32.8
TIQEVAGYVLIALNTVER(+2)	67.23	75.23	995.0544	1127.678	32.8
TIQEVAGYVLIALNTVER(+2)	67.23	75.23	995.0544	1028.61	32.8
TPAQFDADELR (heavy)(+2)	38.98	46.98	636.8084	1171.562	21.9
TPAQFDADELR (heavy)(+2)	38.98	46.98	636.8084	1003.472	21.9
TPAQFDADELR (heavy)(+2)	38.98	46.98	636.8084	875.4133	21.9
TPAQFDADELR (heavy)(+2)	38.98	46.98	636.8084	728.3449	21.9
TPAQFDADELR(+2)	38.98	46.98	631.8042	1161.553	21.9
TPAQFDADELR(+2)	38.98	46.98	631.8042	993.4636	21.9
TPAQFDADELR(+2)	38.98	46.98	631.8042	865.405	21.9
TPAQFDADELR(+2)	38.98	46.98	631.8042	718.3366	21.9
TQTESSTPPGIPGGSR(+2)	33.29	41.29	786.3866	1025.537	26.5
TQTESSTPPGIPGGSR(+2)	33.29	41.29	786.3866	938.5054	26.5
TQTESSTPPGIPGGSR(+2)	33.29	41.29	786.3866	837.4577	26.5
TQTESSTPPGIPGGSR(+2)	33.29	41.29	786.3866	740.405	26.5
TQTESSTPPGIPGGSR(+2)	33.29	41.29	786.3866	473.2467	26.5
TVISNLRPFTLYR(+3)	47.25	55.25	527.3033	796.4352	22.3
TVISNLRPFTLYR(+3)	47.25	55.25	527.3033	699.3824	22.3
TVISNLRPFTLYR(+3)	47.25	55.25	527.3033	552.314	22.3
TYSKPFHPK(+2)	23.83	31.83	552.7955	840.4726	19.5
TYSKPFHPK(+2)	23.83	31.83	552.7955	753.4406	19.5
TYSKPFHPK(+2)	23.83	31.83	552.7955	625.3457	19.5
VAAQNSAEVVR(+2)	28.47	36.47	572.3095	774.4104	20.1
VAAQNSAEVVR(+2)	28.47	36.47	572.3095	660.3675	20.1
VAAQNSAEVVR(+2)	28.47	36.47	572.3095	573.3355	20.1
VEQVVKPPQNK(+2)	27.89	35.89	633.3642	909.5516	21.9
VEQVVKPPQNK(+2)	27.89	35.89	633.3642	810.4832	21.9
VEQVVKPPQNK(+2)	27.89	35.89	633.3642	711.4148	21.9
VEQVVKPPQNK(+2)	27.89	35.89	633.3642	583.3198	21.9
VEQVVKPPQNK(+2)	27.89	35.89	633.3642	486.2671	21.9
VEQVVKPPQNK(+3)	27.89	35.89	422.5786	711.4148	18.3
VEQVVKPPQNK(+3)	27.89	35.89	422.5786	583.3198	18.3
VEQVVKPPQNK(+3)	27.89	35.89	422.5786	486.2671	18.3
VIESGPHC[+57.0]ANTEIIVK(+3)	35.55	43.55	589.6417	1281.662	24.7
VIESGPHC[+57.0]ANTEIIVK(+3)	35.55	43.55	589.6417	816.4825	24.7
VIESGPHC[+57.0]ANTEIIVK(+3)	35.55	43.55	589.6417	702.4396	24.7

VIESGPHC[+57.0]ANTEIIVK(+3)	35.55	43.55	589.6417	601.3919	24.7
VLDSGAPIK(+2)	32.8	40.8	450.2635	687.3672	16.4
VLDSGAPIK(+2)	32.8	40.8	450.2635	572.3402	16.4
VLDSGAPIK(+2)	32.8	40.8	450.2635	485.3082	16.4
VLDSGAPIK(+2)	32.8	40.8	450.2635	357.2496	16.4
VLISTDVWAR(+2)	45.91	53.91	580.3271	834.4104	20.3
VLISTDVWAR(+2)	45.91	53.91	580.3271	747.3784	20.3
VLISTDVWAR(+2)	45.91	53.91	580.3271	646.3307	20.3
VLQGLPR(+2)	34.94	42.94	391.7478	683.4199	14.7
VLQGLPR(+2)	34.94	42.94	391.7478	570.3358	14.7
VLQGLPR(+2)	34.94	42.94	391.7478	442.2772	14.7
VLSPESK(+2)	24.49	32.49	380.216	660.3563	14.3
VLSPESK(+2)	24.49	32.49	380.216	547.2722	14.3
VLSPESK(+2)	24.49	32.49	380.216	460.2402	14.3
VLSSIEQK (heavy)(+2)	29.81	37.81	456.268	699.3763	16.5
VLSSIEQK (heavy)(+2)	29.81	37.81	456.268	612.3443	16.5
VLSSIEQK (heavy)(+2)	29.81	37.81	456.268	525.3122	16.5
VLSSIEQK(+2)	29.81	37.81	452.2609	691.3621	16.5
VLSSIEQK(+2)	29.81	37.81	452.2609	604.3301	16.5
VLSSIEQK(+2)	29.81	37.81	452.2609	517.298	16.5
VTTHPLAK(+2)	22.85	30.85	433.7584	767.441	15.9
VTTHPLAK(+2)	22.85	30.85	433.7584	666.3933	15.9
VTTHPLAK(+2)	22.85	30.85	433.7584	565.3457	15.9
VTTHPLAK(+2)	22.85	30.85	433.7584	428.2867	15.9
VTVAGLAGK (heavy)(+2)	34.47	42.47	412.26	623.3966	15.2
VTVAGLAGK (heavy)(+2)	34.47	42.47	412.26	524.3282	15.2
VTVAGLAGK (heavy)(+2)	34.47	42.47	412.26	453.2911	15.2
VTVAGLAGK(+2)	34.47	42.47	408.2529	615.3824	15.2
VTVAGLAGK(+2)	34.47	42.47	408.2529	516.314	15.2
VTVAGLAGK(+2)	34.47	42.47	408.2529	445.2769	15.2
WVQDSMK(+2)	31.72	39.72	447.2129	707.3393	16.3
WVQDSMK(+2)	31.72	39.72	447.2129	608.2708	16.3
WVQDSMK(+2)	31.72	39.72	447.2129	480.2123	16.3
YADGTIDIEEVTENPK(+2)	43.68	51.68	897.4256	1173.563	29.8
YADGTIDIEEVTENPK(+2)	43.68	51.68	897.4256	1058.536	29.8
YADGTIDIEEVTENPK(+2)	43.68	51.68	897.4256	945.4524	29.8
YGSQVEDQR(+2)	25.92	33.92	541.2491	774.3741	19.1
YGSQVEDQR(+2)	25.92	33.92	541.2491	646.3155	19.1
YGSQVEDQR(+2)	25.92	33.92	541.2491	547.2471	19.1
YIEHLEAVTC[+57.0]K(+2)	35.15	43.15	681.8397	957.4822	23.4
YIEHLEAVTC[+57.0]K(+2)	35.15	43.15	681.8397	820.4233	23.4
YIEHLEAVTC[+57.0]K(+2)	35.15	43.15	681.8397	707.3393	23.4
YIEHLEAVTC[+57.0]K(+3)	35.15	43.15	454.8956	707.3393	19.6

YIEHLEAVTC[+57.0]K(+3)	35.15	43.15	454.8956	578.2967	19.6
YIEHLEAVTC[+57.0]K(+3)	35.15	43.15	454.8956	507.2595	19.6
YLAEVATGDDK(+2)	34.08	42.08	591.2879	834.384	20.6
YLAEVATGDDK(+2)	34.08	42.08	591.2879	705.3414	20.6
YLAEVATGDDK(+2)	34.08	42.08	591.2879	606.2729	20.6
YLAEVATGEK(+2)	33.78	41.78	540.7822	804.4098	19.1
YLAEVATGEK(+2)	33.78	41.78	540.7822	733.3727	19.1
YLAEVATGEK(+2)	33.78	41.78	540.7822	604.3301	19.1
YQEALAK(+2)	27.25	35.25	411.7214	659.3723	15.3
YQEALAK(+2)	27.25	35.25	411.7214	531.3137	15.3
YQEALAK(+2)	27.25	35.25	411.7214	402.2711	15.3
YQEALAK(+2)	27.25	35.25	411.7214	331.234	15.3
YYIHDHFIPIEK(+3)	40.13	48.13	525.6049	883.5036	22.3
YYIHDHFIPIEK(+3)	40.13	48.13	525.6049	746.4447	22.3
YYIHDHFIPIEK(+3)	40.13	48.13	525.6049	599.3763	22.3
YYIHDHFIPIEK(+3)	40.13	48.13	525.6049	486.2922	22.3

Database Links

dbGAP: http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/dataset.cgi?study_id=phs000007.v27.p10&pht=1415

MassIVE: https://massive.ucsd.edu/ProteoSAFe/static/massive.jsp

Panorama Public:
https://panoramaweb.org/labkey/project/Carr/Plasma_TSQQuantiva_AptamerMRM/begin.view