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Wound Status Early Outcome Sensor and 3D Construct Development

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14. ABSTRACT Early identification of the specific proteins, which indicate delayed healing are critical to long-term success of the patient and the development of new treatments. It is the objective of this research to correlate changes in the proteome of wounds with clinical outcome and develop technology to sense these changes. A technique to classify a sampling timepoint based on a sliding 3 timepoint scale was developed. Proteomic analysis of the wound fluid utilized antibody dependent and independent techniques. The quantitative microarray demonstrated significantly different levels of S100A8 and TGFBR3 between healing and worsening wounds. The utilization of SRM-MS for wound fluid analysis is a significant development in the path to wound outcome diagnosis. Ultimately this work may allow the development of personalized wound care based on the proteomic characteristics of the wound.					
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Table of Contents

Introduction	4
Keywords.....	4
Overall Project Summary	4
Key Research Accomplishments	29
Conclusion	29
Publications, Abstracts, and Presentations.....	30
Inventions, Patents, Licenses	N/A
Reportable Outcomes	31
Other Achievements	31
References	31
Appendices	32

INTRODUCTION:

Early identification of the specific proteins, which indicate delayed healing are critical to long-term success of the patient and the development of new treatments. It is our hypothesis that real time sensing of the wound proteome can be used to predict wound outcome, resulting in tailored treatment that improve acute and chronic wound healing. The focus of this proposal is to correlate protein targets and wound outcome and develop a technology that can sense the microenvironment in acute and chronic wounds.

KEYWORDS:

Wound healing, proteomics, biomarkers, microarray, xerogel, SRM-MS, wound fluid, S100A8, S100A9, CXCL9, L-selectin, wound trajectory, MMP-9, TGFB3, RBP4

OVERALL PROJECT SUMMARY:

Statement of Work

Technical Objective 1:

Develop technologies for sensing multiple proteins in the wound microenvironment, in real time.

Subtask 1.1 Develop xerogel-based elements.

Subtask 1.2 Develop PBG-based sensor platforms.

Subtask 1.3 Sensor design and evaluation using wound fluids.

Technical Objective 2:

Test the suitability of our technology for the detection of multiple proteins from acute and chronic wounds in vitro and in vivo, and correlate results with clinical outcomes.

Subtask 2.1 Collect fluid from subjects with pressure ulcers

Subtask 2.2 Collect samples from wounds in porcine model

Subtask 2.3 Proteomic analysis of wound fluid

Technical Objective 1:

Subtask 1.1 Develop xerogel-based elements.

Luminescence based detection is frequently used in chemical, medical, and biomedical diagnostic applications. These sensors have several advantages including fast response and high efficiency. They are less prone to contamination, and display high sensitivity and specificity compared to competing approaches. Sol-gel derived xerogels have been widely used as the platforms for immobilization of active agents. They are meso-porous materials that encapsulate the optically active recognition elements while providing maximum surface interaction area. New integrated sensors that included the xerogel as the selective sensing element were fabricated and the polymer porous photonic bandgap (P³BG) structure as a tunable, high efficiency and noise-free bandpass filter and wavelength selector. This integration provided a template for luminescence based sensing with enhanced analytical signals (AS).

Subtask 1.2 Develop PBG-based sensor platforms.

Monitoring of the biochemical environment on the curved surface of animal and human skin requires the development of a new class of sensing platform. A flexible optical sensing element that conforms to the curved surfaces could potentially be integrated into a bandage. Porous polymeric photonic bandgap (P³BG) structures have been demonstrated to be excellent platforms for gas and liquid analyte sensing. Two main mechanisms are generally used for sensing with these structures: 1) detecting the wavelength shift of the photonic bandgap caused by the refractive index change induced by filling the pores with gaseous or liquid analytes; and 2) embedding analyte specific luminophores within the pores and detecting the quenching of their luminescence due to binding with the analyte. Porous polymeric PBG structures were fabricated on large area flexible substrates (Figure 1).

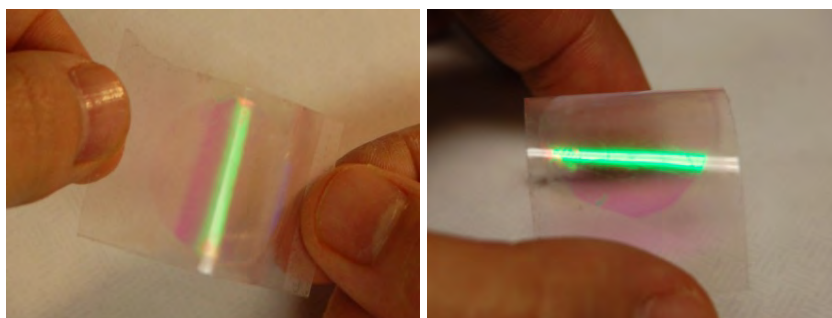


Figure 1. Images of flexible PBG structures.

The optical properties were characterized and compared as a function of angle of incidence for curved and flat porous polymer PBG structures. Specifically, samples were illuminated with the white light beam at positions with a displacement of d ($d=0\text{mm}, 2\text{mm}, 4\text{mm}, \dots$) from the center of the curved flexible PBG structure attached to the column of radius 12mm. The resulting transmission spectra, as a function of displacement, are plotted (Figure 2a). This result can be directly compared to the measurement of the transmission spectra of a flat PBG structure at angles $\alpha = \sin^{-1}(d/R)$ (Figure 2b). The colors in the graph stand for the transmission efficiency. The dispersion curves from these two sets of data are in a good agreement with each other.

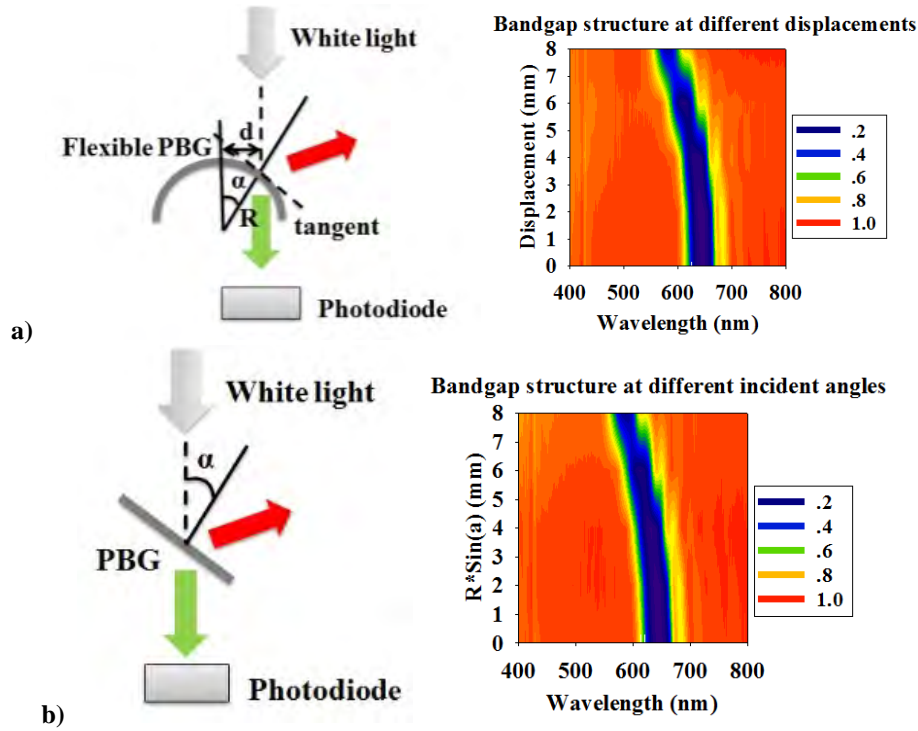


Figure 2. Measurement geometry and dispersion curves of a) flexible PBG structure for different displacements, d , and b) flat PBG structure at the corresponding incident angle $\alpha = \sin^{-1}(d/R)$.

Optical concentrators in the micron scale are important components for photonics devices. These micro-concentrators can be used to enhance the detection of fluorescence signals in biosensors. Micro-concave shaped Bragg reflector were fabricated using holographic photo-patterning by recording the interference of plane wave and divergent wave from the reflection of a spherical surface. The fabrication of these structures with dimensions down to several microns was successfully completed (Figure 3). The resulting structures demonstrate good light focusing (Figure 4). This method is more efficient and lower-cost when compared to other fabrication methods such as atomic layer deposition and electrochemical anodisation.

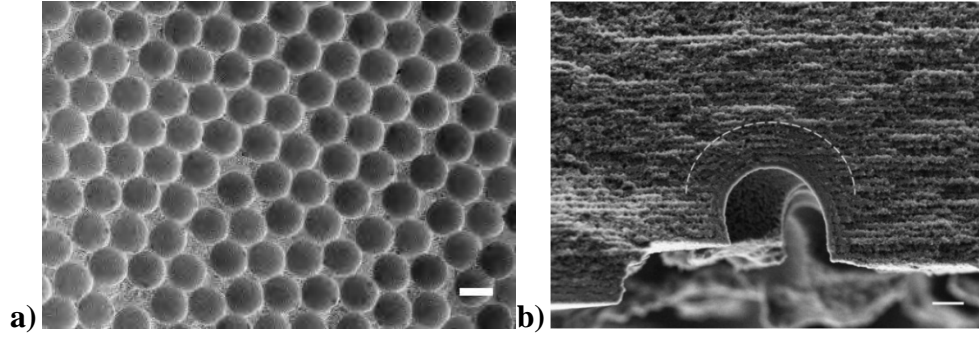


Figure 3. The SEM images of a) the top-view of the formed concave shaped Bragg reflector array (Scale bar: 5 μm); b) the cross-section of one concave shaped Bragg reflector (Scale bar: 1 μm), the white dash line indicates the profile of the concave layers.

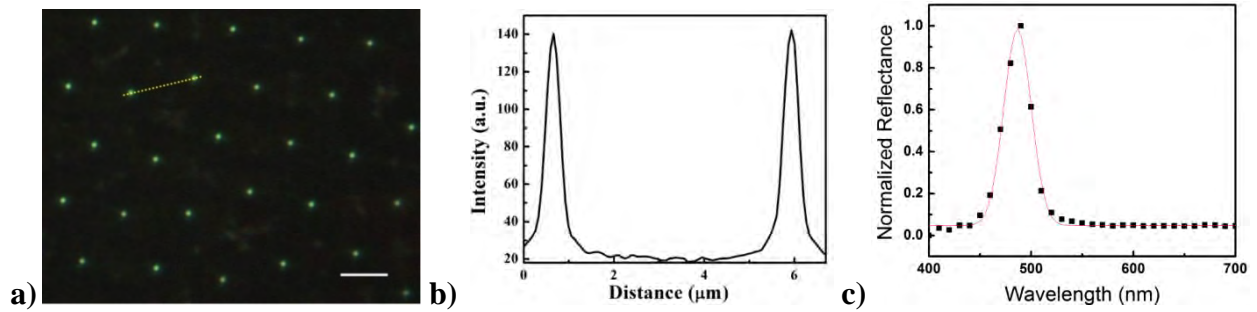


Figure 4. The microscope images of a) the microscopic image of the micro-spherical array illuminated using white light (scale bar: 5 μm); b) The variation of the gray value across the centers of two concave shaped Bragg reflectors and c) The normalized reflectance spectrum of the focusing points.

A one-step fabrication method was used to create a graded holographic photopolymer reflection grating by using cylindrical lens. The period of the Bragg reflector at different lateral positions along the structure is varied gradually, leading to a unique rainbow-colored reflection image in the same viewing angle (Figure 5). Compared to previously reported graded photonic or plasmonic structures prepared by expensive focus ion beam (FIB) milling or electron beam lithography techniques, this holographic photopatterning method is low-cost and amenable to large area fabrication. The dimension of these grating is scalable by using cylindrical lenses with different focal lengths and diameters.

These graded holographic photopolymer reflection gratings provide a low-cost and light-weight solution for multispectral imaging technology. By integrating these grating filters with other imaging devices, they can be applied in bio-imaging and sensing. Sensing for wound healing involves analyzing multiple proteins and growth factors in the wound microenvironment. The graded grating has the potential to serve as multiplexed-channel analyte sensors. Series of fluorescent labels with distinctive emission wavelengths can be employed to detect multiple analytes on one sensor.

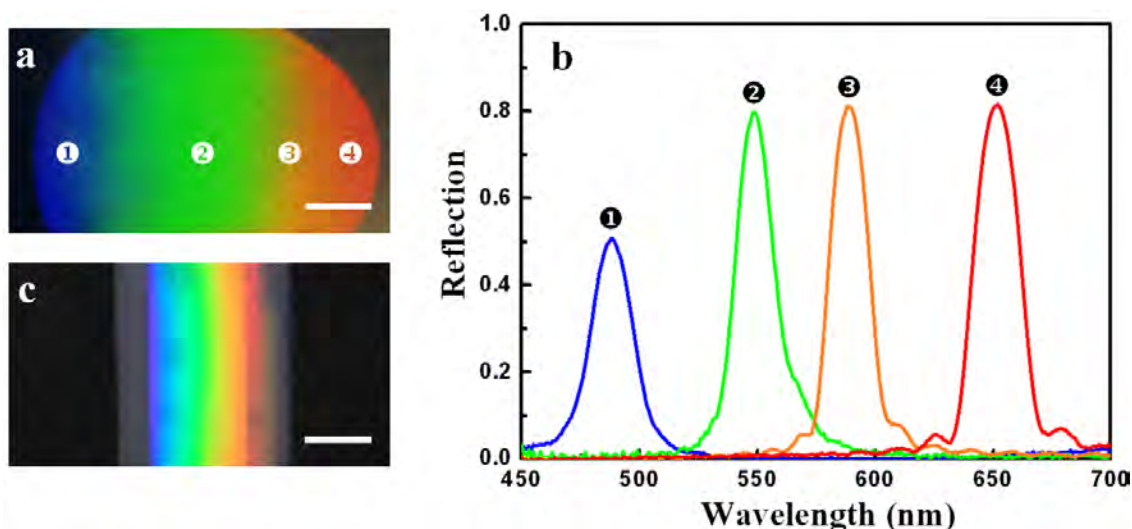


Figure 5. a) The reflection image of the graded holographic photopolymer grating under white light illumination; b) The reflection spectra measured at different positions indicated by circles in (a); c) A second example of a graded holographic photopolymer grating fabricated using a shorter focal length cylindrical lens. Scale bar: 5 mm.

Subtask 1.3 Sensor design and evaluation using wound fluids.

Oxygen responsive sensor platforms were fabricated by pin printing tris (4,7-diphenyl-1,10-phenanthroline) ruthenium(II) ($[\text{Ru}(\text{dpp})_3]^{2+}$) doped sols onto reflective Bragg gratings. The polymeric reflective Bragg gratings were fabricated using holographic lithography method. In an epi-luminescence configuration, these Bragg gratings were designed to reflect selectively the O_2 responsive $[\text{Ru}(\text{dpp})_3]^{2+}$ emission toward the detector to enhance the emission signal intensity. The results show that this hybrid sensor platform exhibits linear, statistically equivalent O_2 sensitivities and yields up to an eight fold increase in analytical signal in comparison to the original sensor platform consists only with pin printing tris(4,7-diphenyl-1,10 phenanthroline) ruthenium(II) ($[\text{Ru}(\text{dpp})_3]^{2+}$) doped sols (Figure 6).

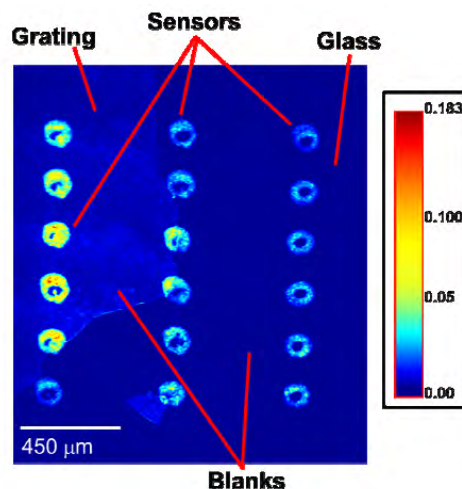


Figure 6. False-color image at 610 nm in the presence of 50% N₂; an O₂ responsive hybrid pin printed sol-gel sensor array comparing with an original pin printed sol-gel sensor array.

The PIXIES (protein imprinted xerogels with integrated emission site) platform was used to detect cytokines of both in vitro and in vivo wound fluids. Porcine wound fluids were analyzed for KGF, IL-1, IL-6, IL-12, TNF α TGF-beta, VEGF and EGF. Detection limits were ≤ 2 pg/ml and results were compared with ELISA.

Preliminary studies were undertaken to evaluate novel amino acid-modified hydrogel materials for wound healing. HaCaT keratinocyte cells were tested for ability to attach and proliferate on these materials and culture fluid was collected for growth factor/cytokine analysis using PIXIES.

Ultimately issues remain with implementation of PIXIES for wound sensing. The primary issue is the long timeline ahead of the technology. The PIXIES sensor technology must be integrated into another platform for use. Ultimately, it is not a common technology and has a long road to bedside use due to the early stages of the technology. Additionally, the wound bed presents an extremely challenging environment for any type of proteomic technology. Wound fluid is a complex mixture of proteins and protein fragments due to the aggressive proteolysis in the environment. PIXIES is a molecular imprinting technology and although it has been shown to work well with intact proteins, but protein fragments are likely abundant in wound fluid and it may prove difficult to keep the fragments necessary for fluorescence change to occur in a timely fashion. During the analysis of samples using iTRAQ technology as part of the planned workflow for the proteomic analysis, a new potential tool for analysis of the wound fluid in a cost effective, low sample usage technology came to light. Selected reaction monitoring mass

spectrometry (SRM-MS) is a targeted proteomics technology used to identify and quantify proteins with high sensitivity, specificity and high reproducibility. SRM-MS is ideally matched to analysis of intact proteins and peptides. SRM-MS is a much more sensitive and reproducible method for quantifying lower abundance proteins in complicated biological samples. It is a targeted technique that differs from the mass spectrometry approaches widely used in discovery proteomics. Furthermore, SRM-MS is being developed for use in a wide variety of applications including the diagnosis of disease processes including different types of cancer (1-3). The technique identifies and quantifies the proteins present and it allows much greater flexibility for samples analyzed. Rather than requiring sample collection directly from the wound bed, wound exudate collected as part of treatment using negative pressure wound therapy (NPWT) could be analyzed. This common treatment is widely used in chronic, acute, and burn wounds. SRM-MS is a repeatable technique across laboratories and does not require development of new technology for the platform, thus allowing a faster track to development and bedside application.

SRM-MS findings are in section *Subtask 2.3* of this report.

Technical Objective 2:

Subtask 2.1 Collect fluid from subjects with pressure ulcers

Enrollment was below the target set even though no cost extensions allowed additional time for recruitment. Final enrollment was 15 men and 2 women with an average age of 63.2 years.

Wound surface area (WSA) measurements were completed for each subject and weekly time point using VeVMD software. The percent change in WSA from the original timepoint was calculated and plotted as the wound trajectory. A combined plot of all wounds is shown below (Figure 7).

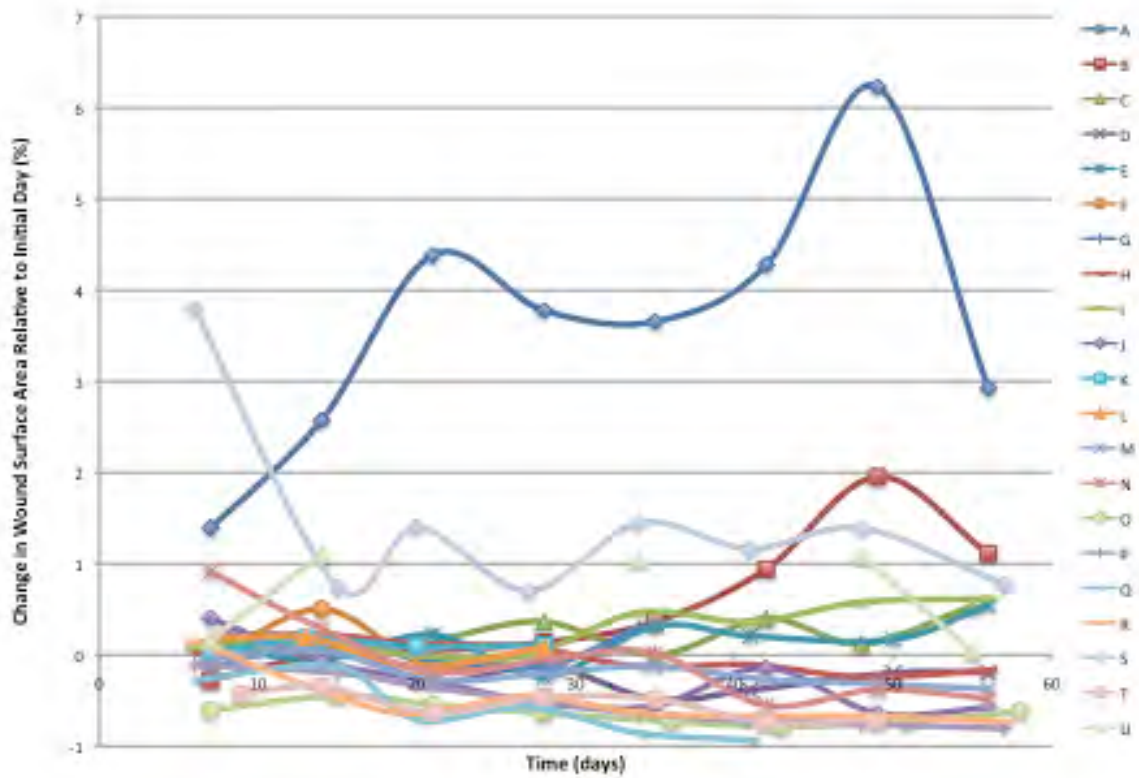


Figure 7. Wound trajectories, the change in wound surface area relative to the initial area, for chronic wounds observed for up to 8 continuous weeks.

This second plot of WSA (Figure 8) differs by the exclusion of 3 wounds (A,S, and U) that increased dramatically in area or were intermittently sampled and is shown to illustrate the trend in area changes for the remaining chronic wounds enrolled.

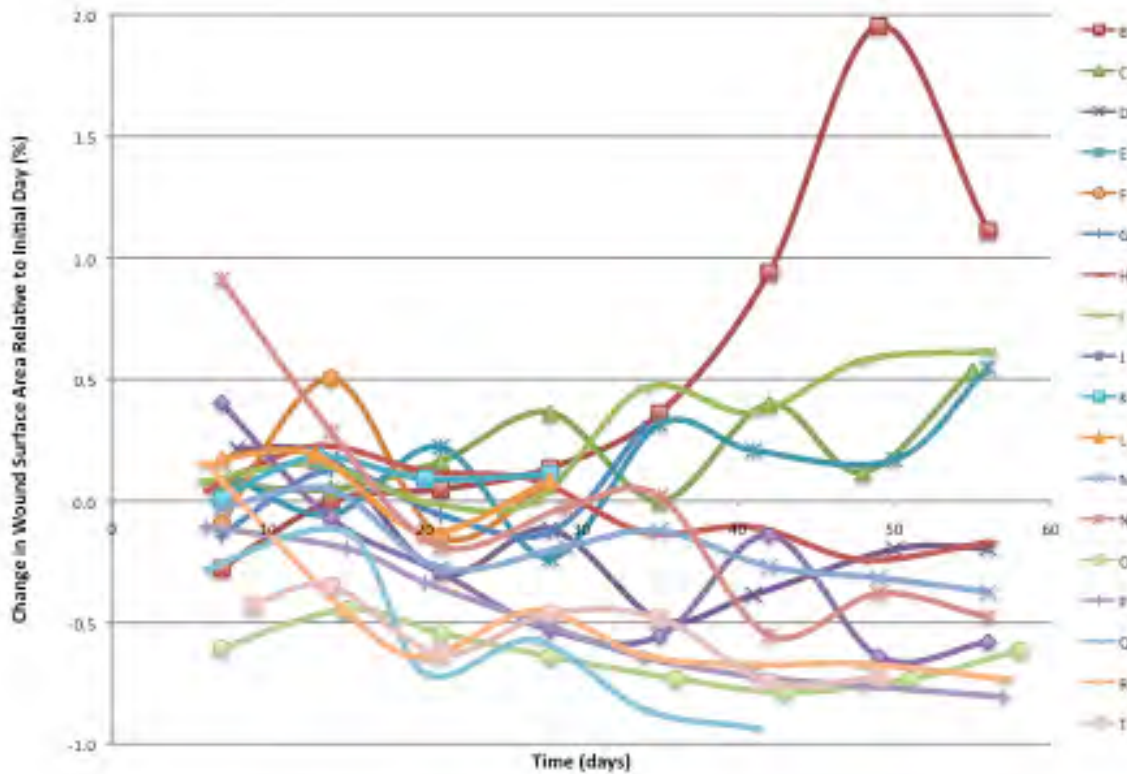


Figure 8. Wound trajectories with wounds with large-scale area changes (n=3) removed to illustrate fine scale differences for the remaining and majority of enrolled wounds.

Evaluation of wound fluids for markers of clinical outcomes is a rapidly expanding field, but the determination of outcome for subjects and sample timepoints is not generally agreed upon. Many studies rely on subjective clinical appearance when classifying wounds and samples (4). Previously, we determined that tissue type does not predict wound outcome for chronic wounds (5). Additionally, although wound healing trajectories can be indicative of healing (6), the overall trend of a wound does not accurately reflect the status of the wound at any single timepoint. Use of measurements comparing initial size to subsequent timepoints, healing trajectories, are generally accepted for tracking progress (tracking). There is no known rate of healing in chronic wounds.

Commonly, chronic wounds experience fluctuations in wound dimensions, both decreasing and increasing in size during the overall path to wound closure. Figure 9 shows 2 wounds sampled in this study. One wound is clearly healing throughout and the other is fluctuating, which makes

the determination of status for the timepoints difficult to classify. If overall a wound heals, but during a period the wound worsens should that point be a healing or worsening sample?

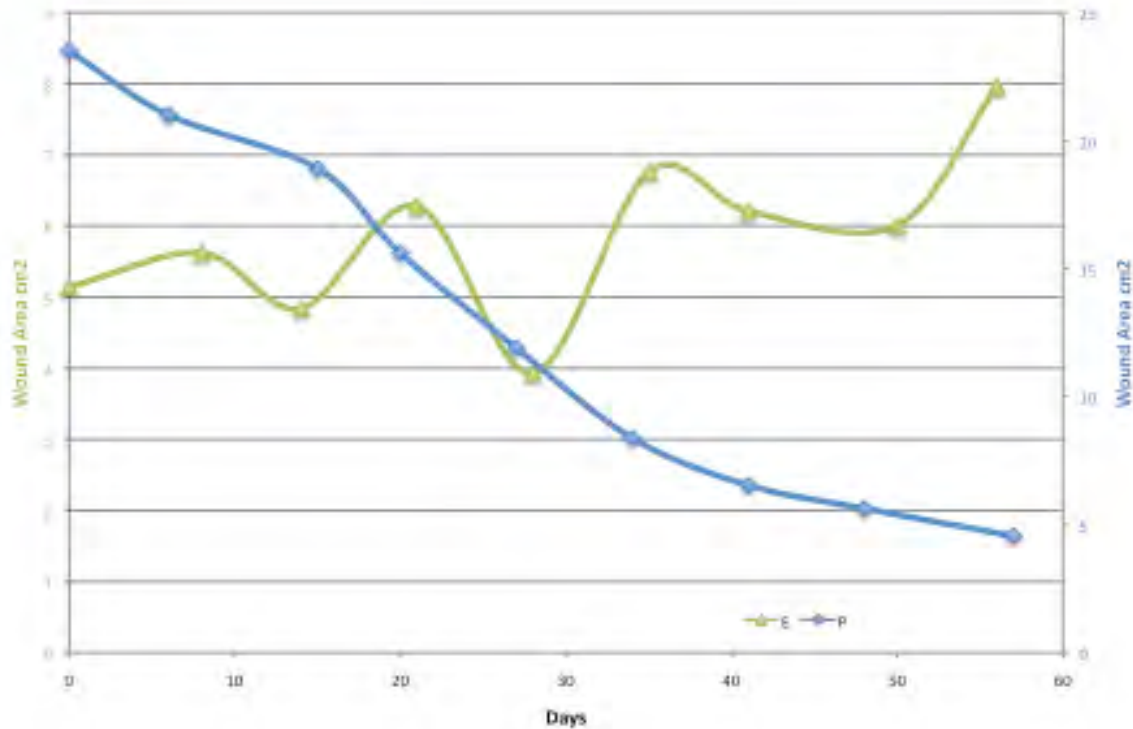


Figure 9. Trends in wound surface area changes for two wounds. Wound E has oscillating area changes, but after 8 weeks is larger than when initially measured. Wound P remains on a healing course throughout the 8 weeks of observation.

Clearly the wounds have varying surface area trends and amplitudes. Commonly, wound outcomes are determined by final percentage of healing, ignoring healing and declining phases throughout the study. When using wound fluid samples to evaluate potential biomarkers it is critical that the samples be sorted into healing and non-healing cohorts correctly. Without any standard in the literature, we sought to define a technique to classify a sampling timepoint based on a sliding 3 timepoint scale that uses the prior and following timepoint data to describe the trend for the wound during the middle timepoint. We divided the timepoints into categories for analysis and comparison using the area changes calculated on a weekly basis with the week prior as the standard to measure changes in WSA rather than the initial measurement. A sliding scale

was used to identify wound timepoints that serve as representative samples for wounds that are decreasing in area or increasing in area. A 2 point sliding scale considers only area changes from the last timepoint, The 3 point sliding scale uses 3 consecutive area measurements and evaluates if the wound was following a constant trajectory of increased or decreased area. Three consecutive wound area data measurements must be consistently increasing or decreasing for the middle timepoint to be assigned to a cohort. The scale slides down the temporal scale considering each set of 3 data measurements in turn. The first and last samples are never considered for cohort inclusion since their immediate history and future are unknown. If the middle point decrease in size and the next point increases in size it is not possible to determine the status of the middle point. The 3rd point is being used to confirm the direction of the middle point and allow sorting of the samples. The middle timepoint is selected as a potential representative of closing or expanding wound healing processes.

Further refinement of the data requires a minimum change in WSA. A threshold is used to filter the wound timepoints based on a minimum change in wound area. Filtering in one direction, single threshold, requires the threshold to be true for only one direction from the middle timepoint. Filtering on the percent change in area before and after, dual threshold, further refines the potential representatives. As the degree of change filter increases (more stringent), fewer wound timepoints are included as representative samples. A one-way or single threshold of 15% yields 10 or more samples in each category (Figures 10 and 11). 15% was chosen based on the pressure ulcer and chronic wound healing literature, which indicates 20-40% healing over a course of 2-4 weeks is indicative of healing (6).

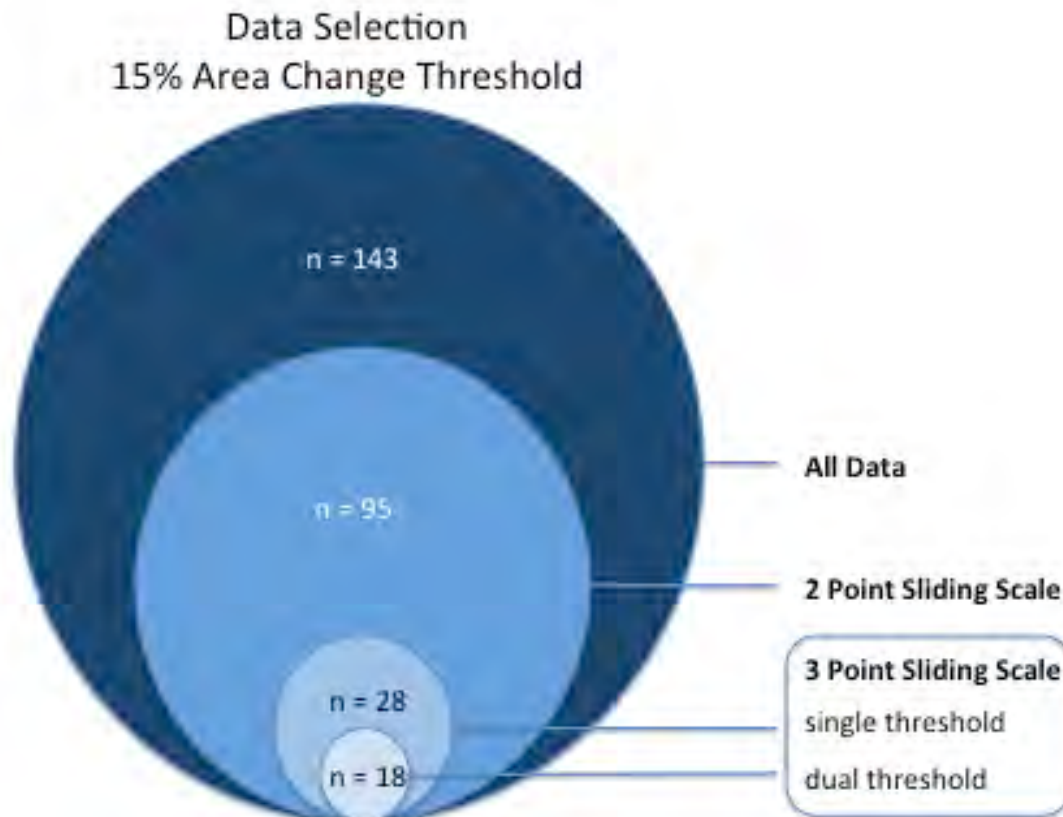


Figure 10. The sampling space for enrolled wounds begins with 143 timepoints. The application of a 2 point sliding scale and imposing a minimum 15% change in wound area relative to the previous measurement reduces the number of timepoints to 95. Further refining the data by applying a 3 point sliding scale where the trajectory must be unidirectional increases the confidence that the wound fluid proteins are representative of a healing or worsening wound. Applying a one-way threshold of 15% reduces the number of data points to 28. The highest confidence is achieved with a dual threshold, applied to both the previous and following area measurement but the data is reduced to 18 timepoints.

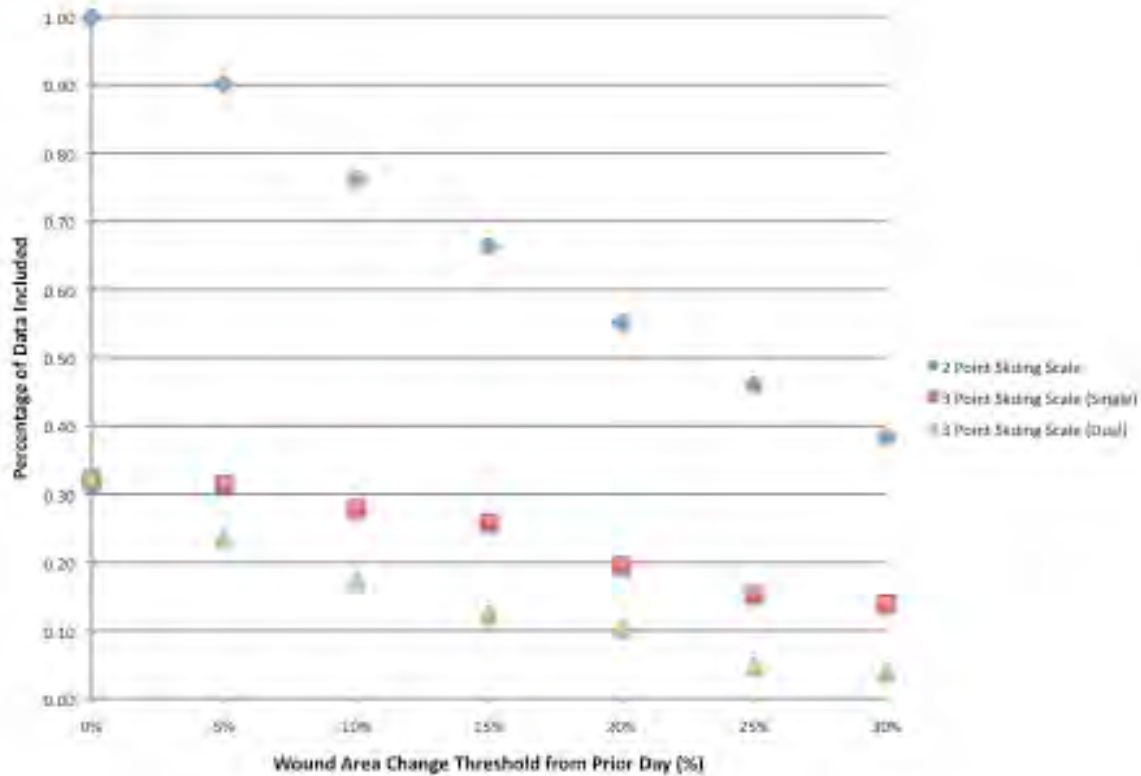


Figure 11. Effect of scale and threshold on data inclusion. As the inclusion criterion increases in stringency from a 2 point to a 3 point scale the amount of data used in each analysis is reduced. This relationship is true also for the threshold set for increasing levels of area change between measurements. With increased stringency comes greater confidence, but fewer data points.

A technology to evaluate the proteome for biomarkers of healing would not be particularly useful in wounds that are obviously healing, but for chronic wounds that are slow to respond to treatment, a biomarker would allow for identification of improving or worsening wounds. In order to identify and validate these biomarkers samples from wounds must include points throughout the wounds progress. The classification technique described is applicable to all wounds. All wound samples were evaluated using the above analysis and divided into bigger (worsening) or smaller (healing). Samples were then group accordingly for proteomic analysis (Figure 12).



Figure 12. Using wound area measurements, the samples were divided into healing or smaller and increasing or larger sample groups. The groups were built using a 2 point scale and 15% threshold, a 3 point scale with single 15% threshold and a 3 point scale with dual 15% threshold before proteomic analyses.

Subtask 2.2 Collect samples from wounds in porcine model

A partial-thickness dermatome-induced wounds were generated in a porcine model and wound healing parameters included wound fluid cytokine analysis.

Subtask 2.3 Proteomic analysis of wound fluid

Porcine wound fluid samples were analyzed using PIXES see section *Subtask 1.3*

Human wound fluid samples were analyzed in using both antibody dependent and antibody independent techniques. The workflow for the analysis is shown in Figure 13.

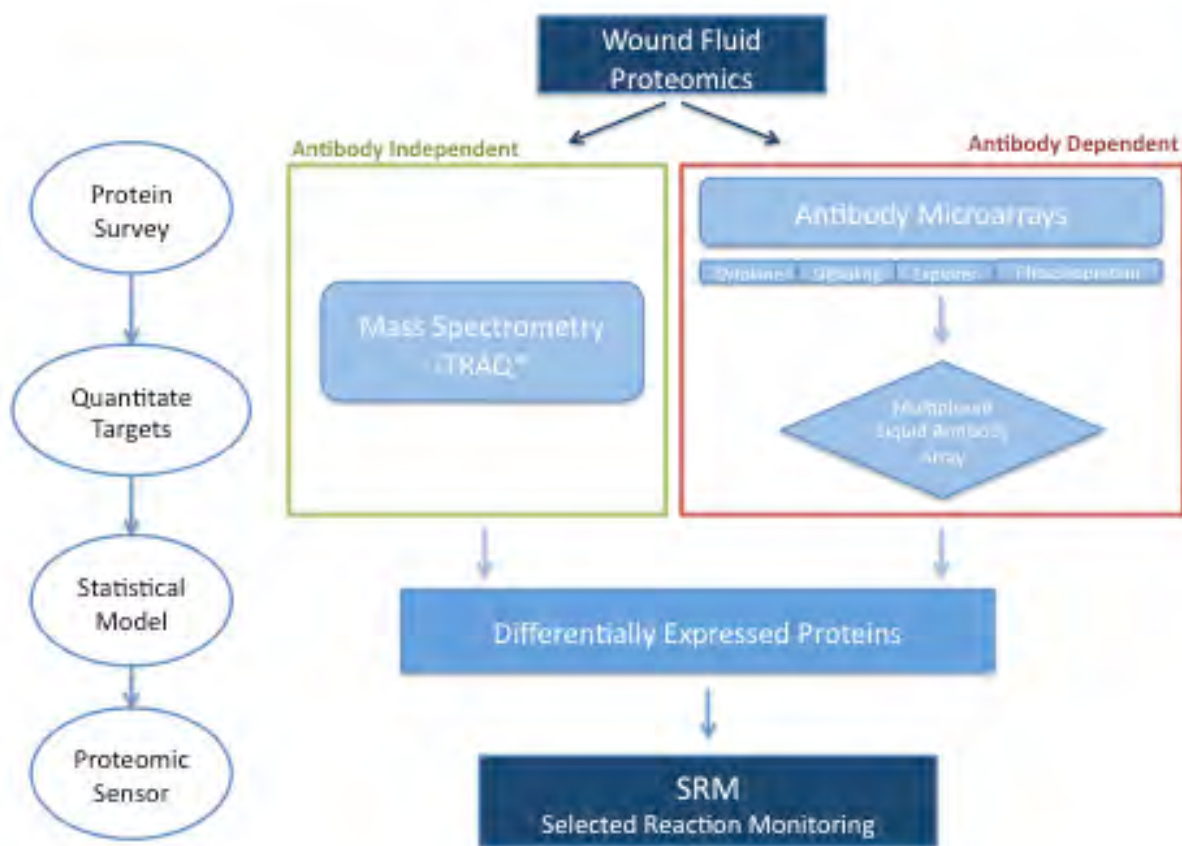


Figure 13. Pooled wound fluid samples were subjected to antibody independent and antibody dependent surveys to identify new potential biomarkers.

Antibody Independent

iTRAQ Analysis

Two sets of pooled samples, one representing wounds increasing in area and the other representing wounds decreasing in area were submitted for mass spectrometry using iTRAQ methodology. The iTRAQ experiments included a biological replicate as well as a technical replicate and data was normalized for direct comparison. Through iTRAQ labeling quantitative proteomics analysis, the expression levels of 2561 proteins were analyzed.

For the plots below, the technical replicates are defined as Experiment 1 and Experiment 2 and in each experiment, there were two ratios, a Larger/Smaller ratio (corresponding to 115/114 ratios in both datasets) and a biological repeat of Larger/Smaller ratio (corresponding to 117/116 ratios

in both datasets). See Appendices A and B for data. The experimental matrix is represented in Figure 14.

	Experiment 1		Experiment 2	
Protein Accession	Larger /Smaller	Larger /Smaller (biological repeat)	Larger /Smaller	Larger /Smaller (biological repeat)
126032350	0.949	1.093	0.967	1.169
...

Figure 14. Technical repeat data are shown with 4 relative ratios from 2 datasets corresponding to a unique protein ID.

Outliers were observed from comparisons of biological repeats in both technical replicate experiments and the data were manually inspected. Outliers were identified as not reproducible in biological replicates, which indicates the possibility of random bias for certain proteins with iTRAQ channel specificity. Raw spectrum data of the outliers were checked and their data qualities were confirmed. Median normalization was chosen to apply to raw data and normalize the reported ratios of the proteins comparing Larger Wound group to Smaller Wound group. Histograms were made to compare the data before and after normalization (Figures 15a and 15b).

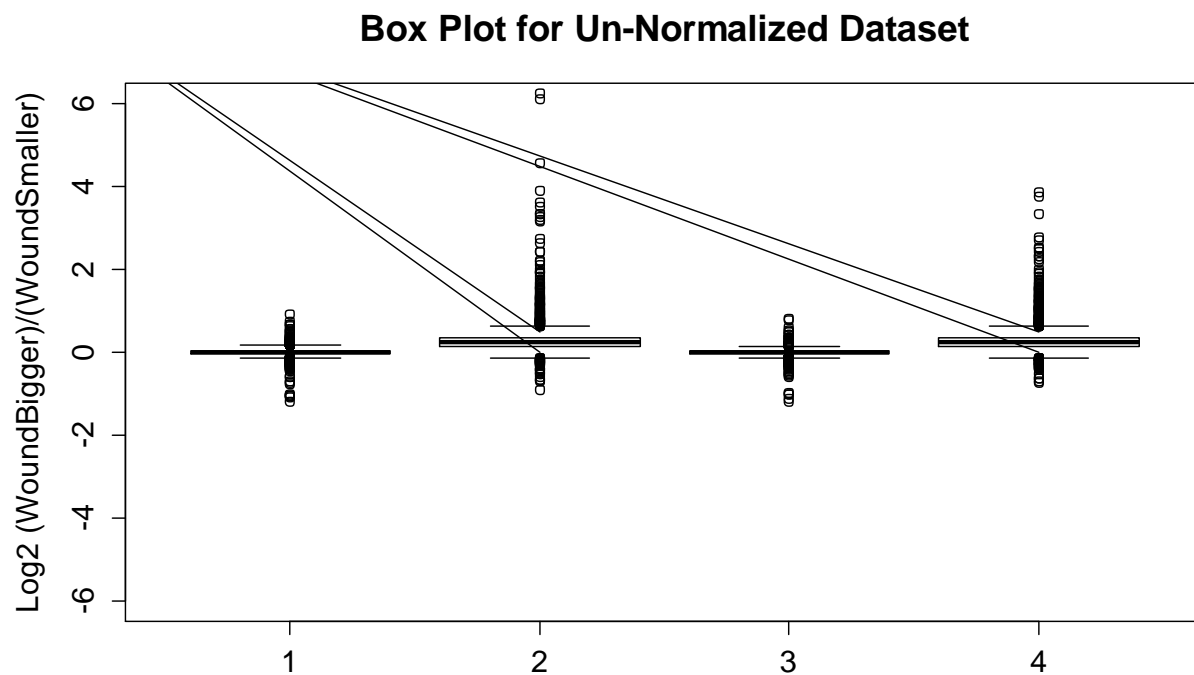


Figure 15a. Histogram of data prior to normalization.

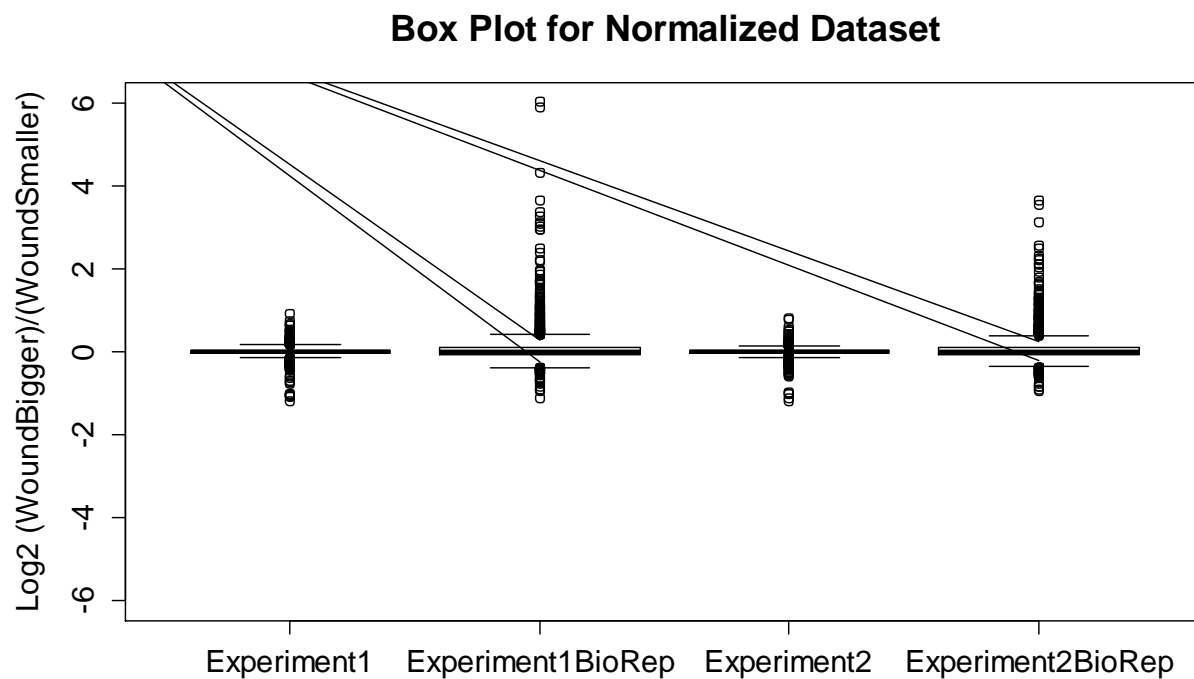


Figure 15b. Histogram of data after normalization.

From the different expression levels of 2561 proteins analyzed by iTRAQ, the top 20 proteins overexpressed in wound fluid from the wounds that are worsening are shown in Figure 16.

GI	Protein Names	EXP 1	EXP 1 BioRep	EXP 2	EXP 2 BioRep
14790190	msx2-interacting protein [Homo sapiens]	NA	NA	1.2659	2.5466
530373465	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 isoform X1 [Homo sapiens]	1.3928	2.5876	NA	NA
4557831	pterin-4-alpha-carbinolamine dehydratase isoform 1 [Homo sapiens]	1.1306	2.3861	NA	NA
578806381	PREDICTED: kinesin-like protein KIF15 isoform X2 [Homo sapiens]	1.5623	2.1505	1.7042	2.4234
578805065	PREDICTED: protein TANC1 isoform X8 [Homo sapiens]	1.2014	1.5009	NA	NA
556503347	vacuolar protein sorting-associated protein VTA1 homolog isoform c [Homo sapiens]	1.1944	1.4609	0.9064	1.0607
40354201	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 isoform 2 [Homo sapiens]	1.2841	1.4524	NA	NA
7657381	pre-mRNA-processing factor 19 [Homo sapiens]	1.1834	1.4294	1.0737	1.7417
578818239	PREDICTED: CUGBP Elav-like family member 2 isoform X22 [Homo sapiens]	1.5374	1.4107	NA	NA
578836106	PREDICTED: retinoblastoma-like protein 1 isoform X1 [Homo sapiens]	1.2901	1.3265	NA	NA
578811945	PREDICTED: large proline-rich protein BAG6 isoform X12 [Homo sapiens]	1.1216	1.2781	NA	NA
5453914	phospholipid transfer protein isoform a precursor [Homo sapiens]	1.1595	1.2381	NA	NA
530398960	PREDICTED: dynamin-1-like protein isoform X2 [Homo sapiens]	1.0499	1.2372	1.0030	1.1129
578827454	PREDICTED: AP-3 complex subunit beta-2 isoform X2 [Homo sapiens]	1.4237	1.2185	NA	NA
12056473	sialic acid synthase [Homo sapiens]	1.0249	1.1539	NA	NA
93204867	probable G-protein coupled receptor 158 precursor [Homo sapiens]	1.4516	1.1182	1.5050	1.3661
4557313	angiogenin precursor [Homo sapiens]	1.2682	1.1156	NA	NA

Figure 16. Top 20 proteins overexpressed in wound fluid from the wounds that are getting larger over the 8 week period.

Antibody Dependent

Antibody Microarrays

Antibody arrays are a high-throughput ELISA based platform for efficient protein expression profiling in chronic wound fluid. A large number of targets can be profiled using a small volume of sample leading to the identification of differentially expressed proteins. The wound fluid proteins are biotin labeled, incubated with the antibody array, and detected using dye or fluorescent-tagged streptavidin. Because the proteins remain non-denatured, false positives may result from protein-protein interactions and non-specific binding and follow-up validations are necessary. Pooled samples using a dual threshold of 15% and a 3 point sliding scale were used on the arrays.

Four antibody arrays were utilized to test for differentially expressed proteins from chronic wound fluid. The cytokine profiling array (Appendix C) features 310 unique antibodies for profiling cytokines and related biomarkers in human cells, tissues, serum or culture media. The explorer antibody array (Appendix D) is a broad-scope antibody array with 656 highly specific and well-characterized antibodies from more than ten signaling pathways. The signaling explorer array (Appendix E) features 1358 unique antibodies covering twenty biological signaling pathways and is ideal for high-throughput biomarker screening and discovery. Targets with a greater than 2 fold difference in expression are differentially given in Figure 17.

Protein Target	Expression Ratio	Array
Vascular Endothelial Growth Factor(VEGF)	4.59	E
Tubulin alpha	4.41	SE
Actin beta	3.40	E
Survivin	2.78	E
Beta actin	2.62	C
CD57	2.47	E
CD2	2.33	E
ADP-ribosylation Factor (ARF-6)	2.28	E
TGF beta Receptor III	2.27	C
HPV 16-E7	2.23	E
FSH	2.20	E
Golgi Complex	2.20	E
Total PSA	2.18	C
BAD	2.15	SE
CD1	2.12	E

Laminin-s	2.11	E
Catenin-alpha1	2.02	C
CEA	2.01	C
MHC I (HLA25 and HLA-Aw32)	2.01	E
Thymidylate Synthase	2.00	E
p18INK4c	0.50	E
DFF40 (DNA Fragmentation Factor 40) / CAD	0.50	E
c-Src	0.50	E
PARP	0.50	E
Endostatin	0.49	E
Cullin-1 (CUL-1)	0.49	E
PARP (Poly ADP-Ribose Polymerase)	0.49	E
XRCC2	0.48	E
MyD88	0.48	E
Cdk3	0.44	E
MMP-23	0.44	E
Cullin-2 (CUL-2)	0.42	E
Stat-1	0.42	E
CDC34	0.41	E
BRCA2 (aa 1323-1346)	0.35	E
PTHrP	0.10	C

* Cytokine (C), Explorer (E), Signaling Explorer (SE)

Figure 17. Targets with a greater than 2 fold difference in expression.

Finally, a phosphoprotein array was used to look for differences in protein abundance, phosphorylation and protein-protein interactions. The array utilizes ~510 pan-specific antibodies for protein expression and ~340 phosphosite-specific antibodies for phosphorylation. The antibodies profile 287 different phosphosites, 189 protein kinases, 31 protein phosphatases and 142 regulatory subunits of these enzymes and other cell signaling proteins that regulate cell proliferation, stress and apoptosis. Two strategies were used to explore differences between healing and worsening wound fluid, evaluation of the 15% dual threshold pooled sample groups (Appendix F) and individual testing of 10 wounds in each category (Appendix G). Differentially expressed targets from the microarrays are pre-validated using western blots to confirm antibody specificity by including molecular weight of the target. In all, 11 pre-validation blots tested 238 antibodies for their sensitivity and specificity. The blot images and potential targets are given in (Appendix H). Forty-four known and 41 cross-reactive unknown targets were identified as potential biomarkers from the pre-validation western blots. Eighteen antibodies were probed

using pooled samples to identify proteins with significant changes between sample groups (Figure 18).

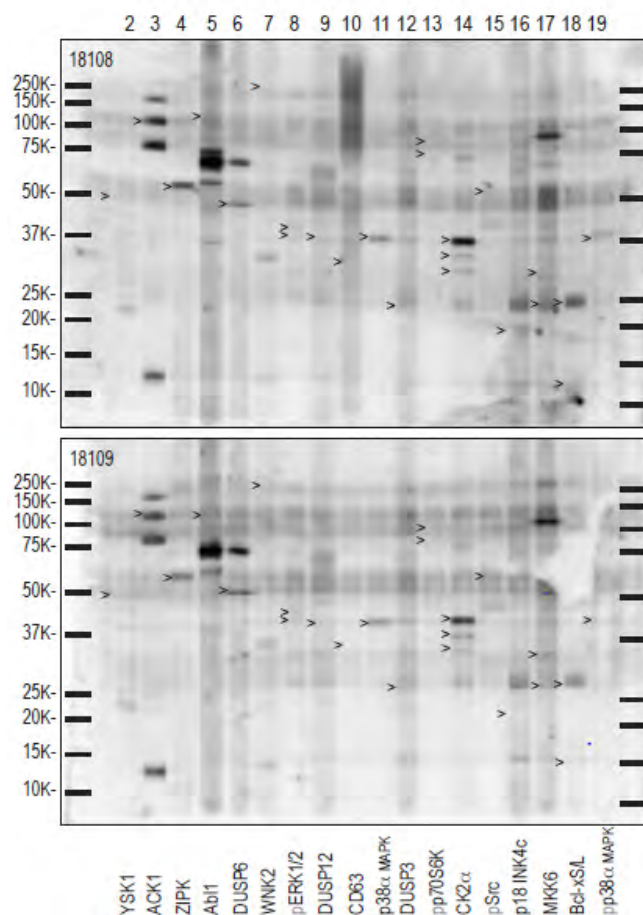


Figure 18. Eighteen antibodies probed using pooled samples to identify proteins with significant changes between sample groups.

Overlays of the gel images were used to highlight similarities and differences in the samples (Figure 19).

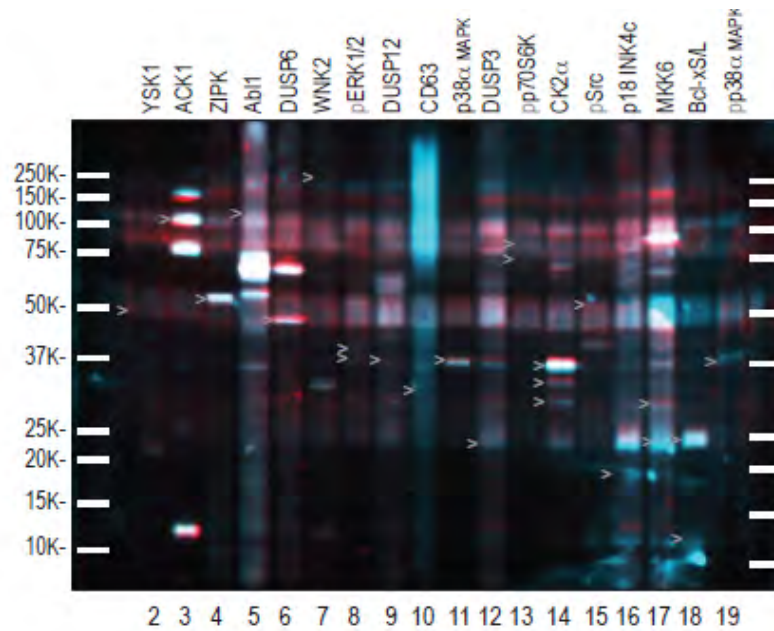


Figure 19. Overlay of the gel images, the blue color represents the pooled “worsening” samples and the red color the pooled “healing” samples. When the protein bands are of the same magnitude in both samples, then the protein bands show up as white.

Differences in expression for targets of the 18 antibodies are shown Figure 20. Eleven targets were measurable with 9 differentially expressed with a 25% minimum threshold.

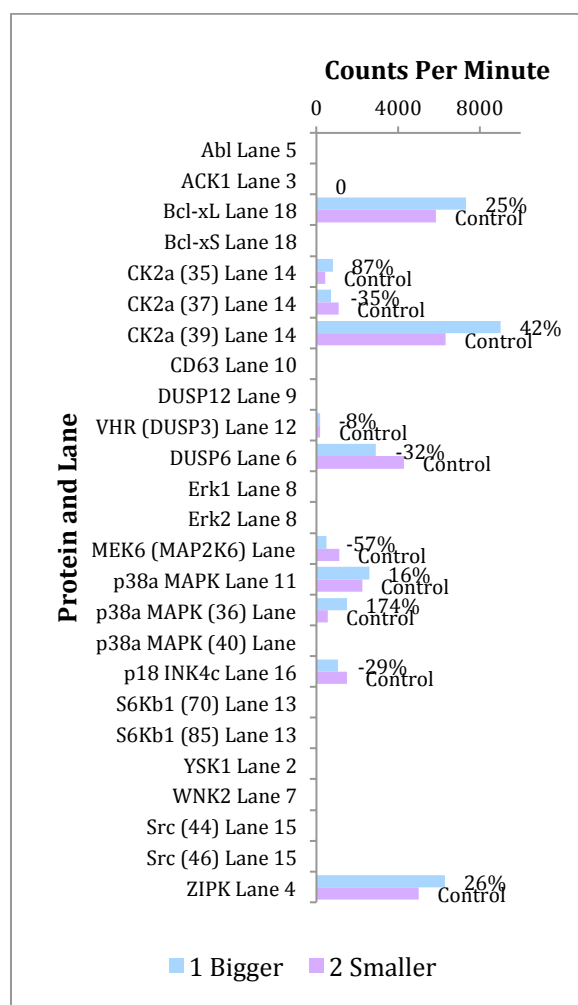


Figure 20. Differences in expression for targets of the 18 antibodies. Eleven targets were measurable with 9 differentially expressed with a 25% minimum threshold.

A microsphere-based suspension microarray was used to simultaneously measure the concentration of 7 analytes, C-X-C motif chemokine 9 (CXCL9), L-selectin (SELL), matrix metalloproteinase-9 (MMP9), protein S100-A8 (S100A8), protein S100-A9 (S100A9), Transforming growth factor beta receptor type 3 (TGFB3), and retinol binding protein 4 (RBP4) in 96 wound fluid samples. The assay methodology is based upon the Luminex® bead-based immunoassay platform. Samples were measured in duplicate and standardized using the wound fluid total protein concentration (Appendix I). The three cohorts of healing and worsening wounds were tests for differential expression and p values are given in Figure 21. Of the 6 targets, S100A8 and TGFB3 were significantly different between healing and worsening wounds.

Scale	Threshold	p value					
		CXCL9	MMP9	RBP4	S100A8	S100A9	TGFBR3
2 point	15%	1.000	0.347	0.097	0.029	0.149	0.035
3 point	15% Single	0.785	0.379	0.205	0.644	0.750	0.575
3 point	15% Dual	0.525	0.351	0.226	0.022	0.062	0.093

Figure 21. Quantitative Microarray for 7 analytes, C-X-C motif chemokine 9 (CXCL9), L-selectin (SELL), matrix metalloproteinase-9 (MMP9), protein S100-A8 (S100A8), protein S100-A9 (S100A9), Transforming growth factor beta receptor type 3 (TGFB3), and retinol binding protein 4 (RBP4).

SRM-MS Analysis

Through iTRAQ labeling quantitative proteomics analysis, the different expression levels of 2561 proteins were evaluated and 6 proteins out of these were selected as SRM-MS protein targets. 14 proteins were further added into the SRM-MS quantification panel using data from previous research and the microarray results of this study. Four individual samples and 2 pooled samples were prepared and subject to SRM-MS analysis using algorithm based and/or iTRAQ data dependent SRM-MS methods. The pooled samples were taken from the highest confidence cohort, 15% dual threshold and 3 point sliding scale. The potential clinical diagnostic utility of the panel was further evaluated.

The abundance of each of the 20 SRM-MS target proteins was represented by a single peptide mapped uniquely to the target protein (Appendix J). Each protein was independently quantified in 6 wound fluid samples, containing 2 samples from the larger or worsening group and 2 samples from the healing group in addition to the pooled samples derived from the 3 point sliding scale and dual 15% threshold. Relative expression levels and a p value for each protein target is shown in Figure 22. The abundance of a target protein is represented by the relative ratios normalized to abundance in the pooled sample.

	Larger Wounds			Smaller Wounds			p-value
	A-14	B-35	15% Dual Threshold Pooled	N-14	O-28	15% Dual Threshold Pooled	
<i>Previous Research</i>							
Protein S100-A7	2.1374	1.9030	1.9051	0.6081	1.1605	1.0000	0.0115
Protein S100-A9	2.6713	2.2497	2.1554	1.0347	1.5528	1.0000	0.0085
Retinol binding protein 4 (RBP4)	0.2684	0.3491	0.2202	0.9024	1.4188	1.0000	0.0292
Matrix Metalloproteinase-9 (MMP9)	7.8121	3.3984	5.9998	0.6842	1.6546	1.0000	0.0626
Profilin-1 (PFN1)	0.3224	0.4516	0.3517	0.6439	1.1512	1.0000	0.0578
TGFBR3	3.8634	4.0737	3.0818	0.9321	1.8031	1.0000	0.0042
L-selectin	0.3167	0.2136	0.2701	0.5844	0.8289	1.0000	0.0401
<i>Microarrays</i>							
VEGF-A	0.0652	0.1433	0.1512	0.4367	1.1530	1.0000	0.0740
Beta actin (ACTB)	0.1352	0.1965	0.0658	0.6448	0.7958	1.0000	0.0136
ADP-ribosylation Factor (ARF-6)	0.1927	0.1765	0.2414	1.1945	1.0360	1.0000	0.0023
Cdk3	0.3652	0.2209	0.3525	0.9531	0.9833	1.0000	0.0026
Cullin-2 (CUL-2)	5.6360	6.6595	4.4842	0.8459	2.3464	1.0000	0.0073
STAT1	6.0845	7.3875	6.2529	0.6372	1.0247	1.0000	0.0028
CDC34	6.8297	7.5555	5.6390	0.7289	1.3683	1.0000	0.0054
<i>iTRAQ</i>							
kinesin-like protein KIF15 isoform X2	9.2240	11.9660	7.8970	1.0777	2.7340	1.0000	0.0102
DCC-interacting protein 13-alpha	2.2750	0.6348	2.7902	0.8614	1.9063	1.0000	0.4422
26S proteasome non-ATPase regulatory subunit 6 isoform X1	7.8246	6.2612	5.1769	0.6427	1.2660	1.0000	0.0153
CUGBP Elav-like family member 2 isoform X22	3.5516	4.9279	3.2949	0.5281	1.3657	1.0000	0.0149
pre-mRNA-processing factor 19	4.1619	5.6161	3.2654	0.5665	2.2474	1.0000	0.0259
pterin-4-alpha-carbinolamine dehydratase isoform 1	4.2906	4.8014	3.9016	0.4900	2.1487	1.0000	0.0107

Figure 22. Selected reaction monitoring (SRM-MS) analysis of 20 proteins in chronic wound fluid from pressure ulcers.

KEY RESEARCH ACCOMPLISHMENTS:

- Fabricated a new integrated sensor that included a xerogel as a selective sensing element
- Fabricated a porous polymeric PBG on large flexible substrates
- Methodology developed and refined during this project was employed in a project evaluating pressure ulcer fluid in people with and without SCI
 - Edsberg LE, Wyffels JT, Ogrin R, Craven C, Houghton P. A pilot study evaluating protein abundance in pressure ulcer fluid from people with and without spinal cord injury. J Spinal Cord Med. 2014 Jun 26. [Epub ahead of print] PMID: 24968005 [PubMed - as supplied by publisher]
- 3 Point sliding scale threshold sample classification system

CONCLUSION:

The goal of this research was to evaluate the wound proteome and outcome and develop a technology to measure protein targets. The analysis of the proteome started with the development of a classification system for wound fluid samples. A technique to classify a sampling timepoint based on a sliding 3 timepoint scale that uses the prior and following timepoint data to describe the trend for the wound during the middle timepoint was developed. This technique offers the potential to standardize and objectively classify samples from a variety of wound types, rather than utilizing subjective clinical judgement. Classification of the samples is integral to the identification of targets.

The proteomic analysis utilized antibody dependent and independent techniques. Of the 6 targets analyzed using a quantitative microarray, S100A8 and TGFBR3 were significantly different between healing and worsening wounds. This finding further supports work by this team investigating the levels of S100 calcium binding proteins in chronic wounds.

PIXIES technology was fabricated, but ultimately it was decided that this novel technology has a longer timeline to clinical use due to the early stages of the technology. Additionally, the wound bed presents an extremely challenging environment for any type of proteomic technology due to the complex mixture of proteins and protein fragments. SRM-MS, cost effective, low sample usage technology, is well suited to analysis of intact proteins and peptides. Additionally, the technology has been shown to be suitable for a diagnostic tool in disease processes. The SRM-

MS data indicated several intriguing findings, but can be utilized in follow-up studies for panel marker confirmation. Validation of this technology is integral to the final development of a bedside collection sample being evaluated for markers of healing. The utilization of SRM-MS for wound fluid analysis is a significant development in the path to bedside wound outcome diagnosis. Ultimately this work may allow the development of personalized wound care based on the proteomic characteristics of the wound.

PUBLICATIONS, ABSTRACTS, AND PRESENTATIONS

- “Bring Revised NPUAP Guidelines and Research to the Bedside”, 20th Annual Symposium to Promote Clinical Excellence, Saratoga Springs, NY, May 22, 2015
- “Proteomic Characterization of Pressure Ulcers”, Invited Lecture, World Union of Wound Healing Societies (WUWHS), 4th Congress, Yokohama, Japan, September 2012.
- Ka Yi Yung, Huina Xu, Ke Liu, Gregory J Martinez, Frank V. Bright, Michael R Detty, and Alexander N. Cartwright, “Hybrid Oxygen-responsive Reflective Bragg Grating Platforms”, *Analytical Chemistry* 2012; 84 (3):1402–1407.
- Liu, K., Xu, H., Hu, H., Gan, Q. and Cartwright, A. N. (2012), One-Step Fabrication of Graded Rainbow-Colored Holographic Photopolymer Reflection Gratings. *Adv. Mater.*, 24:1604–1609. doi:10.1002/adma.201104628
- Huina Xu, Ke Liu, Qiaoqiang Gan, and Alexander N. Cartwright, “Flexible Porous Polymer Photonic Bandgap Structures for Chemical and Biomedical Sensing”, *IEEE Photonics 2011 Conference*, Oct. 2011, Arlington, Virginia.
- Ke Liu, Huina Xu, Qiaoqiang Gan, and Alexander N. Cartwright, “Polymeric Concave Bragg Reflectors Fabricated using Optical Lithography”, *Materials Research Society*, Nov. 2011, Boston, Massachusetts.
- “What Are the Effects of Load on Tissue?”, *Scientific Basis of Wound Healing, Wound Principles & Assessment*, Wound Management Track, Master’s Clinical Science (MCISc) Program, School of Physical Therapy, University of Western Ontario, London, Ontario, September 2011.
- Ke Liu, Huina Xu, Qiaoqiang Gan, and Alexander N. Cartwright, “One-step Holographic Lithography Fabrication of a Rainbow-colored Photonic Bandgap Structure”, *IEEE Photonics 2011 Conference*, Oct. 2011, Arlington, Virginia

- “Proteins and Pressure Ulcer Outcomes”, Chronic Wounds – Mechanisms and Diagnostics, 2nd Meeting of the Australian Wound and Tissue Repair Society, Perth, Western Australia, March 2010.

INVENTIONS, PATENTS AND LICENSES: Nothing to report

REPORTABLE OUTCOMES:

- Utilization of selected reaction monitoring mass spectrometry (SRM-MS) for wound fluid samples

OTHER ACHIEVEMENTS:

- Graduate Certificate in Bioinformatics & Computational Biology (May 2014) University of Delaware (not funded by award, but admission to program supported by need from funded grant for data analysis).
- Pilot studies (not funded by this award, but based on the work in this award) are being conducted to evaluate genomic methodology to identify genes involved with proteins present in healing and non-healing wounds. Sample type (fluid vs. tissue) is also being assessed.
- Novel Compounds From Shark and Stingray Epidermal Mucus With Antimicrobial Activity Against Wound Infection Pathogens. Department of Defense, U.S. Army Medical Research & Materiel Command (USAMRMC), Congressionally Directed Medical Research Programs. Basic Research Award W81XWH-11-2-0110. Non-traditional model antibody independent evaluation of mucus based on the methodology developed in this award.
- Integrated Proteomic Analysis and siRNA Therapy for Treatment of Heterotopic Ossification. Department of Defense, U.S. Army Medical Research & Materiel Command (USAMRMC), Congressionally Directed Medical Research Programs. Idea Development Award, W81XWH-10-2-0139. Wound fluid and tissue analysis based on the methodology developed in this award.
- A Randomized Controlled Pilot Study of Hyperbaric Oxygen Therapy versus Sham Controls in the Early Treatment of Deep Partial Thickness Burns. U.S. Army Medical Research and Materiel Command Broad Agency Announcement, 2014. Proteomics work flow and updated technology will be utilized for this project.

REFERENCES:

1. Mehdi Mesri, Advances in Proteomic Technologies and Its Contribution to the Field of Cancer, *Advances in Medicine*, vol. 2014, Article ID 238045, 25 pages, 2014. doi:10.1155/2014/238045
2. Hembrough T1, Thyparambil S, Liao WL, Darfler MM, Abdo J, Bengali KM, Hewitt SM, Bender RA, Krizman DB, Burrows J. Application of selected reaction monitoring for multiplex

quantification of clinically validated biomarkers in formalin-fixed, paraffin-embedded tumor tissue. *J Mol Diagn*. 2013 Jul;15(4):454-65. doi: 10.1016/j.jmoldx.2013.03.002. Epub 2013 May 11.

3. Xiao-jun Li, Clive Hayward, Pui-Yee Fong, et al. A Blood-Based Proteomic Classifier for the Molecular Characterization of Pulmonary Nodules. *Sci Transl Med* 16 October 2013 5:207ra142. [DOI:10.1126/scitranslmed.3007013]

4. Taverna D, Nanney LB, Pollins AC, Sindona G, Caprioli R. Multiplexed molecular descriptors of pressure ulcers defined by imaging mass spectrometry. *Wound Repair Regen*. 2011 Nov;19(6):734-44. doi: 10.1111/j.1524-475X.2011.00738.x. Epub 2011 Oct 19.

5. Wyffels JT, Edsberg LE. Granulation tissue of chronic pressure ulcers as predictive indicator of wound closure. *Advances in Skin & Wound Care* 2011;24(10):464-473.

6. Edsberg LE, Wyffels JT, Ha D. Longitudinal study of stage III and stage IV pressure ulcer area and perimeter as healing parameters to predict wound closure. *Ostomy Wound Management* 2011;57(10):50-62.

APPENDICES:

Appendix A. iTRAQ Set 1

Appendix B. iTRAQ Set 2

Appendix C. Cytokine

Appendix D. Explorer

Appendix E. Signaling

Appendix F. Pooled Microarray

Appendix G. Individual Microarray

Appendix H. Pre-screen Results

Appendix I. Quantitative Microarray

Appendix J. SRM-MS Transition Parameters

Appendix A

iTRAQ Set 1

Accession	Description	2Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
109715837	protein NDNF precursor [Homo sapiens]		1	1	2	3	1.874	1		1.016	1		22.30	2.82	2	3	568	64.6	8.94	
578807153	PREDICTED: basic helix-loop-helix domain-containing protein KIAA2018 isoform X1 [Homo sapiens]		3	1	7	18	1.881	1		1.180	1		28.33	3.17	10	18	2211	237.6	7.52	
63032616	DNA-3-methyltransferase glycosylase isoform a [Homo sapiens]		3	1	3	7	1.601	1		1.275	1		61.21	9.06	7	7	206	38.2	9.57	
578806381	PREDICTED: kinesin-like protein KIF15 isoform X2 [Homo sapiens]		36	1	10	21	1.567	1		2.529	1		69.08	7.24	17	21	1285	147.9	6.89	
578818239	PREDICTED: CUGBP Elav-like family member 2 isoform X22 [Homo sapiens]		17	1	3	11	1.542	1		1.659	1		145.25	13.65	7	11	403	42.4	8.85	
93204867	probable G-protein coupled receptor 158 precursor [Homo sapiens]		4.69	1	1	6	35	1.456	4	1.8	1.315	4	3.3	66.33	4.69	8	35	1215	135.4	8.28
578827454	PREDICTED: AP-3 complex subunit beta-2 isoform X2 [Homo sapiens]		3.37	5	1	4	6	1.428	1		1.433	1		33.18	3.37	4	6	1038	114.4	5.72
530373465	PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 isoform X1 [Homo sapiens]		6	1	3	7	1.997	1		3.043	1		160.84	9.02	7	7	410	48.0	5.54	
578824847	PREDICTED: neurabinin isoform X10 [Homo sapiens]		10	1	7	21	1.396	3		49.1	0.995	3	5.6	41.54	1.57	10	21	2938	326.8	6.16
578822417	PREDICTED: SUMO-conjugating enzyme UBC9 isoform X4 [Homo sapiens]		7	1	3	7	1.096	1		51.6	1.095	1		158.46	30.38	7	7	156	18.0	8.66
555943926	heme oxygenase 2 isoform c [Homo sapiens]		6.62	3	1	1	2	1.348	1		1.024	1		43.84	6.62	2	2	287	32.8	5.91
578817959	PREDICTED: collagen alpha-1(XVII) chain isoform X3 [Homo sapiens]		4	1	3	12	1.301	3		2.7	1.207	3	35.8	95.72	2.85	5	12	1087	107.8	7.85
578836106	PREDICTED: retinoblastoma-like protein 1 isoform X1 [Homo sapiens]		4.35	12	2	5	8	1.294	2	5.2	1.560	2	21.0	43.95	4.35	5	8	896	101.1	7.56
403542051	2'-deoxynucleoside 5'-phosphate N-hydrolase 1 isoform 2 [Homo sapiens]		22.30	2	1	1	3	1.288	1		1.708	3		196.54	22.30	3	3	148	16.2	6.79
149363656	exocyst complex component 68 [Homo sapiens]		4.44	2	1	4	9	1.274	1		1.040	1		30.99	4.44	4	9	811	94.1	6.46
45573113	angiogenin precursor [Homo sapiens]		19.73	1	1	2	3	1.272	1		3.312	1		50.70	19.73	3	3	147	16.5	9.64
48675813	transpartin-2 isoform 2 [Homo sapiens]		2.48	1	3	44	1.254	1		1.059	1		33.30	2.48	3	44	887	100.3	4.98	
55495586	replication protein A 32 kDa subunit isoform 2 [Homo sapiens]		17.82	3	1	2	4	1.250	1		1.188	1		145.96	17.82	4	4	174	19.1	5.73
50053795	eukaryotic translation initiation factor 4B [Homo sapiens]		9.49	2	2	4	13	1.249	3	8.3	1.047	1		395.67	9.49	10	13	611	69.1	5.73
625180307	hemocentin-2 precursor [Homo sapiens]		2.58	2	1	11	16	1.232	1		1.043	1		26.28	2.58	11	16	5079	543.7	5.81
14277685	protodactherin gamma-C5 isoform 2 precursor [Homo sapiens]		1.14	2	1	1	2	1.229	1		1.141	1		35.31	1.14	2	2	878	95.1	5.11
11559929	costarmer subunit gamma-1 [Homo sapiens]		1.78	2	1	2	4	1.209	1		1.135	1		285.60	3.78	4	4	874	97.7	5.47
578805065	PREDICTED: protein TANC1 isoform X8 [Homo sapiens]		6.20	8	1	9	320	1.205	1		1.765	1		4107.27	6.20	13	320	1677	183.3	8.85
4502491	complement component 1 G subcomponent-binding protein, mitochondrial precursor [Homo sapiens]		14.18	1	1	2	7	1.200	2	6.4	1.052	2	57.1	473.33	14.18	4	7	282	31.3	4.84
556053347	vacuolar protein sorting-associated protein VTA1 homolog isoform c [Homo sapiens]		10.81	3	1	1	3	1.198	1		1.718	1		109.96	10.81	3	3	222	24.5	5.29
6912280	activator of 90 kDa heat shock protein ATPase homolog 1 [Homo sapiens]		8.88	1	1	2	5	1.193	1		1.394	1		122.63	8.88	4	5	338	38.3	5.53
4557663	immunoglobulin-binding protein 1 [Homo sapiens]		6.49	1	1	1	25	1.193	2	12.6	1.187	2	24.4	379.65	6.49	3	25	339	39.2	5.38
40535729	ras and Rab interactor 3 [Homo sapiens]		10	1	7	10	1.133	1		1.189	1		286.23	8.43	9	10	985	107.8	6.41	
7657381	pre-mRNA-processing factor 19 [Homo sapiens]		6.94	1	1	4	17	1.187	1		1.681	1		79.05	6.94	9	17	504	55.1	6.61
190341024	SPARC-like protein 1 isoform 1 precursor [Homo sapiens]		13.10	2	2	4	11	1.186	2	1.7	0.929	2	23.0	412.48	13.10	8	11	664	75.2	4.81
21361176	retinal dehydrogenase 1 [Homo sapiens]		3.39	10	2	2	5	1.186	2	28.1	1.025	2	7.5	143.73	3.39	5	501	54.8	6.73	
4506715	40S ribosomal protein S28 [Homo sapiens]		40.58	1	2	3	6	1.184	2	17.7	1.070	2	69.1	153.54	40.58	6	6	69	7.8	10.70
612407822	carcinoembryonic antigen-related cell adhesion molecule 6 preproprotein [Homo sapiens]		6.69	1	2	6	1.180	2		33.0	1.017	2	12.6	130.86	6.69	6	6	344	37.2	5.82
47458820	signal transducer and activator of transcription 3 isoform 3 [Homo sapiens]		16.90	6	2	11	27	1.180	3	1.5	1.330	3	14.3	362.34	16.90	16	27	722	83.1	7.12
4793379	alpha-soluble NSF attachment protein [Homo sapiens]		5.68	1	1	2	4	1.179	1		1.251	1		146.99	5.08	4	4	295	33.2	5.36
200657509	arF-GAP domain and FG repeat-containing protein 1 isoform 4 [Homo sapiens]		1.92	8	1	3	3	1.174	1		1.714	1		84.54	1.92	3	3	522	54.1	8.92
209180448	target of Myb protein 1 isoform 3 [Homo sapiens]		18.70	3	5	15	1.173	1		2.013	1		155.75	18.70	12	15	460	50.2	4.78	
385731627	UPF0687 protein C20orf27 isoform 2 [Homo sapiens]		19.54	2	2	3	7	1.171	2	6.1	1.217	2	17.7	263.66	19.54	7	7	174	19.3	6.84
5453914	phospholipid transfer protein isoform a precursor [Homo sapiens]		4.06	4	2	2	22	1.163	1		1.356	2	20.6	257.35	4.06	5	22	493	54.7	7.01
16933567	ras-related protein Rab-8A [Homo sapiens]		27.54	21	1	6	72	1.163	3	1.3	1.028	3	17.7	1235.51	27.54	17	72	207	23.7	9.07
7177329	annexin A4 isoform 1 [Homo sapiens]		74.14	2	1	46	438	1.163	3	10.4	1.286	3	15.2	14778.62	74.14	438	473	79.8	8.60	
116734849	glycogen debranching enzyme isoform 2 [Homo sapiens]		3.83	3	2	6	17	1.163	3		1.134	3	2.7	344.63	3.83	11	17	1515	172.5	6.71
530362188	PREDICTED: microtubule-associated serine/threonine-protein kinase 2 isoform X3 [Homo sapiens]		4.51	10	1	8	42	1.162	2	1.6			85.93	4.51	17	42	1797	196.2	8.16	
578811543	PREDICTED: dishevelled-associated activator of morphogenesis 2 isoform X2 [Homo sapiens]		3.17	8	1	4	8	1.158	1		1.365	1		30.38	3.17	7	8	1167	134.2	6.73
388240770	reticulon-3 isoform f [Homo sapiens]		1.74	5	1	2	8	1.154	2	12.8	1.059	2	37.2	221.29	1.74	4	8	920	100.8	4.93
46389554	alpha-endosulfine isoform 4 [Homo sapiens]		31.62	8	2	2	9	1.153	3	0.1	1.053	3	7.4	503.07	31.62	6	9	117	13.0	8.25
578823793	PREDICTED: nucleosome assembly protein 1-like 1 isoform X10 [Homo sapiens]		11.89	2	3	6	1	1.293	2	21.6	1.293	2	28.1	194.77	11.89	2	3	328	38.2	6.56
17586001	major histocompatibility complex, class I, B precursor [Homo sapiens]		13.54	12	2	3	10	1.151	3	13.9	1.131	3	5.9	307.53	13.54	7	10	362	40.4	8.87
4507797	ubiquitin-conjugating enzyme E2 variant 2 [Homo sapiens]		42.07	6	1	7	39	1.150	1		1.144	1		674.87	42.07	21	39	145	16.4	8.09
530411696	PREDICTED: probable ATP-dependent RNA helicase DDX5 isoform X1 [Homo sapiens]		14.66	4	1	10	24	1.147	1		1.027	1		505.74	14.66	24	24	614	69.1	8.92
156564401	vesicle-fusing ATPase [Homo sapiens]		3.49	2	1	2	4	1.147	1		1.059	1		113.19	3.49	4	4	744	82.5	6.95
5729850	guanine nucleotide-binding protein G(i) subunit alpha [Homo sapiens]		21.19	14	1	7	21	1.146	1		1.383	1		688.56	21.19	17	21	354	40.5	5.69
91208426	pre-mRNA-processing-splicing factor 8 [Homo sapiens]		5.05	1	2	11	26	1.142	2	0.2	1.306	2	38.2	298.99	5.05	18	26	2335	273.4	8.84
53032450	PREDICTED: dystonin isoform X17 [Homo sapiens]		6.07	5	1	30	87	1.140	3		1.023	3		49.02	6.07	45	87	3186	348.9	6.76
578838069	PREDICTED: protein-cysteine N-palmitoyltransferase porcupine isoform X10 [Homo sapiens]		4.33	14	1	2	17	1.139	1		1.116	1		86.12	4.33	17	323	36.3	7.99	
578833709	PREDICTED: AP-3 complex subunit delta-1 isoform X1 [Homo sapiens]		3.82	3	2	4	7	1.136	2	10.9	1.276	2	9.1	160.70	3.82	7	7	1203	135.3	7.64
4885153	crk-like protein [Homo sapiens]		12.87	1	2	3	23	1.135	2	17.8	1.362	2	3.6	232.95	12.87	30	23	303	33.8	6.74
578833911	PREDICTED: tubulin-folding cofactor B isoform X1 [Homo sapiens]		12.95	2	1	2	6	1.134	1		1.210	1		249.49	12.95	4	6	193	21.8	4.94
4557851	pterin-4-alpha-carbinodamine dehydratase isoform 1 [Homo sapiens]		20.19	2	1	2	6	1.134	1		2.806	1		89.69	20.19	4	6	104	12.0	6.80
221631991	pentothese precursor [Homo sapiens]		12.92	3	3	5	134	1.134	1		2.438	1		233.37	12.92	5	5	513	57.0	9.55
69122931	TAFs-like RNA polymerase II p200/CBP-associated factor-associated factor 65 kDa subunit 5L h		11.38	3	3	3	48	1.132	1		1.329	1		85.76	11.38	5	48	325	37.0	6.18
239735600	Ictct1 domain-containing protein 1 [Homo sapiens]		4.47	1	1	1	3	1.132	1		1.416	1		26.10	4.47	3	3	179	20.7	8.95
115495445	ankyrin repeat domain-containing protein 30A [Homo sapiens]		7.61	2	1	10	41	1.129	7	3.2	1.288	7	24.8	137.24	7.61	13	41	1341	152.6	6.33
539848098	biogenesis of lysosome-related organelles complex 1 subunit 2 isoform 3 [Homo sapiens]		28.42	1	1	2	1	1.128	1		1.006	1		103.60	28.42	2	2	95	11.1	9.23
578804706	PREDICTED: putative GTP cyclohydrolase 1 type 2 NIF3L1 isoform X2 [Homo sapiens]		5.61	5	1	2	9	1.127	1		1.189	1		173.23	5.61	5	9	285	32.1	8.68
530384981	PREDICTED: aminocyclase RNA synthase complex-interacting multifunctional protein 2 isoform X1		9.58	5	1	3	8	1.126	1		1.269	1		131.20	9.58	8	313	34.6	8.02	
414148872	costarmer subunit zeta-1 isoform 3 [Homo sapiens]		6.25	3	1	1	2	1.126	1		0.987	1		42.33	6.25	2	2	160	18.4	4.91
578811945	PREDICTED: large proline-rich protein BAG6 isoform X1																			

Accession	Description	2Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
116063568	torsin-4A (Homo sapiens)	2.60	1	1	1	2	1.106	1		1.250	1		31.26	2.60		2	423	46.9	9.94	
163659918	sacsin isoform 1 (Homo sapiens)	6.16	3	1	29	102	1.104	1		0.946	1		75.94	6.16	38	102	4579	520.8	7.05	
4506467	40S ribosomal protein S15 (Homo sapiens)	24.14	1	2	3	5	1.104	2	6.2	1.161	2	22.7	133.14	24.14	5	5	145	17.0	10.39	
8923417	poly(ADP-ribose) glycohydrolase ARH3 (Homo sapiens)	8.54	1	1	3	5	1.103	1		1.213	1		178.66	8.54	5	5	363	38.9	5.07	
4507065	antileukoproteinase precursor (Homo sapiens)	9.09	1	1	1	2	1.103	1		0.813	1		97.39	9.09	2	2	132	14.3	8.75	
42718017	DNA endonuclease RBBP8 isoform b (Homo sapiens)	2.65	4	1	3	9	1.102	1					36.00	2.65	3	9	867	98.4	6.64	
352962174	osteopontin isoform 4 precursor (Homo sapiens)	6.96	5	1	1	3	1.101			1.239	1		151.08	6.96	3	3	273	30.8	4.59	
30375357	PREDICTED: ADP-ribosyl cyclase 2 isoform X3 (Homo sapiens)	25.26	4		5	20	1.100	6	4.7	1.019	6	3.4	499.73	25.26	13	20	289	32.7	7.08	
122937185	protein LCNH (Homo sapiens)	4.40	1	1	2	2	1.100	1		0.946	1		39.95	4.40	2	2	485	51.4	5.31	
51815866	PREDICTED: elongation factor 1-delta isoform X9 (Homo sapiens)	15.21	1	8	33	1.100				1.248	1		880.50	15.21	19	33	464	73.0	6.34	
530373508	PREDICTED: serine/threonine-protein kinase OSR1 isoform X1 (Homo sapiens)	9.78	2	2	5	14	1.099	2	2.4	1.266	2	6.7	141.48	9.78	9	14	460	50.6	7.02	
578837470	PREDICTED: DNA topoisomerase 3-beta-1 isoform X8 (Homo sapiens)	4.99	3	1	1	10	1.098	1		0.922	1		17.01	4.99	5	10	862	96.6	8.12	
530426177	PREDICTED: transport and Golgi organization protein 2 homolog isoform X5 (Homo sapiens)	25.23	13	1	2	9	1.097	1		1.387	1		247.04	25.23	5	9	214	24.2	5.30	
530402403	PREDICTED: protocadherin-9 isoform X3 (Homo sapiens)	2.85	5	1	4	7	1.097	1		1.335	1		38.83	2.85	6	7	1019	112.0	5.45	
5730027	KH domain-containing, RNA-binding, signal transduction-associated protein 1 isoform 1 (Homo sapiens)	5.93	5	3	5	17	1.096	2	2.1	1.176	2	29.9	173.10	5.93	11	17	443	48.2	8.66	
15447374	Isoform (Homo sapiens)	12.16	1	2	2	5	1.095	2		0.848	2	5	249.87	12.16	2	5	232	25.7	5.78	
530419646	PREDICTED: MORC family CW-type zinc finger protein 2 isoform X2 (Homo sapiens)	7.29	3	1	10	21	1.095	1		0.844	1		30.52	7.29	11	21	1029	117.4	8.44	
530364823	PREDICTED: nitrilase homolog 1 isoform X3 (Homo sapiens)	24.40	7	3	4	9	1.095	3	7.3	1.212	1		135.70	24.40	9	9	291	31.8	6.87	
211059425	small integral membrane protein 24 precursor (Homo sapiens)	15.38	1	1	1	3	1.094	1		1.205	1		102.74	15.38	3	3	130	15.0	5.29	
578809385	PREDICTED: extracellular matrix protein FRAS1 isoform X4 (Homo sapiens)	1.15	5	1	7	13	1.093			1.464	1		28.41	1.15	7	13	3897	430.3	5.66	
378548190	40S ribosomal protein S3 isoform 1 (Homo sapiens)	11.93	3	2	3	26	1.093	2	1.4	1.696	2	17.5	132.47	11.93	9	26	243	26.7	9.66	
45025933	non-Histone chromosomal protein HMG-14 (Homo sapiens)	64.00	7	43	131	1.093	14	9.2		1.131	14		1324.63	64.00	43	100	107	9.60		
4504011	glutamate--cysteine ligase regulatory subunit (Homo sapiens)	15.69	2	2	4	17	1.092	2	5.8	1.371	2	1.2	339.37	15.69	10	17	274	30.7	6.02	
41281564	WD repeat-containing protein 37 (Homo sapiens)	4.05	1	1	2	4	1.092	1		1.218	1		142.70	4.05	4	4	494	54.6	7.23	
300388183	26S proteasome non-ATPase regulatory subunit 1 isoform 2 (Homo sapiens)	1.95	2	1	1	3	1.091	1		0.738	1		220.18	1.95	3	3	922	102.2	5.27	
648216291	N-myc proto-oncogene protein isoform 2 (Homo sapiens)	5.93	2	1	2	4	1.091	1		1.185	1		45.30	5.93	2	4	253	28.3	8.95	
530402424	PREDICTED: ADP-ribosylation factor-like protein 1 isoform X1 (Homo sapiens)	11.85	2	1	1	3	1.090	1		1.135	1		136.57	11.85	3	3	135	15.4	5.34	
8922911	radical S-adenosyl methionine domain-containing protein 1, mitochondrial precursor (Homo sapiens)	5.43	1	1	3	7	1.090	1		0.960	1		29.32	5.43	6	7	442	48.7	7.78	
24111444	MAM domain-containing glycosylphosphatidylinositol anchor protein 1 precursor (Homo sapiens)	2.62	2	1	3	26	1.090	2	4.5	1.238	2	18.0	36.20	2.62	3	26	955	105.7	8.34	
635172849	beta-hexosaminidase subunit beta isoform 2 (Homo sapiens)	22.05	2	3	6	14	1.089	3	5.7	1.330	3	7.0	296.13	22.05	11	14	331	38.2	6.44	
5031839	keratin, type II cytoskeletal 6A (Homo sapiens)	27.30	11	1	18	84	1.088	1		0.984	1		2038.21	27.30	50	84	564	60.0	8.00	
530386260	PREDICTED: coiled-coil domain-containing protein 146 isoform X3 (Homo sapiens)	5.10	5	2	7	13	1.088	1		1.481	1		35.37	5.10	7	13	823	97.2	9.20	
495528154	collagen alpha-1(V) chain isoform 2 preproprotein (Homo sapiens)	2.50	2	2	4	8	1.087	2	8.6	1.154	1		137.01	2.50	7	8	1838	183.5	5.07	
170765500	protein SET isoform 1 (Homo sapiens)	35.17	5	6	6	27	1.086	8	7.2	1.117	8	8.5	1084.55	35.17	18	27	290	33.5	4.32	
145312241	differentially expressed in TDP-4 homolog (Homo sapiens)	15.53	18	3	11	39	1.085	6	6.8	1.486	6	21	417.10	15.53	39	631	73.9	6.05		
5774661	protein S100-A2 (Homo sapiens)	9.28	1	1	1	3	1.084	1		0.968	1		181.27	9.28	3	3	97	11.0	4.78	
4507123	U2 small nuclear ribonucleoprotein B" (Homo sapiens)	23.11	2	1	5	15	1.084	1		1.266	1		153.73	23.11	11	15	225	25.5	9.72	
262118216	coiled-coil domain-containing protein 88B precursor (Homo sapiens)	5.08	3	2	7	13	1.084	3	2.9	1.586	3	48.8	147.97	5.08	12	14	1476	164.7	5.11	
7661734	mGppxph diphosphatase (Homo sapiens)	12.46	1	3	4	16	1.083	4	12.6	1.232	4	0.7	372.40	12.46	12	16	337	38.6	6.38	
4503097	casein kinase II subunit alpha (Homo sapiens)	7.43	8	1	3	9	1.083	1		1.015	1		95.26	7.43	9	9	350	41.2	8.56	
530396150	PREDICTED: switch-associated protein 70 isoform X2 (Homo sapiens)	11.70	2	1	5	9	1.083	1		2.279	1		84.12	11.70	9	9	436	51.4	6.00	
530407994	PREDICTED: hemoglobin subunit zeta isoform X2 (Homo sapiens)	30.99	2	3	96	1.082	1			1.512	1		2709.18	30.99	7	96	142	15.6	8.21	
226056130	prostaglandin reductase 1 isoform 2 (Homo sapiens)	10.63	2	2	4	10	1.082	2	11.3	1.301	2	25.4	169.82	10.63	4	4	301	32.9	7.20	
149773456	uncharacterized protein KIAA0754 (Homo sapiens)	2.17	1	1	3	6	1.082	1		1.264	1		41.14	2.17	3	6	1427	150.4	4.32	
116875826	HD domain-containing protein 1 (Homo sapiens)	9.80	1	1	2	6	1.080	1		1.036	1		123.27	9.80	6	6	204	23.4	5.49	
578833510	PREDICTED: syntaxin-binding protein 2 isoform X1 (Homo sapiens)	31.63	7	11	13	45	1.079	11	10.2	1.165	11	25.1	1740.54	31.63	37	45	566	63.3	6.51	
35022214	protein transport protein Sec22A (Homo sapiens)	9.93	1	3	6	10	1.079	3	9.4	1.075	3	0.3	349.86	9.93	2	3	165	86.1	7.08	
6830349	argininosuccinate lyase isoform 3 (Homo sapiens)	10.96	4	5	25	107	1.078	2	0.7	1.285	2		314.77	10.96	13	25	438	48.7	6.31	
13129078	tether containing UBX domain for GLUT4 isoform 1 (Homo sapiens)	4.16	2	1	1	1	1.079	1		2.401	1		29.87	4.16	1	1	553	60.1	6.64	
530375442	PREDICTED: E3 ubiquitin-protein ligase CBL-B isoform X2 (Homo sapiens)	5.19	5	1	6	12	1.078	1		1.282	1		79.20	5.19	9	12	982	109.4	7.88	
2832531	serine/threonine-protein phosphatase 4 regulatory subunit 2 (Homo sapiens)	6.76	1	1	2	4	1.078	1		1.119	1		153.11	6.76	4	4	417	46.9	4.54	
132566536	voltage-dependent calcium channel subunit alpha-2deltaA (Homo sapiens)	1.47	1	1	3	11	1.078	1		1.092	1		45.69	1.76	6	11	1137	127.9	5.35	
530421763	PREDICTED: protein RDC1 isoform X1 (Homo sapiens)	57.38	2	1	2	105	1.077	2		1.107	2		57.38	57.38	2	2	232	26.6	9.36	
7657015	RNA-splicing ligase RtcH homolog (Homo sapiens)	12.08	1	1	4	14	1.077	1		1.407	2	28.1	302.22	12.08	8	14	505	55.2	7.23	
530415691	PREDICTED: NACHT, LRR and PYD domains-containing protein 13 isoform X1 (Homo sapiens)	5.12	2	1	5	10	1.077	1		1.005	1		35.88	5.12	5	10	1036	118.1	5.54	
55749779	DIEN domain-containing protein 14 isoform 1 (Homo sapiens)	2.97	6	1	4	6	1.077	2	13.1	2.471	2		37.3	39.34	2.97	4	6	1009	110.5	6.96
24431935	reticulon-4 isoform A (Homo sapiens)	4.19	5	2	5	14	1.076	4	1.4	1.166	4		11.4	448.23	4.19	8	14	1192	129.9	4.50
5803092	methionine aminopeptidase 2 (Homo sapiens)	10.25	1	1	4	19	1.076	1		1.110	1		221.44	10.25	9	19	478	52.9	5.82	
530396980	PREDICTED: lysosomal Pro-X carboxypeptidase isoform X1 (Homo sapiens)	19.69	3	5	5	33	1.076	11	7.4	1.197	11	43.9	194.82	19.69	15	33	391	43.9	6.30	
184971213	peptidyl peptidase 2 (Homo sapiens)	5.76	6	7	6	12	1.076	7	5.7	1.074	7	21.0	344.87	5.76	12	12	1249	138.3	6.32	
127139033	NADPH--cytochrome P450 reductase (Homo sapiens)	15.74	1	5	8	21	1.075	5	14.7	1.102	5		16.2	471.11	15.74	19	21	680	77.0	5.58
4504893	kininogen-1 isoform 2 precursor (Homo sapiens)	63.70	2	2	29	500	1.074	7	4.9	1.236	7		13.7	15792.50	63.70	82	500	427	47.9	6.65
4609584	cAMP-dependent protein kinase catalytic subunit alpha isoform 2 (Homo sapiens)	27.70	18	6	12	29	1.074	7	7.8	1.219	7		10.9	552.02	27.70	24	29	343	39.8	8.66
27501446	density-regulated protein (Homo sapiens)	9.60	1	2	2	12	1.074	4	2.7	1.021	4		13.9	923.88	9.60	6	12	198	22.1	5.30
530380424	PREDICTED: protein diaphanous homolog 1 isoform X1 (Homo sapiens)	11.92	3	5	15	53	1.073	6	9.2	1.134	6		6.1	626.73	11.92	28	53	1250	139.3	5.31
4758440	gla maturation factor gamma (Homo sapiens)	44.37	3	4	6	78	1.073	13	6.8	1.162	13		10.3	2557.68	44.37	18	78	142	16.8	9.26
20702439	histone-binding protein RBBP4 isoform c (Homo sapiens)	22.05	3	2	7	20	1.073	3	2	1.498	2	45.2	352.20	22.05	6	20	390	43.5	4.96	
530371599	PREDICTED: THAP domain-containing protein 4 isoform X1 (Homo sapiens)	2.95	21	4	4	27	1.073	1		1.298	1		130.96	2.95	10	27	711	76.0	9.58	

Accession	Description	Score	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
194363758	signal recognition particle 9 kDa protein isoform 1 [Homo sapiens]	23.17	2	2	2	14	1.064	3	1.0	1.248	3	11.0	287.79	23.17	6	14	82	9.1	7.80	
4505087	protein mago nashi homolog [Homo sapiens]	17.12	2	1	2	10	1.063	3	5.0	1.210	3	3.9	271.84	17.12	4	10	146	17.2	6.11	
57808451	PREDICTED: lipase member 1 isoform X7 [Homo sapiens]	1.00	1	1	2	0.982	1	1	1.00	0.982	1	2	4.00	4.00	2	2	398	45.5	9.35	
287324622	tyrosine-protein kinase HCK isoform d [Homo sapiens]	11.90	100	3	6	23	1.063	3	1.5	1.010	3	11.4	330.32	11.90	16	23	504	57.2	6.86	
4506743	40S ribosomal protein S8 [Homo sapiens]	5.77	3	2	2	6	1.063	2	4.9	0.990	2	6	308.10	5.77	6	6	208	24.2	10.32	
46094058	bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 [Homo sapiens]	4.01	1	1	2	7	1.063	1	1	1.341	1	1	147.40	4.01	4	7	624	70.8	6.86	
21314660	carcinoembryonic antigen-related cell adhesion molecule 8 precursor [Homo sapiens]	24.64	11	5	6	27	1.062	9	10.5	1.07	9	12.1	716.87	24.64	15	27	349	38.1	7.39	
56111324	HAUS augmin-like complex subunit 3 [Homo sapiens]	1.66	1	1	1	2	1.062	1	1	1.089	1	1	37.95	1.66	2	2	603	69.6	5.55	
4912356	echinoderm microtubule-associated protein-like 2 isoform 2 [Homo sapiens]	8.63	5	4	5	7	1.062	4	10.8	1.126	4	7.9	496.77	8.63	15	17	649	80.6	6.32	
91718902	histone-lysine N-methyltransferase 2C [Homo sapiens]	2.40	9	1	2	24	1.061	1	1	1.781	1	1	40.09	2.40	10	20	4911	541.0	6.49	
4507129	small nuclear ribonucleoprotein E [Homo sapiens]	27.17	1	1	1	20	1.061	6	10.3	1.500	6	23.1	1122.27	27.17	3	20	92	10.8	9.44	
6912618	glutaminyl-peptide cyclotransferase precursor [Homo sapiens]	22.44	39	4	5	29	1.061	8	5.8	1.086	8	20.5	1009.80	22.44	13	29	361	40.9	6.61	
5579478	dual specificity mitogen-activated protein kinase kinase 1 [Homo sapiens]	26.46	3	4	11	37	1.061	5	2.3	1.302	5	5.3	810.44	26.46	27	37	393	43.4	6.62	
419635906	tRNA-dihydrouridine(20) synthase [NAD(P)+]-like isoform 2 [Homo sapiens]	4.15	2	1	3	5	1.061	1	1	1.695	1	1	20.93	4.15	3	5	458	51.4	7.33	
45593144	homobox protein GBX-2 [Homo sapiens]	2.59	1	1	2	3	1.061	1	1	1.707	1	1	28.26	2.59	3	3	348	37.3	8.38	
530424789	PREDICTED: myosin regulatory light chain 12A isoform X1 [Homo sapiens]	72.51	7	1	12	155	1.061	2	10.8	1.647	2	64.5	5180.12	72.51	36	155	171	19.8	4.81	
94721241	isoleucine--tRNA ligase, cytoplasmic [Homo sapiens]	4.68	1	1	5	13	1.060	1	1	1.684	1	1	107.96	4.68	11	13	1262	144.4	6.15	
530405396	PREDICTED: tyrosine-protein kinase CSK isoform X1 [Homo sapiens]	30.22	2	8	10	35	1.060	9	6.4	1.149	9	15.0	912.28	30.22	26	35	450	50.7	7.06	
578801274	PREDICTED: histone-lysine N-methyltransferase ASH1L isoform X6 [Homo sapiens]	2.31	2	1	9	62	1.060	1	2.31	1.060	1	1	192.22	2.31	18	62	2904	325.3	9.39	
14249158	hepatoma-derived growth factor-related protein 2 isoform 2 [Homo sapiens]	5.22	9	1	3	10	1.060	2	5.3	1.271	2	17.4	435.91	5.22	10	20	670	74.9	7.42	
4826972	RNA-binding protein 8A [Homo sapiens]	20.69	1	2	3	13	1.060	3	16.0	1.227	3	22.1	575.14	20.69	9	13	174	19.9	5.79	
56114699	infratubular purine biosynthetic protein adenosine-3 isoform 2 [Homo sapiens]	12.47	3	2	5	13	1.060	2	0.7	1.133	2	0.7	125.29	12.47	13	13	433	46.0	6.79	
4506005	serine/threonine-protein phosphatase PP1-beta catalytic subunit isoform 1 [Homo sapiens]	28.75	4	7	7	38	1.059	5	5.3	1.223	5	1.8	1206.33	28.75	21	38	327	37.2	6.19	
34089946	nuclease-sensitive element-binding protein 1 [Homo sapiens]	23.46	5	2	6	23	1.059	4	13.5	0.933	4	13.5	575.93	23.46	12	23	324	35.9	9.88	
321400142	CD44 antigen isoform 8 precursor [Homo sapiens]	13.27	19	3	4	20	1.059	7	14.3	1.104	6	16.2	547.31	13.27	10	20	294	32.1	5.21	
530384106	PREDICTED: fibronectin type III domain-containing protein 1 isoform X1 [Homo sapiens]	3.46	2	1	5	90	1.059	1	1	2.444	1	1	94.69	3.46	9	90	1819	197.6	9.29	
530403927	PREDICTED: protein 2-dependent protease inhibitor isoform X1 [Homo sapiens]	22.97	2	4	8	21	1.059	5	4.5	1.168	5	7.5	616.18	22.97	18	21	444	50.7	8.27	
45076469	translationally-controlled tumor protein isoform 2 [Homo sapiens]	62.71	6	8	8	57	1.058	12	16	1.162	12	1308.53	10.9	1308.53	62.71	162	172	19.6	4.90	
14249348	thrombosin domain-containing protein 17 [Homo sapiens]	30.08	1	3	3	10	1.058	4	11.2	1.089	4	11.1	508.08	30.08	8	10	123	13.9	5.52	
4506217	26S proteasome non-ATPase regulatory subunit 10 isoform 1 [Homo sapiens]	26.11	1	1	3	8	1.058	2	0.0	1.208	2	0.0	366.03	26.11	5	8	226	24.4	6.10	
530387887	PREDICTED: serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform 1 [Homo sapiens]	12.11	20	3	5	17	1.058	3	6.6	0.987	3	12.1	296.40	12.11	13	17	446	51.6	6.20	
66879662	ADP-ribosylation factor 1 [Homo sapiens]	62.98	3	4	10	56	1.057	10	5.5	1.331	10	16.7	2153.53	62.98	26	56	181	20.7	6.80	
4506181	proteasome subunit alpha type-2 [Homo sapiens]	48.29	1	7	8	52	1.057	13	7.5	1.187	13	16.1	1836.76	48.29	21	52	234	25.9	7.43	
312717435	stromal membrane-associated protein 2 isoform 4 [Homo sapiens]	1.29	5	1	1	2	1.057	1	1	2.207	1	2	40.81	2.29	2	2	349	37.7	9.11	
118150618	epithelial cell transforming sequence 2 oncogene-like [Homo sapiens]	8.85	2	1	6	14	1.057	1	1	0.852	1	10	40.87	8.85	10	14	904	104.8	8.40	
530369318	PREDICTED: ras-related protein Ral-B isoform X4 [Homo sapiens]	13.59	1	1	4	8	1.057	1	1	1.437	1	1	208.69	13.59	7	8	206	23.4	6.62	
126362971	serine/threonine-protein kinase 10 isoform 1 [Homo sapiens]	17.77	1	9	14	58	1.057	11	6.4	1.221	11	12.0	1642.06	17.77	37	58	968	112.1	6.95	
4758516	hepatoma-derived growth factor isoform A [Homo sapiens]	70.00	12	15	17	149	1.057	48	8.0	1.086	48	13.9	5596.40	70.00	51	149	240	26.8	4.73	
20336761	heme-binding protein 1 [Homo sapiens]	8.47	1	1	2	8	1.057	2	4.0	1.113	2	42.3	166.24	8.47	5	8	189	21.1	5.80	
4502205	ADP-ribosylation factor 4 [Homo sapiens]	34.44	1	1	4	76	1.056	5	1.1	1.396	5	10.1	659.85	34.44	11	76	180	20.5	7.14	
21344375	AT-rich interactive domain-containing protein 1A isoform b [Homo sapiens]	5.58	2	1	4	10	1.056	1	1	1.091	1	1	217.31	5.58	10	14	2048	218.2	6.40	
4758356	flap endonuclease 1 [Homo sapiens]	22.89	1	4	8	26	1.056	6	5.1	1.130	6	5.2	636.17	22.89	17	26	380	42.6	8.62	
530385605	PREDICTED: leucine-rich repeat and WD repeat-containing protein 1 isoform X1 [Homo sapiens]	5.21	3	1	3	5	1.056	1	1	2.261	1	1	33.50	5.21	3	5	595	65.3	6.81	
307746865	excitatory amino acid transporter 2 isoform 2 [Homo sapiens]	1.42	5	1	1	5	1.056	1	1	0.956	1	1	47.24	1.42	3	5	565	61.2	6.67	
530367188	PREDICTED: coiled-coil domain-containing protein 104 isoform X2 [Homo sapiens]	12.39	1	1	3	7	1.056	1	1	1.768	1	1	32.16	12.39	3	7	218	25.0	4.51	
578080866	PREDICTED: gamma-interferon-inducible protein 16 isoform X2 [Homo sapiens]	13.44	4	5	10	48	1.056	6	11.9	1.056	6	7.8	583.17	13.44	21	48	677	76.3	9.38	
530377842	PREDICTED: MAP kinase-activating death domain protein isoform X1 [Homo sapiens]	1.45	1	1	1	3	1.056	1	1	1.156	1	1	71.75	1.45	1	3	217	23.2	10.92	
90669511	quinone oxidoreductase-like protein 1 [Homo sapiens]	2.16	1	1	3	12	1.056	2	2.3	1.081	2	3.6	197.91	2.16	6	12	349	38.7	5.78	
530416417	PREDICTED: apolipoprotein C-1 isoform X1 [Homo sapiens]	38.55	7	4	5	27	1.056	8	6.0	1.164	8	15.5	809.66	38.55	14	27	83	9.3	8.47	
530366904	PREDICTED: isomyl acetate-hydrolyzing esterase 1 homolog isoform X1 [Homo sapiens]	18.39	2	1	4	12	1.056	1	1	1.094	1	1	144.45	18.39	9	12	223	25.0	5.43	
22748877	class E basic helix-loop-helix protein 22 [Homo sapiens]	1.84	1	1	1	1	1.055	1	1	1.296	1	1	0.00	1.84	1	1	381	37.0	7.39	
530369184	PREDICTED: interleukin-1 receptor antagonist protein isoform X1 [Homo sapiens]	13.29	4	1	1	3	1.055	1	1	0.693	1	1	122.73	13.29	3	3	143	16.1	4.88	
17795451	translation machinery-associated protein 7 [Homo sapiens]	15.63	1	1	1	6	1.055	2	11.0	1.167	2	3	245.72	15.63	3	6	64	7.1	9.99	
55741709	RNA-binding protein 25 [Homo sapiens]	5.58	23	6	6	25	1.055	2	0.5	1.098	2	15	50.8	5.58	18	25	843	100.1	6.32	
578821511	PREDICTED: synaptotagmin-like protein 2 isoform X12 [Homo sapiens]	5.42	4	1	14	37	1.055	3	9.7	2.124	3	17.8	85.90	5.42	19	37	2196	34.1	6.20	
8922498	pyridoxine 5'-phosphate oxidase [Homo sapiens]	14.56	2	1	3	19	1.055	1	1	1.132	1	1	100.96	14.56	5	19	261	30.0	7.06	
530387776	PREDICTED: acid ceramidase isoform X1 [Homo sapiens]	11.26	4	2	3	7	1.054	2	3.0	1.348	2	3.7	217.19	11.26	6	7	373	42.6	6.90	
38327625	citrate synthase, mitochondrial precursor [Homo sapiens]	13.09	3	3	3	23	1.054	3	2.2	1.127	3	27.3	436.70	13.09	8	23	466	51.7	8.32	
394953908	26S proteasome non-ATPase regulatory subunit 11 [Homo sapiens]	9.00	1	2	3	7	1.054	2	2.6	0.817	2	10.0	139.05	9.00	7	7	422	47.4	6.48	
578805817	PREDICTED: regucalcin-1 isoform X5 [Homo sapiens]	34.44	4	4	8	26	1.054	1	1	1.198	1	1	187.44	34.44	15	25	84	110.1	7.96	
15553127	hexokinase-2 [Homo sapiens]	9.16	2	1	9	24	1.054	1	1	1.675	1	1	438.00	9.16	16	24	917	102.3	6.05	
45006986	aminoacyl tRNA synthase complex-interacting multifunctional protein 1 isoform a precursor [Homo sapiens]	8.33	2	1	7	1054	2	2	5.8	1.036	2	16.5	412.57	8.33	2	7	312	34.3	8.43	
578088831	PREDICTED: ras-GEF domain-containing family member 1B isoform X3 [Homo sapiens]	4.86	2	1	2	14	1.054	6	13.2	2.220	6	4.9	90.76	4.86	4	14	432	50.4	8.06	
40254823	phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 isoform b [Homo sapiens]	10.27	2	5	10	25	1.053	5	7.5	1.328	5	11.9	604.40	10.27	23	25	1188	133.1	7.59	
530391261	PREDICTED: TBC1 domain family member 13 isoform X1 [Homo sapiens]	4.63	1	1	2	4	1.053	1	1	1.023	1	1	30.14	4.63	2	4	324	37.7	4.97	
38020480	meiotic recombination protein SPO11 isoform b [Homo sapiens]	9.22	4	1	4	7	1.053	1	1	4.241	1	6	32.13	9.22	1	6	7	358	40.3	9.23

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
145959008	xxa-Pro dipeptidase isoform 1 (Homo sapiens)	16.02	3	3	4	15	1.049	4	11.0	1.505	4	96.1	758.90	16.02	11	15	493	54.5	6.00
530422764	PREDICTED: high mobility group protein B3 isoform X1 (Homo sapiens)	30.18	3	1	7	51	1.049	2	5.0	1.049	2	16.7	784.73	30.18	19	51	222	25.6	8.12
530396338	PREDICTED: alpha-actinin isoform X1 (Homo sapiens)	1.16	2	1	3	21	1.049	2	1.2	1.199	2	4.4	106.06	1.16	7	14	2150	238.8	5.39
4850549	actin, alpha cardiac muscle 1 preproprotein (Homo sapiens)	56.23	27	2	27	2249	1.049	62	9.6	1.240	62	21.8	56764.70	56.23	77	2269	177	42.0	5.39
530390698	PREDICTED: adenylate kinase isoenzyme 1 isoform X3 (Homo sapiens)	18.72	3	1	3	22	1.049	1		1.094	1	7	424.80	18.72	7	22	187	20.7	7.93
31652249	lipopolysaccharide-binding protein precursor (Homo sapiens)	12.27	1	4	5	31	1.048	9	16.6	1.260	9	18.5	1348.47	12.27	14	31	481	53.3	6.70
578833192	PREDICTED: zinc finger protein 844 isoform X2 (Homo sapiens)	4.61	2	1	3	7	1.048	1		1.803	1		25.23	4.61	3	7	499	57.5	8.59
296011001	abi interactor 1 isoform k (Homo sapiens)	6.96	17	2	2	9	1.048	3	0.0	1.146	3	8.0	483.13	6.96	9	9	388	42.6	6.04
578816553	PREDICTED: centrin isoform X2 (Homo sapiens)	7.00	6	1	13	24	1.048	1		1.398	1		40.06	7.00	19	24	1343	155.6	8.40
10000140	histone H2B type 1.8 (Homo sapiens)	14.2	2	13	21	129	1.048	4	5.8	1.129	4	20.8	6662.32	14.2	34	217	124	13.9	10.32
354721179	ras-related protein Rab-5B isoform 2 (Homo sapiens)	28.16	5	2	5	23	1.048	4	15.0	2.310	3	103.5	607.81	28.16	12	23	174	19.1	7.30
10835067	lupus La protein (Homo sapiens)	21.32	1	6	9	41	1.048	8	6.0	1.279	8	9.0	943.95	21.32	24	41	408	46.8	7.12
530406418	PREDICTED: tropomyosin alpha-1 chain isoform X12 (Homo sapiens)	47.76	29	3	17	118	1.047	3	2.3	1.073	3	6.5	3394.57	47.76	48	118	245	28.5	4.78
71274132	phosphoglycerate mutase 4 (Homo sapiens)	40.16	22	1	8	111	1.047	1		1.178	1		3840.54	40.16	24	111	254	28.8	6.65
54607080	carboxypeptidase B preproprotein (Homo sapiens)	3.12	1	1	1	4	1.047	1		1.255	1	1	33.63	3.12	2	4	417	47.3	6.61
530374901	PREDICTED: protein C23G homolog isoform X4 (Homo sapiens)	46.67	6	5	6	16	1.047	5	1.5	1.221	5	24.7	615.52	46.67	15	16	210	21.7	5.54
578795643	PREDICTED: serine--tRNA ligase, cytoplasmic isoform X1 (Homo sapiens)	10.45	2	2	6	17	1.047	3	5.4	1.261	3	46.0	419.39	10.45	12	17	536	61.3	7.06
390635651	ras-related protein Rab-44 (Homo sapiens)	9.11	1	4	6	20	1.047	6	4.5	1.130	6	27.7	1074.55	9.11	14	20	1021	110.8	5.08
4759300	vesicle-associated membrane protein 3 (Homo sapiens)	23.00	1	1	2	5	1.047	1		1.124	1		263.30	23.00	4	5	100	11.3	8.79
42518068	trans-Golgi network integral membrane protein 2 isoform 1 precursor (Homo sapiens)	9.38	3	1	3	6	1.047	1		1.206	1		80.69	9.38	5	6	437	45.9	5.63
4506193	proteasome subunit beta type-1 (Homo sapiens)	45.23	1	8	8	60	1.047	19	6.7	1.132	19	21.1	2622.78	45.23	24	60	241	26.5	8.13
4506137	ribose-phosphate pyrophosphokinasase 1 isoform 1 (Homo sapiens)	25.79	5	4	5	186	1.046	5	4.9	1.186	5	19	678.24	25.79	19	24	316	34.8	6.98
57963298	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1 isoform b (Homo sapiens)	4.29	17	1	9	32	1.046	1		1.157	1		178.76	4.29	15	32	1655	184.7	7.75
145386517	phostensin (Homo sapiens)	7.34	1	2	4	12	1.046	2	2.3	1.068	2	17.6	384.78	7.34	22	613	67.9	5.40	
4758112	spliceosome RNA helicase DXD398 (Homo sapiens)	28.04	1	3	10	57	1.046	4	2.3	0.999	4	38.0	1379.00	28.04	28	57	428	49.0	5.67
578810779	PREDICTED: ras GTPase-activating protein-binding protein 1 isoform X1 (Homo sapiens)	4.94	1	1	6	1.046	2	15.2	1.251	2	2	11.9	143.84	4.94	2	6	466	52.1	5.52
578825985	PREDICTED: proteasome activator complex subunit 2 isoform X1 (Homo sapiens)	63.19	2	1	9	39	1.046	1		1.047	1		1486.84	63.19	27	39	163	18.6	7.99
4506179	proteasome subunit alpha type-1 isoform 2 (Homo sapiens)	60.08	3	12	16	82	1.046	25	13.1	1.118	25	46.7	2637.05	60.08	42	82	263	29.5	6.61
12965178	taste receptor type 2 member 13 (Homo sapiens)	2.44	1	1	6	1.046	2	11.3	1.1	1.046	2	62.20	24.74	2.44	2	30	35.1	9.66	
4758950	peptidyl-prolyl cis-trans isomerase B precursor (Homo sapiens)	40.74	1	8	9	66	1.046	17	5.2	1.147	17	10.5	1407.04	40.74	26	66	216	23.7	9.41
530400291	PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform X9 (Homo sapiens)	16.65	11	7	16	41	1.046	9	6.6	1.179	9	10.3	851.84	16.65	32	431	105.6	5.47	
33239451	proliferating cell nuclear antigen (Homo sapiens)	26.05	1	3	5	16	1.046	3	1.0	1.032	3	14.4	397.62	26.05	13	16	261	28.8	4.69
4885413	histidine triad nucleotide-binding protein 1 (Homo sapiens)	63.49	1	5	6	28	1.045	7	9.4	1.153	7	21.6	865.48	63.49	17	28	126	13.8	6.95
54535599	F-actin-capping protein subunit alpha-2 (Homo sapiens)	46.25	5	9	5	113	1.045	10	6.3	1.101	10	9.0	3428.27	46.25	26	113	286	32.9	5.85
158917236	purpurycin-sensitive aminopeptidase (Homo sapiens)	17.41	8	12	15	57	1.045	17	4.3	1.185	17	16.3	1845.57	17.41	40	57	919	103.2	5.72
5021233	eukaryotic translation initiation factor 1 (Homo sapiens)	25.66	2	1	3	9	1.045	2		1.513	2		154.39	25.66	9	9	113	12.7	7.44
21361399	serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Homo sapiens)	27.67	11	10	13	49	1.045	14	6.9	1.283	14	17.3	1615.79	27.67	33	49	589	65.3	5.11
13027604	28S ribosomal protein S34, mitochondrial (Homo sapiens)	3.21	3	1	1	1	1.045	1		1.105	1		22.66	3.21	1	1	218	25.6	9.98
4506649	60S ribosomal protein L3 isoform a (Homo sapiens)	7.94	1	1	6	28	1.045	1		1.207	1		68.83	7.94	13	28	403	46.1	10.18
55749431	transcription elongation factor A protein-like 3 (Homo sapiens)	18.00	2	2	3	10	1.044	3	10.4	1.161	3	5.6	398.25	18.00	7	10	200	22.5	4.92
22202433	profilin subunit 5 isoform alpha (Homo sapiens)	32.47	1	3	7	1.044	1	1	136.41	0.698	1		136.39	32.47	4	134	154	17.3	6.33
325651836	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 1 (Homo sapiens)	7.70	1	1	7	16	1.044	1		1.317	1		179.35	7.70	11	16	1052	121.8	8.09
32484979	AP-3 complex subunit beta-1 isoform 1 (Homo sapiens)	9.87	3	2	11	27	1.044	2	2.9	0.926	2	29.3	284.58	9.87	20	27	1094	121.2	6.04
13259510	dynactin subunit 1 isoform 1 (Homo sapiens)	6.34	6	2	9	60	1.044	3	1.7	1.143	3	2.9	465.29	6.34	22	60	1278	141.6	5.81
578835493	PREDICTED: glycogen phosphorylase, brain form isoform X1 (Homo sapiens)	12.69	1	1	9	58	1.044	1		1.187	1		1952.14	12.69	24	58	843	96.6	6.86
350529338	protein set-1 homolog 1 isoform 2 precursor (Homo sapiens)	15.61	4	1	3	6	1.043	1		1.267	1		109.72	15.61	6	4	301	33.5	4.83
7661728	regulator complex protein LMN202 isoform 1 (Homo sapiens)	32.40	3	21	30	108	1.043	3	26.0	1.108	3	14.7	263.58	32.40	13	33	125	40.0	6.00
578830342	PREDICTED: baculoviral IAP repeat-containing protein 6 isoform X7 (Homo sapiens)	1.85	12	1	12	24	1.043	1		1.195	1		36.64	28.55	14	24	490	528.0	6.13
344179112	scavenger receptor cysteine-rich type 1 protein M130 isoform b precursor (Homo sapiens)	4.46	16	3	5	13	1.043	2	12.8	1.124	2	39.4	174.92	4.46	11	13	1121	121.5	6.11
33356174	pinin (Homo sapiens)	4.74	1	1	6	9	1.043	1		1.093	1		120.58	4.74	9	9	717	81.6	7.14
315259111	NEDD8-MDP1 protein (Homo sapiens)	21.76	4	1	4	21	1.043	1		0.872	1		534.26	21.76	9	21	193	22.0	6.37
530362892	PREDICTED: leucine-rich repeat-containing protein 8D isoform X1 (Homo sapiens)	3.15	1	1	3	9	1.043	1		2.303	1		27.45	3.15	3	9	858	98.1	7.72
82617634	cytoplasmic FMR1-interacting protein 2 isoform a (Homo sapiens)	9.86	5	6	13	46	1.043	8	6.9	1.285	8	17.3	1006.21	9.86	26	46	1253	145.6	7.05
41406084	glutathione peroxidase 1 isoform 1 (Homo sapiens)	29.56	2	4	4	15	1.043	5	12.8	1.334	5	12.8	334.33	29.56	5	12	178	20.3	6.55
190533935	26S protease regulatory subunit 10B (Homo sapiens)	16.13	1	2	6	18	1.043	3	10.7	1.375	2	34.7	279.57	16.13	12	18	403	45.8	7.78
564473387	actin-related protein 2/3 complex subunit 3 isoform 2 (Homo sapiens)	43.50	2	9	9	89	1.042	26	9.2	1.115	25	15.0	2057.46	43.50	27	89	177	20.4	8.78
71051616	uroporphyrinogen decarboxylase (Homo sapiens)	21.80	2	2	3	17	1.042	2	16.2	1.609	2	14.0	284.27	21.80	6	17	367	40.8	6.14
523704487	ubiquitin-like conjugating enzyme ATG13 isoform 1 (Homo sapiens)	7.40	2	2	2	6	1.042	2	8.5	1.216	2	3.3	322.82	7.40	40	6	311	35.4	4.79
68509926	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 (Homo sapiens)	6.79	6	5	5	18	1.042	7	15.7	1.200	7	11.4	344.33	6.79	13	18	795	90.9	7.46
38788353	regulator complex protein LMN205 (Homo sapiens)	32.47	1	3	7	1.042	1	1	7.4	0.964	1		357.75	32.47	4	13	173	18.1	8.50
14574568	allograft inflammatory factor 1 isoform 3 (Homo sapiens)	36.05	17	3	6	28	1.042	6	11.1	1.352	6	8.1	918.08	36.05	14	28	147	16.7	6.24
4504111	growth factor receptor-bound protein 2 isoform 1 (Homo sapiens)	39.17	2	7	8	54	1.042	18	6.8	1.263	18	15.1	2305.64	39.17	21	54	217	25.2	6.32
578837826	PREDICTED: mottle sperm domain-containing protein 2 isoform X2 (Homo sapiens)	4.00	4	1	2	4	1.042	1		1.119	1		157.82	4.00	4	4	475	54.5	5.83
336176066	RNA-binding protein 39 isoform d (Homo sapiens)	8.96	5	1	5	25	1.042	2	4.0	1.169	2	3.9	227.44	8.96	7	25	502	56.3	10.04
38327039	heat shock 70 kDa protein 4 (Homo sapiens)	34.40	1	17	22	82	1.042	24	5.8	1.067	24	11.7	3029.01	34.40	54	82	840	94.3	5.19
219521928	D153-like exonuclease 1 isoform 1 (Homo sapiens)	3.04	4	1	4	13	1.042	1		1.102	1		20.94	3.04	4	13	1054	120.7	6.54
21450861	attractin isoform 1 preproprotein (Homo sapiens)	9.73	5																

Accession	Description	ZCoverage	Z# Proteins	Z# Unique Peptides	Z# Peptides	Z# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score (A3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
57800460	PREDICTED: complement factor H-related protein 4 isoform X6 [Homo sapiens]	2.89	10	1	2	6	1.038	1		1.045			147.89	2.89	4	6	519	58.5	4.94
5031569	alpha-actinin-1 [Homo sapiens]	32.18	2	3	10	45	1.038	5	5.1	1.033	5	11.1	1433.25	32.18	28	45	376	42.6	6.64
53041126	PREDICTED: zinc finger protein 207 isoform X3 [Homo sapiens]	6.44	5	1	2	4	1.038	1		1.041			126.57	6.44	4	4	466	49.6	6.46
151101404	prothymosin alpha isoform 2 [Homo sapiens]	27.27	25	4	5	35	1.038	10		1.242	9	7.8	1517.58	27.27	15	35	110	12.1	3.79
67190748	complement C4-A isoform 1 precursor [Homo sapiens]	72.36	21	3	103	1598	1.038	10	14.7	0.982	8	95.4	56962.48	72.36	302	1598	1744	192.7	7.08
530406751	PREDICTED: ubiquitin carboxyl-terminal hydrolase 3 isoform X3 [Homo sapiens]	1.99	7	1	1	1	1.038	1		0.973			26.11	1.99	1	1	351	40.1	7.75
530420490	PREDICTED: apolipoprotein L1 isoform X2 [Homo sapiens]	31.05	4	1	10	47	1.038	14	9.3	1.093	13	16.9	1687.30	31.05	28	47	380	42.1	5.80
189181666	beta-hexamidase subunit alpha preproprotein [Homo sapiens]	7.94	1	1	3	11	1.038	1		1.196	1		126.34	7.94	9	11	529	60.7	5.16
295821193	hexon amyloid A-1 protein preproprotein [Homo sapiens]	37.05	11	3	11	131	1.038	15		1.134	15	22.5	5496.18	37.05	33	131	122	13.5	6.79
10129112	ubiquitin-specific chaperone A isoform 2 [Homo sapiens]	44.47	10	11	43	138	1.038	14	8.1	1.038	14	8.1	1468.65	44.47	31	43	108	12.8	5.29
222136639	C-1-tetrahydrofolate synthase, cytoplasmic [Homo sapiens]	10.37	1	9	25	1037		7		1.119	7	13.0	716.82	10.37	25	25	935	101.5	7.30
530397480	PREDICTED: phosphatidylinositol-binding clathrin assembly protein isoform X19 [Homo sapiens]	5.48	26	2	3	11	1.037	3		1.160	3	3.7	498.54	5.48	7	11	547	59.7	8.70
578821054	PREDICTED: protein argonau12-like [Homo sapiens]	3.00	1	1	1	2	1.037	1		1.219	1		39.86	3.00	2	2	233	24.2	11.09
400974227	janus kinase and microtubule-interacting protein 2 isoform 2 [Homo sapiens]	9.51	4	1	9	25	1.037	4	5.7	1.183	4	7.5	335.02	9.51	13	25	799	93.6	5.97
4505145	NAD-dependent malic enzyme, mitochondrial isoform 1 precursor [Homo sapiens]	5.65	1	1	3	6	1.037	1		1.115	1		291.48	5.65	6	6	584	65.4	7.61
530371163	PREDICTED: UDP-GlcNAc 6-epimerase 1, 3-N-acetylglucosaminyltransferase 7 isoform X1 [Homo sapiens]	8.23	2	1	2	2	1.037	1		1.032	1		32.39	8.23	2	2	308	37.9	8.57
530360487	PREDICTED: protein D-1 isoform X1 [Homo sapiens]	89.95	1	17	18	225	1.037	66	8.8	1.196	66	21.0	9052.38	89.95	52	225	189	19.9	6.79
148746218	serine/threonine-protein kinase TAO3 [Homo sapiens]	10.13	3	1	10	53	1.037	1		1.186	1		175.80	10.13	17	53	898	105.3	7.30
4758442	gla maturation factor beta [Homo sapiens]	26.76	3	1	4	37	1.036	1		1.154			1220.35	26.76	10	37	142	16.7	5.29
530370277	PREDICTED: 60 kDa heat shock protein, mitochondrial isoform X1 [Homo sapiens]	7.68	1	2	4	13	1.036	3		1.114	3	18.8	554.65	7.68	10	13	573	61.0	5.87
578837225	PREDICTED: armadillo repeat protein deleted in velo-cardio-facial syndrome isoform X12 [Homo sapiens]	5.49	3	1	4	9	1.036	2		1.582	2	18.4	70.59	5.49	5	9	656	71.3	6.24
167234419	thyroid hormone receptor-associated protein 3 [Homo sapiens]	2.07	15	1	6	15	1.036	2		1.065	2	480.77	6.07	15	15	955	108.6	10.15	
7098049	protein BRPS homolog [Homo sapiens]	2.51	2	1	5	11	1.036	1		1.596	1		25.07	2.51	5	11	1871	208.6	8.87
28827815	protein S100-A7A [Homo sapiens]	53.47	1	1	5	105	1.036	1		1.411			2841.74	53.47	14	105	101	11.3	7.44
14149627	ubiquitin carboxyl-terminal hydrolase 15 isoform 2 [Homo sapiens]	7.88	5	3	9	42	1.036	3	2.2	1.107	3	5.8	294.59	7.88	19	42	952	109.2	5.15
578836895	PREDICTED: protein kinase C and casein kinase substrate in neurons protein 2 isoform X5 [Homo sapiens]	20.22	8	6	11	39	1.036	7	9.9	1.236	7	3.2	684.69	20.22	23	39	445	51.1	5.24
45075059	metalloproteinase inhibitor 1 precursor [Homo sapiens]	11.11	1	1	2	5	1.036	1		1.220	1		171.85	11.11	5	5	207	23.2	8.10
32313593	ultraconserved-4 precursor [Homo sapiens]	21.18	2	10	43	136	1.036	13		1.140	13	13	1714.96	21.18	43	43	510	57.2	5.69
532164704	cltfl lip and platelet transmembrane protein 1 isoform 3 [Homo sapiens]	5.50	1	3	8	1036		2		1.121	2	5.6	33.43	5.50	4	8	655	75.1	6.64
195927020	calcium-binding protein 39 [Homo sapiens]	40.47	1	7	12	66	1.035	10	6.2	1.188	10	13.8	1144.05	40.47	33	66	341	39.8	6.89
6978649	choline/ethanolamine kinase [Homo sapiens]	3.54	1	1	1	3	1.035	1		1.662	1		66.81	3.54	3	3	395	45.2	5.49
5729953	nuclear migration protein nudC [Homo sapiens]	6.95	1	1	3	11	1.035	1		1.159	1		116.33	6.95	7	11	331	38.2	5.38
520975489	ran-specific GTPase-activating protein isoform 4 [Homo sapiens]	36.67	6	2	5	20	1.035	3	4.4	1.087	3	5.7	319.05	36.67	11	20	150	17.5	8.24
530419699	PREDICTED: fructose-bisphosphate adolase C isoform X3 [Homo sapiens]	46.90	3	9	20	168	1.035	11	9.1	1.163	11	5.3	5348.11	46.90	56	168	384	39.4	6.87
2191794	cullin-associated NEDD8-dissociated protein 1 [Homo sapiens]	19.25	1	13	22	56	1.035	15	6.6	1.036	15	27.7	1515.88	19.25	49	56	1230	136.3	5.78
4826659	F-actin-capping protein subunit beta isoform 1 [Homo sapiens]	67.65	5	19	19	193	1.035	67	7.6	1.202	66	19.8	7179.30	67.65	57	193	272	30.6	6.00
530385095	PREDICTED: src kinase-associated phosphoprotein 2 isoform X1 [Homo sapiens]	25.35	1	8	8	42	1.035	14	7.5	1.235	14	12.3	1633.03	25.35	23	42	359	41.2	4.69
578838720	PREDICTED: uncharacterized protein KIAA1210 isoform X1 [Homo sapiens]	1.89	2	1	4	4	1.035	1		1.241			25.04	1.89	4	4	1533	167.9	8.53
5803227	14-3-3 protein theta [Homo sapiens]	63.67	1	9	17	161	1.035	18	10.3	1.175	18	14.8	5422.04	63.67	51	161	245	27.7	4.78
578810593	PREDICTED: calpastatin isoform X11 [Homo sapiens]	27.89	24	15	18	66	1.035	21	8.8	1.134	21	7.2	1658.40	27.89	44	66	735	78.8	5.05
21040371	ATP-dependent RNA helicase/DDX40 [Homo sapiens]	31.18	1	7	46	1634		1		1.034	1		1099.54	31.18	44	47	49	11	5.68
4507323	apolipoprotein C-II precursor [Homo sapiens]	34.34	1	3	3	35	1.034	13	8.8	1.400	13	18.7	1845.37	34.34	9	35	99	10.8	5.41
5902102	small nuclear ribonucleoprotein Sm D1 isoform 1 [Homo sapiens]	54.62	2	4	4	38	1.034	1	7.8	1.259	9	6.5	770.96	54.62	12	38	119	13.3	11.56
56682959	ferritin heavy chain [Homo sapiens]	66.12	1	10	12	105	1.034	30	9.7	1.100	30	11.1	2930.55	66.12	35	105	183	21.2	5.55
334724455	acetyl-coenzyme A synthetase, cytoplasmic isoform 3 [Homo sapiens]	3.96	9	1	4	28	1.034	2	0.9	1.101	2	0.7	321.61	3.96	8	28	606	67.6	6.15
260438860	AP-1 complex subunit beta-1 isoform B [Homo sapiens]	17.68	3	4	14	44	1.034	5	8.5	1.230	5	13.8	752.07	17.68	35	44	939	103.5	5.16
401461824	ribuliding protein particle complex subunit 3 isoform 3 [Homo sapiens]	21.18	1	1	2	1	1.034	1		1.434	1	1	31.19	21.18	1	2	134	15.0	4.88
530336151	PREDICTED: inaa-like protein isoform X5 [Homo sapiens]	4	8	1	9	33	1.033	4	6.6	1.184	4	7.3	268.04	5.57	14	33	1454	160.1	4.87
4503507	eukaryotic translation initiation factor 2 subunit 3 [Homo sapiens]	4.24	1	2	3	7	1.033	2	0.5	1.247	2	13.1	87.87	4.24	7	7	472	51.1	8.40
1356962	ras-related protein Rab-1B [Homo sapiens]	41.79	21	2	7	60	1.033	6	3.6	1.182	6	14.1	2735.97	41.79	21	60	201	22.2	5.73
530379378	PREDICTED: phosphatidylinositol 3-kinase regulatory subunit alpha isoform X1 [Homo sapiens]	4.56	4	1	4	9	1.033	1		1.136	1		30.86	4.56	6	9	724	83.5	6.16
530422933	PREDICTED: zinc finger protein 185 isoform X16 [Homo sapiens]	8.10	19	1	1	10	1.033	1		1.157	1		92.78	8.10	9	10	630	67.2	7.01
62122917	flaggrin-2 [Homo sapiens]	2	1	1	4	8	1.033	1		1.093	1		91.02	2	6	8	2391	247.9	8.31
578820364	PREDICTED: AP-2 complex subunit alpha-2 isoform X3 [Homo sapiens]	8.71	3	7	20	1.033	2		0.6	1.402	2	26.0	421.83	8.71	14	20	941	104.3	6.80
62912466	C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	23.11	3	5	5	26	1.033	9	2.8	1.403	9	8.5	730.78	23.11	15	26	251	28.3	5.14
530364287	PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sapiens]	13.03	3	6	7	31	1.033	9	2.2	1.217	9	19.4	957.27	13.03	18	31	660	75.3	6.48
120433590	acyl-CoA-binding protein isoform 3 [Homo sapiens]	72.41	7	4	7	45	1.033	13	4.7	1.019	13	13.2	1436.88	72.41	18	45	87	10.0	6.57
5570902	opioid growth factor receptor-like protein 1 [Homo sapiens]	15.74	7	2	7	17	1.033	3	10.2	1.073	3	3.7	598.81	15.74	13	17	451	51.2	6.13
9910460	omega-amidase NT12 [Homo sapiens]	47.83	1	9	10	28	1.033	9	3.5	1.117	9	21.7	1046.22	47.83	26	28	276	30.6	7.21
11214873	cave-binding factor subunit beta isoform 2 [Homo sapiens]	15.74	4	15	4	15	1.033	4	5.2	1.080	4		345.23	15.74	15	15	182	21.5	6.60
530381587	PREDICTED: FYVE, RhoGEF and PH domain-containing protein 2 isoform X1 [Homo sapiens]	2.74	2	1	2	3	1.033	2		1.031	2		34.76	2.74	2	3	620	70.8	7.30
195976777	dyserferlin isoform 1 [Homo sapiens]	3.34	16	1	7	26	1.032	3	4.6	1.066	3	1.3	525.31	3.34	11	26	2067	235.8	5.82
167900484	pentraxin-related protein PTX3 precursor [Homo sapiens]	13.65	1	3	4	15	1.032	3	3.2	1.085	3	9.3	543.29	13.65	12	15	381	41.9	5.01
4503481	elongation factor 1-gamma [Homo sapiens]	45.77	1	14	15	99	1.032	31	5.9	1.221	31	22.5	3330.32	45.77	42	99	437	50.1	6.67
148536853	coatamer subunit alpha isoform 2 [Homo sapiens]	6.78	3	3	11	60	1.032	3	3.1	1.111	3	2.6	584.24	6.78	22	60	1224	138.3	7.66
530406263	PREDICTED: ras-related protein Rab-27A isoform X3 [Homo sapiens]	28.57	2	4	5	19	1.032	6	4.3	1.079	6	11.0	689.36	28.57	14	19	168	19.2	5.38
115527062	collagen alpha-2(VI) chain isoform 2C2 precursor [Homo sapiens]	13.35	3	3	9	19	1.032	3	1.7	1.271	3	9.1	361.07	13.35	16	19	1019	108.5	6.21
2																			

Accession	Description	SCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
119395754	keratin, type II cytoskeletal 5 [Homo sapiens]	23.05	10	3	16	70	1.029	6	6.2	1.085	6	3.8	1632.39	23.05	44	70	590	62.3	7.74	
226443152	alpha/beta hydrolase domain-containing protein 14B isoform 1 [Homo sapiens]	24.76	5	4	7	21	1.029	4	4.6	1.146	4	51.3	379.13	24.76	17	21	210	22.3	6.40	
578821106	PREDICTED: CIV domain-containing protein 1 isoform X1 [Homo sapiens]	27.15	4	12	14	48	1.029	21	4.5	1.191	21	21.5	2015.02	27.15	40	66	124	66.1	6.63	
6912586	6-phosphogluconolactonase [Homo sapiens]	69.77	2	12	12	59	1.029	20	6.1	1.136	19	21.1	2177.54	69.77	34	59	258	27.5	6.05	
4504483	hypoxanthine-guanine phosphoribosyltransferase [Homo sapiens]	28.90	6	6	6	29	1.029	9	8.4	1.130	9	17.2	1169.85	28.90	16	29	118	24.6	6.68	
203575529	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 [Homo sapiens]	17.65	5	3	5	32	1.029	2	4.2	1.760	2	66.5	514.07	17.65	14	32	340	37.3	6.00	
578834138	PREDICTED: serine/threonine-protein phosphatase 6 regulatory subunit 1 isoform X3 [Homo sapiens]	5.57	2	1	3	5	1.029	1	1.031				143.75	5.57	5	5	754	82.2	4.55	
578824247	PREDICTED: phosphatidylinositol 5-phosphate 4-kinase type-2 gamma isoform X2 [Homo sapiens]	6.77	5	1	1	3	1.029	1	1.067				158.69	6.77	3	3	251	28.4	6.13	
4885111	calmodulin-like protein 3 [Homo sapiens]	24.16	1	2	3	16	1.029	2	6.0	1.025	2	1.7	593.95	24.16	9	16	149	16.9	4.42	
7641882	rho GTPase-activating protein 25 isoform b [Homo sapiens]	18.50	10	25	10	10	1.029	7	8.9	1.028	7	5.5	491.50	18.50	22	46	438	72.4	6.07	
3045553610	EF-hand calcium-binding domain-containing protein 13 isoform A [Homo sapiens]	2.98	4	1	4	34	1.028	8	1.0	0.842	1		422.57	2.98	8	34	973	110.1	6.57	
530365306	PREDICTED: nuclear ubiquitin casein and cyclin-dependent kinase substrate 1 isoform X1 [Homo sapiens]	13.64	2	2	4	12	1.028	2	3.3	0.955	2	23.2	118.07	13.64	9	12	242	27.2	5.08	
33457316	pleckstrin homology domain-containing family O member 2 isoform 1 [Homo sapiens]	9.59	2	4	5	13	1.028	4	4.8	1.220	4	17.4	499.17	9.59	13	13	490	53.3	5.43	
530370925	PREDICTED: X-ray repair cross-complementing protein 5 isoform X1 [Homo sapiens]	35.67	7	15	23	130	1.028	29	8.3	1.183	29	16.1	5342.84	35.67	59	130	827	93.5	8.10	
4504445	heterogeneous nuclear ribonucleoprotein A1 isoform a [Homo sapiens]	53.75	10	13	19	156	1.028	30	4.6	1.152	30	9.0	5075.21	53.75	56	156	320	34.2	9.23	
12056473	slalic acid synthase [Homo sapiens]	11.42	1	3	3	9	1.028	3	6.4	1.357	3	25.3	414.59	11.42	8	9	359	40.3	6.74	
530403051	PREDICTED: putative ATP-dependent RNA helicase TDRD9 isoform X1 [Homo sapiens]	4.21	4	1	6	19	1.028	2	6.9	1.500	2	10.3	41.75	4.21	11	19	1330	149.7	7.05	
5031593	actin-related protein 2/3 complex subunit 5 isoform 1 [Homo sapiens]	80.13	3	9	11	92	1.028	29	8.4	1.159	29	10.1	3838.50	80.13	29	92	151	16.3	5.67	
34147513	ras-related protein Rab-7a [Homo sapiens]	71.98	1	12	14	143	1.028	46	5.5	1.150	46	15.1	4984.48	71.98	40	143	207	23.5	6.70	
262231791	complement factor H-related protein 3 isoform 2 precursor [Homo sapiens]	16.36	3	2	4	79	1.028	6	12.8	1.385	5	8.1	1436.05	16.36	11	79	269	30.7	7.78	
10880979	lymphocyte-specific protein 1 isoform 1 [Homo sapiens]	50.44	6	11	12	107	1.027	31	6.2	1.101	31	17.9	4759.62	50.44	34	107	339	37.2	4.74	
140972063	neurabin-2 [Homo sapiens]	3.43	8	3	2	6	1.027	1	1	0.63	1		133.62	3.43	9	8	817	89.3	4.97	
117320537	1-phosphoglycinolactol 4,5-bisphosphate phosphoglycerate gamma-2 [Homo sapiens]	9.88	1	5	9	23	1.027	5	10.4	1.094	5	6.7	700.25	9.88	22	23	1265	147.8	6.64	
14251209	chloride intracellular channel protein 1 [Homo sapiens]	76.76	8	14	14	162	1.027	53	7.9	1.201	49	20.1	5836.57	76.76	41	162	241	26.9	5.17	
354983501	protein-L-isopartate(D-aspartate) O-methyltransferase isoform 1 [Homo sapiens]	53.33	5	9	11	74	1.027	21	8.0	1.261	20	16.1	2240.38	53.33	29	74	285	30.3	7.52	
530393565	PREDICTED: insulin-degrading enzyme isoform X4 [Homo sapiens]	1.48	3	1	1	2	1.026	1					47.52	1.48	2	2	609	69.9	6.89	
530403615	PREDICTED: DNA-(apurinic or apyrimidinic site) lyase isoform X1 [Homo sapiens]	55.03	2	16	18	85	1.026	26	3.5	1.133	26	17.2	3438.31	55.03	51	85	318	35.5	8.12	
22538465	proteasome subunit beta type-3 [Homo sapiens]	31.17	1	5	5	30	1.026	10	10	1.154	10	10.4	919.84	31.17	15	30	205	22.2	6.56	
571324877	carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	6	13	6	6	22	1.026	6	13.2	1.299	6	32.0	407.50	13.21	15	22	384	44.0	7.71	
578834433	PREDICTED: uncharacterized protein C19orf68 isoform X3 [Homo sapiens]	6.12	6	1	8	18	1.026	3	8.3	1.803	3	26.5	54.42	6.12	12	18	947	104.7	8.40	
19401857	phosphoribosyl pyrophosphate synthase-associated protein 1 [Homo sapiens]	7.79	1	1	2	4	1.026	1	1	1.358	4		116.88	7.79	4	4	385	42.4	8.47	
300360515	actin-related protein 2/3 complex subunit 1A isoform 2 [Homo sapiens]	3.37	2	1	1	2	1.026	1		0.960	1		41.64	3.37	2	2	356	39.6	8.22	
121114302	culin-4B isoform 2 [Homo sapiens]	11.17	6	1	8	27	1.026	1	1	1.137	1		186.99	11.17	14	27	895	102.2	7.94	
530384039	PREDICTED: atropin isoform X7 [Homo sapiens]	6.13	7	1	26	205	1.026	1		1.450	1		973.26	6.13	50	205	3424	393.2	5.33	
530380347	PREDICTED: glucosamine-6-phosphate isomerase 1 isoform X1 [Homo sapiens]	25.16	9	5	7	27	1.026	7	7	1.202	7		926.87	25.16	19	27	318	36.1	7.61	
4557587	fumarylacetoacetase [Homo sapiens]	18.38	1	6	6	25	1.026	8	3.3	1.111	8	15.4	455.20	18.38	17	25	419	46.3	6.95	
55741719	liprin [Homo sapiens]	3.10	2	4	4	19	1.026	3	5.9	2.362	3	51.5	43.86	3.10	4	19	1516	161.1	6.62	
7657069	ERO1-like protein alpha precursor [Homo sapiens]	16.03	1	3	7	15	1.025	3	0.7	1.076	3	1.7	482.55	16.03	3	15	15	468	54.4	5.68
4181453	STE20-like serine/threonine-protein kinase [Homo sapiens]	13.28	17	6	16	45	1.025	5	13.2	1.051	5	17.8	855.10	13.28	37	45	1235	142.6	5.15	
24430132	VW domain-binding protein 2 [Homo sapiens]	8.81	1	3	8	1.025	1	1	1	1.068	1		96.26	8.81	7	8	261	28.1	5.91	
530380347	acidopropionin A-II precursor [Homo sapiens]	41.35	23	26	200	1.025	61	7.0	1.245	1.245	58	16.3	5910.78	41.35	73	200	396	45.3	5.38	
24430192	keratin, type I cytoskeletal 16 [Homo sapiens]	38.90	20	6	21	75	1.025	8	7.7	1.136	8	11.0	2335.21	38.90	56	75	473	51.2	5.05	
344030204	ras-related protein Rab-6A isoform c [Homo sapiens]	11.43	19	1	2	9	1.025	1		1.118	1		335.11	11.43	6	9	175	19.9	5.07	
5031571	actin-related protein 2 isoform b [Homo sapiens]	61.17	25	16	20	238	1.025	65	9.0	1.221	59	20.5	8489.39	61.17	56	238	394	44.7	6.74	
256222019	ras-related protein Rab-10 [Homo sapiens]	25.50	20	2	5	34	1.025	5	5.6	1.405	5	21.8	1619.89	25.50	13	34	200	22.5	8.38	
8051584	ficollin-1 precursor [Homo sapiens]	24.85	2	6	6	30	1.025	10	5.2	1.046	10	13.4	1020.75	24.85	18	30	326	35.1	6.86	
4504061	N-acetylglucosamine-4-epimerase precursor [Homo sapiens]	15.47	6	6	26	1.025	16	13	14.6	1.211	13	8	965.34	15.47	18	26	552	60.0	8.31	
34577063	adenylsuccinate synthetase isozyme 2 [Homo sapiens]	39.25	4	14	17	90	1.025	27	7.8	1.176	26	25.4	2651.68	39.25	45	90	456	50.1	6.55	
4575826	beta-2-microglobulin precursor [Homo sapiens]	49.58	2	4	4	26	1.025	8	2.7	1.142	8	8.3	1084.87	49.58	12	26	119	13.7	6.52	
4507949	14-3-3 protein beta/alpha [Homo sapiens]	81.30	1	9	21	260	1.025	40	7.1	1.205	39	18.6	8374.54	81.30	59	260	246	28.1	4.83	
4503477	elongation factor 1-beta [Homo sapiens]	42.22	1	4	7	26	1.025	7	1.9	1.235	7	12.0	908.14	42.22	17	26	225	24.7	4.67	
530392285	PREDICTED: sickle tail protein homolog isoform X14 [Homo sapiens]	3.28	30	1	7	9	1.025	1	3.28	1.229	1		33.21	3.28	7	9	170	194.6	6.95	
53038685	PREDICTED: CREB3 regulatory factor isoform X1 [Homo sapiens]	2	2	4	7	1.025	2	2	11.3	1.460	2		39.1	34.02	7	7	631	71.3	4.87	
578834710	PREDICTED: spectrin beta chain, non-erythrocytic 4 isoform X1 [Homo sapiens]	7.81	1	23	61	1.025	2	2	1.1	1.380	2	2.9	306.49	7.81	60	61	2394	270.1	5.67	
4575900	calreticulin precursor [Homo sapiens]	74.34	1	21	23	182	1.025	57	7.7	1.116	54	17.8	6259.99	74.34	64	182	417	48.1	4.44	
197382664	eukaryotic translation initiation factor 4E type 3 isoform b [Homo sapiens]	14.41	2	1	1	6	1.024	2	7.2	1.080	2	5.2	235.06	14.41	3	6	118	13.3	5.78	
4504901	importin subunit alpha-3 [Homo sapiens]	6.33	1	1	3	6	1.024	1		1.224	1		144.60	6.33	5	6	521	57.9	4.96	
4506787	ras GTPase-activating protein 1 G0GAP1 [Homo sapiens]	54.44	5	63	70	400	1.024	122	6.9	1.168	117	17.4	1938.30	54.44	198	400	1657	189.1	6.46	
156616294	N-acetylmuramoyl-L-alanine amidase precursor [Homo sapiens]	34.55	2	11	17	10	1.024	23	11.7	1.024	20	7.5	114.75	34.55	32	70	576	62.2	7.58	
47132320	keratin, type II cytoskeletal 2 epidermal [Homo sapiens]	17.41	13	21	13	79	1.024	4	19.4	1.024	4	10.8	1598.28	17.41	19	43	399	45.4	8.00	
4575818	V-type proton ATPase subunit G 1 [Homo sapiens]	35.59	1	4	4	17	1.024	5	3.0	1.095	5	9.4	589.90	35.59	11	17	118	13.7	8.79	
19923497	echinoderm microtubule-associated protein-like 4 isoform a [Homo sapiens]	6.63	6	2	7	14	1.024	2	3.4	1.123	2	14.7	167.40	6.63	14	14	981	108.8	6.32	
33519455	methionine adenosyltransferase 2 subunit beta isoform 2 [Homo sapiens]	5.88	2	1	2	33	1.024	1		0.920	1		52.30	5.88	6	33	323	36.4	6.65	
4507651	tropomyosin alpha-4 chain isoform 2 [Homo sapiens]	53.23	14	5	22	152	1.024	6	1.0	1.046	6	5.5	3983.62	53.23	64	152	248	28.5	4.69	
57889860	PREDICTED: serine/threonine-protein kinase NIM1 isoform X1 [Homo sapiens]	6.42	2	1	3	8	1.024	3	5.8	1.039	3	5.8	535.77	6.42	3	8	436	49.6	8.35	
9257257	WD repeat-containing protein 1 isoform 1 [Homo sapiens]	59.74	3	27	31	284	1.024	84	5.8											

Accession	Description	LCoverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI		
4502565	calpain small subunit 1 [Homo sapiens]	48.88	4	9	10	95	1.021	23					11.1	2669.60	48.88	28	95	268	28.3	5.20	
355594753	clusterin preproprotein [Homo sapiens]	41.65	2	13	14	134	1.021	40	5.3	1.251	22		16.9	5046.73	41.65	39	134	449	52.5	6.27	
724747917	anligent peptide transporter 2 [Homo sapiens]	8.12	3	1	6	19	1.021	3	5.3	10.199	2		245.5	100.16	8.12	9	19	653	70.0	7.64	
5453597	F-actin-capping protein subunit alpha-1 [Homo sapiens]	68.18	5	10	13	212	1.021	46	10	1.247	42		29.0	8308.36	68.18	38	212	286	32.9	5.69	
530376754	PREDICTED: acyl-CoA synthetase family member 4 isoform X6 [Homo sapiens]	3.93	8	1	4	34	1.021	6	5.5	1.108	6		3.5	351.49	3.93	9	34	789	89.0	7.97	
21313638	leucine-rich repeat LGI family member 2 precursor [Homo sapiens]	1.28	1	1	1	2	1.021	1		1.214	1			38.44	1.28	2	2	545	62.3	6.93	
4507145	sorting nexin-4 [Homo sapiens]	2.00	1	1	1	2	1.021	1		1.079	1			47.05	2.00	2	2	450	51.9	5.99	
156151392	heterogeneous nuclear ribonucleoprotein R isoform 4 [Homo sapiens]	10.71	7	2	6	24	1.021	2		1.192	2		3.7	610.14	10.71	18	24	532	59.6	9.16	
197927454	protein DKK isoform 1 [Homo sapiens]	20.41	3	5	8	134	1.021	8		1.134	8		16.6	901.24	21.41	21	32	341	38.7	8.15	
73014819	X-ray repair cross-complementing protein 6 isoform 3 [Homo sapiens]	32.38	7	15	17	60	1.021	16		1.113	16		16.3	1445.40	32.38	17	60	559	44.2	9.28	
578798632	PREDICTED: tyrosine-protein kinase Fgr isoform X1 [Homo sapiens]	34.03	92	10	12	61	1.021	16		1.209	16		16	27.7	1781.27	34.03	34	61	529	59.4	5.59
154759259	spectrin alpha chain, non-erythrocytic L isoform 2 [Homo sapiens]	38.03	20	62	75	291	1.021	86		1.186	86		16.5	10470.93	38.03	200	291	2472	284.4	5.35	
4504523	10 kDa heat shock protein, mitochondrial [Homo sapiens]	18.63	1	2	2	9	1.021	3		1.002	3		3.5	195.69	18.63	6	9	102	10.9	8.92	
4503977	starch-binding domain-containing protein 1 [Homo sapiens]	3.63	1	1	2	3	1.020	1		1.167	1			31.67	3.63	3	3	358	39.0	5.73	
4502133	serum amyloid P-component precursor [Homo sapiens]	34.53	1	8	8	89	1.020	30		1.386	29		15.1	2992.18	34.53	23	89	223	25.4	6.54	
530389997	PREDICTED: GDP-L-fucose synthase isoform X2 [Homo sapiens]	13.61	4	4	7	17	1.020	4		1.127	4		8.8	337.81	13.61	17	441	48.3	6.79		
60097902	flaggrin [Homo sapiens]	16.55	1	14	21	100	1.020	23		1.101	23		8.3	2590.94	16.55	47	100	4061	434.9	9.25	
578803915	PREDICTED: heterogeneous nuclear ribonucleoprotein A3 isoform X4 [Homo sapiens]	30.51	6	7	11	84	1.020	15		1.152	15		6.1	1971.90	30.51	32	84	331	35.4	9.17	
530406069	PREDICTED: transient receptor potential cation channel subfamily M member 7 isoform X3 [Homo sapiens]	4.29	6	1	7	27	1.020	2		1.145	2		3.2	101.93	4.29	27	1864	212.5	7.88		
6806898	alpha-synuclein isoform NACP112 [Homo sapiens]	19.64	4	2	2	8	1.020	3		1.005	3		8.8	373.94	19.64	6	8	112	11.4	8.29	
5031877	lamin-B1 isoform 1 [Homo sapiens]	52.05	2	21	27	114	1.020	33		1.163	33		10.9	4715.70	52.05	72	114	586	66.4	5.16	
4758484	glutathione S-transferase omega-1 isoform 1 [Homo sapiens]	85.06	3	18	62	191	1.020	59		1.162	59		13.7	5142.34	85.06	64	191	241	29.5	6.60	
530381195	PREDICTED: docking protein 3 isoform X2 [Homo sapiens]	7.95	5	2	2	6	1.020	2		1.165	2		31.5	234.22	7.95	6	6	440	47.6	7.61	
10947139	arginase-1 isoform 2 [Homo sapiens]	61.80	7	14	16	92	1.020	27		1.196	26		16.6	2738.86	61.80	48	92	322	34.7	7.21	
14702180	eukaryotic translation initiation factor 4H isoform 2 [Homo sapiens]	18.42	2	2	2	9	1.020	3		1.002	3		19.5	323.96	18.42	6	9	228	25.2	8.09	
19923142	importin subunit beta-1 isoform 1 [Homo sapiens]	22.49	2	17	66	1.020	23		7.1	1.185	21		12.1	2020.35	22.49	48	66	876	97.1	4.78	
530384863	PREDICTED: probable palmitoyltransferase ZDHHC4 isoform X1 [Homo sapiens]	6.40	1	1	2	9	1.020	1		1.144	1			23.87	6.40	2	9	344	39.8	7.36	
530384472	PREDICTED: chromobox protein homolog 3 isoform X1 [Homo sapiens]	49.73	3	6	7	38	1.020	13		1.220	13		36.1	1114.49	49.73	11	38	183	20.8	5.33	
5453990	proteasome activator complex subunit 1 isoform 1 [Homo sapiens]	63.05	4	14	15	87	1.019	23		1.203	23		17.3	2625.39	63.05	21	87	249	28.7	6.02	
40353734	nucleophosmin isoform 2 [Homo sapiens]	36.98	5	7	8	46	1.019	15		1.130	15		11.9	2153.29	36.98	22	46	265	29.4	4.61	
18375644	tyrosine-protein phosphatase non-receptor type 11 isoform 2 [Homo sapiens]	9.35	4	2	4	10	1.019	2		1.348	2		13.1	168.38	9.35	20	10	460	52.8	7.44	
578830584	PREDICTED: protein unc-13 homolog D isoform X1 [Homo sapiens]	13.63	3	5	10	35	1.019	5		1.172	5		26.2	909.55	13.63	23	35	1071	120.6	6.40	
12025678	alpha-actinin-4 [Homo sapiens]	75.08	5	33	56	692	1.019	102		1.148	98		19.7	25500.34	75.08	163	692	911	104.8	5.44	
375331941	diacylglycerol phosphatase 3 isoform 2 [Homo sapiens]	14.29	2	5	7	33	1.019	8		1.150	8		23.0	1433.71	14.29	19	33	707	79.3	5.03	
109484945	serpin B3 [Homo sapiens]	35.44	2	10	14	56	1.019	15		1.042	15		16.5	1615.74	35.44	37	56	390	44.5	6.81	
14790115	casepase-3 propeptide [Homo sapiens]	11.55	1	3	4	9	1.019	3		1.178	3		8.1	183.83	11.55	3	9	277	31.6	6.54	
87196339	collagen alpha-1(VI) chain precursor [Homo sapiens]	11.58	2	9	10	42	1.019	14		1.072	14		7.7	1416.33	11.58	28	42	1028	108.5	5.43	
17149844	peptidyl-prolyl cis-trans isomerase FKBP2 precursor [Homo sapiens]	14.79	1	1	2	10	1.019	3		1.045	3		9.5	133.26	14.79	4	10	142	15.6	9.19	
4501891	alpha-actinin-4 isoform b [Homo sapiens]	78.59	40	41	65	953	1.019	169		1.166	164		18.2	34229.23	78.59	194	953	892	103.0	5.41	
10863927	peptidyl-prolyl cis-trans isomerase A [Homo sapiens]	74.55	20	12	13	436	1.019	117		1.191	116		19.8	14043.41	74.55	39	436	165	18.0	7.81	
109484945	transient receptor potential cation channel subfamily M member 8 [Homo sapiens]	27.2	1	4	14	1.019	1		4.2	1.351	1			43.45	2.72	7	14	1104	127.4	7.24	
4506613	60S ribosomal protein L22 preprotein [Homo sapiens]	20.31	3	1	1	6	1.018	2		1.473	2		38.3	409.64	20.31	3	6	128	14.8	9.19	
530372330	PREDICTED: Golgin subfamily A member 4 isoform X7 [Homo sapiens]	5.83	10	1	16	54	1.018	1		1.062	1			56.80	5.83	26	54	2214	259.0	5.36	
4507555	thymopoietin isoform alpha [Homo sapiens]	16.28	5	7	8	43	1.018	13		1.206	13		8.0	2129.17	16.28	22	43	694	75.4	7.66	
4557797	nucleoside diphosphate kinase A isoform b [Homo sapiens]	53.29	2	1	8	98	1.018	2		1.154	2		24.4	3126.20	53.29	23	98	152	17.1	6.19	
58218968	calmodulin [Homo sapiens]	81.21	2	10	13	140	1.018	38		1.176	38		14.5	5582.30	81.21	23	36	140	149	16.8	4.22
7661920	cytoskeletal initiation factor 4B III [Homo sapiens]	14.17	1	6	11	13	1.018	1		1.099	1		1	143.53	14.17	13	11	431	45.6	6.73	
530385393	PREDICTED: nicotinamide phosphoribosyltransferase isoform X1 [Homo sapiens]	69.86	1	26	27	302	1.018	87		1.234	87		20.0	9255.69	69.86	79	302	491	55.5	7.15	
23110939	proteasome subunit alpha type-3 isoform 2 [Homo sapiens]	24.19	21	7	7	41	1.018	12		1.180	12		11.6	1418.61	24.19	21	41	248	27.6	5.33	
156231037	kininogen-1 isoform 4 precursor [Homo sapiens]	48.91	1	4	34	510	1.018	9		1.230	9		17.6	15980.92	48.91	94	510	644	71.9	6.81	
4502261	antithrombin-III precursor [Homo sapiens]	65.95	2	32	33	467	1.018	128		1.131	126		12.9	13604.88	65.95	94	467	464	52.6	6.71	
153791507	leucine-rich repeat neuronal protein 3 precursor [Homo sapiens]	3.25	1	1	3	4	1.018	1		1.182	1			35.42	3.25	3	4	708	79.4	7.83	
50595952	U2 small nuclear ribonucleoprotein A' [Homo sapiens]	25.49	1	3	5	12	1.018	3		1.324	3		13.4	475.51	25.49	3	12	12	255	28.4	8.62
5174735	ubiquitin beta-B chain [Homo sapiens]	55.73	20	20	195	1.018	11		5.6	1.232	11		22.4	6804.17	55.73	56	195	445	49.8	4.89	
530410446	PREDICTED: alpha-2-antiplasmin isoform X6 [Homo sapiens]	40.73	7	11	13	83	1.018	27		1.153	27		16.1	3088.17	40.73	35	83	464	51.7	6.29	
194248072	heat shock 70 kDa protein 1A/1B [Homo sapiens]	71.61	61	30	40	802	1.018	196		1.195	182		17.4	29008.35	71.61	114	802	641	70.0	5.66	
29150261	gamma-interferon-inducible lysosomal thiol reductase preproprotein [Homo sapiens]	11.60	1	1	1	8	1.018	1		1.018	1			105.76	11.60	3	8	250	27.9	4.88	
13489054	dual specificity mitogen-activated protein kinase kinase 2 [Homo sapiens]	17.75	2	2	8	23	1.018	2		1.125	2		0.0	503.77	17.75	18	23	400	44.4	6.55	
166235148	osteoclast-stimulating factor 1 [Homo sapiens]	38.79	4	6	6	56	1.018	18		1.252	18		24.4	2718.26	38.79	18	56	214	23.8	5.68	
164197460	complement component C3 gamma chain precursor [Homo sapiens]	85.94	7	48	54	1.017	7		8.2	1.317	7		9.0	1476.33	85.94	20	48	202	23.2	8.31	
21624607	coactivator-like protein [Homo sapiens]	78.87	1	11	12	105	1.017	31		1.173	31		12.4	2794.79	78.87	35	105	142	15.9	5.67	
14141161	heterogeneous nuclear ribonucleoprotein U isoform b [Homo sapiens]	22.70	2	17	121	1.017	28		4.8	1.213	28		22.5	4097.87	22.70	45	121	806	88.9	5.78	
71565154	alcohol dehydrogenase class-3 [Homo sapiens]	6.42	1	3	4	14	1.017	3		1.227	3		4.6	249.31	6.42	10	14	374	39.7	7.49	
55956788	nucleolin [Homo sapiens]	23.10	1	12	17	76	1.017	21		1.115	21		14.4	2754.22	23.10	43	76	710	76.6	4.70	
578825752	PREDICTED: heterogeneous nuclear ribonucleoproteins C1/C2 isoform X2 [Homo sapiens]	35.49	7	10	12	78	1.017	23		1.240	23		17.3	2158.36	35.49	35	78	293	32.3	5.08	
5788																					

Accession	Description	2Coverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
19923106	serum paraoxonase/arylesterase 1 precursor [Homo sapiens]	55.21	2	11	12	114	1.015	32	9.9	1.358	30	40.0	5024.35	55.21	36	114	355	39.7	5.22	
4759160	small nuclear ribonucleoprotein Sm D3 [Homo sapiens]	26.19	1	1	4	9	1.015	1	1.082	1	1	13.9	138.17	26.19	7	9	126	13.9	10.32	
55799814	AP-2 complex subunit mu [Homo sapiens]	6.31	2	2	5	9	1.015	2	1.8	1.216	2	3.5	107.38	6.31	9	9	433	49.4	9.54	
3820144	homeodomain-interacting protein kinase 1 isoform 4 [Homo sapiens]	2.08	1	1	2	3	1.015	1	1.354	1	1	2.08	29.41	2.08	2	3	816	87.2	8.59	
10834978	interleukin-8 precursor [Homo sapiens]	25.25	1	2	2	9	1.015	2	3.8	1.248	2	10.9	228.63	25.25	6	9	99	11.1	8.84	
31742503	histone H3.2 [Homo sapiens]	58.82	3	1	11	112	1.015	7	13.1	1.030	4	12.7	2320.74	58.82	33	112	136	15.4	11.27	
23110962	cathepsin S isoform 1 preproprotein [Homo sapiens]	34.44	12	8	12	90	1.015	13	8.0	1.217	13	14.2	1143.67	34.44	29	90	331	37.5	8.34	
74136549	AT-rich interactive domain-containing protein 5B isoform 1 [Homo sapiens]	2.78	2	1	4	6	1.015	1	1.04	2.075	1	29.80	2.78	1	4	6	1188	132.3	8.72	
21955465	myoglobin [Homo sapiens]	61.86	1	7	7	55	1.015	18	5.7	1.104	18	11.0	1622.54	61.86	20	55	118	12.9	5.52	
51828075	PREDICTED: pyruvate kinase X1 [Homo sapiens]	1.97	2	2	7	13	1.014	2	1.6	1.133	2	3.3	395.41	1.97	12	27	780	88.3	7.94	
545158	valine--tRNA ligase [Homo sapiens]	8.86	3	6	8	23	1.014	6	1.2	1.185	6	24.0	497.82	8.86	21	23	1264	140.4	7.59	
112790163	metal regulatory transcription factor 1 [Homo sapiens]	1.20	1	1	1	8	1.014	1			1		68.75	1.20	3	8	753	80.9	5.30	
5031863	galactin-3-binding protein precursor [Homo sapiens]	24.79	1	9	10	45	1.014	15	3.7	1.243	15	33.4	1788.59	24.79	30	45	585	65.3	5.27	
21735621	malate dehydrogenase, mitochondrial isoform 1 precursor [Homo sapiens]	24.26	3	6	25	1.014	8	4.1	1.162		8	20.2	979.89	24.26	18	38	355	58.6	8.68	
40254866	charged multivesicular body protein 2b isoform 1 [Homo sapiens]	21.13	2	1	5	9	1.014	1	1.141		1	9	127.79	21.13	1	9	213	23.9	8.76	
4506549	non-secretory ribonuclease precursor [Homo sapiens]	19.88	1	3	3	35	1.014	12	12.8	1.225	12	22.5	1479.42	19.88	1	35	161	18.3	8.73	
15272659	bactericidal permeability-increasing protein [Homo sapiens]	59.14	7	19	21	250	1.014	66	9.3	1.285	55	31.7	7690.95	59.14	63	250	487	53.9	9.38	
15325120	calcineurin-like phosphatohydrolase domain-containing protein 1 isoform a [Homo sapiens]	55.41	2	13	14	55	1.014	16	5.8	1.163	16	9.1	2085.40	55.41	42	55	314	35.5	6.20	
222352151	poly(C)-binding protein 1 [Homo sapiens]	29.49	1	4	7	20	1.014	5	5.4	1.302	5	17.7	671.63	29.49	18	20	356	37.5	7.09	
4503471	elongation factor 1-alpha 1 [Homo sapiens]	56.71	2	17	18	200	1.014	62	6.2	1.157	57	13.1	7118.03	56.71	53	200	462	50.1	9.01	
8923210	nuclear distribution protein nucle homology 1 [Homo sapiens]	8.66	8	1	4	13	1.014	1	1.229		1		164.37	8.66	10	13	335	37.7	5.15	
402478626	low affinity immunoglobulin gamma Fc region receptor III-B isoform 4 [Homo sapiens]	31.94	9	6	29	1.014	8	5.5	1.206	1.014	8	24.1	812.75	31.94	19	29	216	24.4	6.71	
4506695	40S ribosomal protein S19 [Homo sapiens]	6.21	1	1	1	29	1.014	1	1.214		1		167.90	6.21	3	29	145	16.1	10.32	
223890219	RNA-binding motif protein, X-linked-like-3 [Homo sapiens]	4.69	2	1	5	25	1.014	1	0.935		1		574.27	4.69	8	25	1067	114.9	9.10	
530402176	PREDICTED: sister chromatid cohesion protein PD55 homolog B isoform X2 [Homo sapiens]	6.30	11	1	10	30	1.014	2	3.1	0.983	2	11.0	567.97	6.30	20	30	1445	164.3	8.43	
4557894	lysosome C precursor [Homo sapiens]	72.30	1	12	12	479	1.014	143	8.0	1.245	141	16.7	13782.83	72.30	36	143	148	16.5	9.16	
55743122	retinoid-binding protein 4 precursor [Homo sapiens]	76.12	2	11	12	239	1.013	76	6.9	1.143	74	16.9	8428.62	76.12	36	239	201	23.0	6.07	
58533161	POZ and LIM domain protein 5 isoform e [Homo sapiens]	4.54	7	1	1	2	1.013	1	0.964		1		44.82	4.54	1	2	216	23.8	9.92	
38019414	deoxynucleoside triphosphate triphosphohydrolase SAMHD1 [Homo sapiens]	15.97	2	3	8	38	1.013	5	2.0	1.222	5	9.2	923.34	15.97	16	38	626	72.2	7.14	
530398067	PREDICTED: apolipoprotein A-1 isoform X1 [Homo sapiens]	86.89	35	31	36	1347	1.013	432	8.5	1.317	418	22.1	43488.15	86.89	106	1347	267	30.8	5.76	
578837549	PREDICTED: DEP domain-containing protein 5 isoform X10 [Homo sapiens]	3.83	8	1	5	31	1.013	10	3.8	1.997	10	19.9	78.09	3.83	7	31	1490	168.2	6.80	
170016081	protein XRP2 [Homo sapiens]	8.29	1	4	4	13	1.013	4	4.0	1.243	4	9.5	328.67	8.29	12	13	350	39.6	5.12	
167234422	hematopoietic lineage cell-specific protein isoform 1 [Homo sapiens]	25.51	2	12	14	93	1.013	25	6.2	1.115	25	9.0	2406.12	25.51	39	93	486	54.0	4.81	
576809106	PREDICTED: immunoglobulin J chain isoform X1 [Homo sapiens]	41.51	1	6	6	83	1.013	27	7.3	1.179	27	20.1	2862.58	41.51	18	83	159	18.1	5.24	
4506429	40S ribosomal protein L29 [Homo sapiens]	18.87	1	1	3	8	1.013	2	4.9	1.224	2	1.0	279.75	18.87	5	8	159	17.7	11.66	
75709200	phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform A precursor [Homo sapiens]	18.27	3	1	4	8	1.013	1	1.342		1		56.28	18.27	8	8	197	22.2	8.37	
578832788	PREDICTED: thioredoxin-like protein 1 isoform X2 [Homo sapiens]	27.06	3	4	4	12	1.013	4	4.0	1.083	4	3.3	643.72	27.06	12	12	255	28.5	4.83	
4505753	phosphoglycerate mutase 1 [Homo sapiens]	84.65	23	13	20	343	1.013	76	10.4	1.167	75	27.7	13563.24	84.65	59	343	254	28.8	7.18	
578804376	PREDICTED: bifunctional purine biosynthesis protein PURH isoform X1 [Homo sapiens]	19.14	2	7	8	46	1.013	10	6.6	1.156	9	6.8	838.80	19.14	22	46	533	58.6	6.84	
39812055	beta-arrestin-2 isoform 2 [Homo sapiens]	12.94	7	4	22	1.013	6	6	4.3	1.139	6	3.5	783.55	12.94	12	22	394	44.4	7.88	
5032059	protein S100-A12 [Homo sapiens]	91.30	10	60	60	319	1.013	180	10.3	1.139	166	28.2	23513.49	91.30	64	319	624	62.5	6.25	
530379453	PREDICTED: chromodomain-helicase-DNA-binding protein 1 isoform X1 [Homo sapiens]	4.62	23	1	10	14	1.013	1	1.762		1		30.47	4.62	10	14	1798	207.3	7.23	
47271443	serine/arginine-rich splicing factor 2 [Homo sapiens]	18.55	2	3	5	14	1.013	4	9.0	1.273	4	13.5	667.23	18.55	11	14	221	25.5	11.85	
62420888	dipeptidyl peptidase 2 preproprotein [Homo sapiens]	8.74	3	2	3	8	1.013	2	1.6	1.303	2	10.2	372.49	8.74	7	8	492	54.3	6.32	
55749932	desmin [Homo sapiens]	14.89	4	1	9	129	1.013	1	1.192		1		1543.77	14.89	22	129	470	53.5	5.27	
530407832	PREDICTED: protein CLEC16A isoform X7 [Homo sapiens]	6.05	8	1	7	16	1.013	1	1.186		1		91.12	6.05	11	16	925	105.6	6.51	
4912388	granulysin [Homo sapiens]	44.76	6	2	9	65	1.013	21	4.4	1.182	21	21.3	2373.19	44.76	21	65	217	24.0	5.21	
530376092	PREDICTED: protein phosphatase 2, regulatory subunit B, gamma isoform X3 [Homo sapiens]	5.26	1	2	9	1.013	2	2	16.0	1.127	2	6	168.17	5.26	6	9	342	39.5	6.65	
4503689	fibrinogen alpha chain isoform alpha-E preproprotein [Homo sapiens]	51.15	52	47	49	1390	1.013	415	7.6	1.177	395	16.9	33979.80	51.15	145	1390	866	94.9	6.01	
4506185	proteasome subunit alpha type-4 isoform 1 [Homo sapiens]	44.44	2	9	9	41	1.013	14	5.5	1.119	14	9.6	1364.77	44.44	27	119	41	261	29.5	7.72
530409962	PREDICTED: WD repeat-containing protein 16 isoform X2 [Homo sapiens]	3.58	2	1	2	2	1.013	1	0.805		1		27.86	3.58	2	2	531	58.6	7.42	
4507793	ubiquitin-conjugating enzyme E2 N [Homo sapiens]	34.87	2	4	4	23	1.013	6	5.5	1.186	6	12.7	698.40	34.87	12	23	152	17.1	6.57	
45022317	V-type proton ATPase subunit E 1 isoform a [Homo sapiens]	36.28	4	5	7	27	1.013	4	22.0	1.142	4	22.0	492.26	36.28	18	27	226	26.1	8.00	
579831314	PREDICTED: transcription elongation factor SPI1 isoform X3 [Homo sapiens]	5.48	2	3	15	1.013	3	3	1.5	1.077	3	4.8	146.13	5.48	15	27	1603	184.6	5.11	
66629216	mitogen-activated protein kinase 1 [Homo sapiens]	27.50	27	7	8	36	1.012	11	9.0	1.244	11	44.1	925.50	27.50	23	36	360	41.4	6.98	
209842911	peroxisome biogenesis factor 2 precursor [Homo sapiens]	45.57	6	23	25	204	1.012	54	8.1	1.266	54	29.2	6831.68	45.57	69	204	779	87.0	7.81	
32483377	thioredoxin-dependent peroxide reductase, mitochondrial isoform b [Homo sapiens]	39.08	2	6	6	23	1.012	8	4.7	1.127	8	9.1	880.19	39.08	18	23	238	25.8	7.46	
10645195	histone H2A type 1-B/E [Homo sapiens]	60.00	5	1	6	70	1.012	2	1.2	1.131	2	9.6	2076.11	60.00	18	70	130	14.1	11.05	
4506005	regulator of G-protein signaling 10 isoform b [Homo sapiens]	1.79	1	1	1	1	1.012	1	1.251		1		239.31	1.79	1	1	167	19.6	5.87	
77320143	protein FAM83B [Homo sapiens]	70.06	16	18	108	1.012	9	35	1.9	1.169	34	22.0	4234.79	70.06	108	224	38.7	6.06		
4503987	gamma-glutamyl hydrolase precursor [Homo sapiens]	27.99	1	8	8	41	1.012	12	6.5	1.220	12	10.0	1334.62	27.99	24	41	318	35.9	7.11	
194394158	nicotinate phosphoribosyltransferase isoform 1 [Homo sapiens]	54.83	2	18	82	1.012	27	27	7.7	1.227	24	19.7	3262.18	54.83	50	82	538	57.5	5.68	
6912516	mitochondrial peptide methionine sulfoxide reductase isoform a precursor [Homo sapiens]	21.70	4	4	5	12	1.012	4	5.5	1.140	4	24.1	339.64	21.70	12	12	235	26.1	8.09	
189163532	alpha-1-antitrypsin precursor [Homo sapiens]	81.10	2	40	43	3605	1.012	957	9.6	1.171	942	20.6	115931.48	81.10	124	3605	418	46.7	5.59	
148596990	copper homeostasis protein CUC1 homolog [Homo sapiens]	10.62	1	1	2	6	1.012	1	1.2	1.131	1		242.79	10.62	6	6	273	29.3	8.18	
26016612	hydroperoxide isomerase ALOXES isoform 1 precursor [Homo sapiens]	2.37	1	1	2	2	1.011	1	0.883		1		27.45	2.37	2	2	843	95.1	7.75	
1154																				

Accession	Description	2Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
12408675	prefoldin subunit 2 [Homo sapiens]	29.87	1	2	5	9	1.010	2	5.3	0.986	2	30.4	146.77	29.87	9	9	154	16.6	5.58
539845980	protein phosphatase 1 regulatory subunit 7 isoform 6 [Homo sapiens]	36.21	7	7	8	29	1.010	10	6.6	1.462	2	20.5	1194.73	36.21	21	29	301	35.1	6.31
4506191	proteasome subunit beta type-10 precursor [Homo sapiens]	27.84	1	4	5	7	1.010	6	5.7	1.254	6	21.5	940.31	27.84	11	17	203	28.9	7.01
530418509	PREDICTED: eukaryotic translation initiation factor 2 subunit 2 isoform X1 [Homo sapiens]	10.83	2	1	4	11	1.010	1	1.0	1.213	1		130.37	10.83	7	11	314	36.2	5.48
5031695	complement factor H-related protein 2 precursor [Homo sapiens]	25.93	3	4	6	38	1.010	8	3.2	1.238	8	8.5	1375.40	25.93	18	38	270	30.6	6.38
6912486	U6 snRNA-associated Sm-like protein LSM4 isoform 1 [Homo sapiens]	17.27	1	2	3	7	1.010	2	5.9	1.251	2	19.1	104.09	17.27	7	7	139	15.3	9.99
30410792	proteasome activator complex subunit 2 [Homo sapiens]	43.93	2	1	9	39	1.010	1	1.0	1.330	1		1674.95	43.93	27	39	239	27.4	5.73
530415994	PREDICTED: rRNA 2'-O-methyltransferase fibrillarin isoform X1 [Homo sapiens]	6.56	2	1	2	17	1.009	1		1.141	1		111.55	6.56	6	17	320	33.7	10.18
4505257	moesin [Homo sapiens]	81.46	4	6	63	1133	1.009	225	19.3	1.181	216	19.3	29002.28	81.46	179	1133	577	67.8	6.40
42544239	complement factor D propeptide [Homo sapiens]	45.06	1	5	7	24	1.009	19	14.6	1.213	6	38.5	702.53	45.06	18	24	253	27.0	7.71
290504188	hyaluronan-binding protein 2 isoform 2 [Homo sapiens]	12.55	2	5	6	33	1.009	7	5.5	1.130	7	2.4	416.92	12.55	18	33	534	59.8	6.43
25777602	26S proteasome non-ATPase regulatory subunit 2 [Homo sapiens]	24.23	3	13	15	53	1.009	17	7.9	1.118	17	31.4	2157.26	24.23	41	53	908	100.1	5.20
58219792	ras-related protein Rap-1b isoform 1 precursor [Homo sapiens]	58.70	5	8	11	54	1.009	17	5.9	1.310	12	29.4	1772.71	58.70	30	54	184	20.8	5.78
578818565	PREDICTED: vimentin isoform X1 [Homo sapiens]	55.36	6	31	36	477	1.009	122	7.9	1.114	122	11.1	15988.79	55.36	105	477	466	53.6	5.12
4502599	carboxyl reductase [NADH] 1 isoform 1 [Homo sapiens]	25.99	3	5	7	18	1.009	6	4.8	1.295	6	15.7	731.82	25.99	15	18	277	30.4	8.32
5803187	transaldolase [Homo sapiens]	78.04	1	30	32	441	1.009	137	6.9	1.171	137	13.1	12433.78	78.04	95	441	337	37.5	6.81
71037379	glycogen phosphorylase, liver form isoform 1 [Homo sapiens]	59.39	4	38	46	403	1.009	104	7.0	1.197	104	16.1	13061.54	59.39	131	403	847	97.1	7.17
578815682	PREDICTED: phosphoprotein associated with glycosphingolipid-enriched microdomains 1 isoform X1 [Homo sapiens]	6.48	1	2	2	12	1.009	4	4.5	1.130	4	7.2	693.54	6.48	6	12	432	47.0	4.65
578827537	PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 isoform X1 [Homo sapiens]	15.50	5	5	7	16	1.009	5	6.9	1.427	5	37.5	287.43	15.50	16	16	413	47.3	5.45
530397816	PREDICTED: probable ATP-dependent RNA helicase DDX6 isoform X1 [Homo sapiens]	12.84	2	2	4	20	1.009	5	14.0	1.011	5	16.3	600.10	12.84	8	20	483	54.4	8.66
11342680	beta-actinin [Homo sapiens]	26.33	2	2	8	28	1.009	3	0.4	2.229	3	71.9	651.70	26.33	21	28	376	42.3	6.40
450171070	T-complex protein 1 subunit theta isoform 3 [Homo sapiens]	28.17	4	11	13	43	1.009	19	4.0	1.156	19	14.4	2476.41	28.17	37	63	497	54.1	5.31
4503727	peptidyl-prolyl cis-trans isomerase FKBP3 [Homo sapiens]	9.82	1	2	2	6	1.009	2	0.2	1.164	2	3.8	165.79	9.82	6	6	224	25.2	9.28
221316614	extracellular matrix protein 1 precursor [Homo sapiens]	14.81	3	5	6	17	1.009	5	10.6	1.123	4	19.3	651.66	14.81	15	17	540	60.6	6.71
530387774	PREDICTED: nuclear GTPase SLIP-GC isoform X3 [Homo sapiens]	3.72	2	1	4	9	1.009	1		1.173	1		30.80	3.72	4	9	672	76.8	8.40
154146191	heat shock protein HSP 90-alpha isoform 2 [Homo sapiens]	51.09	13	24	43	369	1.009	59	7.5	1.173	56	16.6	12796.32	51.09	125	369	732	84.6	5.02
336391093	ras-related protein Rab-2A isoform b [Homo sapiens]	14.36	4	2	2	6	1.009	2	4.4	1.185	2	6.9	443.06	14.36	6	6	188	20.8	6.11
205277441	thymidine-binding globulin precursor [Homo sapiens]	34.22	3	13	13	80	1.009	25	5.1	1.157	25	33.7	2688.33	34.22	37	80	415	46.3	6.30
38454326	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1 [Homo sapiens]	2.67	1	1	8	1.009	3	3	16.6	1.041	3	8	104.91	2.67	3	3	300	34.3	7.66
530402208	PREDICTED: zinc finger CCH domain-containing protein 13 isoform X12 [Homo sapiens]	4.99	5	1	10	21	1.008	4	2.5	1.204	4	21.2	68.86	4.99	13	21	1564	184.8	9.47
9966777	resistin precursor [Homo sapiens]	35.19	1	3	3	62	1.008	21	6.1	1.242	21	13.1	2866.07	35.19	9	62	108	11.4	6.86
59859885	40S ribosomal protein S6 [Homo sapiens]	23.73	1	4	4	11	1.008	5	3.7	1.103	4	15.5	366.19	23.73	9	11	295	32.8	4.87
124944254	proliferation-associated protein 2G4 [Homo sapiens]	36.55	1	10	13	61	1.008	18	7.2	1.102	17	6.2	1838.00	36.55	35	61	394	43.8	6.55
530361334	PREDICTED: complement C1q subcomponent subunit B isoform X1 [Homo sapiens]	46.64	1	8	10	133	1.008	32	10.0	1.273	31	22.6	3746.24	46.64	29	133	253	26.7	8.63
530418349	PREDICTED: double-stranded RNA binding protein Staufen homolog 1 isoform X6 [Homo sapiens]	4.85	11	1	4	8	1.008	2	14.2	1.217	2	10.5	42.95	4.85	4	8	496	54.9	9.51
88702793	vasenin precursor [Homo sapiens]	4.90	1	1	3	11	1.008	1		2.147	1		256.71	4.90	7	11	673	71.7	7.39
109148508	ubiquitin thioesterase OTUB1 [Homo sapiens]	27.68	1	5	5	26	1.008	7	3.6	1.180	7	7.6	698.03	27.68	15	26	271	31.3	4.94
51702222	protein SPT2 homolog [Homo sapiens]	7.45	13	2	8	39	1.008	6	7.1	1.038	4	16.5	53.58	7.45	14	39	685	75.6	9.79
23238211	actin-related protein 2/3 complex subunit 2 [Homo sapiens]	74.00	2	23	24	314	1.008	97	6.6	1.184	96	13.5	10936.34	74.00	70	314	300	34.3	7.36
24822872	EF-hand domain-containing protein D2 [Homo sapiens]	42.92	4	11	12	55	1.008	16	6.2	1.095	16	12.4	2161.32	42.92	34	55	240	26.7	5.20
50317389	inositol monophosphatase 1 isoform 1 [Homo sapiens]	26.35	3	4	6	22	1.008	6	4.0	1.242	6	16.7	987.11	26.35	22	27	30.2	5.26	
123173757	ribonucleoprotein PTB-binding 1 [Homo sapiens]	1.72	1	1	1	3	1.008	1		1.033	1		185.46	1.72	3	3	756	79.5	8.92
194097323	enoyl-CoA hydratase, mitochondrial [Homo sapiens]	12.07	1	2	2	4	1.008	2	13.4	1.582	2	0.1	135.01	12.07	4	4	290	31.4	8.07
4826760	heterogeneous nuclear ribonucleoprotein F [Homo sapiens]	21.45	2	3	7	30	1.008	5	3.8	1.074	5	2.2	855.98	21.45	19	30	415	45.6	5.58
32483399	serine/threonine-protein kinase PAK 2 [Homo sapiens]	28.44	7	8	10	46	1.008	8	6.2	1.160	7	13.5	1044.34	28.44	30	46	524	58.0	5.96
289063417	AMP deaminase 3 isoform 4 [Homo sapiens]	21.55	6	10	12	41	1.008	12	9.0	1.197	10	16.9	1221.00	21.55	33	41	608	71.2	6.99
578810352	PREDICTED: regulator of G-protein signaling 2-binding protein isoform X2 [Homo sapiens]	12.18	1	1	1	1	1.008	1		1.161	1		20.33	12.18	1	1	204	22.7	7.36
223972653	aldohydroxy dehydrogenase family 16 member A1 isoform 2 [Homo sapiens]	13.18	4	6	20	1.008	4	4	4.1	1.358	20	11.6	564.71	13.18	16	20	751	79.9	7.58
5031635	cofilin-1 [Homo sapiens]	80.12	20	22	22	389	1.008	119	6.7	1.190	119	19.6	12256.22	80.12	66	389	166	18.5	8.09
255918200	serine/threonine-protein phosphatase 6 regulatory subunit 3 isoform 3 [Homo sapiens]	1.26	16	1	1	1	1.008	1		1.26	1		28.32	1.26	1	1	791	88.9	4.58
11863154	coatomer subunit delta isoform 1 [Homo sapiens]	12.52	3	5	7	24	1.008	7	9.4	1.120	7	18.2	817.24	12.52	19	24	511	57.2	6.21
42822872	ribonuclease inhibitor [Homo sapiens]	48.59	1	12	15	90	1.008	27	8.8	1.111	27	9.8	4056.96	48.59	41	90	461	49.9	6.82
530373049	PREDICTED: isolectin B4 isoform X4 [Homo sapiens]	4.69	3	4	6	11	1.008	4	8.0	1.095	4	6.1	520.82	4.69	11	11	323	58.9	5.05
190041728	kinesin light chain 2 isoform 2 [Homo sapiens]	8.44	4	1	7	12	1.008	1		3.563	1		43.95	8.44	12	12	545	60.0	7.28
226498466	T-cell immunoglobulin and mucin domain-containing protein 4 isoform 2 precursor [Homo sapiens]	6.57	2	1	3	7	1.008	1		1.119	1		31.27	6.57	3	7	350	38.5	6.15
188497671	serum amyloid A-2 protein isoform a precursor [Homo sapiens]	71.31	11	4	11	117	1.007	19	6.9	1.111	19	28.0	3984.90	71.31	32	117	122	13.5	9.14
58530845	zyxin [Homo sapiens]	17.13	3	6	6	42	1.007	12	12	1.091	12	11.6	1335.70	17.13	18	42	572	61.2	6.67
216548487	protein-arginine deiminase type-4 [Homo sapiens]	57.01	5	27	34	362	1.007	97	6.9	1.158	94	16.6	9906.90	57.01	91	362	663	74.0	6.58
144226251	chitinase-3-like protein 1 precursor [Homo sapiens]	52.48	1	13	16	113	1.007	35	14.8	1.049	34	26.0	4948.70	52.48	44	113	383	42.6	8.46
7106423	U6 snRNA-associated Sm-like protein LSM7 [Homo sapiens]	7.0423	2	2	4	13	1.007	3	3.9	1.037	3	3.2	325.39	7.04	13	13	103	11.6	8.27
7657603	heme-binding protein 2 [Homo sapiens]	32.68	1	6	6	29	1.007	9	6.0	1.178	9	10.0	1188.05	32.68	18	29	205	22.9	4.63
530417131	PREDICTED: vasodilator-stimulated phosphoprotein isoform X1 [Homo sapiens]	53.83	3	15	16	149	1.007	40	7.7	1.210	36	8.5	5040.61	53.83	47	149	379	39.7	8.94
4502337	zinc-alpha-2-glycoprotein precursor [Homo sapiens]	59.40	1	19	21	266	1.007	85	5.9	1.229	81	16.2	9247.82	59.40	61	266	298	34.2	6.05
4506387	UV excision repair protein RAD23 homolog B isoform 1 [Homo sapiens]	17.11	39	4	6	32	1.007	6	6.1	1.032	6	17.9	829.80	17.11	18	32	409	43.1	4.84
578804845	PREDICTED: WAS/WASL-interacting protein family member 1 isoform X1 [Homo sapiens]	27.44	1	6	8	43	1.007	11	5.4	1.043	11	11.1	27.0	1049.17	27.44	43	503	51.2	11.47
7657532	protein S100-A6 [Homo sapiens]	66.67	33	9	10	100	1.												

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
4503971	rab GDP dissociation inhibitor alpha [Homo sapiens]	40.27	8	6	16	109	1.005	10	4.2	1.727	10	10.9	3403.24	40.27	46	109	447	50.6	5.14	
612407849	integrin alpha-8 isoform 2 preproprotein [Homo sapiens]	1.72	2	1	2	8	1.005	1	2	3.763	1	26.67	1.72		2	8	1048	115.9	5.68	
4826643	annexin A2 [Homo sapiens]	81.73	2	29	32	507	1.005	157	7.1	1.216	153	15.4	16349.26	81.73	89	507	323	36.4	5.93	
525342616	acyl-protein thioesterase 1 isoform 6 [Homo sapiens]	21.08	7	3	3	13	1.005	3	7.0	1.362	3	0.2	365.32	21.08	9	13	166	18.0	5.06	
306922420	trophoblast glycoprotein-like precursor [Homo sapiens]	9.42	1	1	3	8	1.005	2	5.0	11.390	1	35.10	9.42		3	8	382	40.4	8.27	
4507791	NEDD8-conjugating enzyme Ubc12 [Homo sapiens]	12.02	1	2	3	9	1.005	2	2.2	1.040	2	1.6	198.61	12.02	9	9	183	20.9	7.69	
41393561	cytosol aminopeptidase [Homo sapiens]	11.75	1	4	5	17	1.005	4	10.7	1.056	4	8.2	423.86	11.75	13	17	519	56.1	7.93	
4503303	neutrophil defensin 4 preproprotein [Homo sapiens]	5.15	1	1	1	2	1.005	1	1	1.218	1	28.57	5.15		2	2	97	10.5	8.02	
119468182	40S ribosomal protein S18 [Homo sapiens]	23.03	1	4	4	10	1.005	2	6.5	1.251	2	10.1	22.0	175.67	23.03	10	10	152	17.7	10.99
53030796	PREDICTED: formin-binding protein 1 isoform X20 [Homo sapiens]	17.06	23	5	11	35	1.005	7	14.8	1.074	7	14.8	526.54	17.06	38	531	44.0	5.24		
381342476	heterogeneous nuclear ribonucleoprotein H [Homo sapiens]	19.82	8	5	8	38	1.005	9	6.0	1.226	9	16.4	998.31	19.82	22	38	449	49.2	6.30	
578829418	PREDICTED: piezo-2 type mechanosensitive ion channel component 1 isoform X2 [Homo sapiens]	1.16	8	2	4	8	1.005	2	2.6	1.195	2	8.9	47.53	1.16		8	2497	283.9	7.43	
7664942	glyceraldehyde-3-phosphate dehydrogenase isoform 1 [Homo sapiens]	91.64	3	4	27	2870	1.005	47	11.4	1.317	45	26.0	97872.33	91.64	81	2870	335	36.0	8.46	
4758638	peroxiredoxin-6 [Homo sapiens]	74.55	1	16	16	124	1.004	40	8.5	1.116	40	12.3	4245.82	74.55	46	124	224	25.0	6.38	
63055049	phosphoglucuronatase-2 [Homo sapiens]	40.20	2	16	20	96	1.004	25	5.2	1.237	25	13.2	2625.47	40.20	58	96	612	68.2	6.73	
260099723	L-lactate dehydrogenase A chain isoform 3 [Homo sapiens]	67.04	10	25	29	525	1.004	137	8.1	1.206	137	17.2	16802.63	67.04	83	525	361	39.8	8.43	
4557325	apolipoprotein E precursor [Homo sapiens]	55.84	2	15	16	169	1.004	55	6.4	1.407	55	29.7	7419.73	55.84	48	169	317	36.1	5.73	
115298678	complement C3 precursor [Homo sapiens]	88.51	5	153	160	5899	1.004	1787	9.0	1.259	1667	25.2	22403.34	88.51	468	5899	1663	187.0	6.40	
4557351	cholinesterase precursor [Homo sapiens]	5.32	2	2	2	6	1.004	3	3.3	1.255	3	50.3	295.19	5.32	4	6	602	68.4	7.42	
530397403	PREDICTED: cleavage and polyadenylation specificity factor subunit 7 isoform X5 [Homo sapiens]	12.07	6	1	2	4	1.004	1	1	1.889	1	172.06	12.07		4	4	381	41.9	9.57	
503672599	annexin A11 isoform 2 [Homo sapiens]	39.19	6	17	17	97	1.004	33	5.9	1.158	33	12.1	3752.64	39.19	51	97	472	51.2	7.66	
503964148	isocitrate dehydrogenase [NADP], mitochondrial isoform 2 [Homo sapiens]	21.25	5	5	9	44	1.004	7	9.0	1.161	7	9.0	1004.83	21.25	20	44	600	40.5	7.75	
371918873	CORO7-FAM16 protein [Homo sapiens]	9.73	8	6	8	35	1.004	7	11.3	0.953	7	25.0	794.86	9.73	19	35	1048	114.1	6.33	
530372834	PREDICTED: cAMP-dependent protein kinase type II-alpha regulatory subunit isoform X1 [Homo sapiens]	13.12	3	3	5	23	1.004	5	6.9	1.245	5	7.2	598.52	13.12	13	23	404	45.5	5.07	
21071008	transcobalamin-1 precursor [Homo sapiens]	28.18	1	8	31	304	1.004	10	5.0	1.165	10	11.1	1264.12	28.18	23	31	433	48.2	5.03	
578818421	PREDICTED: amyloid beta A4 precursor protein-binding family B member 1-interacting protein	18.92	1	9	11	59	1.004	15	4.3	1.180	14	15.2	1382.09	18.92	29	59	666	73.1	5.59	
385251392	minor histocompatibility protein HA-1 isoform 2 precursor [Homo sapiens]	4.60	11	2	7	12	1.004	2	2.7	1.184	2	7.4	135.99	4.60	12	12	1152	126.4	6.05	
554320095	1-phosphoglycerate-4,5-bisphosphate phosphoglycerate beta-2 isoform 3 [Homo sapiens]	5.21	9	2	6	31	1.004	2	6.7	1.104	2	0.5	110.29	5.21	12	1170	132.4	6.29		
57880044	PREDICTED: inter-alpha-trypsin inhibitor heavy chain H3 isoform X3 [Homo sapiens]	34.41	6	24	118	1.004	35	16	6.0	1.209	35	16.9	3593.18	34.41	61	118	896	100.7	5.91	
21071030	alpha-18-glycoprotein precursor [Homo sapiens]	59.39	1	17	18	499	1.004	149	7.1	1.259	142	26.0	15923.34	59.39	54	499	495	54.2	5.86	
4504067	aspartate aminotransferase, cytoplasmic [Homo sapiens]	39.71	30	9	11	44	1.004	9	6.6	1.038	9	23.7	963.57	39.71	30	44	413	46.2	7.01	
388240801	lamin-B2 [Homo sapiens]	17.42	1	6	12	41	1.004	7	6.7	1.290	7	19.9	1156.16	17.42	29	41	620	69.9	5.59	
162809334	pregnancy zone protein precursor [Homo sapiens]	26.86	1	16	33	608	1.004	26	6.1	1.379	26	35.1	34596.07	26.86	90	608	1482	163.8	6.38	
7524546	adenylate kinase 2, mitochondrial isoform b [Homo sapiens]	44.40	3	5	9	31	1.004	8	12.7	1.277	8	15.0	973.52	44.40	21	31	232	25.6	7.88	
15431301	60S ribosomal protein L7 [Homo sapiens]	16.94	4	2	4	11	1.004	3	11.6	1.196	3	7	281.14	16.94	7	11	246	29.2	10.65	
55743106	collagen alpha-3(VI) chain isoform 5 precursor [Homo sapiens]	12.05	8	19	27	111	1.004	28	9.3	1.079	26	12.7	2803.36	12.05	71	111	297	321.2	7.30	
578811455	PREDICTED: leukocyte elastase inhibitor isoform X1 [Homo sapiens]	58.84	5	19	22	162	1.003	50	7.2	1.066	50	8.3	5825.22	58.84	61	162	379	42.7	6.28	
4506381	ras-related C3 botulinum toxin substrate 2 [Homo sapiens]	52.60	6	5	10	93	1.003	14	4.1	1.352	13	31.5	2591.99	52.60	30	33	192	21.4	7.61	
52487191	endoplasmic reticulum resident protein 44 precursor [Homo sapiens]	13.55	1	3	5	16	1.003	4	5.0	1.080	4	19.4	474.84	13.55	13	16	406	46.9	5.26	
578822199	PREDICTED: neutrophil collagenase isoform X1 [Homo sapiens]	38.29	2	13	13	188	1.003	60	4.7	1.180	60	16.8	7784.50	38.29	39	188	444	50.8	6.16	
4502315	V-type proton ATPase subunit c1 [Homo sapiens]	4.54	2	2	4	11	1.003	2	24.0	6	102	14.1	248.32	4.54	2	4	382	43.9	7.46	
578813531	PREDICTED: MAGUK p55 subfamily member 6 isoform X3 [Homo sapiens]	6.67	5	1	4	22	1.003	1	6.7	1.006	1	44.19	6.67		6	22	540	61.1	6.18	
6912396	glyoxylate reductase/hydroxypruvate reductase [Homo sapiens]	36.89	2	6	7	20	1.003	6	3.1	1.326	6	27.3	861.75	36.89	20	20	328	35.6	7.39	
530400688	PREDICTED: rho GTPase-activating protein 9 isoform X4 [Homo sapiens]	10.03	8	3	5	12	1.003	3	0.3	1.180	3	17.0	461.92	10.03	11	12	798	88.5	8.07	
4557361	BH3-interacting domain death agonist isoform 2 [Homo sapiens]	38.46	3	5	6	28	1.003	9	9.5	1.215	9	20.1	1146.41	38.46	16	28	195	22.0	5.44	
5730023	ruvB-like 2 [Homo sapiens]	8.86	1	1	4	13	1.003	1	1	1.301	1	183.54	8.86		6	13	463	51.1	5.64	
41327364	afatinib B1 aldehyde reductase member 2 [Homo sapiens]	16.38	5	3	5	11	1.003	3	2.4	0.918	3	487.60	16.38		11	11	359	6.9	7.46	
133778974	transketolase-like protein 2 [Homo sapiens]	4.31	9	1	3	5	1.003	1	3.3	1.362	1	33.33	4.31		3	5	626	67.8	6.33	
530428415	PREDICTED: proteasome subunit beta type-8 isoform X1 [Homo sapiens]	49.79	3	8	8	48	1.003	14	3.6	1.212	14	13.9	1395.72	49.79	24	48	243	27.0	7.18	
260436922	suprabasin isoform 1 precursor [Homo sapiens]	26.10	3	6	6	27	1.003	9	5.1	1.046	9	7.9	1413.37	26.10	18	27	590	60.5	7.01	
315075331	SAH2-SAH2 protein precursor [Homo sapiens]	42.79	3	5	10	149	1.003	22	4.9	1.306	21	20.8	3600.82	42.79	28	149	208	23.3	8.98	
11716121	mannose-1-phosphate guanylttransferase beta isoform 2 [Homo sapiens]	10.56	2	3	4	17	1.003	5	3.3	1.188	5	9.8	397.60	10.56	11	17	360	39.8	6.78	
145099123	dedicator of cytokinesis protein 11 [Homo sapiens]	2.60	4	1	6	10	1.003	1	1	1.086	1	26.17	2.60		10	2073	237.5	7.74		
530370210	PREDICTED: mannosyl-1-phosphate guanylttransferase alpha isoform X4 [Homo sapiens]	9.05	3	3	9	9	1.003	3	4.1	1.212	3	7.9	360.59	9.05	3	9	420	46.3	7.21	
165905601	proline-serine-threonine phosphatase-interacting protein 2 [Homo sapiens]	14.67	1	5	5	13	1.003	3	0.5	1.172	3	29.4	197.07	14.67	12	13	334	38.8	8.48	
45439306	aspartate--tRNA ligase, cytoplasmic isoform 1 [Homo sapiens]	18.56	2	5	9	21	1.003	5	11.6	1.143	5	10.7	186.04	18.56	18	21	501	57.1	6.55	
540344555	complement C2 isoform 5 [Homo sapiens]	40.11	6	21	25	127	1.003	37	4.9	1.226	35	22.0	3132.95	40.11	69	127	723	80.1	7.46	
4507725	transferrin precursor [Homo sapiens]	77.55	1	13	13	596	1.003	191	12.1	1.198	188	27.3	26394.27	77.55	38	596	147	15.9	5.75	
6059542	translational endoplasmic reticulum ATPase [Homo sapiens]	61.29	6	35	39	217	1.003	67	6.7	1.134	67	16.2	6702.37	61.29	111	217	806	89.3	5.26	
5901998	US snRNP associated Sm-like protein 5nm [Homo sapiens]	71.50	4	5	7	26	1.003	4	5	1.380	4	7	482.98	71.50	13	26	81	9.1	9.58	
4505227	myeloid cell nuclear differentiation antigen [Homo sapiens]	74.20	57	3	32	641	1.003	179	7.1	1.179	175	15.8	21345.79	74.20	95	641	407	45.8	9.76	
530368148	PREDICTED: macrophage-capping protein isoform X1 [Homo sapiens]	77.01	2	13	16	191	1.002	52	5.0	1.200	49	16.4	7926.37	77.01	49	191	348	38.5	6.19	
11386147	prospapilin isoform a preproprotein [Homo sapiens]	28.63	3	13	14	130	1.002	39	8.8	1.173	38	12.0	3810.05	28.63	40	130	524	58.1	5.17	
503774159	sorting nexin-2 isoform 2 [Homo sapiens]	14.93	7	2	5	12	1.002	2	1.4	1.025	2	0.5	364.94	14.93	12	12	102	46.1	7.24	
543583725	prostaglandin E synthase 3 isoform 1 [Homo sapiens]	19.27	8	2	3	14	1.002	6	12.3	1.309	6	24.2	618.48	19.27	6	14	109	12.7	5.59	
145309326	laminin subunit gamma-1 precursor [Homo sapiens]</																			

Accession	Description	Score	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
57809103	PREDICTED: complement factor I isoform X4 [Homo sapiens]	42.75	5	21	26	179	1.001	52	8.5	1.231	52	16.4	5355.17	42.75	72	179	531	60.0	7.93
39995109	ganglioside GM2 activator isoform 1 precursor [Homo sapiens]	18.65	1	2	3	10	1.050	3	13.1		3	5.3	364.36	18.65	7	10	193	20.8	5.31
11929293	RTB/POZ domain-containing protein KCTD12 [Homo sapiens]	28.92	2	8	9	32	1.001	9	2.9	1.206	9	11.3	911.96	28.92	27	33	325	35.7	5.64
194688133	high mobility group protein 82 [Homo sapiens]	60.77	1	10	17	241	1.001	51	4.2	1.144	51	14.4	6327.02	60.77	51	241	209	24.0	7.81
530410617	PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens]	61.67	2	17	20	158	1.001	38	7.2	1.124	38	16.5	6164.96	61.67	60	158	240	27.4	4.89
530412282	PREDICTED: ATP-citrate synthase isoform X1 [Homo sapiens]	35.15	4	26	30	133	1.001	43	8.2	1.131	43	15.0	5206.74	35.15	81	133	1155	126.1	8.18
4504981	galectin-1 [Homo sapiens]	35.56	1	5	5	17	1.001	6	4.5	1.087	6	7.7	560.17	35.56	14	17	135	14.7	5.50
530397175	PREDICTED: signal-induced proliferation-associated protein 1 isoform X1 [Homo sapiens]	5.37	30	1	6	13	1.000	1		1.525	1		68.45	5.37	9	13	1042	112.1	6.60
530364900	PREDICTED: ubiquitin-fold modifier-conjugating enzyme 1 isoform X1 [Homo sapiens]	22.13	2	3	3	9		3		1.104	3	9	124	255.56	22.13	9	122	14.6	5.59
2136121	phosphoglucomutase-1 isoform 1 [Homo sapiens]	68.33	1	21	181	1.000		51	8.3	1.196	48	17.0	7013.48	68.33	72	181	562	81.4	6.76
54792071	small ubiquitin-related modifier 2 isoform b precursor [Homo sapiens]	36.62	5	2	2	15	1.000	3	1.9	1.100	3	13.0	400.17	36.62	6	15	71	8.1	5.41
4506925	SH3 domain-binding glutamic acid-rich-like protein [Homo sapiens]	68.42	1	8	8	67	1.000	22	9.2	1.186	21	15.2	2534.96	68.42	24	67	114	12.8	5.25
515869348	hsc70-interacting protein isoform 2 [Homo sapiens]	18.11	2	5	7	24	1.000	6	8.2	1.070	6	7.7	687.69	18.11	21	24	359	40.1	5.30
325652042	transcription elongation factor B polypeptide 1 isoform b [Homo sapiens]	42.71	2	3	3	15	1.000	5	2.2	1.201	5	13.4	740.40	42.71	9	15	96	10.8	5.36
530391028	PREDICTED: gelsolin isoform X6 [Homo sapiens]	70.45	10	37	41	975	1.000	264	8.4	1.161	257	19.5	34080.66	70.45	121	975	731	80.6	5.85
73058566	heparin cofactor 2 precursor [Homo sapiens]	62.73	2	22	24	226	1.000	71	5.9	1.284	69	20.0	4434.13	62.73	68	226	499	57.0	6.90
4713262	5-methyl-5'-thioadenosine phosphorylase [Homo sapiens]	26.86	1	4	6	15	1.000	4	3.2	1.164	4	7.7	692.21	26.86	15	15	283	31.2	7.18
16418467	leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]	52.74	1	14	15	194	1.000	52	9.0	1.148	48	23.4	6431.95	52.74	44	194	347	38.2	6.95
530376957	PREDICTED: sulfotransferase family cytosolic 18 member 1 isoform X3 [Homo sapiens]	21.66	3	2	5	12	1.000	3	0.4	1.566	3	30.7	458.45	21.66	9	12	277	32.7	6.62
157649073	adenylyl cyclase-associated protein 1 [Homo sapiens]	82.32	3	36	39	613	1.000	198	7.6	1.191	186	16.4	24129.03	82.32	113	613	475	55.2	8.02
375493534	casein kinase 2, alpha 1 polypeptide-like [Homo sapiens]	8.18	7	3	4	21	1.000	6	6.8	1.230	6	15.8	507.88	8.18	12	21	391	45.1	8.50
29408770	ubiquitin-like modifier-activating enzyme ATG7 isoform 1 [Homo sapiens]	10.43	8	5	3	18	1.000	5	5.2	1.186	5	5	641.53	10.43	18	623	68.6	6.48	
4502163	apolipoprotein D precursor [Homo sapiens]	37.57	1	8	8	128	1.000	46	8.2	1.516	45	21.2	5244.38	37.57	24	128	189	21.3	5.15
574584836	mannose-6-phosphate isomerase isoform 2 [Homo sapiens]	9.41	1	1	2	1	1.000	1		1.100	1		47.37	9.41	2	2	287	31.9	6.74
348041314	cathelicidin antimicrobial peptide preproprotein [Homo sapiens]	54.91	1	11	12	141	1.000	41	4.6	1.248	41	11.4	3733.95	54.91	34	141	173	19.6	9.41
384367993	COP9 signalosome complex subunit 4 isoform 2 [Homo sapiens]	29.26	31	3	8	16	1.000	3	7.9	1.078	3	5.5	476.65	29.26	16	16	352	40.2	6.95
30581135	structural maintenance of chromosomes protein 1A isoform 1 [Homo sapiens]	20.60	30	8	26	84	1.000	8	7.7	1.334	8	21.3	1288.20	20.60	56	84	1233	143.1	7.64
294080770	platelet-activating factor acetylhydrolase II subunit beta isoform d [Homo sapiens]	25.76	4	2	2	12	1.000	4	8.7	1.271	4	4	548.91	25.76	6	12	132	14.9	5.10
345197264	tumor protein D54 isoform b [Homo sapiens]	14.11	2	2	6	11	1.000	2	4	1.179	2	6	294.91	14.11	2	6	163	17.5	6.60
645912966	major vault protein isoform 3 [Homo sapiens]	46.19	3	27	30	125	0.999	37	5.9	1.101	35	14.9	4086.67	46.19	82	125	827	91.9	5.41
60279268	splicing factor U2AF 65 kDa subunit isoform b [Homo sapiens]	13.16	3	5	5	16	0.999	5	6.7	1.121	5	35.5	405.07	13.16	13	16	471	53.1	9.09
530380257	PREDICTED: core histone macro-H2A.1 isoform X3 [Homo sapiens]	47.28	6	13	13	114	0.999	37	5.4	1.192	36	11.6	4760.09	47.28	39	114	368	39.0	9.80
4826898	profilin-1 [Homo sapiens]	75.00	4	11	11	912	0.999	289	9.6	1.184	285	16.6	34773.89	75.00	33	912	140	15.0	8.27
57404397	slaphyococcal nuclease domain-containing protein 1 [Homo sapiens]	12.75	1	7	11	25	0.999	7	5.3	1.127	7	12.6	712.43	12.75	25	25	910	101.9	7.17
530410036	PREDICTED: eukaryotic translation initiation factor 5A-1 isoform X5 [Homo sapiens]	71.43	4	8	48	0.999	14	13.4	1.115	13	5.4	1288.96	71.43	24	48	154	16.8	5.24	
578846043	PREDICTED: uncharacterized protein LOC102725101 [Homo sapiens]	7.52	2	1	3	333	0.999	10	6.9	1.402	10	24.0	4976.52	7.52	9	333	359	39.1	8.47
18104989	tyrosine-protein phosphatase non-receptor type 6 isoform 1 [Homo sapiens]	45.21	4	22	24	164	0.999	48	8.5	1.148	48	16.9	5801.62	45.21	71	164	595	67.5	7.78
4502119	membrane primary amine oxidase isoform 1 [Homo sapiens]	4.19	2	1	4	4	0.999	1		1.294	1		25.36	4.19	4	4	763	84.6	6.52
4503635	prothrombin preproprotein [Homo sapiens]	60.29	1	24	29	235	0.999	75	6.6	1.276	73	21.1	8902.55	60.29	80	235	622	70.0	5.90
5453555	GTP-binding nuclear protein Ran isoform 1 [Homo sapiens]	40.74	1	10	11	82	0.999	26	5.3	1.205	26	13.7	3300.65	40.74	31	82	216	24.4	7.49
4507581	fatty acid binding protein, epidermal [Homo sapiens]	65.93	9	8	9	88	0.999	27	8.1	1.089	27	7.4	2900.13	65.93	88	135	15.2	7.01	
4504301	histone H4 [Homo sapiens]	59.22	1	7	8	246	0.999	78	6.0	1.250	78	21.9	8688.50	59.22	24	246	103	11.4	11.36
4506691	40S ribosomal protein S16 [Homo sapiens]	29.45	2	2	5	25	0.999	2	3.4	1.112	2	0.3	415.58	29.45	11	25	146	16.4	10.21
9951915	adenosylhomocysteine isomerase isoform 1 [Homo sapiens]	37.04	2	15	16	75	0.999	24	6.7	1.178	23	19.2	2961.11	37.04	46	75	432	47.7	6.34
48762920	6-phosphofructokinase, liver type isoform b [Homo sapiens]	33.59	12	16	20	64	0.999	18	7.3	1.179	18	14.0	2118.70	33.59	55	64	780	85.0	7.50
5453567	craniofacial development protein 1 [Homo sapiens]	7.02	1	1	3	12	0.999	1		1.161	1		38.45	7.02	4	12	299	33.6	4.81
578085319	PREDICTED: protein kinase C, delta type isoform X2 [Homo sapiens]	15.99	13	11	31	121	0.999	6	6.0	1.199	6	6	618.99	15.99	6	6	618	67.5	7.75
4506203	proteasome subunit beta type-7 preprotein [Homo sapiens]	18.77	1	4	4	16	0.999	4	6.7	0.997	4	5.8	338.64	18.77	12	16	277	29.9	7.68
485385	histone H3.3 [Homo sapiens]	58.82	3	1	11	106	0.999	5	8.2	1.418	3	2.6	2359.60	58.82	3	106	136	15.3	11.27
23308577	D-3-phosphoglycerate dehydrogenase [Homo sapiens]	5.25	1	3	3	12	0.999	4	5.9	1.166	4	10.5	252.46	5.25	9	12	533	56.6	6.71
6912494	microtubule-associated protein RP/EB family member 1 [Homo sapiens]	46.64	8	9	12	58	0.999	17	5.3	1.186	17	12.2	1567.48	46.64	30	58	268	30.0	5.14
343887374	glutaredoxin-1 [Homo sapiens]	80.19	3	7	7	237	0.999	46	10.4	1.123	44	18.4	6701.22	80.19	21	237	106	11.8	8.09
53495701	vacuolar protein sorting-associated protein 13B isoform 1 [Homo sapiens]	0.90	3	5	5	16	0.999	1		1.038	1		94.96		12	16	3997	445.7	6.46
4826762	hepatoglycin isoform 1 preproprotein [Homo sapiens]	18.08	8	19	38	5608	0.998	1039	9.5	1.315	908	29.8	16271.17	18.08	111	5608	404	45.2	6.98
29332611	tyrosine-protein kinase SYK isoform Syk(S) [Homo sapiens]	14.38	2	5	9	25	0.998	7	4.3	1.153	7	26.0	560.30	14.38	19	25	612	69.5	7.56
578823780	PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X10 [Homo sapiens]	25.58	7	4	4	20	0.998	6	4.8	1.069	6	28.7	574.06	25.58	12	20	215	23.4	4.56
7657315	U6 snRNA-associated Sm-like protein LSM3 [Homo sapiens]	28.43	1	1	3	12	0.998	3	6.3	1.488	3	37.3	140.82	28.43	6	12	102	11.8	4.70
11293277	dnaJ homolog subfamily C member 8 [Homo sapiens]	21.74	1	3	4	14	0.998	4	7.2	1.232	4	4.6	333.69	21.74	11	14	253	29.9	9.06
578813467	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X5 [Homo sapiens]	43.13	10	21	12	173	0.998	36	5.1	1.169	36	10.3	5086.10	43.13	61	173	313	33.9	9.03
57114447	guanine nucleotide-binding protein subunit beta-2 like 1 [Homo sapiens]	31.85	10	6	10	104	0.998	7	17.8	1.058	7	17.8	4702.64	31.85	32	104	35.1	7.49	
4506189	proteasome subunit alpha type-7 [Homo sapiens]	51.61	8	10	13	80	0.998	20	8.4	1.051	20	9.2	2783.71	51.61	61	80	248	27.9	8.46
116284394	myosin-14 isoform 2 [Homo sapiens]	15.39	92	1	35	154	0.998	1		1.154	1		3023.50	15.39	39	154	1995	227.7	5.60
5032057	protein S100-A11 [Homo sapiens]	88.57	1	9	9	181	0.998	55	7.7	1.260	54	16.9	6657.37	88.57	27	181	105	11.7	7.12
578821773	PREDICTED: fermitin family homolog 3 isoform X1 [Homo sapiens]	45.10	4	22	24	102	0.998	31	4.3	1.160	30	16.3	3350.88	45.10	67	102	663	75.4	6.77
578821284	PREDICTED: bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cycling) is	6.93	4	2	3	7	0.998	2	7.3	1.202	2	19.8	139.09	6.93	6	7	505	51.9	6.81
255918077	versican core																		

Accession	Description	SCoverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
19913428	V-type proton ATPase subunit B, brain isoform [Homo sapiens]	40.12	3	13	15	75	0.996	24	9.7	1.242	23	22.2	2785.10	40.12	41	75	511	56.5	5.81	
160507237	78 kDa glucose-regulated protein precursor [Homo sapiens]	48.32	1	23	29	257	0.996	48	7.3	1.159	47	11.3	7994.48	48.32	79	257	654	72.3	5.16	
5116459	malic dehydrogenase, cytoplasmic isoform 2 [Homo sapiens]	40.42	3	11	12	57	0.996	19	8.7	1.124	19	32.6	2517.42	40.42	32	57	334	36.4	7.36	
332470717	basic leucine zipper and WZ domain-containing protein 1 isoform 1 [Homo sapiens]	20.05	4	4	6	16	0.996	4	3.2	1.215	4	33.2	470.39	20.05	15	16	419	48.0	5.92	
530393496	PREDICTED: hexokinase 1 isoform X1 [Homo sapiens]	7.92	6	4	9	28	0.996	4	3.0	1.224	4	34.1	556.40	7.92	22	28	960	106.9	6.98	
5031749	non-histone chromosomal protein HMG-17 [Homo sapiens]	57.78	1	4	9	85	0.996	11	6.8	1.180	11	6.2	1412.96	57.78	22	85	90	9.4	9.99	
586798161	general vesicular transport factor p115 isoform 2 [Homo sapiens]	9.15	42	2	8	18	0.996	2	3.0	1.056	2	3.0	306.18	9.15	17	18	962	107.8	4.91	
13129110	methylosome protein S0 [Homo sapiens]	4.39	1	1	1	3	0.996	1	1.0	1.009	1	3	120.74	4.39	3	3	342	36.7	5.17	
576812708	PREDICTED: engulfment and cell motility protein 1 isoform X3 [Homo sapiens]	6.46	33	5	2	5	0.996	3	24.2	1.159	4	4.3	340.31	6.46	3	10	727	83.8	6.28	
37647430	T-complex protein 1 subunit delta isoform B [Homo sapiens]	10	10	10	40	0.995	12	48	33.9	1.129	46	29.27	1129.46	29.27	16	47	509	54.7	7.83	
67514036	SH3 domain-containing kinase-binding protein 1 isoform b [Homo sapiens]	16.08	6	5	7	19	0.995	6	3.7	1.203	6	19.6	783.14	16.08	16	19	628	68.5	7.50	
83700220	geranylgeranyl pyrophosphate synthase [Homo sapiens]	5.00	1	1	2	7	0.995	1	4.0	1.590	1	32.79	5.00	4	7	300	34.8	6.14		
156523970	alpha-2-HS-glycoprotein preproprotein [Homo sapiens]	54.77	1	14	14	443	0.995	132	8.6	1.236	127	24.2	14123.93	54.77	42	443	367	39.3	5.72	
4501987	afamin precursor [Homo sapiens]	54.92	2	22	26	219	0.995	68	5.9	1.225	66	24.2	7085.17	54.92	72	219	599	69.0	5.90	
4557287	angiotensinogen preproprotein [Homo sapiens]	53.20	1	16	16	191	0.995	57	9.9	1.304	54	24.2	6268.17	53.20	48	191	485	53.1	6.32	
228008398	heterogeneous nuclear ribonucleoprotein C isoform 3 [Homo sapiens]	26.38	9	12	4	12	0.995	5	5.3	1.403	5	23.5	906.33	26.38	31	44	527	58.7	7.56	
530362677	PREDICTED: voltage-gated potassium channel subunit beta-2 isoform X4 [Homo sapiens]	36.83	12	7	10	46	0.995	12	6.0	1.072	12	41.2	977.08	36.83	26	46	353	39.3	8.62	
40316951	aminopeptidase B [Homo sapiens]	34.62	4	15	16	100	0.995	31	7.5	1.224	31	15.3	3764.13	34.62	46	100	650	72.5	5.74	
578819756	PREDICTED: xaa-Pro aminopeptidase 1 isoform X4 [Homo sapiens]	7.07	6	3	4	9	0.995	3	4.2	1.152	3	12.8	232.26	7.07	9	9	552	62.1	5.73	
4885379	histone H1.4 [Homo sapiens]	55.25	4	5	18	328	0.995	14	4.7	1.091	14	7.1	12667.80	55.25	51	328	219	21.9	11.03	
56786155	complement C1q subcomponent subunit C precursor [Homo sapiens]	25.31	1	5	5	54	0.995	19	8.4	1.392	19	30.6	2054.30	25.31	15	54	245	25.8	8.41	
45025091	glucosylase 2 subunit beta isoform 2 precursor [Homo sapiens]	20.95	6	8	34	137	0.995	12	8.4	1.137	12	33.0	1303.66	20.95	34	525	291	44.2	6.42	
192447438	vitamin K-dependent protein S preproprotein [Homo sapiens]	41.57	2	17	24	142	0.995	36	8.8	1.209	35	13.7	4444.64	41.57	65	142	676	75.1	5.67	
38455402	neutrophil gelatinase-associated lipocalin precursor [Homo sapiens]	69.70	1	16	16	577	0.995	156	8.7	1.249	151	19.7	15936.06	69.70	47	577	198	22.6	8.91	
50301238	glutathione reductase, mitochondrial isoform 1 precursor [Homo sapiens]	48.66	4	14	15	84	0.995	26	12.1	1.161	24	21.7	3539.05	48.66	42	84	522	56.2	8.50	
324021743	vitamin D-binding protein isoform 1 precursor [Homo sapiens]	83.12	12	35	42	764	0.995	245	7.5	1.211	239	22.4	27346.69	83.12	122	764	474	52.9	5.45	
45580868	complement component C7 precursor [Homo sapiens]	42.82	1	22	24	158	0.995	51	7.5	1.168	51	24.2	6139.32	42.82	69	158	84	93.1	6.16	
530376637	PREDICTED: protein fury homolog-like isoform X9 [Homo sapiens]	2.51	47	1	11	71	0.995	2	2.1	1.140	2	6.1	113.60	2.51	2	29	3028	341.1	5.98	
73858570	plasma protease C1 inhibitor precursor [Homo sapiens]	42.60	6	21	23	340	0.995	106	10.6	1.219	103	15.6	18025.54	42.60	66	340	500	55.1	6.55	
4507149	superoxide dismutase [Cu-Zn] [Homo sapiens]	83.77	1	9	10	52	0.995	18	8.2	1.024	17	17.1	1971.45	83.77	26	52	154	15.9	6.13	
605051969	protein FAM228B isoform B [Homo sapiens]	6.42	1	3	16	994	1	1	83.23	6.42	1	83.23	6.42	6	16	187	21.9	8.37		
4885287	guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 precursor [Homo sapiens]	13.24	1	1	1	3	0.994	1	54.46	13.24	3	1.040	3	3	68	7.3	9.85			
282847455	glutamate-rich protein 5 isoform 1 [Homo sapiens]	3.21	1	1	1	1	0.994	1	29.69	3.21	1	1	29.69	3.21	1	3	374	39.9	4.49	
47189970	neutrophil cytosol factor 2 isoform 1 [Homo sapiens]	42.21	5	17	20	101	0.994	28	10.8	1.180	26	17.0	3038.48	42.21	36	101	526	59.7	6.16	
54460120	lactotransferin isoform 1 precursor [Homo sapiens]	88.17	21	63	68	3813	0.994	1128	12.7	1.175	1079	17.7	13495.92	88.17	199	3813	710	78.1	8.12	
33356148	formin-like protein 1 [Homo sapiens]	10.45	10	3	10	29	0.994	3	1.7	1.131	3	14.8	293.56	10.45	20	1100	121.8	57.2	5.72	
5174449	histone H1x [Homo sapiens]	50.70	1	8	12	61	0.994	14	7.7	1.206	14	14.0	1269.39	50.70	29	61	213	22.5	10.76	
7706541	regulator of telomere elongation helicase 1 isoform 1 [Homo sapiens]	5.66	4	9	40	0.994	3	3	1.1	1.223	3	16.5	29.90	5.66	23	40	1219	133.6	8.29	
4502067	protein AMBP preproprotein [Homo sapiens]	42.90	2	15	15	202	0.994	62	7.6	1.142	62	16.1	6363.57	42.90	44	202	352	39.0	6.25	
4505701	pyridoxal kinase [Homo sapiens]	48.72	5	8	9	66	0.994	26	4.5	1.196	26	20	3171.46	48.72	26	66	312	35.1	6.13	
21614544	protein S100-A8 [Homo sapiens]	100.00	27	28	468	0.994	27	1466	100.00	1.223	87	1423	178718.01	100.00	83	468	93	10.8	7.03	
194097330	hexokinase-3 [Homo sapiens]	59.05	7	24	35	199	0.994	51	7.1	1.246	49	28.7	6924.50	59.05	97	199	923	99.0	5.40	
116063573	flutamin-A isoform 1 [Homo sapiens]	52.10	2	89	101	854	0.994	249	9.1	1.152	244	13.3	34211.11	52.10	296	854	2639	279.8	6.05	
574287947	sex hormone-binding globulin isoform 5 [Homo sapiens]	8.14	5	1	2	5	0.994	1	4.8	1.708	1	288.06	8.14	5	5	344	37.5	6.23		
27544941	unconventional myosin-II [Homo sapiens]	34.79	5	19	25	138	0.994	34	8.3	1.192	32	17.1	3847.61	34.79	67	138	1098	124.8	9.11	
27436948	lamin isoform A-delta10 [Homo sapiens]	13.09	6	6	8	29	0.994	9	4.0	1.125	9	22.4	630.20	13.09	20	29	634	70.6	8.40	
4507125	small nuclear ribonucleoprotein-associated protein B and B' isoform B [Homo sapiens]	40.42	6	3	6	33	0.994	7	2.6	1.077	7	19.6	452.44	40.42	18	33	231	26.4	10.90	
17865802	vacuolar protein sorting-associated protein 4B [Homo sapiens]	10.36	2	1	3	7	0.994	1	10.6	1.324	1	7	129.66	10.36	7	7	444	49.3	7.23	
108773793	glucose-6-phosphate 1-dehydrogenase isoform b [Homo sapiens]	71.65	8	33	36	373	0.994	115	7.7	1.209	112	18.2	12464.56	71.65	104	373	515	59.2	6.84	
4885393	hemoglobin subunit epsilon [Homo sapiens]	18.37	1	1	3	234	0.994	5	5.3	1.085	5	1.1	4358.15	18.37	9	234	147	16.2	8.63	
578830426	PREDICTED: collagen alpha-1(I) chain isoform X3 [Homo sapiens]	12.94	6	8	9	85	0.994	26	6.9	1.157	26	12.6	2482.61	12.94	26	85	1000	99.7	5.50	
216149808	RNA-binding protein 20 [Homo sapiens]	4.26	4	2	4	18	0.994	4	23.4	1.580	4	23.4	83.68	4.26	7	18	1227	134.2	5.69	
4506195	prolactinoma subunit beta type-2 isoform 1 [Homo sapiens]	36.31	3	5	8	44	0.993	9	10.0	1.756	9	10.0	756.19	36.31	22	40	201	22.8	7.02	
4506467	radixin isoform 2 [Homo sapiens]	32.59	7	4	26	317	0.993	6	6.7	1.100	6	6.7	6818.90	32.59	37	317	583	68.5	6.37	
4557871	serotransferrin precursor [Homo sapiens]	82.38	54	69	72	4685	0.993	1372	9.3	1.300	1277	26.9	160152.09	82.38	214	4685	698	77.0	7.12	
578839125	PREDICTED: putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-B-4	30.97	1	3	4	276	0.993	47	4.8	1.307	46	23.3	13985.21	30.97	12	276	155	17.4	9.11	
31563514	N-alpha-acetyltransferase 20 isoform c [Homo sapiens]	6.31	3	1	1	16	0.993	5	3.8	1.302	5	4.0	129.74	6.31	2	16	111	12.7	4.67	
55170842	C-reactive protein precursor [Homo sapiens]	34.82	1	9	9	109	0.993	35	7.7	1.231	34	26.5	2829.77	34.82	27	109	224	25.0	5.63	
530402326	PREDICTED: keratin, type I cuticular H6 isoform X1 [Homo sapiens]	4.102	7	1	3	18	0.993	4	10.6	1.271	4	4	1.81	191.56	4.102	6	18	563	62.0	6.37
379317149	secrin isoform D [Homo sapiens]	40.00	1	2	4	13	0.992	2	4	1.123	2	7.4	71.79	40.00	10	10	180	20.0	9.63	
530412767	PREDICTED: signal transducer and activator of transcription 5B isoform X2 [Homo sapiens]	8.45	7	3	4	10	0.993	3	4.5	1.830	3	31.4	203.55	8.45	10	10	497	56.8	6.37	
58219054	bcl-2-like protein 15 [Homo sapiens]	13.50	1	1	2	12	0.993	3	5.3	1.161	3	36.2	211.13	13.50	6	12	163	3.7	4.41	
66392203	NME1-NME2 protein [Homo sapiens]	73.41	3	7	15	154	0.993	19	5.2	1.179	19	8.1	4240.51	73.41	44	154	267	30.1	8.92	
530407092	PREDICTED: aminopeptidase N isoform X1 [Homo sapiens]	3.62	1	4	4	12	0.993	4	5.5	1.060	4	14.9	583.00	3.62	12	12	967	109.5	5.48	
578804605	PREDICTED: UDP-glucose-glycoprotein glucosyltransferase 1 isoform X3 [Homo sapiens]	4.47	4	1	5	24	0.993	1	1.913	4.47	1	47.82	4.47	7	24	1544	176.2	5.63		

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
557878742	long-chain-fatty-acid-CoA ligase 1 isoform f [Homo sapiens]	7.40	14	2	5	10	0.991	2	0.9	1.615	2	14.3	221.26	7.40	9	10	527	58.5	7.53	
5453880	acidic leucine-rich nuclear phosphoprotein 32 family member A [Homo sapiens]	37.35	4	4	10	86	0.991	17	11.7	1.268	14	11.0	3112.76	37.35	30	86	249	28.6	4.09	
16933542	fibronectin isoform 3 precursor [Homo sapiens]	49.24	27	80	100	1001	0.991	280	8.0	1.184	274	15.1	33251.20	184	240	101	2355	259.1	5.73	
485831	histone H1.5 [Homo sapiens]	50.88	2	15	20	324	0.991	89	7.1	1.204	89	17.5	11547.02	50.88	59	324	226	22.6	10.92	
57808622	PREDICTED: multifunctional protein ADE2 isoform X1 [Homo sapiens]	13.40	3	6	12	30	0.991	8	6.5	1.290	8	30.4	968.31	13.40	24	30	836	93.9	8.06	
7662502	malignant T-cell-amplified sequence 1 isoform 1 [Homo sapiens]	30.94	2	4	4	14	0.990	5	1.5	1.259	5	7.0	522.26	30.94	11	14	181	20.5	8.82	
578814728	PREDICTED: uncharacterized aaF domain-containing protein kinase 2 isoform X1 [Homo sapiens]	6.83	2	1	4	14	0.990	1		2.246			23.47	6.83	4	4	542	60.0	9.31	
149999611	signal recognition particle 14 kDa protein [Homo sapiens]	27.21	1	3	3	22	0.990	7	5.7	1.188	7	14.9	1070.62	27.21	9	22	136	14.6	10.00	
4504469	histidine-rich glycoprotein precursor [Homo sapiens]	42.24	2	18	18	228	0.990	70	17.3	1.166	68	54	21.6	4954.80	43.24	54	228	525	99.5	7.50
39230709	receptor type tyrosine protein phosphatase C isoform 2 precursor [Homo sapiens]	21.41	6	15	21	41	0.990	18	20.3	1.164	18	23.1	1795.75	21.41	13	61	111	131.0	6.33	
57808863	PREDICTED: eukaryotic translation initiation factor 4E isoform X1 [Homo sapiens]	24.49	6	4	6	16	0.990	4	2.1	1.011	4	12.4	484.81	24.49	16	16	245	28.5	8.12	
10716563	calnexin precursor [Homo sapiens]	23.65	1	11	12	62	0.990	18	7.3	1.118	18	12.6	2135.56	23.65	33	62	592	67.5	4.60	
295844834	N-acetyl-D-glucosaminase kinase [Homo sapiens]	40.51	3	12	13	59	0.990	17	5.9	1.307	17	23.1	1818.47	40.51	37	59	390	42.0	6.68	
530364307	PREDICTED: farnesyl pyrophosphate synthase isoform X2 [Homo sapiens]	18.13	3	4	5	21	0.990	5	1.5	1.429	5	20.5	577.76	18.13	15	21	353	40.5	5.17	
209969703	protein RCC2 [Homo sapiens]	13.60	1	3	7	27	0.990	3	14.2	1.231	3	28.5	186.88	13.60	13	27	522	56.0	8.78	
4506201	proteasome subunit beta type-5 isoform 1 [Homo sapiens]	8.37	4	2	2	6	0.990	2	2.8	1.095	2	6.6	269.28	8.37	6	6	263	28.5	6.92	
7662314	zinc finger protein 432 [Homo sapiens]	3.68	4	3	14	14	0.990	2	2.7	1.142	2	19.4	58.80	3.68	3	14	652	74.8	8.75	
578827386	PREDICTED: endonuclease 8-like 1 isoform X6 [Homo sapiens]	3.46	5	1	2	6	0.989	1		1.058	1		20.74	3.46	2	6	433	48.8	10.11	
40806221	thymocyte nuclear protein 1 isoform 1 [Homo sapiens]	21.78	4	3	5	16	0.989	3	11.1	0.991	3	8.9	330.83	21.78	13	16	225	25.7	9.25	
530395269	PREDICTED: hemopexin isoform X1 [Homo sapiens]	78.14	4	33	33	1862	0.989	556	7.4	1.293	534	26.0	53094.00	78.14	97	1862	462	51.6	7.02	
38201710	probable ATP-dependent RNA helicase DDX17 isoform 1 [Homo sapiens]	14.13	5	3	13	32	0.989	3	4.0	0.939	3	3.4	720.24	14.13	32	32	729	80.2	8.27	
45580723	histoglinin-related protein precursor [Homo sapiens]	62.64	6	27	2216	1	0.989	17	4.9	1.105	17	17.6	66442.15	62.64	66	2216	348	39.0	7.09	
9845511	ras-related C3 botulinum toxin substrate 1 isoform Rac1 [Homo sapiens]	42.19	8	6	8	59	0.989	5	8.3	1.035	3	4.0	1879.26	42.19	24	59	192	21.4	8.50	
5901926	cleavage and polyadenylation specificity factor subunit 5 [Homo sapiens]	7.49	1	2	2	6	0.989	2	2.5	1.218	2	2.8	120.20	7.49	2	6	227	26.2	8.82	
4557759	myeloperoxidase precursor [Homo sapiens]	61.48	3	44	50	939	0.989	279	7.2	1.156	277	14.0	31187.87	61.48	142	939	745	83.8	8.97	
526479824	dynactin subunit 3 isoform 4 [Homo sapiens]	16.88	5	1	3	12	0.989	1		0.995	1		108.33	16.88	8	12	154	17.2	8.68	
122939159	protein-arginine deiminase type-2 [Homo sapiens]	21.50	1	11	14	66	0.989	15	4.8	1.347	15	21.2	2226.00	21.50	39	66	665	75.5	5.59	
45055229	signal-regulatory protein beta-1 isoform 3 precursor [Homo sapiens]	12.06	13	4	4	27	0.989	3	3.5	1.122	3	3.1	420.86	12.06	13	27	398	43.3	7.83	
91520973	phosphoserine aminotransferase isoform 1 [Homo sapiens]	10.27	3	3	5	13	0.989	3	10.7	1.117	3	9.1	190.62	10.27	3	13	190	40.4	7.66	
530371139	PREDICTED: 1-Myc-interactor isoform X1 [Homo sapiens]	24.10	1	6	6	29	0.989	8	4.3	1.155	8	17.5	785.08	24.10	17	29	307	35.0	5.34	
4885377	histone H1.3 [Homo sapiens]	35.29	4	3	13	250	0.989	3	4.6	1.156	3	5.0	11027.36	35.29	38	250	221	32.3	11.02	
578838605	PREDICTED: cohesin subunit SA-2 isoform X7 [Homo sapiens]	4.42	3	1	2	4	0.989	1		1.664	1		61.12	2.42	3	4	1199	138.4	5.41	
5803181	stress-induced-phosphoprotein 1 isoform b [Homo sapiens]	2.52	3	15	19	79	0.989	20	3.4	1.114	20	6.8	1674.56	40.52	49	79	543	62.6	6.80	
45055229	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	51.24	1	7	14	645	0.989	109	9.5	1.240	108	27.0	18887.96	51.24	42	645	201	23.6	5.11	
262206315	L-selectin precursor [Homo sapiens]	14.55	1	2	6	27	0.989	2	1.5	1.179	2	12.4	152.08	14.55	10	27	385	43.6	7.15	
7706425	LSMB homolog, U6 small nuclear RNA associated [Homo sapiens]	23.96	2	2	2	6	0.989	2	1.5	1.151	2	25.1	267.01	23.96	6	6	96	10.4	4.48	
578828789	PREDICTED: cholesterol ester transfer protein isoform X1 [Homo sapiens]	6.77	3	1	2	10	0.989	3	0.6	1.545	3	34.3	53.09	6.77	2	10	266	29.1	6.52	
4503011	carboxypeptidase N catalytic chain precursor [Homo sapiens]	20.96	1	6	7	38	0.989	11	6.2	1.243	11	11.4	1572.63	20.96	21	38	458	52.3	7.34	
32189394	ATP synthase subunit beta, mitochondrial precursor [Homo sapiens]	14.74	1	4	5	18	0.989	5	5.0	1.236	5	17.9	939.90	14.74	15	19	529	56.5	5.40	
8051595	Ga-binding protein subunit beta-1 isoform beta 2 [Homo sapiens]	9.14	8	1	4	5	0.988	1		1.228	1		38.89	9.14	5	5	383	41.3	4.84	
530420952	PREDICTED: male-specific lethal 3 homolog isoform X2 [Homo sapiens]	1.49	5	1	1	2	0.988	1		1.990	1		38.90	1.49	2	2	355	40.6	8.85	
530395059	PREDICTED: glycoyltransferase-like protein LARGE2 isoform X3 [Homo sapiens]	4.03	3	1	3	6	0.988	1		1.485	1		0.00	4.03	3	6	494	56.9	8.13	
5031855	lymphocyte cytosolic protein 2 [Homo sapiens]	10.51	1	4	5	19	0.988	5	4.5	1.270	5	13.1	603.28	10.51	5	19	533	60.2	6.27	
530378251	PREDICTED: rho GTPase-activating protein 24 isoform X1 [Homo sapiens]	5.21	16	2	6	22	0.988	5	2.8	1.073	5	4.2	67.49	5.21	6	22	748	84.2	6.67	
19923483	ras-related protein Rab-14 [Homo sapiens]	36.28	16	4	5	19	0.988	4	4.1	1.178	4	17.5	811.86	36.28	15	19	215	23.9	6.21	
74722287	matrix metalloproteinase-9 propeptide [Homo sapiens]	65.91	1	41	41	591	0.988	199	19.9	1.208	194	22.7	21992.85	65.91	121	591	707	78.4	6.06	
578824102	PREDICTED: histoglinin-1 RNA ligase, cytoplasmic isoform X4 [Homo sapiens]	29.10	17	19	43	27	0.988	20	3.6	1.195	20	11.8	2765.58	29.10	50	67	471	53.1	6.21	
225498192	delta-aminolevulinic acid dehydratase [Homo sapiens]	10.59	5	1	4	4	0.988	1		1.4	1		28.87	10.59	4	4	321	34.6	10.21	
189083849	delta-aminolevulinic acid dehydratase [Homo sapiens]	25.15	2	6	6	28	0.988	10	11.1	1.005	10	10.4	1147.04	25.15	18	28	330	36.3	6.79	
28416940	ribosome maturation protein SBDS [Homo sapiens]	12.40	10	1	5	28	0.988	1		1.183	1		263.51	12.40	11	28	250	28.7	8.75	
15011972	rho guanine nucleotide exchange factor 1 isoform 2 [Homo sapiens]	21.93	9	14	17	66	0.988	20	8.2	1.156	20	25.3	1930.62	21.93	44	66	912	102.4	5.66	
4557389	complement component C8 alpha chain precursor [Homo sapiens]	38.70	1	16	18	88	0.988	25	8.6	1.204	24	16.7	3243.49	38.70	49	88	584	65.1	6.47	
568815719	clathrin heavy chain 1 isoform 2 [Homo sapiens]	22.75	3	22	31	160	0.988	30	8.5	1.157	28	21.3	3993.77	22.75	82	160	1679	191.9	5.69	
19923227	neuroepithelial cell-transforming gene 1 protein isoform 2 [Homo sapiens]	2.40	7	1	2	2	0.988	1		1.222	1		32.67	2.40	2	2	542	61.8	8.88	
22208975	high mobility group protein HMG-1/HMG-V isoform b [Homo sapiens]	37.50	1	3	16	16	0.988	5	8.6	1.149	5	13.0	256.67	37.50	6	16	96	10.7	10.32	
5902134	coronin-1A [Homo sapiens]	63.12	13	28	31	491	0.987	151	9.3	1.215	140	18.2	14866.54	63.12	93	491	461	51.0	6.68	
23238188	testin isoform 2 [Homo sapiens]	6.80	3	1	2	4	0.987	1		1.037	1		191.47	6.80	4	4	412	46.9	7.59	
530426780	PREDICTED: TNF receptor-associated factor 1 isoform 2 X2 [Homo sapiens]	1.88	1	1	1	5	0.987	1		1.179	1		72.39	1.88	1	3	5	233	59.1	7.52
530434491	PREDICTED: uncharacterized protein LOC101930119 [Homo sapiens]	1.88	2	1	1	4	0.987	1		1.230	1		22.33	1.88	1	4	520	24.5	9.77	
547234776	BRP12 like protein isoform 3 [Homo sapiens]	3.01	4	4	315	5	0.987	80	6.3	1.514	75	37.5	1744.06	3.01	315	1197	132.6	8.48		
315221152	60S ribosomal protein L11 isoform 2 [Homo sapiens]	26.55	2	1	7	46	0.987	1		1.309	1		219.28	26.55	16	46	177	20.1	9.60	
4504349	hemoglobin subunit beta [Homo sapiens]	95.24	12	19	5142	0.987	1026	11.0	10.74		1026	10.1	230073.47	95.24	57	5142	147	16.0	7.28	
530397196	PREDICTED: syntrophin 3 isoform X5 [Homo sapiens]	16.23	6	2	5	78	0.987	2	5.2	1.103	2	16.4	162.72	16.23	11	78	265	30.6	5.56	
578803212	PREDICTED: protein dpy-30 homolog isoform X3 [Homo sapiens]	32.50	2	1	3	9	0.987	2	19.1	1.120	2	21.1	315.97	32.50	5	9	120	13.9	7.50	
156071465	rho GTPase-activating protein 4 isoform 2 [Homo sapiens]	18.50	2	7	13	45	0.987	7	8.7	1.106	8	7.6	1133.31	18.50	30	45	946	105.0	6.34	
578829954	PREDICTED: phosphoribosylformylglycanide synthase isoform X1 [Homo sapiens]	5.49	2	4	13	0.987	3	3	11.6	1.023	3									

Accession	Description	2Coverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
34147630	elongation factor Tu, mitochondrial precursor [Homo sapiens]	5.27	1	1	2	23	0.985	2	5.1	1.047	2	8.6	294.89	5.27	6	23	455	49.8	7.61
28195394	histone H2A type 2-B [Homo sapiens]	45.38	2	1	6	57	0.985	2	6.0	1.219	2	16.3	1679.20	45.38	18	57	130	14.0	10.89
70995211	delta(2,5)-delta(2,4)-delta(2,3)-acyl-CoA isomerase, mitochondrial precursor [Homo sapiens]	1.96	1	1	2	9	0.985	1	5.47	1.370	1	5.2	52.47	3.93	2	9	326	35.8	6.50
4503117	cystatin-B [Homo sapiens]	59.18	1	4	5	35	0.985	10	3.4	1.090	10	8.0	938.17	59.18	14	35	96	11.1	7.56
578815934	PREDICTED: triple CxxK/R motif-containing protein isoform X1 [Homo sapiens]	6.98	1	1	1	4	0.985	1	1.127	1.127	1	90.72	6.98	3	4	86	9.7	9.36	
4503529	eukaryotic initiation factor 4A-1 isoform 1 [Homo sapiens]	35.22	3	10	14	59	0.985	16	4.7	1.103	16	11.8	1480.36	35.22	38	59	406	46.1	5.48
5174411	CD5 antigen-like precursor [Homo sapiens]	43.23	2	13	13	104	0.985	34	5.8	1.193	34	17.6	4678.47	43.23	38	104	347	38.1	5.47
58331240	fetuin-B precursor [Homo sapiens]	15.45	3	4	5	15	0.984	4	5.8	1.327	3	11.0	495.98	15.45	13	15	382	42.0	6.83
578818360	PREDICTED: arkyrin repeat domain-containing protein 26 isoform X3 [Homo sapiens]	7.24	9	1	17	36	0.984	1	1.369	1.369	1	42.56	7.24	25	36	2031	233.5	5.87	
1177819	vascular protein sorting associated protein 26A isoform 1 [Homo sapiens]	1.96	1	1	2	8	0.984	2	0.0	1.242	2	12.9	182.21	2.42	2	8	327	38.1	6.57
4757760	adiponectin precursor [Homo sapiens]	6.15	1	1	1	9	0.984	3	1.2	1.246	3	6.8	446.23	6.15	3	9	244	26.4	5.74
4506003	serine/threonine-protein phosphatase PP1-alpha catalytic subunit isoform 1 [Homo sapiens]	25.45	6	3	37	38	0.984	5	2.3	1.059	5	3.6	1322.64	25.45	21	38	330	37.5	6.33
530382085	PREDICTED: ribosyl-dihydrofolate reductase (quinone) isoform X3 [Homo sapiens]	51.95	2	7	8	46	0.984	13	8.4	1.161	13	7.2	1657.10	51.95	23	46	231	25.9	6.29
224028248	non-POU domain-binding protein isoform 2 [Homo sapiens]	18.59	2	4	6	32	0.984	9	13.6	1.118	9	20.1	1197.18	18.59	15	32	382	43.8	8.63
5453760	NEDD8 precursor [Homo sapiens]	37.04	1	1	3	20	0.984	2	6.6	1.402	2	16.7	814.48	37.04	7	20	81	9.1	8.43
260914167	transmembrane emp24 domain-containing protein 6 precursor [Homo sapiens]	4.17	3	1	1	9	0.984	1	1	0.730	1	29.91	4.17	1	9	240	27.6	8.27	
33350932	cytoplasmic dynein 1 heavy chain 1 [Homo sapiens]	5.41	1	5	22	51	0.984	5	11.9	1.088	4	37.8	475.81	4.41	37	51	4646	532.1	6.40
578810877	PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 isoform X14 [Homo sapiens]	3.29	5	1	4	19	0.983	4	5.3	1.553	4	31.2	291.09	3.29	8	19	882	100.8	7.97
530363148	PREDICTED: splicing factor, proline- and glutamine-rich isoform X5 [Homo sapiens]	20.93	2	10	28	0.983	8	9.6	1.082	8	6.1	854.82	20.93	24	28	669	72.2	9.23	
542133044	zinc finger protein 343 isoform 3 [Homo sapiens]	6.09	14	1	3	9	0.983	3	0.9	1.052	3	4.6	30.14	6.09	5	9	509	58.8	8.98
106796653	phosphoglycolate phosphatase [Homo sapiens]	16.51	1	3	3	14	0.983	4	6.9	0.903	4	9.6	633.25	16.51	9	14	321	34.0	6.14
555290081	3' (2', 5'-bisphosphate nucleotidase 1 isoform 2 [Homo sapiens]	1.32	1	1	1	3	0.983	1	0.846	0.983	1	270.47	6.32	3	3	253	29.5	5.33	
18379349	synaptic vesicle membrane protein VAT-1 homolog [Homo sapiens]	62.09	2	15	18	152	0.983	49	12.3	1.198	48	25.2	7590.79	62.09	52	152	393	41.9	6.29
189458812	1,4-alpha-glucan-branching enzyme [Homo sapiens]	36.18	1	13	18	135	0.983	27	5.6	1.247	27	11.3	3653.86	36.18	48	135	702	80.4	6.32
124028517	transcription factor PU 1 isoform 2 [Homo sapiens]	13.70	2	2	4	10	0.983	2	3.4	1.213	2	34.2	199.60	13.70	8	10	270	31.1	6.80
530379128	PREDICTED: ly6M and putative peptidoglycan-binding domain-containing protein 3 isoform X1 [Homo sapiens]	5.23	10	1	3	8	0.983	2	7.0	1.190	2	4.2	95.26	5.23	7	8	306	34.5	5.97
11641247	Golgi-associated plant pathogenesis-related protein 1 isoform a [Homo sapiens]	51.30	5	5	6	25	0.983	8	5.3	1.213	8	8.6	1449.02	51.30	16	25	154	17.2	9.41
530379765	PREDICTED: eukaryotic peptide chain release factor subunit 1 isoform X2 [Homo sapiens]	8.42	3	2	4	10	0.983	2	2.0	1.135	2	17.1	235.22	8.42	9	10	404	45.4	5.57
4826902	serpin B10 [Homo sapiens]	70.03	1	23	23	150	0.982	51	6.9	1.143	51	18.6	5090.16	70.03	69	150	397	45.4	6.16
586798140	bridging integrator 2 isoform 2 [Homo sapiens]	30.43	39	9	13	53	0.982	15	6.0	1.114	15	20.7	1937.22	30.43	33	53	539	59.2	5.00
24308273	costars family protein ABRACL [Homo sapiens]	38.27	1	2	3	18	0.982	4	4.5	1.112	4	31.8	119.65	38.27	7	18	81	9.1	6.29
578821763	PREDICTED: calpain-1 catalytic subunit isoform X1 [Homo sapiens]	37.25	1	19	20	101	0.982	33	9.6	1.205	31	25.5	3533.10	37.25	59	101	714	81.8	5.67
578813403	PREDICTED: glycine--tRNA ligase isoform X1 [Homo sapiens]	18.18	2	4	7	18	0.982	4	6.4	1.039	4	14.2	298.36	18.18	16	18	616	69.9	6.13
578809641	PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 3 isoform X1 [Homo sapiens]	5.50	3	1	6	7	0.982	1	1	1.501	1	44.56	5.50	6	7	873	100.8	8.06	
4505185	macrophage migration inhibitory factor (Homo sapiens)	87.43	3	5	5	140	0.982	23	9.4	1.183	16	6.4	1225.55	87.43	15	140	115	12.5	7.88
6912352	protein argonaute-1 [Homo sapiens]	1.97	1	1	4	6	0.982	1	1	1.191	1	58.38	3.97	6	6	857	97.2	9.16	
384229049	thymidine phosphorylase isoform 1 proprotein [Homo sapiens]	48.34	2	13	16	73	0.982	23	7.6	1.170	23	17.4	3356.63	48.34	44	73	482	49.9	5.53
4758256	eukaryotic translation initiation factor 2 subunit 1 [Homo sapiens]	6.03	1	2	2	6	0.982	2	0.5	1.218	2	0.5	219.18	6.03	6	6	315	36.1	5.08
629266054	probable G-protein coupled receptor 179 precursor [Homo sapiens]	2.92	1	1	7	25	0.982	4	2.9	1.100	4	30.2	130.78	2.92	9	25	2367	257.2	5.71
4503149	cathepsin G preproprotein [Homo sapiens]	59.61	3	15	17	282	0.982	78	5.6	1.174	78	14.0	7393.72	59.61	90	282	255	28.8	11.19
20070130	transcription factor BTG3 isoform B [Homo sapiens]	10.49	2	1	2	8	0.982	2	2.2	1.896	2	153.36	10.49	8	162	17.7	7.50		
11342670	aurousin preproprotein [Homo sapiens]	53.39	1	9	9	253	0.982	63	8.4	1.152	60	19.2	7395.83	53.39	27	253	251	26.9	9.50
38201684	ribonuclease pancreatic precursor [Homo sapiens]	14.74	1	1	1	6	0.982	2	21.8	1.245	2	4.6	202.93	14.74	3	6	156	17.6	8.79
88703045	proline-rich protein 11 [Homo sapiens]	6.94	1	1	5	152	0.981	20	4.1	1.438	20	28.1	680.02	6.94	10	152	360	40.1	10.11
530402140	PREDICTED: 5-formylglutathione hydrolase isoform X1 [Homo sapiens]	65.25	1	11	12	65	0.981	17	9.6	1.180	16	14.1	1850.36	65.25	36	65	282	31.4	7.02
115529463	serine/threonine-protein kinase D1 [Homo sapiens]	1.21	2	1	3	14	0.981	2	9.0	1.823	2	3.1	62.68	1.21	5	14	912	101.6	6.62
7106254	nucleolar protein 58 [Homo sapiens]	1.73	1	1	3	173	0.981	1	1	1.077	1	151.63	1.73	4	3	59	59.5	8.92	
4504351	hemoglobin subunit delta [Homo sapiens]	95.24	1	8	17	2380	0.981	86	9.5	1.072	86	10.9	114443.61	95.24	50	2380	147	16.0	8.05
530405979	PREDICTED: pyruvate kinase PKM isoform X3 [Homo sapiens]	84.93	25	4	49	1109	0.981	34	7.4	1.245	34	24.6	45692.09	84.93	145	1109	531	57.9	7.84
162287326	tyrosine-protein kinase Lyn isoform B [Homo sapiens]	9.98	97	3	5	22	0.981	4	7.8	1.072	4	6.8	542.34	9.98	14	22	491	56.0	6.49
530365780	PREDICTED: rab GTPase-activating protein 1-like isoform X2 [Homo sapiens]	6.51	24	1	7	19	0.981	2	2.2	1.074	2	4.7	101.36	6.51	12	19	1014	115.3	5.47
530383216	PREDICTED: ras-related GTP-binding protein D isoform X1 [Homo sapiens]	2.31	4	1	1	2	0.981	4	1	1.178	1	42.37	2.31	2	12	2	303	34.2	4.44
4504345	hemoglobin subunit alpha [Homo sapiens]	96.48	2	17	18	4565	0.981	1418	10.6	1.088	1424	10.6	229789.54	96.48	54	4565	142	15.2	8.68
15343229	26S proteasome non-ATPase regulatory subunit 9 isoform 1 [Homo sapiens]	13.45	2	4	4	13	0.981	5	2.8	1.094	5	5.6	312.19	13.45	12	15	223	24.7	6.95
185429681	26S protease regulatory subunit B isoform 2 [Homo sapiens]	23.12	3	5	8	20	0.981	5	20.6	1.226	5	20.6	516.30	23.12	20	398	44.8	8.18	
4504255	histone H2A.2 [Homo sapiens]	53.91	7	3	6	50	0.980	7	16.2	1.051	6	11.9	1359.90	53.91	16	50	128	13.5	10.58
4503649	coagulation factor IX preproprotein [Homo sapiens]	9.33	3	3	4	14	0.980	4	3.5	1.518	4	15.8	453.74	9.33	10	14	461	51.7	5.47
11999541	vacuolar protein sorting-associated protein 35 [Homo sapiens]	21.23	5	14	70	0.980	24	5	5.7	1.184	24	16.0	2344.43	21.23	40	70	796	91.6	5.45
530370136	PREDICTED: solute carrier family 2, facilitated glucose transporter member 8 isoform X1 [Homo sapiens]	2.87	4	1	2	2	0.980	1	1	1.024	1	7.1	2.87	2.87	2	2	314	34.3	7.36
518831041	PREDICTED: cytokine receptor like factor 3 isoform X1 [Homo sapiens]	1.96	4	1	2	15	0.980	4	7.7	1.165	4	2.6	490.51	1.96	4	14	488	50.6	5.56
24234756	interleukin enhancer-binding factor 3 isoform c [Homo sapiens]	18.84	10	11	38	0.980	11	5	7.2	1.154	11	15.1	1372.95	18.84	32	38	690	74.6	8.24
5032315	dystrophin Pd427p2 isoform [Homo sapiens]	5.56	47	1	25	63	0.980	1	1	1.525	1	246.04	5.56	38	63	3562	412.1	5.83	
304555581	elongation factor 1-delta isoform 1 [Homo sapiens]	16.07	12	1	8	36	0.980	2	2.0	1.192	2	7.2	1216.35	16.07	19	36	647	71.4	6.42
20149583	nucleoside diphosphate-linked moiety X motif 6 isoform a [Homo sapiens]	5.70	2	1	2	4	0.980	1	42.11	5.70	4	4	42.11	5.70	4	4	316	35.7	8.00
20357559	galactin-10 [Homo sapiens]	47.89	1	3	6	70	0.980	14	12.0	1.066	14	7.7	1343.89	47.89	13	70	142	16.4	7.37
24307939	T-complex protein 1 subunit epsilon [Homo sapiens]	31.98	1	9	12	44	0.980	11	4.0	1.099	10	10.9	1311.37	31.98	31</				

Accession	Description	LCoverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
5453710	LIM and SH3 domain protein 1 isoform a [Homo sapiens]	72.80	4	10	12	63	0.977	20	10.8	1.154	20	20.8	1205.96	72.80	32	63	261	29.7	7.05
5912238	peroxiredoxin-5, mitochondrial isoform a precursor [Homo sapiens]	61.21	4	10	12	175	0.977	52	9.8	1.157	51	17.6	6489.83	61.21	34	175	214	22.0	8.57
53037475	PREDICTED: isopentenyl isomerase X5 [Homo sapiens]	1.06	1	1	1	1	0.977	1	1	1.06	1	1	20.02	1.06	1	1	461	50.2	8.25
56499409	RNA-binding motif protein, X chromosome isoform 1 [Homo sapiens]	17.14	4	4	8	42	0.977	8	5.1	1.272	8	12.6	1272.48	17.14	19	42	391	42.3	10.05
57883547	PREDICTED: NSF1 cofactor p47 isoform X4 [Homo sapiens]	23.17	6	3	5	19	0.977	4	3.9	1.051	4	1.9	519.60	23.17	13	19	259	28.5	9.38
380837121	vesicle-trafficking protein SEC22b precursor [Homo sapiens]	30.70	1	4	6	32	0.977	5	3.5	1.203	5	15.0	600.24	30.70	15	32	215	24.7	8.51
4507511	metalloproteinase inhibitor 2 precursor [Homo sapiens]	20.91	1	3	4	14	0.977	3	1.3	1.218	3	20.7	257.01	20.91	11	14	220	24.4	7.49
22091452	apolipoprotein M isoform 1 [Homo sapiens]	57.98	3	7	9	48	0.977	14	9.5	1.145	14	41.8	1497.72	57.98	25	48	188	21.2	6.01
180595677	integrin beta-2 precursor [Homo sapiens]	17.56	2	9	13	42	0.976	12	3.7	1.144	12	11.0	1227.07	17.56	30	42	769	84.7	6.95
300931782	transportin 3 isoform 2 [Homo sapiens]	4.31	4	4	8	1	0.976	1	1	1.295	1	1	157.26	4.31	8	8	859	97.3	5.44
66933014	inosine-5'-monophosphate dehydrogenase 2 [Homo sapiens]	17.51	2	4	5	13	0.976	4	6.6	1.105	3	4.7	475.16	17.51	13	13	514	55.8	6.90
578838944	PREDICTED: NF-kappa-B essential modulator isoform X6 [Homo sapiens]	6.72	6	1	3	12	0.976	1	32.01	1.469	1	12	6.72	6.72	17	12	461	7.1	6.62
4504041	guanine nucleotide-binding protein G(i) subunit alpha-2 isoform 1 [Homo sapiens]	42.54	22	6	13	59	0.976	13	6.4	1.266	12	24.0	2305.68	42.54	34	59	355	40.4	5.54
21281677	WD repeat-containing protein 36 [Homo sapiens]	1.68	1	1	2	5	0.976	1	1	1.472	1	14.81	1.68	1.68	2	5	951	105.3	7.53
237649049	small nuclear ribonucleoprotein Sm D2 isoform 2 [Homo sapiens]	25.93	2	3	3	9	0.976	3	1.7	1.215	3	27.8	236.08	25.93	9	9	108	12.4	9.89
4503625	coagulation factor X propeptide [Homo sapiens]	18.24	3	7	9	34	0.976	10	5.5	1.095	10	12.1	711.98	18.24	22	34	486	54.7	5.94
530411225	PREDICTED: Gq12 SNAP receptor complex member 1 isoform X3 [Homo sapiens]	23.24	5	1	4	9	0.976	1	0.9	0.975	1	9	140.37	23.24	9	9	185	21.2	9.61
258679498	carbonic anhydrase 1 isoform a [Homo sapiens]	83.52	3	12	14	752	0.976	140	9.3	1.085	140	9.0	20643.20	83.52	42	752	261	28.9	7.12
578789051	PREDICTED: uncharacterized protein LOC100293211 [Homo sapiens]	23.33	2	5	7	445	0.976	50	6.0	1.243	49	24.5	8614.25	23.33	21	445	270	29.5	8.59
530422109	PREDICTED: RNA-binding protein LOC100293211 [Homo sapiens]	7.36	7	2	5	19	0.976	1	57.52	1.101	1	5.9	117.52	7.36	5	19	394	44.9	9.60
4547469	AP-2 complex subunit beta isoform b [Homo sapiens]	14.94	3	6	13	40	0.976	7	2.5	1.167	7	5.9	1131.86	14.94	34	40	937	104.5	5.38
323510705	signal recognition particle 19 kDa protein isoform b [Homo sapiens]	24.75	3	1	2	5	0.976	1	50.26	1.075	1	2	50.26	24.75	2	2	101	11.5	9.04
530412701	PREDICTED: band 3 anion transport protein isoform X2 [Homo sapiens]	9.57	2	5	6	25	0.976	9	2.6	1.183	9	26.6	988.10	9.57	16	25	846	94.1	6.16
83700231	cytosolic T-lymphocyte protein 4 isoform CTLA-4deltaTM precursor [Homo sapiens]	7.47	2	1	2	3	0.976	1	30.69	1.152	1	3	7.47	7.47	3	3	174	19.1	8.47
544186046	protein disulfide-isomerase A6 isoform b [Homo sapiens]	23.16	8	7	9	36	0.975	10	6.9	1.151	10	6.2	1443.32	23.16	23	36	488	53.2	5.53
530408977	PREDICTED: sulfotransferase 1A1 isoform X1 [Homo sapiens]	39.66	7	9	10	54	0.975	18	4.7	1.454	18	18.0	1866.71	39.66	27	54	295	34.1	6.62
530425195	PREDICTED: neutrophil elastase isoform X1 [Homo sapiens]	55.06	1	8	11	317	0.975	86	8.7	1.258	77	20.3	11655.41	55.06	32	317	267	28.5	9.35
546235986	beta-glucuronidase isoform 2 precursor [Homo sapiens]	7.52	5	1	5	9	0.975	1	45.17	1.150	1	5	7.52	7.52	7	5	505	58.3	6.99
578822219	PREDICTED: nuclear factor related to kappa B-binding protein isoform X5 [Homo sapiens]	2.40	1	3	5	0.975	1	3	41.99	1.032	3	5	12.94	2.40	3	5	1294	139.9	8.87
94721252	vesicle-associated membrane protein-associated protein A isoform 2 [Homo sapiens]	15.66	2	3	3	10	0.975	4	7.9	1.111	4	20.5	208.56	15.66	6	10	249	27.9	8.62
118442839	complement factor H-related protein 1 precursor [Homo sapiens]	38.18	3	2	10	72	0.975	3	1.8	1.094	3	1.8	1717.31	38.18	29	72	330	37.6	7.39
342349321	interleukin-18 isoform 2 proprotein [Homo sapiens]	9.52	2	1	3	10	0.975	2	3.9	1.273	2	8.8	56.24	9.52	6	10	189	21.9	4.78
50428935	microtubule-associated protein 15 [Homo sapiens]	4.34	1	4	12	0.975	3	0.6	1.214	3	3	29.2	222.22	4.34	11	12	1059	112.1	7.30
15431295	60S ribosomal protein L13 isoform 1 [Homo sapiens]	14.69	2	1	4	13	0.974	3	2.0	1.095	3	6.8	356.10	14.69	6	13	211	24.2	11.65
578840723	PREDICTED: V-set and immunoglobulin domain-containing protein 1-like [Homo sapiens]	24.80	1	8	6	264	0.974	78	4.1	1.307	73	14.4	2855.67	24.80	25	264	250	27.2	8.54
299758394	dyxamin-2 isoform 5 [Homo sapiens]	19.10	23	12	17	51	0.974	12	20.8	1.191	12	20.8	797.51	19.10	46	51	869	97.9	7.44
255958306	perilipin-3 isoform 3 [Homo sapiens]	39.10	3	11	12	59	0.974	14	7.1	1.146	14	15.2	1413.80	39.10	32	59	422	45.8	5.43
26051231	serine beta-lactamase-like protein LACTB, mitochondrial isoform a precursor [Homo sapiens]	4.02	4	3	14	0.974	1	3	1.222	1	1	28.34	4.02	3	14	547	60.7	8.53	
23111047	sorting nexin-5 isoform a [Homo sapiens]	7.18	1	2	3	9	0.974	3	1.0	0.944	3	11.7	324.06	7.18	6	9	404	46.8	6.76
21361659	importin-9 [Homo sapiens]	6.53	2	1	5	10	0.974	1	1	1.521	1	7	210.24	6.53	7	10	1041	115.9	4.81
46346485	plasminogen activator inhibitor 1 RNA-binding protein isoform 4 [Homo sapiens]	13.18	4	3	5	13	0.974	4	5.6	1.217	4	8.1	251.47	13.18	10	13	387	42.4	8.44
4885583	rho-associated protein kinase 1 [Homo sapiens]	10.78	1	4	15	40	0.974	4	1.7	1.161	3	6.1	454.74	10.78	30	40	1354	158.1	5.90
530391093	PREDICTED: protein prenyltransferase alpha subunit repeat-containing protein 1 isoform X2 [Homo sapiens]	9.73	17	2	4	36	0.974	3	12.4	5.364	2	425.9	209.56	9.73	9	36	401	46.3	6.99
530425592	PREDICTED: putative hydrolase RBBP9 isoform X1 [Homo sapiens]	10.16	2	1	1	3	0.974	1	1	1.283	1	91.25	10.16	3	3	128	14.7	5.72	
578813594	PREDICTED: actin, cytoplasmic 1 isoform X1 [Homo sapiens]	97.23	23	3	30	4096	0.974	3	6.6	2.422	2	50.7	165999.28	97.23	86	4096	253	28.2	5.34
4502171	adenine phosphoribosyltransferase isoform a [Homo sapiens]	49.44	2	7	7	45	0.974	15	9.3	1.133	14	31.8	1870.46	49.44	21	45	180	19.6	6.02
51477708	heterogeneous nuclear ribonucleoprotein D0 isoform 1 [Homo sapiens]	24.74	6	4	6	17	0.974	11	8.4	1.177	11	823.10	24.74	24.74	42	42	807	70.7	8.41
530407875	PREDICTED: RNA-binding protein FUS isoform X3 [Homo sapiens]	14.64	6	3	3	15	0.974	4	7.0	1.053	4	3.4	772.78	14.64	9	15	321	33.2	9.17
404211881	obscurin isoform IC [Homo sapiens]	3.79	43	3	34	88	0.974	2	12.4	1.398	2	28.7	310.94	3.79	54	88	8923	972.4	5.99
537361067	armadillo repeat-containing protein 8 isoform 5 [Homo sapiens]	6.67	8	5	14	0.973	1	1	26.71	1.155	1	6.71	6.67	6.67	11	14	600	67.1	6.73
78191798	plasma kallikrein propeptide [Homo sapiens]	31.97	3	16	18	80	0.973	22	7.9	1.299	21	13.3	2269.15	31.97	51	80	638	71.3	8.22
320202986	alcohol dehydrogenase [NAD(P)+] [Homo sapiens]	49.54	3	11	14	50	0.973	14	8.7	1.241	13	8.7	1959.97	49.54	35	50	325	36.5	6.79
57881012	PREDICTED: hematological and neurological expressed 1 protein isoform X1 [Homo sapiens]	28.11	5	3	2	10	0.973	3	5.9	1.129	3	8.5	312.21	28.11	7	10	185	19.4	8.48
38158015	maternin-like protein 3 [Homo sapiens]	1.50	3	1	2	3	0.973	1	1	1.50	1	1	25.71	1.50	3	3	1133	121.6	7.52
55956899	kuratin, type 1 cytoskeletal 9 [Homo sapiens]	30.34	2	6	10	37	0.973	6	3.6	1.095	6	3.6	1237.10	30.34	26	37	623	62.0	5.24
530394359	PREDICTED: mini-chromosome maintenance complex-binding protein isoform X1 [Homo sapiens]	1.36	3	1	1	12	0.973	3	8.4	1.114	3	2.4	88.75	1.36	2	12	587	66.5	5.95
578814467	PREDICTED: tyrosine-protein phosphatase non-receptor type 12 isoform X2 [Homo sapiens]	4.41	5	2	3	7	0.973	2	1.4	1.084	2	1.4	157.54	4.41	7	7	748	84.4	5.60
44890052	stathmin isoform a [Homo sapiens]	45.64	5	6	9	29	0.973	8	6.2	1.174	8	4	928.66	45.64	23	29	149	17.3	5.97
530365819	PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Homo sapiens]	21.11	2	4	4	5	0.973	4	17.7	1.226	4	15.8	392.40	21.11	15	15	289	32.1	5.85
761862	protein phosphatase 1F [Homo sapiens]	15.52	2	5	25	13	0.973	6	5.1	1.114	6	11.1	704.77	15.52	9	25	454	49.8	5.10
112382370	folate receptor gamma precursor [Homo sapiens]	15.51	3	2	4	8	0.973	2	4.6	1.003	2	3.7	166.23	15.51	7	8	245	27.9	7.66
19920317	cytoskeleton-associated protein 4 [Homo sapiens]	3.49	1	1	2	6	0.972	1	6.6	1.205	6	6	602	3.49	6	6	602	66.0	5.92
2786588	protein-tyrosine kinase 2-beta isoform b [Homo sapiens]	10.96	3	3	10	20	0.972	3	1.5	1.155	3	9.3	173.40	10.96	17	20	967	111.1	5.91
4502165	apolipoprotein F precursor [Homo sapiens]	7.36	1	1	2	8	0.972	2	32.5	270.53	2	32.5	270.53	7.36	24	8	326	35.4	5.64
530414265	PREDICTED: cytosolic non-specific dipeptidase isoform X2 [Homo sapiens]	17.05	2	5	6	21	0.972	7	3.7	1.131	7	21.4	587.93	17.05	15	21	475	52.8	5.97
57879625	PREDICTED: NAD kinase isoform X5 [Homo sapiens]	19.50	5	6	6	21	0.972	7	6	1.184	7	24.2	111						

Accession	Description	LCoverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
578831699	PREDICTED: UPF0378 protein KIAA1001 isoform X2 [Homo sapiens]	5.93	3	1	13	28	0.969	1					45.58	5.93	13	28	2092	237.2	6.99
4503771	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha [Homo sapiens]	16.62	1	2	5	40	0.969	3	8.5	1.443	3	15.6	111.25	16.62	13	40	379	44.4	5.88
579698844	colloid-collagen-containing protein 51 isoform 2 [Homo sapiens]	2.62	2	2	5	5	0.969	2	1.5	1.358	2	43.6	46.73	2.62	15	5	302	33.6	6.86
118402586	lactoyglutathione lyase [Homo sapiens]	46.74	1	9	37	0.969		12	9.6	1.039	12	13.9	845.93	46.74	25	37	184	20.8	5.31
530407070	PREDICTED: tyrosine-protein kinase Fes/Fps isoform X6 [Homo sapiens]	8.11	4	2	8	45	0.969	7	2.6	1.287	7	18.7	421.22	8.11	16	45	752	85.4	6.90
11056044	inorganic pyrophosphatase [Homo sapiens]	24.57	1	5	6	22	0.968	6	6.6	1.076	6	2.8	599.11	24.57	16	22	289	32.6	5.86
4757804	copper transport protein ATOX1 [Homo sapiens]	32.35	7	3	3	14	0.968	5	5.6	1.344	5	22.3	158.80	32.35	8	14	68	7.4	7.24
2754778	ficolin-3 isoform 2 precursor [Homo sapiens]	25.35	2	6	6	36	0.968	12	5.6	1.138	12	20.4	1030.16	25.35	18	36	288	31.7	6.84
40789206	protein ZNF365 isoform C [Homo sapiens]	3.46	2	1	2	3	0.968	1	1.114		1	3	24.52	3.46	3	3	462	53.5	6.77
38788372	iron binding protein aquargus [Homo sapiens]	6.37	1	1	9	370	0.968	1	1	1.132	1	19.98	3.70	6.37	9	9	1486	171.2	6.37
19913416	AP-2 complex subunit alpha-1 isoform 2 [Homo sapiens]	13.40	2	3	12	28	0.968	3	4.3	1.042	3	3.1	660.27	13.40	23	28	955	105.3	7.66
64762445	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 isoform b [Homo sapiens]	6.16	5	1	3	5	0.968	1		1.110			149.59	6.16	5	5	471	54.4	7.56
154355000	far upstream element-binding protein 2 [Homo sapiens]	7.31	2	1	5	15	0.968	1		0.918	1		70.12	7.31	9	15	711	73.1	7.30
662033927	astrocytic phosphoprotein PEA-15 isoform c [Homo sapiens]	9.26	3	1	1	3	0.968	1		1.063	1		175.23	9.26	3	3	108	12.5	5.17
93277088	mediator of RNA polymerase II transcription subunit 12-like protein [Homo sapiens]	2.70	2	1	7	21	0.967	1		1.023	1		71.39	2.70	12	21	2145	240.0	7.77
24234489	stress 70 protein, mitochondrial precursor [Homo sapiens]	8.39	1	1	6	22	0.967	1		1.057	1		113.40	8.39	12	22	679	73.6	6.16
530412652	PREDICTED: HEAT repeat-containing protein 6 isoform X2 [Homo sapiens]	1.18	2	1	2	8	0.967	2	0.7	1.025	2	3.4	95.14	1.18	5	8	1013	110.2	7.23
148612803	keratin, type II, cytoskeletal 74 [Homo sapiens]	13.42	9	1	11	33	0.967	1		1.434	1		243.06	13.42	21	33	529	57.8	7.71
530361304	PREDICTED: ribosomal protein S6 kinase alpha-1 isoform X2 [Homo sapiens]	4.04	17	2	3	6	0.967	2	4.4	1.459	2	18.1	137.53	4.04	6	6	643	72.7	8.25
148727247	ubiquitin carboxyl-terminal hydrolase 5 isoform 2 [Homo sapiens]	4.31	2	2	3	14	0.967	2	5.9	0.871	2	17.0	160.93	4.31	8	14	835	93.2	5.08
578826513	PREDICTED: putative V-set and immunoglobulin domain-containing like protein IGHV4OR15-B1	19.69	2	1	3	165	0.967	3	1.0	1.136	3	1.0	8808.59	19.69	8	165	127	14.1	8.84
56237029	integrin alpha-5 precursor [Homo sapiens]	1.05	1	1	9	1	0.967	1		1.730	1		19.36	1.05	9	9	1049	114.5	5.77
8922601	ADP-ribosylation factor-like protein 8B [Homo sapiens]	4.84	1	1	1	3	0.966	1		1.017	1		164.11	4.84	3	3	186	21.5	8.43
4506209	26S protease regulatory subunit 7 isoform 1 [Homo sapiens]	11.55	2	4	5	15	0.966	4	8.1	1.234	4	14.7	384.49	11.55	13	15	433	48.6	5.95
18141299	zinc finger and BTB domain-containing protein 26 [Homo sapiens]	2.27	1	1	1	3	0.966	3	10.6	2.899	1		61.58	2.27	1	3	441	49.9	7.08
11386157	cytidine deaminase [Homo sapiens]	86.99	1	6	6	48	0.966	14	8.5	1.540	10	29.0	1414.08	86.99	18	48	146	16.2	6.92
530413109	PREDICTED: hepatocyte growth factor-regulated tyrosine kinase substrate isoform X1 [Homo sapiens]	7.42	2	1	8	19	0.966	2	4.6	1.399	2	13.6	216.98	7.42	14	19	768	85.2	6.06
7176675	V-type proton ATPase subunit D [Homo sapiens]	12.15	1	3	7	0.966	1	1		1.227	1		74.98	12.15	7	7	247	28.2	9.36
28558975	mediator of RNA polymerase II transcription subunit 17 [Homo sapiens]	4.45	1	1	3	5	0.966	1					33.48	4.45	3	5	35	72.8	7.44
38202255	threonine--RNA ligase, cytoplasmic isoform 1 [Homo sapiens]	6.22	4	4	6	21	0.966	4	4.7	1.216	4	15.2	167.25	6.22	13	21	723	83.4	6.67
11022798	phospholipase B-like 1 precursor [Homo sapiens]	34.36	1	11	13	95	0.966	24	8.3	1.159	23	12.9	2123.81	34.36	37	95	553	63.2	9.06
170932494	syntaxin-7 [Homo sapiens]	22.61	1	4	5	17	0.966	5	4.3	1.217	5	10.8	913.36	22.61	12	17	261	29.8	5.55
34734066	fibulin-1 isoform D precursor [Homo sapiens]	17.78	4	9	9	33	0.966	12	5.8	1.077	12	10.8	1114.54	17.78	25	33	703	77.2	5.26
47132587	protein kinase C delta-binding protein [Homo sapiens]	14.56	1	1	5	9	0.965	1		1.067	1		27.91	14.56	6	9	261	27.7	6.43
223972612	protein cramped-like [Homo sapiens]	2.44	1	4	5	24	0.965	1		1.368	1		29.07	2.44	4	5	1269	134.6	7.87
530393330	PREDICTED: zinc finger SWIM domain-containing protein 8 isoform X8 [Homo sapiens]	1.00	10	1	2	10	0.965	3	5.9	1.721	3	9.8	154.06	1.00	4	10	1800	193.4	6.99
40353564	bisphosphoglycerate mutase [Homo sapiens]	34.36	1	6	6	23	0.965	8	10.0	1.135	8	15.8	701.08	34.36	17	23	259	30.0	6.54
162329583	cleavage and polyadenylation specificity factor subunit 6 [Homo sapiens]	8.35	4	1	4	25	0.965	1		1.052	1		281.64	8.35	10	25	551	59.2	7.15
5454096	serine/threonine-protein kinase 4 [Homo sapiens]	20.53	5	4	8	36	0.965	4	5.5	1.020	4	23.6	502.15	20.53	20	20	487	55.6	5.07
5453607	T-complex protein 1 subunit eta isoform a [Homo sapiens]	22.84	4	8	9	47	0.965	12	10.1	1.138	12	22.5	1168.15	22.84	23	47	543	59.3	7.65
4557101	keratin, type I, cytoskeletal 17 [Homo sapiens]	41.44	14	6	19	49	0.965	4	6	1.126	4	13.1	1492.72	41.44	48	49	432	48.1	5.03
7705653	ras-related protein Rab-8B [Homo sapiens]	30.92	22	2	6	39	0.964	4	8.7	1.178	4	6.7	1726.82	30.92	18	39	207	23.6	9.07
578814724	PREDICTED: maltase-glucoamylase, intestinal isoform X1 [Homo sapiens]	4.07	3	3	6	12	0.964	3	17.6	1.355	3	80.3	306.33	4.07	12	12	2753	311.8	5.41
578808151	PREDICTED: alpha-L-iduronidase isoform X2 [Homo sapiens]	1.73	3	1	1	1	0.964	1		2.067	1		20.12	1.73	1	1	521	57.8	8.82
530412093	PREDICTED: interferon-induced 35 kDa protein isoform X1 [Homo sapiens]	26.57	2	8	10	43	0.964	10	3.3	1.133	10	21.5	972.89	26.57	27	43	286	31.5	6.09
530362562	PREDICTED: protein S100-A7 isoform X1 [Homo sapiens]	66.34	1	5	9	162	0.964	19	8.2	1.137	19	6.5	5485.19	66.34	26	162	101	11.5	6.77
530403277	PREDICTED: aspartic chitinase endonuclease inducer in the nucleus isoform X4 [Homo sapiens]	19.54	19	5	16	94	0.964	1		1.041	1		72.97	19.54	9	16	503	57.5	7.59
392512662	interleukin enhancer-binding factor 2 isoform 2 [Homo sapiens]	18.47	2	2	3	15	0.964	2	1.9	1.200	3	21.4	399.61	18.47	8	15	352	38.9	4.94
311771547	RBM14-RBM4 protein isoform 2 [Homo sapiens]	18.64	5	1	2	8	0.964	2	0.8	1.046	2	16.3	245.76	18.64	5	8	118	12.9	8.21
578808923	PREDICTED: protein transport protein Sec31A isoform X23 [Homo sapiens]	7.58	12	2	6	11	0.964	2	12.8	1.114	2	14.7	215.14	7.58	2	11	897	99.1	6.80
4506017	serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform [Homo sapiens]	44.66	5	7	7	30	0.963	9	8.1	1.153	9	17.0	1117.08	44.66	20	30	309	35.6	5.54
4557395	carbonic anhydrase 2 isoform 1 [Homo sapiens]	67.31	2	11	12	106	0.963	32	8.8	1.052	32	8.1	4440.98	67.31	34	106	260	29.2	7.40
530364071	PREDICTED: BRD1 domain-containing protein BRDXX isoform X5 [Homo sapiens]	10.67	6	1	7	23	0.963	1		1.217	1		72.50	10.67	16	23	356	40.3	7.17
26263314	cytidine 4 precursor [Homo sapiens]	4.83	1	1	1	3	0.963	2	7.3	1.496	2	64.0	144.11	4.83	3	3	145	15.4	8.48
11067747	cell division cycle 5-like protein [Homo sapiens]	5.86	12	1	6	34	0.963	1		1.436	1		83.02	5.86	10	34	802	92.2	8.18
300244560	cysteine-rich secretory protein 3 isoform 1 precursor [Homo sapiens]	39.15	2	6	8	37	0.963	11	6.5	1.118	11	15.0	784.70	39.15	21	37	258	29.0	7.80
118601081	heterogeneous nuclear ribonucleoprotein U-like isoform 2 [Homo sapiens]	21.82	8	10	14	48	0.963	10	4.9	1.163	10	12.7	1314.91	21.82	35	48	747	85.1	4.91
578819487	PREDICTED: mannose-binding protein C isoform X3 [Homo sapiens]	18.15	3	2	5	11	0.962	2	2.5	1.333	2	31.5	102.65	18.15	11	11	248	26.1	5.91
118882255	ATP-binding cassette 5 family C member 8 isoform 2 [Homo sapiens]	2.72	3	1	6	30	0.962	3	0.1	1.157	3	6.3	232.54	2.72	9	30	1581	176.9	7.89
14277700	60S ribosomal protein S12 [Homo sapiens]	4.98	1	1	3	4	0.962	1		1.092	1		121.99	4.98	1	3	132	14.5	7.21
4502955	collagen alpha-5(V) chain isoform 1 precursor [Homo sapiens]	1.78	4	1	3	8	0.962	1		1.547	1		41.58	1.78	3	8	1685	160.9	7.62
4557892	phosphatidylcholine-sterol acyltransferase precursor [Homo sapiens]	7.27	1	2	3	8	0.962	2	9.8	1.707	2	29.6	292.41	7.27	7	8	440	49.5	6.11
530375762	PREDICTED: carboxypeptidase N subunit 2 isoform X1 [Homo sapiens]	31.19	1	11	11	73	0.962	18	5.0	1.239	18	23.6	1905.22	31.19	33	73	545	60.5	5.99
13676857	heat shock-related 70 kDa protein 2 [Homo sapiens]	22.54	1	1	14	207	0.961	1		1.096	1		6169.50	22.54	37	207	639	70.0	5.74
4502951	collagen alpha-1(III) chain prepropeptide [Homo sapiens]	7.30	1	5	8	22	0.961	6	7.5	1.119	6	7.9	1037.12	7.30	19	22	1466	138.5	6.57
578825257	PREDICTED: DNA ligase 4 isoform X4 [Homo sapiens]	5.71	8	2	1	7	0.961	8	7.6	1.208	7	1.1	35.03	5.71	4	7	911	103.9	7.96
212549536	regulator of G-protein signaling protein-like [Homo sapiens]	7.53	5	1	11	34	0.961	1		1.244	1		40.44	7.53	20				

Accession	Description	2Coverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
378744212	GTP-binding protein RIT1 isoform 3 [Homo sapiens]	4.37	3	1	1	11	0.956	3	0.7	1.527	3	12.2	65.03	4.37	3	11	183	21.6	9.09
29626323	alpha-adducin isoform c [Homo sapiens]	12.68	12	3	7	20	0.956	3	9.6	1.056	3	1.7	246.83	12.68	16	20	631	69.9	6.46
41393614	ras-related protein Rab-5C isoform a [Homo sapiens]	25.00	1	2	4	16	0.956	2	6.5	1.348	2	5.1	545.27	25.00	12	16	216	20.5	8.41
115430223	galactin-3 isoform 1 [Homo sapiens]	22.40	4	5	5	41	0.956	12	4.6	1.147	12	18.8	1107.48	22.40	15	41	250	26.1	8.56
530420291	PREDICTED: gamma-parvin isoform X2 [Homo sapiens]	7.85	1	2	2	6	0.956	2	5.3	1.105	2	3.8	246.74	7.85	6	6	331	37.5	5.49
150170699	kinesin-like protein KIF26A [Homo sapiens]	2.50	1	2	6	19	0.956	2	1.5	1.156	1	11	111.05	2.50	11	19	1882	194.5	8.81
183603931	serine/threonine-protein phosphatase 6 catalytic subunit isoform c [Homo sapiens]	16.96	4	4	4	19	0.956	1	1.492	1.492	1	19	129.48	16.96	8	19	283	32.5	6.04
5901956	folistatin-related protein 1 precursor [Homo sapiens]	11.69	1	1	2	4	0.956	1	1	1.033	1	1	104.32	11.69	6	7	308	35.0	5.52
344179106	regulator complex protein LAMTOR3 isoform 2 [Homo sapiens]	28.21	2	1	2	4	0.955	1	1	0.965	1	1	85.93	28.21	3	4	117	12.9	8.13
254222415	fibulin-8 isoform 4 [Homo sapiens]	14.92	9	14	75	0.955	3	2.7	1.209	0.955	3	1.0	1586.72	4.93	3	75	2578	275.5	5.78
296179399	outer dense fiber protein 2-like isoform d [Homo sapiens]	15.74	24	1	12	52	0.955	1	1	2.577	1	1	148.06	15.74	24	52	591	68.6	6.55
62241042	bifunctional glutamate/proline-tRNA ligase [Homo sapiens]	7.08	1	4	11	34	0.955	6	3.5	1.298	6	18.4	811.54	7.08	24	34	1512	64.6	7.33
21269877	cysteine-tRNA ligase, cytoplasmic isoform a [Homo sapiens]	7.99	6	2	5	11	0.955	2	3.7	1.056	2	1.9	185.86	7.99	11	11	726	82.8	7.02
5454088	acidic leucine-rich nuclear phosphoprotein 32 family member B [Homo sapiens]	40.24	13	4	11	78	0.955	12	10.1	1.124	11	7.0	2250.48	40.24	32	78	251	28.8	4.06
66529407	tenasin-1 [Homo sapiens]	2.02	4	1	4	4	0.955	4	1	1.025	4	1	19.68	2.02	4	4	1735	185.6	7.75
38002257	neutral alpha-glucosidase AB isoform 2 precursor [Homo sapiens]	16.74	5	8	11	32	0.955	9	8.7	1.260	9	27.1	846.14	16.74	29	32	944	106.8	6.14
62243048	insulin-like growth factor-binding protein 3 isoform b precursor [Homo sapiens]	14.09	55	3	4	24	0.955	3	8.1	1.489	3	12.6	533.30	14.09	12	24	291	31.7	8.69
51873055	fibulin-2 isoform b precursor [Homo sapiens]	6.50	3	1	2	7	0.955	1	1	1.178	1	1	128.42	6.50	5	7	1184	126.5	4.82
578832396	PREDICTED: trafficking protein particle complex subunit 8 isoform X4 [Homo sapiens]	2.84	5	1	4	9	0.954	1	2.84	0.954	1	4	44.95	2.84	4	9	1338	150.1	6.83
195972866	keratin, type I cytoskeletal 10 [Homo sapiens]	34.93	21	14	19	92	0.954	27	15.0	1.054	27	6.6	4024.07	34.93	50	92	584	58.8	5.21
7661880	ar-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 [Homo sapiens]	15.00	2	5	9	41	0.954	6	6.7	1.342	6	13.4	728.13	15.00	21	41	740	81.5	7.66
17149653	FKBP-binding protein-like [Homo sapiens]	1.30	14	1	2	10	0.954	1	1.309	0.954	1	44.31	10	1.309	14	10	349	38.2	5.50
31543385	choline-phosphate cytidylyltransferase A [Homo sapiens]	5.18	4	2	2	4	0.953	2	1.0	1.099	2	9.4	67.84	5.18	4	4	367	41.7	7.25
578799003	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X	3.35	7	9	26	0.953	3	3.35	2.2	1.189	3	11.9	447.06	3.35	18	26	4057	433.5	6.55
212165400	acyl-coenzyme A thioesterase 11 isoform 2 [Homo sapiens]	5.72	2	1	4	6	0.953	1	1	0.981	1	1	28.99	5.72	4	6	594	67.1	7.64
56788356	tufelin-interacting protein 11 [Homo sapiens]	3.58	1	1	4	14	0.953	1	1	1.051	1	1	35.37	3.58	8	14	837	96.8	5.67
4557485	ceruloplasmin precursor [Homo sapiens]	74.37	1	2	63	1125	0.953	12	8.2	1.316	12	25.8	38070.30	74.37	184	1125	1065	122.1	5.72
4865399	structural maintenance of chromosomes protein 3 [Homo sapiens]	12.24	7	2	16	103	0.953	2	16.7	1.345	2	16.4	477.81	12.24	30	103	1217	141.5	7.18
383872480	ubiquitin-conjugating enzyme E2 variant 1 isoform a [Homo sapiens]	51.18	12	3	10	50	0.953	4	8.8	1.106	4	17.7	749.62	51.18	28	50	170	19.3	8.54
374253794	B-cell receptor-associated protein 31 isoform b [Homo sapiens]	8.54	9	1	3	11	0.953	1	1	1.201	1	1	123.55	8.54	8	11	246	28.0	8.44
46094009	melanoma inhibitory activity protein 2 precursor [Homo sapiens]	2.60	1	2	7	0.953	2	15.0	1.881	2	48.0	113.04	2.60	2	7	654	74.0	4.34	
578806133	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Homo sapiens]	17.92	6	4	5	17	0.953	4	9.6	1.069	4	11.0	284.84	17.92	12	17	625	70.6	7.61
6912286	casein-14 precursor [Homo sapiens]	14.88	1	2	3	9	0.953	2	8.9	0.994	2	8.0	122.57	14.88	9	9	242	27.7	5.58
109148542	alanine-tRNA ligase, cytoplasmic [Homo sapiens]	10.74	2	3	8	17	0.953	3	2.8	1.286	3	27.2	436.38	10.74	14	17	968	106.7	5.53
301171467	arleykin-1 isoform 2 [Homo sapiens]	4.65	2	1	7	25	0.953	2	4.65	1.125	2	5.4	311.32	4.65	25	1719	188.9	6.62	
301171467	ATP-dependent RNA helicase DDX3X isoform 2 [Homo sapiens]	11.50	6	1	6	25	0.952	3	0.1	1.006	3	4.9	451.02	11.50	11	25	661	73.1	7.18
222144309	prenylated Rab acceptor protein 1 [Homo sapiens]	7.03	10	1	2	27	0.952	1	1	2.033	1	1	89.74	7.03	6	27	185	20.6	7.34
8393638	junctional adhesion molecule A precursor [Homo sapiens]	4.01	1	1	1	2	0.952	2	3.4	1.052	2	3.4	54.92	4.01	1	2	299	32.6	7.90
23097308	nesprin-1 isoform 2 [Homo sapiens]	5.85	22	4	55	158	0.952	7	5.9	1.415	7	17.7	518.98	5.85	84	158	8749	1004.6	5.52
289547524	rab11 family-interacting protein 1 isoform 3 [Homo sapiens]	7.40	2	3	8	22	0.951	3	12.6	1.205	3	1.5	388.55	7.40	17	22	1283	137.1	5.43
41327171	probable ATP-dependent RNA helicase DDX21 [Homo sapiens]	8.29	1	7	17	0.951	2	1.9	1.098	0.951	2	8.3	180.89	8.29	13	17	820	95.5	9.55
530421644	PREDICTED: mediator of RNA polymerase II transcription subunit 14 isoform X2 [Homo sapiens]	2.06	4	1	4	10	0.951	3	4.1	2.103	3	5.7	58.03	2.06	4	10	1410	156.3	8.69
98986457	host cell factor 1 [Homo sapiens]	2.06	3	5	21	0.951	3	2.4	1.093	0.951	3	1.1	270.14	2.06	13	21	2035	208.6	7.46
7657313	U6 snRNA-associated Sm-like protein LSM1 [Homo sapiens]	5.26	1	1	1	2	0.951	1	1	1.258	1	1	36.87	5.26	2	2	133	15.2	5.22
308737003	origin recognition complex subunit 3 isoform 3 [Homo sapiens]	5.99	5	1	2	6	0.951	1	1	2.004	1	1	29.41	5.99	2	6	568	65.9	7.62
578832501	PREDICTED: methyl-CpG-binding domain protein 1 isoform X28 [Homo sapiens]	9.34	38	1	6	10	0.951	1	1	0.870	1	1	131.85	9.34	10	10	610	67.5	9.54
5031961	26S proteasome non-ATPase regulatory subunit 14 [Homo sapiens]	21.23	16	5	23	0.951	16	5	6.4	1.068	16	8.5	562.25	21.23	5	16	310	34.6	6.52
31657142	integrin alpha-1 precursor [Homo sapiens]	5.26	1	1	8	18	0.950	2	3.3	1.153	2	4.0	31.56	5.26	8	18	1179	130.8	6.29
578818505	PREDICTED: zinc finger protein 248 isoform X2 [Homo sapiens]	9.50	1	1	7	7	0.950	1	1	1.263	1	1	28.97	9.50	7	7	579	67.0	8.25
7706511	methylionine-S-sulfoxide reductase B1 [Homo sapiens]	7.76	1	1	1	2	0.950	1	1	0.972	1	1	53.25	7.76	2	2	116	12.8	8.37
530414003	PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 2 isoform X4 [Homo sapiens]	4.73	3	1	1	6	0.950	2	5.7	1.457	2	2.6	100.26	4.73	3	6	169	18.5	5.54
14150155	vacuolar protein-sorting-associated protein 25 [Homo sapiens]	4.55	1	1	1	3	0.950	1	1	1.196	1	1	37.70	4.55	3	3	176	20.7	6.34
530376083	PREDICTED: SH3 domain and tetrapeptide repeat-containing protein 1 isoform X1 [Homo sapiens]	2.9	5	1	5	28	0.949	1	1	1.722	1	1	51.48	2.9	23	23	1260	139.2	6.28
126032350	DNA-dependent protein kinase catalytic subunit isoform 2 [Homo sapiens]	9.67	16	13	35	133	0.949	13	10.9	1.093	12	18.1	996.99	9.67	70	133	4097	465.2	7.17
116875844	phosphogluconate-cysteine ligase isoform a [Homo sapiens]	7.07	3	1	2	4	0.949	3	1	1.253	3	1	112.68	7.07	4	4	311	34.0	6.71
4826665	copper chaperone for superoxide dismutase [Homo sapiens]	5.47	1	2	2	4	0.949	1	1	0.914	1	1	63.97	5.47	4	4	274	29.0	5.58
217416379	heterogeneous nuclear ribonucleoprotein L-like isoform 2 [Homo sapiens]	8.38	5	3	4	10	0.949	3	9.7	1.161	3	9.3	245.42	8.38	10	10	537	59.6	7.72
108347345	PREDICTED: unconventional myosin-XVIIb isoform X4 [Homo sapiens]	3.55	3	1	9	18	0.949	1	1	1.276	1	1	31.10	3.55	9	18	2449	272.2	6.90
578772136	G-protein coupled receptor-associated sorting protein 1 [Homo sapiens]	1.15	2	1	2	1	0.948	1	1	1.016	1	1	27.73	1.15	2	2	1395	156.8	4.68
578809225	PREDICTED: ubiquitin-like modifier-activating enzyme 4 isoform X1 [Homo sapiens]	9.93	2	1	3	13	0.948	2	2.1	1.261	2	11.2	228.85	9.93	13	13	977	110.2	6.24
42794779	unconventional myosin-XVIIa isoform b [Homo sapiens]	8.58	2	5	16	41	0.948	6	7.7	1.255	5	15.7	416.25	8.58	29	41	2039	231.1	6.20
148277022	selenoprotein P isoform 2 [Homo sapiens]	16.30	2	3	6	33	0.948	8	5.6	1.186	8	17.0	1080.55	16.30	12	33	411	46.2	8.03
578807020	PREDICTED: programmed cell death protein 10 isoform X4 [Homo sapiens]	4.72	1	1	1	3	0.947	1	1	1.173	1	1	53.92	4.72	3	3	212	24.7	8.19
31877525	arachidonate 5-lipoxygenase isoform 2 [Homo sapiens]	5.30	3	3	14	0.947	3	3.2	1.163	0.947	3	2.3	492.12	5.30	7	14	642	74.6	5.63
145309304	cadherin EGF LAG seven-pass G-type receptor 3 precursor [Homo sapiens]	3.26	1	1	9	11	0.947	1	1	0.985	1	1	21.21	3.26	9	11	3312	358.0	6.68
21070997	stromal interaction molecule 1 isoform 2 precursor [Homo sapiens]	7.01	2	1	4	20	0.946	1	1	1.053	1	10	194.62	7.01	10	20	685	77.4	6.57
7657647	trigomulin-2 isoform a [Homo sapiens]	8.55	1	1	3	15	0.946	1	1	1.103	1	1							

Accession	Description	LCoverage	#F Proteins	#F Unique Peptides	#F Peptides	#F PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
530414204	PREDICTED: asparagine--tRNA ligase, cytoplasmic isoform X1 [Homo sapiens]	1.46	2	1	1	3	0.939	1		1.499			46.87	1.46	3	3	547	62.8	6.25	
42239885	cytoplasmic dynein 1 intermediate chain 2 isoform 1 [Homo sapiens]	13.64	53	2	6	24	0.939	2	23.0	1.255	2	26.0	309.88	13.64	13	24	638	71.4	5.20	
38327558	interferon-induced guanylate-binding protein 2 [Homo sapiens]	11.60	1	1	6	19	0.938	1		1.626			112.39	11.60	13	19	591	69.2	5.71	
205360947	protein-methionine sulfoxide oxidase MICAL1 isoform 1 [Homo sapiens]	9.18	3	2	9	48	0.938	4		3.2	1.255	4	20.8	665.23	9.18	15	48	1067	117.8	6.40
38505161	tudor domain-containing protein 1 [Homo sapiens]	7.06	3	1	9	31	0.938	5	2.7	1.188	3	18.1	87.39	7.06	17	31	1189	132.8	6.46	
530373793	PREDICTED: multidrug resistance-associated protein 5 isoform X1 [Homo sapiens]	7.03	82	1	8	15	0.938	1		1.215			32.08	7.03	12	15	1437	160.6	8.66	
57880858	PREDICTED: NEDO4-binding protein 2 isoform X2 [Homo sapiens]	1.36	8	1	4	39	0.938	6	11.1	1.153	5	8.9	447.14	1.36	8	39	1690	189.7	5.25	
530375309	PREDICTED: polyhomocytic-like protein 3 isoform X3 [Homo sapiens]	0.56	6	1	1	3	0.938	1		1.254			43.08	0.56	3	3	897	96.5	7.27	
530362657	PREDICTED: zinc finger and SCAN domain-containing protein 16 isoform X2 [Homo sapiens]	10.26	2	1	2	3	0.937	1		24.23	10.26	1	2	10.26	2	3	195	22.7	6.71	
15431733	casepase 1 isoform delta [Homo sapiens]	13.11	5	4	12	1	0.937	4	9.1	1.264	1	3.4	252.92	13.31	4	12	243	29.8	7.91	
13129048	SOSS complex subunit B1 [Homo sapiens]	3.32	1	1	1	1	0.937	1		1.153			26.30	3.32	1	1	211	22.3	9.06	
289547631	leukocyte immunoglobulin-like receptor subfamily A member 3 isoform 1 precursor [Homo sapiens]	29.16	48	5	10	46	0.936	10	13.3	1.153	10	25.8	1498.75	29.16	28	46	439	47.4	8.09	
18104948	60S ribosomal protein L21 [Homo sapiens]	4.38	1	1	1	2	0.936	1		1.265			42.27	4.38	2	2	160	18.6	10.49	
167614502	protein phosphatase 1 regulatory subunit 3A [Homo sapiens]	4.19	2	1	6	23	0.936	2	14.4	1.053	2	3.5	66.29	4.19	10	23	1122	125.7	5.00	
530427505	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X3 [Homo sapiens]	9.02	8	5	7	16	0.936	5	4.7	1.194	5	3.7	281.73	9.02	15	16	676	72.1	8.82	
530382158	PREDICTED: sorbin B1 isoform X1 [Homo sapiens]	8.51	7	2	3	12	0.936	2	6.9	1.101	2	6.5	327.08	8.51	9	12	376	42.4	5.86	
42544123	splicing factor 1 isoform 3 [Homo sapiens]	4.93	11	1	2	6	0.936	1		1.222			79.20	4.93	6	6	548	59.7	9.50	
13129018	gamma-glutamylcyclotransferase [Homo sapiens]	15.96	2	1	3	7	0.936	1		1.011			200.71	15.96	7	7	188	21.0	5.14	
115387104	4-trimethylaminobutyraldehyde dehydrogenase [Homo sapiens]	9.65	1	1	5	31	0.935	1		1.166			271.57	9.65	13	31	518	56.3	6.57	
530393716	PREDICTED: S-adenosylmethionine synthase isoform type-1 isoform X2 [Homo sapiens]	5.93	3	1	3	7	0.935	1		1.140			36.24	5.93	6	7	354	39.1	6.33	
530400856	PREDICTED: centrosomal protein of 290 kDa isoform X4 [Homo sapiens]	9.06	5	1	23	38	0.935	1		1.126			72.34	9.06	23	38	2009	234.7	6.51	
21487129	nucR domain-containing protein 2 [Homo sapiens]	5.92	1	2	4	9	0.935	1		1.139			55.67	5.92	4	4	157	17.7	5.07	
41327773	probable ATP-dependent RNA helicase DDX46 [Homo sapiens]	12.42	19	1	16	56	0.935	1		1.527			234.33	12.42	30	56	1031	117.3	9.29	
33286420	pyruvate kinase PKM isoform b [Homo sapiens]	79.47	23	2	47	1015	0.934	3	0.2	1.343	3	5.5	42000.52	79.47	139	1015	531	58.0	7.71	
225543097	platelet-activating factor acetylhydrolase IB subunit gamma [Homo sapiens]	7.36	1	1	1	3	0.934	1		0.949			93.42	7.36	3	3	231	25.7	6.84	
4826686	ATP-dependent RNA helicase DDX1 [Homo sapiens]	7.84	1	1	6	23	0.934	2	20.7	1.150	1		436.62	7.84	13	23	740	82.4	7.23	
530423920	PREDICTED: zinc finger homeobox protein 1 isoform X1 [Homo sapiens]	1.70	3	1	7	14	0.934	1		1.226			28.12	1.70	7	14	3702	404.0	6.21	
530423421	PREDICTED: serine/threonine-protein kinase 24 isoform X3 [Homo sapiens]	1.71	4	1	1	21	0.933	1		0.834			111.77	1.71	3	3	333	36.8	5.88	
4824952	26S proteasome non-ATPase regulatory subunit 5 isoform 1 [Homo sapiens]	19.05	3	3	7	29	0.933	3	10.0	1.562	3	19.6	290.94	19.05	16	29	504	58.2	5.48	
578804127	PREDICTED: protein unc-89 homolog isoform X3 [Homo sapiens]	3.43	14	1	12	47	0.933	1		1.177			76.78	3.43	16	47	3319	369.7	6.95	
7657214	hormonally up-regulated neu tumor-associated kinase [Homo sapiens]	1.40	1	1	1	2	0.933	1		1.520			29.15	1.40	2	2	714	79.6	9.13	
214832050	dual specificity protein phosphatase 19 isoform 2 [Homo sapiens]	4.82	2	1	1	14	0.933	4	5.0	1.339	4	22.7	148.08	4.82	2	14	166	18.3	8.07	
578800886	PREDICTED: involutionin isoform X1 [Homo sapiens]	23.93	1	8	11	82	0.933	12	15.0	1.091	12	11.3	1202.63	23.93	29	82	585	68.4	4.61	
4506221	26S proteasome non-ATPase regulatory subunit 12 isoform 1 [Homo sapiens]	24.78	2	5	9	29	0.933	7		1.471			760.03	24.78	23	29	456	52.9	7.65	
112380626	lysosome-associated membrane glycoprotein 1 isoform X1 [Homo sapiens]	5.76	3	3	10	0.932	2	2	5.4	1.001	2	6	54.66	5.76	4	10	417	44.9	8.75	
4506631	60S ribosomal protein L30 [Homo sapiens]	28.70	2	1	6	6	0.932	2		1.576			80.4	101.25	28.70	6	115	12.8	9.63	
223278393	protein phosphatase 1 regulatory subunit 3G [Homo sapiens]	3.35	1	1	1	4	0.931	1		1.514			61.66	3.35	2	4	358	38.0	4.93	
530377639	PREDICTED: hydroxacyl-coenzyme A dehydrogenase, mitochondrial isoform X1 [Homo sapiens]	22.96	3	1	5	21	0.931	2	4.1	0.899	2	83.0	297.36	22.96	10	21	318	35.2	7.21	
154146262	IgGfC-binding protein precursor [Homo sapiens]	3.13	1	2	10	17	0.931	2	8.8	1.270	2	4.9	230.92	3.13	15	17	5405	571.6	5.34	
30181236	copine-2 [Homo sapiens]	7.30	18	2	3	21	0.931	2	9.8	1.323	2	12.7	635.35	7.30	9	21	548	61.2	6.07	
7105300	ubiquitin-fold modifier 1 isoform 1 precursor [Homo sapiens]	58.82	1	2	9	9	0.931	3	2.8	1.253	3	5.4	444.69	58.82	9	9	85	9.1	9.31	
578814449	PREDICTED: sodium/potassium/calcium exchanger 2 isoform X3 [Homo sapiens]	3.42	2	1	3	18	0.931	1		1.110			46.14	3.42	4	18	644	71.6	6.27	
348605285	TNFAIP3-interacting protein 3 isoform 1 [Homo sapiens]	4.07	2	1	3	13	0.931	1		3.207			29.77	4.07	5	13	369	44.1	7.61	
199559785	tRNA pseudouridine(38/39) synthase isoform 1 [Homo sapiens]	3.74	1	1	2	2	0.931	1		10.018			31.12	3.74	2	2	481	55.6	7.30	
269847098	phospholipase phosphohistidine inorganic pyrophosphatase isoform 1 [Homo sapiens]	9.63	3	2	2	4	0.930	1		1.251			73.85	9.63	4	4	270	29.1	6.15	
89191868	von Willebrand factor preproprotein [Homo sapiens]	6.33	1	5	12	41	0.930	1	6	1.274	1	16.3	384.40	6.33	26	41	2813	309.1	5.49	
6005757	FACT complex subunit SPT16 [Homo sapiens]	1.02	1	7	10	0.930	30	1		0.536			176.54	1.02	10	1047	119.8	5.66		
339895886	prospero homeobox protein 2 isoform 2 [Homo sapiens]	9.86	3	1	3	10	0.930	1		1.676			91.85	9.86	5	10	365	40.5	8.69	
578807065	PREDICTED: ceruloplasmin isoform X3 [Homo sapiens]	74.37	4	1	62	1095	0.929	1		1.127			37062.08	74.37	181	1095	1065	122.1	5.72	
262050538	inter-alpha-trypsin inhibitor heavy chain H4 isoform 2 precursor [Homo sapiens]	60.89	11	1	41	576	0.929	2	4.3	1.333	2	32.1	19563.32	60.89	122	576	900	99.8	6.47	
7706339	peptidyl-prolyl cis-trans isomerase-like 1 [Homo sapiens]	8.43	1	1	1	3	0.929	1		1.147			138.55	8.43	3	3	166	18.2	7.99	
358356407	60S ribosomal protein L15 isoform 2 [Homo sapiens]	4.83	2	1	1	2	0.928	1		1.489			49.43	4.83	2	2	145	16.7	11.53	
510785740	vacuolar protein sorting-associated protein 13D isoform 2 [Homo sapiens]	2.88	2	1	14	43	0.928	2		2.169			92.80	2.88	26	43	4363	488.8	6.55	
55749515	synectin-1 isoform 3 [Homo sapiens]	18.86	3	2	4	9	0.928	2	9.1	0.846	2	60.9	228.82	18.86	9	9	297	32.3	7.53	
4507131	small nuclear ribonucleoprotein F [Homo sapiens]	24.42	1	2	2	9	0.928	3		1.237	3	10.5	307.89	24.42	6	9	86	9.7	4.67	
223278387	calmodulin-like protein 5 [Homo sapiens]	33.56	1	4	13	0.927	2	1.9	1.9	1.118	2	15.5	246.71	33.56	9	13	146	15.9	4.44	
530410543	PREDICTED: 60S ribosomal protein L26 isoform X1 [Homo sapiens]	15.17	3	1	2	7	0.926	2	10.0	1.154	2	17.4	180.28	15.17	4	7	145	17.2	10.55	
4503269	deoxycytidine kinase 5 [Homo sapiens]	2.69	1	1	1	2	0.926	1		1.027			77.38	2.69	2	2	260	30.5	5.21	
530422603	PREDICTED: rho guanine nucleotide exchange factor 6 isoform X3 [Homo sapiens]	11.42	4	2	7	18	0.926	4	14.2	0.886	4	40.5	149.20	11.42	13	18	727	82.0	5.64	
402794208	poly(ADP-ribose) polymerase 1 isoform b [Homo sapiens]	9.22	6	3	21	229	0.926	2	9.22	1.229	2	68.7	331.26	9.22	27	49	599	54.0	5.33	
24497519	mannosyl-oligosaccharide 1,2-alpha-mannosidase 1A [Homo sapiens]	9.65	2	2	7	45	0.926	2	5.5	1.422	2	15.0	237.29	9.65	16	45	653	72.9	6.47	
40385883	ribulose-phosphate 3-epimerase isoform 1 [Homo sapiens]	54.82	6	6	26	0.925	7	4.3	1.123	6	21.8	1000.80	54.82	54.82	26	26	228	24.9	5.58	
284448551	NADH-cytochrome b5 reductase 3 isoform 3 [Homo sapiens]	5.39	3	1	2	2	0.924	1		1.077			27.56	5.39	2	2	334	38.2	6.90	
530412644	PREDICTED: sodium channel protein type 4 subunit alpha isoform X1 [Homo sapiens]	1.58	1	3	12	0.924	1			0.812			30.18	1.58	3	12	1836	207.9	5.10	
510785740	integrin-linked protein kinase isoform 2 [Homo sapiens]	5.12	2	1	2	4	0.923	1		0.970			112.48	5.12	4	4	391	44.3	7.97	
58001359	complement C1q-like protein 3 precursor [Homo sapiens]	3.53	1	1	10	0.923	1	2	1.5	1.554	2	11.6	72.91	3.53	10	255	28.7	6.79		
83582815	comf-8 [Homo sapiens]	37.08	2	2	2	7	0.923	2	11.0	1.041	2	2.4	195.00	37.08	6	7	89	9.9	8.48	
530395458	PREDICTED: PHD finger protein 21A isoform X9 [Homo sapiens]	3.34	6	1	3	9	0.923	1		1.117			62.89	3.34	5	9				

Accession	Description	2Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
53190811	ubiquitin-conjugating enzyme E2 A isoform 4 [Homo sapiens]	10.08	3	1	2	3	0.908	1		1.355	1		33.37	10.08	3	3	119	13.6	4.75
151301228	pre-mRNA-processing factor 40 homolog A [Homo sapiens]	1.51	4	1	2	4	0.906	1		0.977	1		148.50	1.51	4	4	930	105.9	7.99
578085786	PREDICTED: histyl-ubiquitin-ubiquitinase isoform X4 [Homo sapiens]	6.12	2	1	1	3	0.906	1		1.260	1		110.77	6.12	3	3	147	16.6	7.08
239735492	transcriptional activator Myb isoform 5 [Homo sapiens]	8.86	3	1	8	86	0.906	2	0.7	1.417	2	12.6	83.33	8.86	16	86	745	83.6	7.24
530366140	PREDICTED: protein lin-9 homolog isoform X1 [Homo sapiens]	1.63	1	1	1	2	0.905	1		2.746	1		24.78	1.63	2	2	615	70.0	9.67
578824446	PREDICTED: mitochondrial inner membrane protease ATP23 homolog isoform X2 [Homo sapiens]	6.49	2	1	2	5	0.905	1		1.250	1		33.34	6.49	2	5	185	21.3	7.56
4505215	interstitial collagenase isoform 1 preproprotein [Homo sapiens]	10.87	2	2	5	9	0.902	2	15.6	1.095	2	37.5	125.48	10.87	8	9	469	54.0	6.96
530360517	PREDICTED: serine/threonine-protein kinase mTOR isoform X1 [Homo sapiens]	1.73	2	1	6	13	0.902	1		0.914	1		42.42	1.73	6	13	2549	288.7	7.17
296531459	band 4.1-like protein 5 isoform 2 [Homo sapiens]	6.57	6	1	4	34	0.902	1		1.273	1		27.71	6.57	4	34	687	77.5	6.79
93252551	CMP19-like protein 1 [Homo sapiens]	10.5	1	1	11	234	0.901	2	10.5	1.234	2	28.7	273.21	9.67	11	938	480.6	7.24	
530367362	PREDICTED: IGF-containing fibulin-like extracellular matrix protein 1 isoform X2 [Homo sapiens]	7.55	2	3	4	11	0.901	3	4.3	1.098	3	1.6	352.53	7.55	11	11	543	59.3	7.74
5031815	lysine-tRNA ligase isoform 2 [Homo sapiens]	8.88	2	2	5	27	0.900	2	13.5	1.460	2	3.5	197.38	8.88	27	597	68.0	6.35	
23238231	high mobility group nucleosome-binding domain-containing protein 3 isoform HMGN3b [Homo sapiens]	19.48	7	1	1	16	0.900	3	6.0	1.164	3	9.4	362.67	19.48	3	16	77	8.4	10.26
530382432	PREDICTED: dystonin isoform X8 [Homo sapiens]	4.37	52	1	41	115	0.899	1		0.990	1		188.43	4.37	60	115	7709	875.1	5.35
4758226	transcription factor E2f2 [Homo sapiens]	2.29	1	1	1	2	0.899	1	1	1.237	1	1	25.07	2.29	1	2	437	47.5	4.87
96304457	low molecular weight phosphotyrosine protein phosphatase isoform d [Homo sapiens]	16.07	2	1	1	3	0.899	1	1	1.392	1	3	263.79	16.07	3	3	112	12.2	7.74
530423350	PREDICTED: Importin-5 isoform X2 [Homo sapiens]	6.91	1	6	12	0.899	1	1		1.342	1		183.76	6.91	9	12	1115	125.5	4.92
33188456	ubiquitin-conjugating enzyme E2 D2 isoform 2 [Homo sapiens]	29.66	7	2	2	6	0.897	2	21.3	1.130	1		141.77	29.66	4	6	118	13.6	8.29
5453994	double-strand-break repair protein rad21 homolog [Homo sapiens]	4.91	1	2	3	10	0.897	2	22.2	0.868	2	18.0	322.64	4.91	9	10	631	71.6	4.65
6912638	ras suppressor protein 1 isoform 1 [Homo sapiens]	26.71	3	3	5	15	0.897	4	16.9	1.200	4	23.2	485.10	26.71	12	15	277	31.5	8.25
528524494	dynein light chain roadblock-type 1 isoform b [Homo sapiens]	19.05	7	1	1	3	0.896	1	1	1.275	1		163.34	19.05	3	3	633	73.7	7.65
54792150	zinc finger protein 473 [Homo sapiens]	1.44	1	1	5	12	0.893	1		0.893	1		26.20	1.44	12	871	100.1	6.71	
17105394	60S ribosomal protein L23a [Homo sapiens]	12.18	1	1	2	3	0.895	1	1	1.121	1		43.80	12.18	3	3	156	17.7	10.45
149944590	SRR1-like protein [Homo sapiens]	5.31	1	2	2	2	0.895	1		1.188	1		28.01	5.31	2	2	339	38.5	5.41
17158039	histone deacetylase 9 isoform 1 [Homo sapiens]	3.07	4	1	5	9	0.895	1		14.781	1		29.14	3.07	7	9	1011	111.2	6.89
530418521	PREDICTED: zinc finger SWIM domain-containing protein 1 isoform X2 [Homo sapiens]	1.03	1	1	1	1	0.894	1	1	1.142	1		29.47	1.03	1	1	485	55.0	7.42
4507947	tyrosine-tRNA ligase, cytoplasmic [Homo sapiens]	8.90	1	2	4	9	0.892	2	9.7	0.994	2	6.9	160.71	8.90	9	528	59.1	7.05	
56487420	transcription factor BTF3 homolog 4 isoform 1 [Homo sapiens]	24.48	1	1	2	10	0.891	1		2.205	1		58.08	24.48	4	4	156	17.3	6.35
551729022	ubiquitin carboxyl-terminal hydrolase 7 isoform 3 [Homo sapiens]	11.06	3	1	11	30	0.890	1		1.209	1		209.54	13.06	19	30	1003	116.9	5.90
9506363	SAM and SH3 domain-containing protein 3 [Homo sapiens]	4.21	2	1	1	5	0.889	2	9.3	1.267	2	17.5	141.11	4.21	3	5	380	41.6	5.27
396578115	IQ and AAA domain-containing protein 1 isoform 1 [Homo sapiens]	6.91	3	1	6	18	0.889	1		2.101	1		28.82	6.91	6	18	781	90.4	9.33
565324221	calcium-binding protein 39-like [Homo sapiens]	15.73	1	1	7	44	0.888	1		1.452	1		241.01	15.73	15	44	337	39.1	8.40
19913446	neuron-specific calcium-binding protein hippocalcin [Homo sapiens]	4.15	3	1	1	3	0.886	1	1		1		56.66	4.15	3	3	193	22.4	4.97
578804386	PREDICTED: septin-2 isoform X10 [Homo sapiens]	26.80	6	1	5	9	0.885	1		1.305	1		161.72	26.80	7	9	194	22.6	6.55
530389882	PREDICTED: kinesin-like protein KIF24 isoform X2 [Homo sapiens]	1.19	2	1	2	3	0.885	1	1	1.367	1	2	43.21	1.19	4	3	1007	110.4	7.53
194306543	oxidation resistance protein 1 isoform 2 [Homo sapiens]	2.50	11	1	2	4	0.883	1		0.941	1		109.60	2.50	4	4	839	93.7	5.19
578823270	PREDICTED: oxysterol-binding protein-related protein 8 isoform X6 [Homo sapiens]	6.38	5	1	6	22	0.883	1		0.814	1		130.93	6.38	10	22	847	96.9	7.55
124256474	diacylglycerol kinase gamma isoform 2 [Homo sapiens]	3.52	3	1	3	3	0.883	1	1	1.423	1		21.02	3.52	3	3	766	86.2	6.65
530384769	PREDICTED: integrin beta-8 isoform X2 [Homo sapiens]	5.36	2	1	5	17	0.882	1		1.118	1		67.90	5.36	10	17	634	71.2	7.68
578816120	PREDICTED: sperm-associated antigen 1 isoform X2 [Homo sapiens]	5.09	21	1	6	19	0.880	2	1.4	1.047	2	1.6	184.11	5.09	14	19	884	98.8	6.87
14150098	transmembrane protein 79 [Homo sapiens]	2.01	1	1	4	20	0.880	1		0.880	1		49.68	2.01	2	4	394	43.5	4.93
578803150	PREDICTED: exportin-1 isoform X5 [Homo sapiens]	6.97	5	3	6	15	0.879	3	21.6	1.622	3	1.0	203.56	6.97	14	15	904	104.1	5.78
118572606	hemicentin-1 precursor [Homo sapiens]	1.22	1	7	16	0.879	1	1		1.517	1		34.40	1.22	7	16	5635	613.0	6.49
530403141	PREDICTED: mirror-image polyductyl gene 1 protein isoform X2 [Homo sapiens]	3.29	3	1	2	14	0.878	4	5.2	1.847	4	13.7	111.74	3.29	6	14	365	42.6	6.05
530396574	PREDICTED: C2 domain-containing protein 3 isoform X5 [Homo sapiens]	1.79	6	1	4	27	0.878	7	3	6.92	3	0.8	218.53	1.79	8	27	1676	186.3	8.40
56550081	mitotic checkpoint protein BUB3 isoform b [Homo sapiens]	9.20	2	2	4	11	0.877	2	24.3	1.171	2	20.8	92.58	9.20	8	11	326	36.9	6.84
153791662	colled-coil domain-containing protein 7 [Homo sapiens]	4.22	7	1	7	426	0.876	1		1.426	1		22.57	4.22	7	4	447	49.6	11.80
525313660	24-hydroxycholesterol 7-alpha-hydroxylase isoform 3 [Homo sapiens]	3.70	5	1	2	11	0.875	1		0.974	1		141.91	3.70	5	11	297	34.5	8.37
545478755	protein arginine N-methyltransferase 5 isoform f [Homo sapiens]	11.16	6	1	4	6	0.875	1		1.633	1		210.98	11.16	6	6	466	53.5	6.14
530361637	PREDICTED: splicing factor 3A subunit 3 isoform X1 [Homo sapiens]	5.13	2	1	2	6	0.874	1		1.102	1		62.09	5.13	4	6	448	52.4	5.27
530411988	PREDICTED: granulin isoform X1 [Homo sapiens]	20.91	1	7	9	53	0.874	18	8.9	1.180	18	15.0	1500.57	20.91	21	53	593	63.5	6.83
565324225	tyrosine-protein kinase BTK isoform 3 [Homo sapiens]	9.38	3	1	6	9	0.874	1		1.582	1		35.41	9.38	7	9	693	79.9	7.46
45042497	histone H3.1 [Homo sapiens]	58.82	3	1	11	112	0.874	3	7.2	1.018	1		1749.57	58.82	33	112	136	15.4	11.32
530386428	PREDICTED: myosin regulatory light chain 10 isoform X1 [Homo sapiens]	25.85	1	1	3	7	0.873	1		1.137	1		133.93	25.85	7	7	147	16.9	4.70
242117893	apoptosis regulator BAX isoform sigma [Homo sapiens]	7.26	4	1	3	0.863	1	3		1.337	1		115.17	7.26	3	3	179	19.7	5.40
4506699	40S ribosomal protein S21 [Homo sapiens]	10.84	1	1	1	3	0.861	1		1.336	1		48.68	10.84	3	3	83	9.1	8.50
4759264	COP9 signalosome complex subunit 2 isoform 1 [Homo sapiens]	13.09	2	1	5	8	0.860	1		1.628	1		350.20	13.09	7	8	443	51.6	5.53
5729999	ras-related GTP-binding protein A [Homo sapiens]	15.34	26	2	6	48	0.859	2	17.0	1.167	2	9.8	663.87	15.34	16	48	313	36.5	7.72
167808516	ar-GAP with coiled-coil, ARK repeat and PH domain-containing protein 2 [Homo sapiens]	11.06	3	2	7	26	0.859	3	2	27.5	3	12.4	327.46	11.06	15	26	778	88.0	6.80
26134906	neurabin 1 isoform 5 [Homo sapiens]	7.34	5	1	6	16	0.858	1		1.127	1		27.79	7.34	5	16	1090	122.3	5.15
157671917	colled-coil domain-containing protein 178 isoform 2 [Homo sapiens]	6.88	2	1	7	23	0.856	2		1.168	1		28.49	6.88	7	23	829	97.5	6.25
157694524	plexin-D1 precursor [Homo sapiens]	2.18	1	1	5	18	0.855	1		1.215	1		44.21	2.18	5	18	1925	211.9	7.20
301601630	LIM and senescent cell antigen-like-containing domain protein 1 isoform b [Homo sapiens]	6.77	12	1	2	4	0.853	1		1.334	1		137.90	6.77	4	4	325	37.2	8.05
4505501	oxidized low-density lipoprotein receptor 1 isoform 1 [Homo sapiens]	8.79	3	2	2	4	0.852	2	36.2	2.645	2	89.7	189.19	8.79	4	4	273	30.9	7.28
10864011	sulfide:quinone oxidoreductase, mitochondrial [Homo sapiens]	7.78	1	1	3	4	0.851	1		1.716	1		20.31	7.78	3	4	450	49.9	9.11
530367595	PREDICTED: latent-transforming growth factor beta-binding protein 1 isoform X5 [Homo sapiens]	3.93	11	1	6	18	0.851	1		1.244	1		48.34	3.93	10	18	1247	134.0	7.50
4885099	carbonic anhydrase 3 [Homo sapiens]	13.85	1	2	4	0.850	1	4		1.126	4		47.70	13.85	4	4	260	29.5	7.34
33457348	UPF056 protein C19orf10 precursor [Homo sapiens]	11.56	1	2	2	8	0.847	3	23.5	1.176	3	13.8	201.68	11.56	5	8	173	18.8	6.68
221136806	putative zinc finger CCHC domain-containing protein 18 [Homo sapiens]	3.47	1	2	2	10	0.842	2	2.3	1.132	2	5.0	32.29						

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
578820587	PREDICTED: paired box protein Pax-6 isoform X8 [Homo sapiens]	3.94	1	1	1	3	0.616	1		1.243	1		22.51	3.94	1	3	355	39.2	9.23
300360487	protein canapoy homolog 2 isoform 2 precursor [Homo sapiens]	19.05	2	1	1	3	0.601	1		1.245	1		84.44	19.05	3	3	84	9.1	7.30
578801667	PREDICTED: major facilitator superfamily domain-containing protein 1 isoform X1 [Homo sapiens]	6.11	4	1	3	3	0.588	1		1.050	1		31.80	6.11	3	3	475	51.7	7.36
530391566	PREDICTED: terminal uridylyltransferase 7 isoform X4 [Homo sapiens]	6.59	87	1	11	22	0.494	1		1.068	1		36.90	6.59	11	22	1381	157.7	6.47
94536743	protein DDIX26B [Homo sapiens]	8.71	4	1	8	17	0.479	1					21.17	8.71	10	17	861	96.6	8.73
530378724	PREDICTED: dynein heavy chain 5, axonemal isoform X1 [Homo sapiens]	4.08	47	3	24	198	0.478	5	20.3	1.052	5	10.8	1021.39	4.08	46	198	4609	526.8	6.01
13430848	nuclear receptor subfamily 1 group D member 1 [Homo sapiens]	3.75	1	1	3	4	0.477	1		4.626			24.84	3.75	3	4	614	66.8	8.50
530384633	PREDICTED: uncharacterized protein KIA0895 isoform X3 [Homo sapiens]	5.82	1	1	2	134	0.471	1		1.099	1		152.73	5.82	4	134	275	32.1	7.84
218050779	protocadherin-15 isoform CD1-6 precursor [Homo sapiens]	0.90	8	1	2		0.433	1		1.309	1		42.47	0.90	4	6	1886	208.2	5.11
297203791	fibrous sheath interacting protein 2 [Homo sapiens]	4.26	30	1	32	73							109.07	4.26	45	73	4996	789.4	6.48
353390331	kinesin-like protein KIF21B isoform 4 [Homo sapiens]	6.40	59	2	15	116							916.71	6.40	31	116	1610	179.6	7.09
359718912	probable E3 ubiquitin-protein ligase HECTD4 [Homo sapiens]	2.73	1	1	13	48							54.90	2.73	23	48	4284	469.7	6.15
5453908	phosphatidylinositol transfer protein alpha isoform [Homo sapiens]	6.67	1	1	2	5							192.87	6.67	5	5	270	31.8	6.55
255652953	zinc finger CCH domain-containing protein 18 isoform 2 [Homo sapiens]	0.84	2	1	1	2							27.93	0.84	2	2	953	106.3	8.32
62955803	nucleoporin NUP188 homolog [Homo sapiens]	2.12	3	1	4	13							66.71	2.12	10	13	1749	195.9	6.73
67782362	ATP-dependent RNA helicase DHX29 [Homo sapiens]	3.29	35	1	6	20							150.84	3.29	14	20	1349	155.1	8.09
20070266	GTP-binding protein REM 1 [Homo sapiens]	5.37	6	2	2	7							88.87	5.37	5	7	298	32.9	8.79
222537743	phosphatidylinositol phosphatase PTPRO precursor [Homo sapiens]	1.70	7	1	6	167							347.73	1.70	10	167	2299	257.1	5.73
47578107	nipped-B-like protein isoform B [Homo sapiens]	5.90	7	1	20	74							494.34	5.90	33	74	2697	304.2	7.81
126116589	fibrocystin-L precursor [Homo sapiens]	0.78	3	1	5	17							124.78	0.78	9	17	4243	465.4	6.11
50428940	mediator of RNA polymerase II transcription subunit 25 [Homo sapiens]	0.80	1	1	1	2							31.57	0.80	2	2	747	78.1	8.34
229862308	shugoshin-like 2 isoform 2 [Homo sapiens]	3.65	5	1	6	11							39.27	3.65	10	11	1260	143.9	7.68
4758302	enhancer of rudimentary homolog [Homo sapiens]	5.77	1	1	1	3							78.86	5.77	3	3	104	12.3	5.92
242332527	uncharacterized protein CSorF42 [Homo sapiens]	2.38	6	1	9	19							55.85	2.38	13	19	3197	361.5	6.99
27734719	thiamine transporter 1 [Homo sapiens]	3.62	12	1	2	5							74.91	3.62	4	5	497	55.4	6.74
28827813	NACHT, LRR and PYD domains-containing protein 14 [Homo sapiens]	3.75	2	1	5	27							30.82	3.75	9	27	1093	124.7	6.61
546232151	phosphatidylinositol transfer protein beta isoform 2 [Homo sapiens]	13.60	3	1	5	16							189.66	13.60	12	16	272	31.6	6.25
530380645	PREDICTED: STB/POZ domain-containing protein KCTD16 isoform X1 [Homo sapiens]	6.54	4	1	4	6							46.61	6.54	6	6	428	49.1	8.09
21359947	propep domain-containing protein 3 [Homo sapiens]	2.75	1	1	1	3							43.99	2.75	3	3	291	33.8	7.96
578807537	PREDICTED: serine/threonine-protein phosphatase 2A regulatory subunit B" subunit alpha isoform [Homo sapiens]	3.48	3	1	3	8							26.49	3.48	4	8	1150	130.2	5.21
51896037	G protein-coupled receptor kinase 6 isoform C [Homo sapiens]	4.64	3	1	3	10							75.28	4.64	5	10	560	64.3	8.44
7019435	interleukin-17C precursor [Homo sapiens]	3.05	1	1	1	2							23.75	3.05	2	2	197	21.8	8.12
578814066	PREDICTED: filamin-C isoform X1 [Homo sapiens]	3.99	3	1	12	78							1949.40	3.99	30	78	2632	281.4	6.04
530369681	PREDICTED: striated muscle preferentially expressed protein kinase isoform X2 [Homo sapiens]	3.43	23	1	14	26							35.42	3.43	18	26	3206	347.6	8.50
578836045	PREDICTED: ubiquinol-cytochrome-c reductase complex assembly factor 1 isoform X1 [Homo sapiens]	2.27	10	1	1	9							158.37	2.27	3	9	220	25.0	9.77
530363589	PREDICTED: zinc finger MYM-type protein 4 isoform X1 [Homo sapiens]	6.25	11	1	8	61							42.14	6.25	11	61	1551	173.0	6.79
578817778	PREDICTED: serine/threonine-protein kinase WNK2 isoform X10 [Homo sapiens]	1.03	11	1	3	8							81.77	1.03	6	8	2227	234.8	5.87
530390571	PREDICTED: nucleoredoxin-like protein 2 isoform X2 [Homo sapiens]	4.32	1	1	2	10							48.17	4.32	4	10	139	15.5	7.03
578819920	PREDICTED: polycomb group RING finger protein 5 isoform X5 [Homo sapiens]	5.26	22	1	2	7							90.99	5.26	5	7	190	22.0	5.76
530384400	PREDICTED: nucleotide-binding oligomerization domain-containing protein 1 isoform X9 [Homo sapiens]	5.96	56	1	7	32							242.18	5.96	11	32	705	79.4	8.29
530424332	PREDICTED: epithelial splicing regulatory protein 2 isoform X2 [Homo sapiens]	4.05	2	1	4	8							78.34	4.05	8	8	716	77.2	6.83
530387276	PREDICTED: WD repeat-containing protein 60 isoform X1 [Homo sapiens]	3.42	3	1	4	16							34.28	3.42	7	16	878	98.7	6.86
578822940	PREDICTED: protein asaurin homolog isoform X4 [Homo sapiens]	5.23	2	1	4	10							30.29	5.23	6	10	631	71.9	6.62
530363232	PREDICTED: synaptonemal complex protein 1 isoform X4 [Homo sapiens]	6.30	8	1	8	21							53.86	6.30	15	21	921	107.6	5.69
88703062	40S ribosomal protein S4, Y isoform 2 [Homo sapiens]	2.28	1	1	1	2							47.10	2.28	1	2	263	29.3	10.08
323510690	serine/threonine-protein kinase Nek2 isoform 2 [Homo sapiens]	7.29	4	1	4	5							37.68	7.29	4	5	384	44.9	8.41
578806449	PREDICTED: protein SEC13 homolog isoform X6 [Homo sapiens]	5.19	6	1	2	2							29.21	5.19	2	2	308	34.0	5.72
53831195	splicing factor 3A subunit 1 isoform 2 [Homo sapiens]	5.36	2	1	5	10							29.61	5.36	5	10	728	81.6	5.34
578811795	PREDICTED: exocyst complex component 2 isoform X1 [Homo sapiens]	5.52	1	1	6	44							51.17	5.52	8	44	924	104.0	6.90
295789158	sodium-dependent phosphate transport protein 2B isoform b [Homo sapiens]	4.06	2	1	4	5							22.14	4.06	4	5	689	75.5	8.27
41581463	formin-binding protein 1-like isoform 2 [Homo sapiens]	11.52	4	1	7	39							26.00	11.52	7	39	547	63.5	6.19
222352143	TBC1 domain family member 2A isoform 2 [Homo sapiens]	3.49	3	1	3	4							29.00	3.49	3	4	917	104.0	6.46
9068681	cysteinyl leukotriene receptor 2 [Homo sapiens]	4.34	1	1	2	11							21.69	4.34	2	11	346	39.6	9.55
189409140	isoleucine repeat-binding factor 1 isoform 2 [Homo sapiens]	7.40	7	1	4	7							51.50	7.40	4	7	419	48.2	6.62
22027514	cell division cycle-associated protein 7 isoform 2 [Homo sapiens]	7.55	5	0	4	31							66.20	7.55	7	31	371	42.5	9.45
530416714	PREDICTED: prostate tumor-overexpressed gene 1 protein isoform X1 [Homo sapiens]	6.50	1	1	3	8							22.29	6.50	4	8	431	47.8	9.88
530372667	PREDICTED: plexin-B1 isoform X3 [Homo sapiens]	2.23	3	1	4	13							47.39	2.23	4	13	1211	135.1	6.33
530373023	PREDICTED: CUB domain-containing protein 1 isoform X1 [Homo sapiens]	2.99	2	1	4	6							32.20	2.99	4	6	770	86.0	7.64
95770876	neurogenic locus notch homolog protein 4 preproprotein [Homo sapiens]	0.75	1	1	3	4							24.41	0.75	3	4	2003	209.5	5.73
222352168	protein ANKUB1 [Homo sapiens]	0.92	1	1	1	1							20.17	0.92	1	1	544	61.2	9.20
578832581	PREDICTED: zinc finger protein 532 isoform X14 [Homo sapiens]	2.45	14	1	4	6							40.63	2.45	4	6	1060	114.0	8.54

Appendix B

iTRAQ Set 2

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
13256532	dual oxidase 2 precursor [Homo sapiens]	0.52	35	1	2	4	1.755	1		1.196	1		84.85	0.52	4	4	1548	175.3	7.85
578806381	PREDICTED: kinesin-like protein KIF15 isoform X2 [Homo sapiens]	1.40	31	1	2	3	1.711	1		2.833	1		46.01	1.40	3	3	1285	147.9	6.89
93204067	probable G-protein coupled receptor 158 precursor [Homo sapiens]	1.32	32	1	2	3	1.511	1		1.597	1		39.60	1.32	3	3	1215	135.4	8.28
612407822	carcinoembryonic antigen-related cell adhesion molecule 6 prepropeptide [Homo sapiens]	2.97	1	1	2	1.427	1	1		1.125	1		64.52	2.97	2	2	344	37.2	5.82
55783849	ubiquitin-fold modifier 1 isoform 2 [Homo sapiens]	42.17	3	1	1	3	1.415	1		1.088	1		200.01	42.17	3	3	83	8.9	9.31
57813594	PREDICTED: actin, cytoplasmic 1 isoform X1 [Homo sapiens]	95.26	1	1	23	2814	1.414	1		1.324	1		133155.76	95.26	67	2814	253	28.2	5.34
17865802	vacuolar protein sorting-associated protein 4B [Homo sapiens]	5.18	1	1	1	2	1.349	1			100.74	5.18	2	2	444	49.3	7.23		
530416619	PREDICTED: sodium/potassium-transporting ATPase subunit alpha [Homo sapiens]	0.63	1	1	1	2	1.334	1		1.392	1		29.40	0.63	2	2	1261	136.8	6.05
27501446	density-regulated protein [Homo sapiens]	9.09	1	1	1	3	1.331	1		1.212	1		213.48	9.09	3	3	198	22.1	5.30
14790190	msx2-interacting protein [Homo sapiens]	0.14	1	1	1	3	1.271	2		2.977	2		19.72	0.14	2	3	3664	402.0	7.64
28372531	serine/threonine-protein phosphatase 4 regulatory subunit 2 [Homo sapiens]	4.08	1	1	1	1	1.443	1		1.443	1		44.84	4.08	1	1	417	46.9	4.54
194473714	latenin [Homo sapiens]	4.50	1	1	1	2	1.259	1		0.901	1		39.36	4.50	2	2	222	25.7	5.78
57817959	PREDICTED: collagen alpha-1(OXIII) chain isoform X3 [Homo sapiens]	0.74	4	1	1	8	1.259	4			5.2	31.2	93.93	0.74	2	8	1087	107.8	7.85
14249614	synaptotagmin-like protein 1 isoform 2 [Homo sapiens]	4.55	9	2	2	4	1.245	1		1.152	4		172.61	4.55	4	4	550	60.6	5.48
4507131	small nuclear ribonucleoprotein F [Homo sapiens]	15.12	1	1	1	3	1.230	1		1.133	1		218.00	15.12	3	3	86	9.7	4.67
578836735	PREDICTED: protein dopey-2 isoform X1 [Homo sapiens]	0.44	51	1	2	4	1.220	1		0.645	1		44.37	0.44	4	4	2298	258.1	6.29
21361322	tubulin beta-4A chain isoform 3 [Homo sapiens]	53.15	6	1	16	139	1.189	1		1.178	1		5325.57	53.15	44	139	444	49.6	4.88
530422607	PREDICTED: rho guanine nucleotide exchange factor 6 isoform X5 [Homo sapiens]	2.25	4	1	1	1	1.172	1		1.096	1		26.38	2.25	1	1	622	70.7	6.55
4885099	carbonic anhydrase 3 [Homo sapiens]	3.46	1	1	1	3	1.169	1		1.014	1		87.97	3.46	3	3	260	29.5	7.35
578810535	PREDICTED: transcription factor 7 isoform X10 [Homo sapiens]	2.33	72	1	1	2	1.162	1		2.079	1		27.87	2.33	2	2	258	28.8	9.84
211050425	small integral membrane protein 24 precursor [Homo sapiens]	0.34	1	1	1	3	1.161	1		1.247	1		109.38	0.34	3	3	130	15.0	5.20
116734849	glycogen debranching enzyme isoform 2 [Homo sapiens]	1.52	3	2	2	7	1.159	3		0.962	3		316.88	1.52	4	7	1515	172.5	6.71
40549451	lymphatic vessel endothelial hyaluronate acid receptor 1 precursor [Homo sapiens]	2.80	1	1	1	2	1.154	1		1.388	2		46.78	2.80	2	2	322	35.2	8.28
392494084	eukaryotic translation initiation factor 6 isoform 3 [Homo sapiens]	23.67	2	2	2	8	1.152	3		6.0	1.046		438.89	23.67	6	8	245	26.6	4.68
530394359	PREDICTED: mini-chromosome maintenance complex-binding protein 1 [Homo sapiens]	1.36	3	1	1	1	1.151	1		1.099	1		31.94	1.36	1	1	587	66.5	5.95
46389562	alpha-endosulfine isoform 8 [Homo sapiens]	19.05	5	1	1	6	1.145	2		6.5	0.947		327.52	19.05	3	6	105	12.0	4.91
27886588	protein-tyrosine kinase 2-beta isoform b [Homo sapiens]	1.45	3	1	1	3	1.144	1		0.901	3		129.86	1.45	3	3	967	111.1	5.91
530406156	PREDICTED: uveal autoantigen with coiled-coil domains and ankyrin repeats [Homo sapiens]	0.72	5	1	1	1	1.140	1		1.454	1		22.10	0.72	1	1	1392	160.2	7.18
55749461	transcription elongation factor A protein-like 3 [Homo sapiens]	10.50	1	1	1	3	1.140	1		1.136	1		204.75	10.50	3	3	200	22.5	4.92
5803135	ras-related protein Rab-35 isoform 1 [Homo sapiens]	18.41	21	1	4	22	1.135	1		1.403	11		1079.99	18.41	22	201	23.0	6.89	
134152719	CUGBP Elav-like family member 2 isoform 4 [Homo sapiens]	10.66	17	2	2	4	1.133	2		1.427	2		234.03	10.66	4	4	488	52.0	8.60
47834348	minor histocompatibility protein HA-1 isoform 1 precursor [Homo sapiens]	2.02	5	2	2	8	1.133	3		3.2	0.950		216.85	2.02	6	8	1136	124.5	6.10
578815063	PREDICTED: tyrosine-protein kinase Sgk223 isoform X1 [Homo sapiens]	0.57	1	1	1	1	1.133	1		1.595	1		28.32	0.57	1	1	1406	149.5	7.20
386643034	protein NDRG1 isoform 3 [Homo sapiens]	4.47	3	1	1	3	1.128	1		1.001	3		169.55	4.47	3	3	313	33.6	6.44
298919181	nuclear receptor corepressor 1 isoform 3 [Homo sapiens]	0.21	11	1	1	2	1.125	1		0.863	1		16.70	0.21	2	2	2337	258.4	6.92
530423403	PREDICTED: tripeptidyl-peptidase 2 isoform X4 [Homo sapiens]	1.89	5	2	2	17	1.124	7		39.3	1.054		286.01	1.89	6	17	1162	128.1	6.77
530400854	PREDICTED: centrosomal protein of 290 kDa isoform X3 [Homo sapiens]	2.30	5	1	1	2	1.122	1		1.483	1		27.75	0.30	2	2	2353	275.6	6.10
5037111	eukaryotic translation initiation factor 1a [Homo sapiens]	26.58	2	2	2	4	1.122	2		7.0	1.191		407.90	26.58	4	6	113	12.8	7.37
354721719	ras-related protein Rab-5B isoform 2 [Homo sapiens]	0.71	5	2	4	15	1.122	2		8.8	1.021		621.10	0.71	12	15	174	19.1	7.30
117553580	AP-3 complex subunit delta-1 isoform 2 [Homo sapiens]	1.13	3	1	1	3	1.120	1		1.110	3		161.17	1.13	3	3	1153	130.1	8.48
14110414	heterogeneous nuclear ribonucleoprotein D0 isoform c [Homo sapiens]	29.41	9	1	9	40	1.119	2		17.1	1.129		1708.57	29.41	20	40	306	32.8	8.16
6912242	DCC-interacting protein 13-alpha [Homo sapiens]	3.53	1	1	1	2	1.117	1			79.86	3.53	2	2	709	79.6	5.41		
7662502	malignant T-cell-amplified sequence 1 isoform 1 [Homo sapiens]	19.34	2	2	2	4	1.116	2		22.1	0.881		307.93	19.34	6	6	181	20.5	8.82
578826489	PREDICTED: uncharacterized protein LOC102723683 [Homo sapiens]	2.55	1	1	1	1	1.116	1		1.003	1		27.21	2.55	1	1	353	38.0	9.60
282847388	uncharacterized protein C10orf62 [Homo sapiens]	3.14	1	1	1	1	1.115	1		1.365	1		25.08	3.14	1	1	223	25.1	7.59
578835493	PREDICTED: glycogen phosphorylase, brain form isoform X1 [Homo sapiens]	7.47	1	1	6	48	1.115	1		1.056	16		1923.36	7.47	48	843	96.6	6.86	
302699239	eukaryotic translation initiation factor 4 gamma 1 isoform 4 [Homo sapiens]	0.78	7	1	1	3	1.115	1		1.087	1		97.94	0.78	2	3	1404	154.8	5.16
578838913	PREDICTED: profilin subunit 3 isoform X1 [Homo sapiens]	6.25	2	1	1	1	1.114	1		1.087	1		27.08	6.25	1	1	192	22.2	6.60
10863895	thymosin beta-10 [Homo sapiens]	31.82	1	1	3	23	1.114	1		1.192	1		554.03	31.82	6	23	44	5.0	5.36
578817221	PREDICTED: FK506-binding protein 15 isoform X2 [Homo sapiens]	2.52	3	2	2	4	1.114	1		1.032	1		159.34	2.52	4	4	1151	126.7	5.20
4557663	immunoglobulin-binding protein 1 [Homo sapiens]	6.49	1	1	3	3	1.113	1		1.058	1		294.56	6.49	3	3	339	39.2	5.38
530367723	PREDICTED: HEAT repeat-containing protein 5B isoform X1 [Homo sapiens]	0.37	4	1	1	2	1.113	1		1.392	1		20.91	0.37	2	2	1881	203.3	7.08
530427505	PREDICTED: heterogeneous nuclear ribonucleoprotein M isoform X [Homo sapiens]	6.07	8	4	4	8	1.112	4		6.6	1.114		197.66	6.07	8	8	676	72.1	8.82
166706885	denatulin isoform 3 [Homo sapiens]	5.59	6	1	1	2	1.110	1		1.088	5		5.59	5.59	2	2	358	40.7	8.85
284695137	24S proteasome non-ATPase regulatory subunit 10 isoform 2 [Homo sapiens]	1.95	2	1	1	3	1.109	1		1.113	1		111.53	1.95	3	3	151	16.1	5.95
557786105	vacuolar fusion protein MORN1 homolog B isoform 3 [Homo sapiens]	1.50	1	1	1	2	1.109	2		10.5	2.746		29.56	1.50	1	2	401	44.2	9.10
522838244	angiotensin-like protein 2 isoform 3 [Homo sapiens]	2.32	4	1	1	1	1.109	1		1.003	1		28.22	2.32	1	1	777	85.4	7.18
530400550	PREDICTED: kinesin-like protein KIF21A isoform X9 [Homo sapiens]	1.00	17	1	1	1	1.108	1		1.660	1		26.67	1.00	1	1	1607	179.8	6.51
290543591	YTH domain-containing family protein 2 isoform 2 [Homo sapiens]	1.13	2	1	1	1	1.106	1		1.629	1		24.51	1.13	1	1	529	56.8	8.94
4502165	apolipoprotein F precursor [Homo sapiens]	4.29	1	1	1	3	1.106	1		1.279	1		163.22	4.29	3	3	326	35.4	5.64
578798496	PREDICTED: dihydropyrimidine dehydrogenase (NADP(+)) isoform 1 [Homo sapiens]	1.46	3	1	1	3	1.101	1		1.108	1		140.26	1.46	3	3	889	96.1	6.24
527498299	SLIT and NTRK-like protein 1 precursor [Homo sapiens]	1.44	1	1	1	2	1.100	1		1.031	1		33.34	1.44	2	2	696	77.7	6.44
51702222	protein SP17 homolog [Homo sapiens]	1.46	23	1	2	14	1.099	6		1.801	6		116.85	1.46	14	685	75.6	9.79	
7706663	COMM domain-containing protein 10 [Homo sapiens]	5.94	1	1	1	3	1.099	1		1.205	1		269.18	5.94	3	3	202	23.0	6.54
530420132	PREDICTED: eukaryotic translation initiation factor 3 subunit L isoform 1 [Homo sapiens]	2.79	4	1	1	1	1.099	1		1.197	1		174.81	2.79	3	3	466	55.1	8.95
530403277	PREDICTED: apoptotic chromatin condensation inducer in the nucleus [Homo sapiens]	1.72	7	1	1	3	1.098	1		1.097	1		60.02	1.72	3	3	583	67.5	7.59
530417087	PREDICTED: U1 small nuclear ribonucleoprotein 70 kDa isoform X2 [Homo sapiens]	2.57	2	1	1	3	1.098	1		0.987	1		147.29	2.57	3	3	428	50.6	9.89
530391650	PREDICTED: actin-related protein 2/3 complex subunit 5-like protein [Homo sapiens]	16.99	1	1	3	13	1.097	1		1.172	1		448.78	16.99	8	13	153	16.9	6.60
530368776	PREDICTED: E3 SUMO-protein ligase RanBP2 isoform X5 [Homo sapiens]	0.45	32	1	2	8	1.096	1		1.175	1		103.57	0.45	6	8	3136	348.8	6.16
10880134	beta-arrestin-1 isoform b [Homo sapiens]	6.10	8	1	2	13	1.095	2		13.0	0.953		374.87	6.10	6	13	410	46.3	

Accession	Description	ZCoverage	Z# Proteins	Z# Unique Peptides	Z# Peptides	Z# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
388240801	lamin-B2 [Homo sapiens]	7.90	1	4	4	15	1.082	5	1.2	1.088	5	8.5	838.25	7.90	12	15	620	69.9	5.59
53831995	splicing factor 3A subunit 1 isoform 2 [Homo sapiens]	1.24	2	1	1	1	1.082	1		1.217	1		30.64	1.24	1	1	728	81.6	5.34
578806449	PREDICTED: protein SEC13 homolog isoform X6 [Homo sapiens]	4.87	6	1	1	1	1.082	1		1.102	1		31.60	4.87	1	1	308	34.0	5.72
530407875	PREDICTED: RNA-binding protein FUS isoform X3 [Homo sapiens]	10.28	6	2	2	9	1.082	3	0.9	1.071	3	14.3	404.85	10.28	6	9	321	33.2	9.17
4507129	small nuclear ribonucleoprotein E [Homo sapiens]	27.17	1	1	1	3	1.081	1		0.764	1		232.16	27.17	3	3	92	10.8	9.44
19923236	nuclear autoantigen Sp-100 isoform 2 [Homo sapiens]	3.30	6	1	5	30	1.081	1			1		359.62	3.30	12	30	879	100.4	8.22
578819255	PREDICTED: AP-3 complex subunit mu-1 isoform X1 [Homo sapiens]	5.98	8	2	2	10	1.081	1		1.422	1		237.75	5.98	6	10	418	46.9	6.93
254028213	IQ domain-containing protein F6 [Homo sapiens]	6.54	2	1	1	1	1.081	1		1.263	1		40.23	6.54	1	1	107	13.1	11.71
530387046	PREDICTED: GTPase IMAP family member 4 isoform X2 [Homo sapiens]	2.63	10	1	1	1	1.080	1		1.342	1		0.00	2.63	1	1	190	22.6	5.59
112293277	dnaJ homolog subfamily C member 8 [Homo sapiens]	7.51	1	2	2	8	1.080	3	8.1	1.308	3	22.7	240.32	7.51	6	8	253	29.8	9.06
11225260	DNA topoisomerase 1 [Homo sapiens]	3.92	6	3	3	12	1.080	4	3.1	1.191	4	8.3	446.30	3.92	9	12	765	90.7	9.31
282847476	peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 isoform 2 [Homo sapiens]	9.02	2	1	1	3	1.080	1		1.132	1		181.18	9.02	3	3	133	14.2	10.15
24431933	reticulon-4 isoform B [Homo sapiens]	12.33	3	2	2	11	1.080	4	5.9	1.102	3	16.1	429.67	12.33	5	11	373	40.3	4.78
115495445	ankyrin repeat domain-containing protein 30A [Homo sapiens]	0.75	2	1	1	2	1.080	2	5.0	1.250	2	0.3	33.95	0.75	1	2	1341	152.6	6.33
119703753	keratin, type II cytoskeletal 68 [Homo sapiens]	25.00	16	1	16	89	1.080	2	2.2	1.108	2	6.8	3056.47	25.00	42	89	564	60.0	8.00
4885217	DNA repair endonuclease XPF [Homo sapiens]	1.86	1	1	1	1	1.079	1		1.558	1		28.19	1.86	1	1	916	104.4	6.93
40556376	putative oxidoreductase GLYR1 [Homo sapiens]	3.62	5	2	2	7	1.079	3	0.3	1.095	3	5.6	209.82	3.62	5	7	553	60.5	9.17
530365976	PREDICTED: serologically defined colon cancer antigen 8 isoform X1	1.48	9	2	1	4	1.079	2	1.6	1.384	2		36.20	1.48	3	4	406	47.8	5.96
6669542	paired box protein Pax-8 isoform PAX8E [Homo sapiens]	2.09	4	1	1	2	1.079	1		0.786	1		31.20	2.09	2	2	287	31.0	8.54
6857820	phosphatidylinositol 5-phosphate 4-kinase type-2 alpha [Homo sapiens]	3.45	1	1	1	6	1.078	2	7.8	1.142	2	0.9	319.10	3.45	3	6	406	46.2	6.99
76573881	pre-mRNA-processing factor 19 [Homo sapiens]	4.56	1	1	1	3	1.078	1		1.036	1		163.44	4.56	3	3	504	55.1	6.99
6912356	echinoderm microtubule-associated protein-like 2 isoform 2 [Homo sapiens]	3.39	5	2	2	6	1.078	2	10.1	0.972	2	16.9	272.93	3.39	6	6	649	70.6	6.32
4502961	collagen alpha-1(VII) chain precursor [Homo sapiens]	0.37	1	1	1	1	1.077	1			1		38.71	0.37	1	1	2944	295.0	6.27
4501893	alpha-actinin-2 isoform 1 [Homo sapiens]	18.57	41	1	16	127	1.077	1		1.642	1		5178.23	18.57	41	127	894	103.8	5.45
530419254	PREDICTED: pericentriolar protein X6 [Homo sapiens]	0.25	7	1	1	1	1.077	1		21.43	0.25	1	21.43	0.25	1	1	3139	355.7	5.47
59859885	40S ribosomal protein SA [Homo sapiens]	25.76	1	4	4	10	1.077	4	4.3	1.188	4	24.3	503.63	25.76	10	10	295	32.8	4.87
530387776	PREDICTED: acid ceramidase isoform X1 [Homo sapiens]	1.88	3	1	1	3	1.077	1		1.274	1		130.64	1.88	3	3	373	42.6	6.90
194018522	eukaryotic peptide chain release factor GTP-binding subunit ERF3A	3.21	6	1	1	6	1.076	2	7.6	1.252	2	14.9	255.01	3.21	3	6	499	55.7	5.62
530425819	PREDICTED: adipocyte plasma membrane-associated protein isoform 1	3.11	2	1	1	3	1.076	1		1.116	1		93.31	3.11	3	3	289	32.7	5.85
16564401	vesicle-fusing ATPase [Homo sapiens]	2.82	2	2	2	8	1.076	3		19.1	1.110		241.71	2.82	5	8	744	82.5	6.95
145386517	photostatin [Homo sapiens]	3.75	1	1	1	9	1.075	3	1.8	0.992	3	9.8	583.45	3.75	3	9	613	67.9	5.40
55770888	early endosome antigen 1 [Homo sapiens]	0.99	2	1	1	3	1.075	1		0.816	1		144.21	0.99	3	3	1411	162.4	5.66
11796001	major histocompatibility complex, class I, B precursor [Homo sapiens]	9.39	11	2	2	6	1.075	2	9.1	1.334	2	26.0	325.26	9.39	6	6	362	40.4	5.85
38044112	CAP-Gly domain-containing linker protein 1 isoform B [Homo sapiens]	0.43	8	1	1	3	1.075	1		2.513	1		47.88	0.43	3	3	1392	156.7	5.36
122937345	unconventional myosin-Vb [Homo sapiens]	0.43	1	2	2	16	1.075	2	27.9	1.534	2	2.1	276.74	0.43	4	16	1848	213.5	7.20
4503507	eukaryotic translation initiation factor 2 subunit 3 [Homo sapiens]	7.20	17	3	4	11	1.075	3	0.9	1.163	3	5.7	234.75	7.20	11	11	472	51.1	8.40
254540132	myeloma-overexpressed gene 2 protein isoform 2 [Homo sapiens]	35.09	1	1	1	3	1.074	1		1.113	1		114.93	35.09	3	3	57	6.2	3.83
44090584	CAMP-dependent protein kinase catalytic subunit alpha isoform 2 [Homo sapiens]	13.70	18	6	5	17	1.074	1	6.5	1.334	1	30.9	547.04	13.70	14	17	343	39.8	8.66
578829028	PREDICTED: lysophosphatidylcholine acyltransferase 2 isoform X2	2.46	2	1	1	5	1.074	2	23.2	1.279	2	3	184.24	2.46	3	5	488	54.4	5.91
530360665	PREDICTED: protein LZIC isoform X5 [Homo sapiens]	15.79	2	2	2	9	1.074	3	3.2	1.204	3	6.5	466.47	15.79	6	9	190	21.5	4.94
25777612	26S proteasome non-ATPase regulatory subunit 3 [Homo sapiens]	5.24	1	2	2	5	1.074	2	4.4	0.691	2	68.5	309.17	5.24	5	5	534	60.9	8.44
4506715	40S ribosomal protein S28 [Homo sapiens]	17.39	1	1	1	3	1.074	1		1.133	1		199.62	17.39	3	3	69	7.8	10.70
378404908	glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens]	92.83	3	1	25	1693	1.073	1		1.176	1		89140.91	92.83	74	1693	293	31.5	7.61
47458820	signal transducer and activator of transcription 3 isoform 3 [Homo sapiens]	2.49	6	1	1	5	1.073	2	5.9	0.957	2	6.2	271.50	2.49	3	5	722	83.1	7.12
291190772	platelet glycoprotein Ib alpha chain precursor [Homo sapiens]	1.53	1	1	1	3	1.073	1		1.098	1		74.89	1.53	3	3	652	71.5	6.29
117616270	tumor necrosis factor alpha-induced protein 8 isoform B [Homo sapiens]	14.89	5	2	2	9	1.072	3	0.8	1.395	3	11.3	642.65	14.89	6	9	188	21.9	8.75
112362370	folate receptor gamma precursor [Homo sapiens]	3.27	1	1	1	3	1.072	1		1.036	1		146.16	3.27	2	3	245	27.9	7.66
15826852	Golgi resident protein GCP60 [Homo sapiens]	4.55	1	1	1	3	1.072	1		1.209	1		236.80	4.55	3	3	528	60.6	5.06
530396980	PREDICTED: lysosomal Pro-X carboxypeptidase isoform X1 [Homo sapiens]	7.67	3	2	2	11	1.071	4	5.7	1.236	4	32.8	435.62	7.67	6	11	391	43.9	6.30
530413911	PREDICTED: DNA endonuclease RBBP8 isoform X2 [Homo sapiens]	1.28	4	1	1	1	1.071	1			1		28.83	1.28	1	1	623	70.5	6.51
578818376	PREDICTED: selenide, water kinase 1 isoform X1 [Homo sapiens]	6.92	4	2	2	5	1.070	2	5.2	1.136	2	8.3	289.46	6.92	5	5	390	42.7	5.97
601984520	polyubiquitin-C [Homo sapiens]	80.15	7	9	9	100	1.069	36	11.6	1.127	36	8.2	3936.83	80.15	26	100	685	77.0	7.66
578804376	PREDICTED: bifunctional purine biosynthesis protein PURH isoform 1	7.32	2	3	3	12	1.069	5	4.7	1.152	5	12.3	322.11	7.32	8	12	533	58.6	6.64
16418881	vascular protein sorting-associated protein 26B [Homo sapiens]	5.36	1	1	1	3	1.069	1		1.072	1		191.86	5.36	3	3	286	39.1	7.36
530380612	PREDICTED: histidine--RNA ligase, cytoplasmic isoform X1 [Homo sapiens]	11.14	9	2	5	13	1.069	2	5.5	1.060	2	13	400.68	11.14	13	13	440	49.6	5.41
34734066	fibulin-1 isoform D precursor [Homo sapiens]	10.53	2	1	7	21	1.068	2	1.0	1.116	2	8.9	558.05	10.53	19	21	703	77.2	5.26
530381810	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 1	4.87	3	3	3	8	1.068	2	7.2	1.135	3	4.9	280.12	4.87	3	8	677	73.7	6.16
334278906	vascular non-inflammatory molecule 2 isoform 3 precursor [Homo sapiens]	4.35	4	1	1	3	1.068	1		1.222	1		132.68	4.35	3	3	299	33.2	6.13
194018472	plasma serine protease inhibitor preproprotein [Homo sapiens]	4.68	1	2	2	4	1.068	2	5.7	0.802	2	60.0	110.73	4.68	4	4	406	45.6	9.26
4826932	peptidyl-prolyl cis-trans isomerase D [Homo sapiens]	7.84	6	1	2	7	1.068	1		1.060	1		148.62	7.84	5	7	370	40.7	7.21
4826972	RNA-binding protein 8A [Homo sapiens]	6.32	1	1	1	3	1.068	1		1.234	1		192.61	6.32	3	3	174	19.9	5.72
4557797	nucleoside diphosphate kinase A isoform b [Homo sapiens]	56.58	6	1	9	120	1.067	2	0.8	1.096	2	4.0	4500.07	56.58	26	120	152	17.1	6.19
57879984	PREDICTED: udk pyrenyltransferase domain-containing protein 1 isoform 1	4.74	2	1	1	3	1.067	2	2.4	1.395	2	10.0	31.71	4.74	2	3	211	22.8	7.72
45545435	COMM domain-containing protein 2 [Homo sapiens]	12.06	1	1	6	1	1.067	2	2.3	1.359	2		417.46	12.06	3	6	199	22.7	6.73
578817031	PREDICTED: kinesin-like protein KIF12 isoform X8 [Homo sapiens]	1.10	1	1	1	2	1.066	1		1.873	1		37.77	1.10	2	2	635	69.1	8.73
14790115	casease-3 preproprotein [Homo sapiens]	6.86	1	2	2	6	1.066	1		0.990	2	21.0	190.58	6.86	6	6	277	31.6	6.54
5714655	reticulon-3 isoform a [Homo sapiens]	7.20	5	1	2	7	1.066	2	10.1	1.095	2	1.1	280.10	7.20	4	7	236	25.6	8.51
28416940	ribosome maturation protein SBDS [Homo sapiens]	4.00	1	1	1	3	1.066	1		1.150	1		67.17	4.00	3	3	250	28.7	8.75
578815658	PREDICTED: aspartyl/asparaginyl beta-hydroxylase isoform X18 [Homo sapiens]	1.24	18	1	1	1	1.065	1		1.825	1		24.92	1					

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
7706425	LSM8 homolog, U6 small nuclear RNA associated [Homo sapiens]	7.29	1	1	3	1.060	1	1.157		1.157	1		131.96	7.29	3	3	96	10.4	4.48	
289629267	protein transport protein Sec23b isoform 2 [Homo sapiens]	2.67	4	2	2	5.1060	2	1.056	0.8	1.056	1		247.26	2.67	5	5	749	84.4	6.99	
55956288	nucleolin [Homo sapiens]	17.61	1	10	10	52.1059	18	1.086	10.8	1.086	18		2558.16	17.61	30	52	710	76.6	4.70	
578632299	PREDICTED: N-acetyltransferase ESCO1 isoform X2 [Homo sapiens]	1.24	2	1	1	1.059	1	1.059	2.7	1.059	1		43.15	1.24	1	3	565	63.5	6.45	
14531241	differentially expressed in FDC9 6 homolog [Homo sapiens]	9.35	1	4	4	13.1398	5	1.398	9.35	1.398	5		547.89	9.35	11	13	631	73.9	6.05	
226443152	alpha/beta hydrolase domain-containing protein 14B isoform 1 [Homo sapiens]	11.43	1	2	2	6.1059	2	1.2	1.705	1.705	2	60.8	265.95	11.43	6	6	210	22.3	6.40	
618468299	dynein light chain Tctex-type 1 isoform 3 [Homo sapiens]	19.51	2	1	1	3.1059	2	1.148		1.148	1		194.21	19.51	3	3	82	9.4	4.83	
14161692	calpain small subunit 2 [Homo sapiens]	13.31	1	4	4	18.1058	1	1.090		1.090	1		415.41	13.31	12	18	248	27.6	5.73	
39777604	rho guanine nucleotide exchange factor 1 isoform 3 [Homo sapiens]	11.04	9	8	8	29.1058	11	1.142	3.7	1.142	11	14.4	1009.00	11.04	22	29	879	98.7	5.57	
530385717	PREDICTED: testin isoform X1 [Homo sapiens]	4.17	3	1	1	6.1058	2	1.170	6.8	1.170	2	10.4	316.97	4.17	3	6	336	38.2	7.65	
14574568	allograft inflammatory factor 1 isoform 3 [Homo sapiens]	29.93	10	4	4	30.1058	10	1.070	6.0	1.070	9		1164.03	29.93	12	30	147	16.7	6.24	
284413778	uncharacterized protein C2orf57 [Homo sapiens]	1.52	1	1	3	1.057	1	1.114		1.114	1		54.35	1.52	3	3	395	41.6	5.12	
31542206	charged multivesicular body protein 1b [Homo sapiens]	8.04	1	2	2	4.1057	2	1.216	8.0	1.216	2	12.8	248.28	8.04	6	6	199	22.1	8.10	
4507949	14-3-3 protein beta/alpha [Homo sapiens]	82.93	1	9	20	246.1057	35	1.171	13.7	1.171	35	14.4	8973.61	82.93	57	246	246	28.1	4.83	
530412701	PREDICTED: band 3 anion transport protein isoform X2 [Homo sapiens]	10.87	2	5	5	29.1056	11	1.165	8.7	1.165	11	14.0	1879.45	10.87	14	29	846	94.1	6.16	
38201644	homeodomain-interacting protein kinase 1 isoform 4 [Homo sapiens]	0.86	1	1	1	1.056	1	1.631		1.631	1		29.41	0.86	1	1	816	87.2	8.59	
530424789	PREDICTED: myosin regulatory light chain 12A isoform X1 [Homo sapiens]	72.51	7	1	12	124.1056	2	21.0	5.355				5207.88	72.51	35	124	171	19.8	4.81	
256222019	ras-related protein Rab-10 [Homo sapiens]	22.50	20	2	4	32.1055	5	1.278	3.6	1.278	5	17.2	1668.14	22.50	12	32	200	22.5	8.38	
7662655	sorting nexin-24 [Homo sapiens]	5.33	3	1	1	3.1055	1	1.647		1.647	1		77.49	5.33	3	3	169	19.8	7.78	
578828704	PREDICTED: centrilin coiled-coil protein of 110 kDa isoform X4 [Homo sapiens]	1.13	5	1	1	2.1055	1	1.180		1.180	1		39.10	1.13	2	2	971	109.0	8.14	
38649656	40S ribosomal protein S3 isoform 3 [Homo sapiens]	24.79	3	2	2	4.1055	2	1.148	0.6	1.148	2	0.2	217.75	24.79	4	4	117	12.6	9.28	
14249348	thioredoxin domain-containing protein 17 [Homo sapiens]	30.08	1	3	3	9.1055	3	1.205	2.7	1.205	3	0.7	397.42	30.08	9	9	123	13.9	5.52	
4694058	bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 [Homo sapiens]	1.60	1	1	1	2.1054	1	1.60		1.60	1		36.46	1.60	2	2	624	70.8	6.86	
578819489	PREDICTED: mannose-binding protein C isoform X4 [Homo sapiens]	26.32	3	4	4	10.1054	4	1.214	3.2	1.214	4	13.3	418.68	26.32	10	10	152	16.9	6.13	
13775198	SH3 domain-binding glutamic acid-rich-like protein 3 [Homo sapiens]	83.87	1	7	7	73.1054	28	1.129	6.3	1.129	27	9.4	2836.98	83.87	20	73	93	10.4	4.93	
24497519	mannosyl-oligosaccharide 1,2-alpha-mannosidase IA [Homo sapiens]	1.68	2	1	1	3.1054	1	1.205		1.205	1		161.47	1.68	3	3	653	72.9	6.47	
29826323	alpha-adducin isoform c [Homo sapiens]	2.06	8	1	1	3.1054	1	1.205		1.205	1		164.71	2.06	3	3	631	69.9	6.46	
33519455	methionine adenosyltransferase 2 subunit beta isoform 2 [Homo sapiens]	3.72	2	1	1	1.1054	1	1.153		1.153	1		28.32	3.72	1	1	323	36.4	6.65	
41406082	glutathione peroxidase 1 isoform 2 [Homo sapiens]	1.20	2	1	1	1.1054	1	1.266		1.266	1		138.99	1.20	3	3	98	10.3	10.23	
7616880	cap GAP with coiled-coil, ANK repeat and PH domain containing protein 1 [Homo sapiens]	8.38	2	4	4	14.1054	5	1.096	3.6	1.096	5	15.5	744.10	8.38	12	14	740	81.5	7.66	
578834710	PREDICTED: spectrin beta chain, non-erythrocytic 4 isoform X1 [Homo sapiens]	1.00	6	1	3	11.1054	1	1.537		1.537	1		387.69	1.00	8	11	2394	270.1	5.67	
530400291	PREDICTED: protein phosphatase 1 regulatory subunit 12A isoform 1 [Homo sapiens]	4.08	11	3	3	15.1053	5	1.143	6.5	1.143	5		629.15	4.08	9	15	931	105.6	5.47	
31742503	histone H3.2 [Homo sapiens]	61.03	3	1	9	74.1053	6	1.639	1.7	1.639	5	7.2	2221.05	61.03	26	74	136	15.4	11.27	
530383580	PREDICTED: interactor protein for cytohesin exchange factors 1 isoform 1 [Homo sapiens]	3.20	2	1	1	1.1052	1	1.476		1.476	1		30.32	3.20	1	1	437	49.0	7.52	
14141161	heterogeneous nuclear ribonucleoprotein U isoform b [Homo sapiens]	13.40	2	9	10	43.1052	16	1.212	6.2	1.212	16	13.5	2146.38	13.40	27	43	806	88.9	5.78	
14141193	40S ribosomal protein S9 [Homo sapiens]	4.12	1	9	1	3.1052	1	1.213		1.213	1		126.76	4.12	3	3	194	22.6	10.65	
33186601	protein FAM101B [Homo sapiens]	8.41	1	1	1	3.1051	1	1.190		1.190	1		133.08	8.41	3	3	214	22.9	5.74	
4758516	hepatoma-derived growth factor isoform a [Homo sapiens]	65.83	9	13	14	75.1051	27	1.193	12.4	1.193	26	12.7	3078.56	65.83	75	240	403	26.8	4.73	
4504011	glutamate--cysteine ligase regulatory subunit [Homo sapiens]	5.47	1	1	1	3.1051	1	1.052		1.052	1		247.25	5.47	3	3	274	30.7	6.02	
530372836	PREDICTED: cAMP-dependent protein kinase type II-alpha regulatory subunit 1 [Homo sapiens]	13.35	4	4	4	12.1051	4	1.216	3.6	1.216	4	18.4	751.19	13.35	12	12	382	43.0	5.08	
30795231	brain acid soluble protein 1 [Homo sapiens]	76.65	1	14	14	91.1051	32	1.175	8.0	1.175	32	17.6	3964.37	76.65	41	91	227	22.7	4.63	
11968182	40S ribosomal protein S18 [Homo sapiens]	12.50	1	2	2	5.1051	2	1.170	11.7	1.099	2		130.48	12.50	5	5	152	17.7	10.99	
6912280	activator of 90 kDa heat shock protein ATPase homolog 1 [Homo sapiens]	9.47	1	2	2	5.1050	2	1.4	1.073	1.073	2	8.5	335.07	9.47	5	5	338	38.3	5.53	
50345292	hematological and neurological expressed 1 protein isoform 3 [Homo sapiens]	13.89	5	1	1	3.1050	1	1.034		1.034	1		117.80	13.89	3	3	108	11.0	4.84	
37594461	nucleoside diphosphate-linked moiety X motif 6 isoform b [Homo sapiens]	4.76	2	1	1	2.1050	1	1.789		1.789	1		29.37	4.76	2	2	147	17.1	5.10	
71737110	apoptoprotein A-RV precursor [Homo sapiens]	46.97	1	18	18	140.1050	50	1.192	6.7	1.192	50	18.0	5813.97	46.97	140	386	45.3	5.38	4.73	
5803011	gamma-enolase [Homo sapiens]	17.51	1	5	5	117.1050	1	2.791		2.791	1		6259.71	17.51	15	117	434	47.2	5.03	
209963011	perlestin isoform 3 precursor [Homo sapiens]	46.99	5	2	27	165.1049	3	1.175	3.3	1.175	3		749.78	46.99	79	165	781	29.3	7.81	
578804845	PREDICTED: WAS/WASL-interacting protein family member 1 isoform 1 [Homo sapiens]	26.64	1	7	7	24.1049	11	1.038	11.0	1.038	11	26.4	882.10	26.64	18	24	503	51.2	11.47	
578811929	PREDICTED: protein PRRC2A isoform X1 [Homo sapiens]	0.24	9	1	1	2.1049	1	6.536		6.536	1		25.82	0.24	2	2	2086	221.5	9.42	
4885049	actin, alpha cardiac muscle 1 precursor [Homo sapiens]	48.81	5	2	21	1590.1049	63	1.168	7.9	1.168	63	19.7	53721.09	48.81	62	1590	377	42.0	5.39	
156151392	heterogeneous nuclear ribonucleoprotein R isoform 4 [Homo sapiens]	5.83	7	1	3	15.1049	1	1.219		1.219	1		554.37	5.83	9	15	532	59.6	9.16	
4506613	60S ribosomal protein L22 precursor [Homo sapiens]	20.21	1	1	1	5.1049	2	1.147	9.8	1.147	2	58.7	277.84	20.21	3	5	128	14.8	9.19	
530418950	PREDICTED: bromodomain and WD repeat-containing protein 1 isoform 1 [Homo sapiens]	0.37	3	1	1	1.1048	1	1.227		1.227	1		28.42	0.37	1	1	2422	253.3	8.46	
5196037	G protein-coupled receptor kinase 6 isoform c [Homo sapiens]	1.25	3	2	2	1.1048	2	1.434	1.25	1.434	2		49.68	1.25	3	7	560	64.3	8.44	
578835477	PREDICTED: NSFL1 cofactor p47 isoform X4 [Homo sapiens]	22.01	6	4	4	11.1048	4	1.126	3.9	1.126	4	6.6	521.58	22.01	11	11	259	28.5	9.38	
4504893	kininogen-1 isoform 2 precursor [Homo sapiens]	58.55	2	3	30	363.1048	14	1.197	6.8	1.197	14		15645.66	58.55	83	363	427	47.9	6.65	
301897118	Fanconi anemia group J protein [Homo sapiens]	0.64	1	1	1	1.1048	1	5.006		5.006	1		23.35	0.64	1	1	1249	140.8	6.92	
25777602	26S proteasome non-ATPase regulatory subunit 2 isoform 1 [Homo sapiens]	13.11	3	7	7	20.1048	8	1.099	4.7	1.099	8	17.4	1085.85	13.11	17	20	908	100.1	5.20	
530373049	PREDICTED: biotinidase isoform X4 [Homo sapiens]	4.78	4	2	2	12.1048	4	1.132	8.4	1.132	4	2.2	643.76	4.78	6	12	523	58.9	5.89	
5453597	F-actin-capping protein subunit alpha-1 [Homo sapiens]	58.74	3	8	8	195.1048	40	1.158	8.6	1.158	38		9557.11	58.74	33	195	286	32.9	5.65	
53039698	PREDICTED: adenylate kinase isoenzyme 1 isoform X3 [Homo sapiens]	5.88	3	1	1	1.1048	1	1.066		1.066	1		26.85	5.88	1	1	187	20.7	7.93	
34098946	nucleoside-sensitive element binding protein 1 [Homo sapiens]	18.83	5	3	3	8.1048	4	1.537	3.7	1.537	4	16.1	138.90	18.83	6	8	324	35.9	9.88	
4507651	tropomyosin alpha-4 chain isoform 2 [Homo sapiens]	43.95	8	3	19	119.1047	4	0.963	4.9	0.963	4		3908.00	43.95	48	50	119	248	28.5	4.69
18860831	dynamitin-like 120 kDa protein, mitochondrial isoform 2 [Homo sapiens]	1.62	13	1	2	7.1047	1	1.224		1.224	1		135.73	1.62	4	7	924	107.5	7.99	
118442839	complement factor H-related protein 1 precursor [Homo sapiens]	26.06	3	2	9	71.1047	4	1.024	3.4	1.024	4</									

Accession	Description	ZCoverage	Z# Proteins	Z# Unique Peptides	Z# Peptides	Z# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
123173757	ribonucleoprotein PTB-binding 1 [Homo sapiens]	1.72	1	1	1	2	1.043	1		1.841	1		82.51	1.72	2	2	756	79.5	8.92
530422336	PREDICTED: dedicator of cytokinesis protein 11 isoform X2 [Homo sapiens]	1.07	3	2	2	4	1.043	1		1.028	1		78.11	1.07	4	4	2055	235.7	7.58
530402178	PREDICTED: sister chromatid cohesion protein PDS5 homolog B isoform X1 [Homo sapiens]	1.63	5	2	2	6	1.043	2	0.5	1.045	2	0.2	508.85	1.63	6	6	1411	160.7	8.31
526281405	condensin complex subunit 2 isoform 4 [Homo sapiens]	1.16	7	1	1	3	1.043	1		1.16	1		90.34	1.16	3	3	605	67.5	6.87
11056061	thymosin beta 4 [Homo sapiens]	56.82	1	7	9	91	1.043	29	7.6	1.138	29	12.2	2737.97	56.82	23	91	44	5.0	5.06
5032315	dystrophin Dp427p isoform [Homo sapiens]	0.51	44	1	3	9	1.042	1		1.387	1		190.55	0.51	9	9	3562	412.1	5.83
10716563	calnexin precursor [Homo sapiens]	12.16	1	6	6	33	1.042	12	7.6	1.196	12		1472.41	12.16	18	33	592	67.5	4.60
4502205	ADP-ribosylation factor 4 [Homo sapiens]	34.44	1	1	4	18	1.042	5	3.5	1.439	5	18.7	631.59	34.44	10	18	180	20.5	7.14
578798834	PREDICTED: microtubule-actin cross-linking factor 1 isoform X27 [Homo sapiens]	0.47	40	3	3	5	1.042	1		10.102	1		93.77	0.47	5	5	4720	531.2	5.27
530393302	PREDICTED: cytosolic purine 5'-nucleotidase isoform X10 [Homo sapiens]	12.43	6	3	3	21	1.042	7	5.9	1.310	7	18.3	846.86	12.43	9	21	370	42.7	6.29
62420888	dephosphorylase 2 preproprotein [Homo sapiens]	6.50	3	2	2	6	1.042	2	4.6	0.925	2	2	371.81	6.50	6	6	492	54.3	6.32
5174529	5-adenosylmethionine synthase isoform type-2 [Homo sapiens]	2.78	1	1	1	3	1.042	1		1.116	1		116.95	2.78	3	3	395	43.6	6.48
4759212	tubulin-specific chaperone A isoform 2 [Homo sapiens]	51.85	1	9	9	42	1.042	15	6.9	1.066	15	8.4	1737.68	51.85	26	42	108	12.8	5.29
557878742	long-chain-fatty acid-CoA ligase 1 isoform 2 [Homo sapiens]	3.04	14	2	2	6	1.042	2	5.7	1.392	2	22.9	201.67	3.04	6	6	527	58.5	7.53
530402403	PREDICTED: protocadherin-9 isoform X3 [Homo sapiens]	0.88	5	1	1	3	1.042	2	2.7	1.271	2	5.9	41.92	0.88	2	3	1019	112.0	5.45
145199237	RNA exonuclease 1 homolog [Homo sapiens]	0.41	2	1	1	1	1.041	1		1.168	1		25.21	0.41	1	1	1221	131.4	8.95
7656562	calyculin-binding protein isoform 1 [Homo sapiens]	5.70	1	1	2	18	1.041	1		1.133	1		320.99	5.70	6	18	228	26.2	8.25
530422392	PREDICTED: coagulation factor IX isoform X2 [Homo sapiens]	13.64	3	4	4	11	1.041	4	8.4	1.292	4	24.8	511.66	13.64	11	11	418	47.0	5.43
530406751	PREDICTED: ubiquitin carboxyl-terminal hydrolase 3 isoform X3 [Homo sapiens]	1.99	7	1	1	1	1.041	1		1.091	1		23.33	1.99	1	1	351	40.1	7.75
355594753	clusternin preproprotein [Homo sapiens]	42.09	2	13	13	105	1.041	36	5.5	1.248	36	21.9	4684.56	42.09	35	105	449	52.5	6.27
56331274	sepiin-5 isoform 2 [Homo sapiens]	15.03	2	3	3	11	1.041	4	7.1	1.157	4	19.2	322.49	15.03	4	11	346	39.3	7.8
294923771	nick-associated protein 1-like isoform 2 [Homo sapiens]	1.16	2	1	1	3	1.040	1		1.984	1		305.26	1.16	2	3	1077	122.4	6.62
148536853	costarmer subunit alpha isoform 2 [Homo sapiens]	4.74	2	5	5	17	1.040	6	4.4	1.258	6	5.6	593.98	4.74	14	17	1224	138.3	7.66
154426278	muscular LMNA-interacting protein isoform 3 [Homo sapiens]	1.97	10	1	1	1	1.040	1		1.289	1		29.43	1.97	1	1	458	50.4	6.38
4502209	ADP-ribosylation factor 5 [Homo sapiens]	38.89	1	1	5	25	1.040	1		2.239	1		1050.26	38.89	14	25	180	20.5	6.79
530369968	PREDICTED: cytoplasmic dynein 1 intermediate chain 2 isoform X7 [Homo sapiens]	9.82	9	5	5	14	1.040	5	8.9	1.106	5	23.1	655.96	9.82	14	14	611	68.3	5.29
212276104	leucine-rich repeat flightless-interacting protein 1 isoform 5 [Homo sapiens]	17.95	73	11	11	36	1.040	13	7.3	1.148	13	28.7	1951.32	17.95	28	36	752	82.6	4.61
394953908	26S proteasome non-ATPase regulatory subunit 11 [Homo sapiens]	3.08	1	1	1	2	1.040	1		1.391	1		129.92	3.08	2	2	422	47.4	6.48
110611218	ribosome-binding protein 1 [Homo sapiens]	2.46	4	2	2	7	1.040	3	13.5	1.040	3	1.6	369.47	2.46	5	7	977	108.6	5.54
15431332	casease-1 isoform delta [Homo sapiens]	7.60	5	2	7	1	1.039	3	4.0	1.547	3	6.5	206.37	7.60	5	7	263	29.8	7.91
375331936	protein FAM193A isoform 4 [Homo sapiens]	0.66	6	1	1	1	1.039	1		0.999	1		29.86	0.66	1	1	1211	134.2	6.40
18543329	26S proteasome non-ATPase regulatory subunit 9 isoform 1 [Homo sapiens]	41.26	1	4	4	11	1.039	5	12.6	1.422	4	15.5	332.19	41.26	10	11	223	24.7	6.95
358356407	60S ribosomal protein L15 isoform [Homo sapiens]	6.21	2	1	1	2	1.039	1		0.948	1		58.99	6.21	2	2	145	16.7	11.53
21237808	SWI/SNF complex subunit SMARCC2 isoform b [Homo sapiens]	1.15	7	1	1	3	1.039	1		1.227	1		124.99	1.15	3	3	1130	124.8	5.55
22538467	proteasome subunit beta type-4 [Homo sapiens]	25.76	1	4	4	19	1.039	8	2.0	1.123	8	14.7	908.11	25.76	12	19	264	29.2	5.97
14043026	vesicle-associated membrane protein 8 [Homo sapiens]	10.00	1	1	1	3	1.039	1		1.161	1		195.49	10.00	3	3	100	11.4	7.34
14702780	eukaryotic translation initiation factor 4B isoform 2 [Homo sapiens]	21.05	3	3	3	9	1.039	9	2.7	1.184	2	20.9	261.28	21.05	9	9	228	25.2	8.09
4504183	glutathione S-transferase P [Homo sapiens]	49.52	1	14	14	294	1.039	106	9.3	1.177	106	13.3	13737.31	49.52	23	294	210	5.64	5.64
25777113	S-phase kinase-associated protein 1 isoform b [Homo sapiens]	19.02	2	2	2	6	1.038	2		1.173	2	25.0	318.05	19.02	6	6	163	18.6	4.54
578811110	PREDICTED: heterogeneous nuclear ribonucleoprotein H isoform X [Homo sapiens]	23.31	7	4	4	7	1.038	7	5.2	1.125	7	12.3	1137.00	23.31	21	34	429	47.1	6.34
4557389	complement component C8 alpha chain precursor [Homo sapiens]	30.99	1	13	13	78	1.038	28	7.2	1.145	28	24.4	3791.89	30.99	37	78	584	65.1	6.47
4758012	clathrin heavy chain 1 isoform 1 [Homo sapiens]	16.24	14	19	20	92	1.038	32	5.2	1.116	32	57	4117.48	16.24	57	92	1675	191.5	5.69
197382664	eukaryotic translation initiation factor 4E type 3 isoform b [Homo sapiens]	14.41	2	1	6	1	1.038	2	2.4	1.088	2	38.1	219.45	14.41	3	6	118	13.3	5.78
4507115	fascin [Homo sapiens]	6.29	1	2	2	6	1.038	2	9.9	1.368	2	49.4	365.05	6.29	6	6	493	54.5	7.24
578831752	PREDICTED: probable helicase with zinc finger domain isoform X6 [Homo sapiens]	0.32	7	1	1	1	1.038	1		1.207	1		25.73	0.32	1	1	1578	177.5	8.10
62241042	functional glutathione-proline-4-oxo-ligase [Homo sapiens]	5.97	1	5	5	14	1.038	5	2.5	1.086	5	14	1512.12	5.97	14	14	1512	170.5	7.33
530420490	PREDICTED: apolipoprotein L1 isoform X2 [Homo sapiens]	20.00	4	1	7	30	1.037	10	7	1.020	10	10.5	1152.62	20.00	21	30	389	42.1	5.80
530376756	PREDICTED: acyl-CoA synthetase family member 4 isoform X7 [Homo sapiens]	1.11	8	1	1	1	1.037	4	1.4	1.021	4		226.53	1.11	3	11	721	80.4	7.49
578800742	PREDICTED: dimethylallylamine monooxygenase [N-oxide-forming] 4 [Homo sapiens]	1.31	4	1	1	1	1.037	1		1.255	1		0.00	1.31	1	1	381	43.4	8.48
39812055	beta-arrestin-2 isoform 2 [Homo sapiens]	11.93	11	4	4	5	1.037	4	3.7	1.159	4	18.7	606.11	11.93	14	14	394	44.4	7.88
18702331	OTU domain-containing protein 7A [Homo sapiens]	1.51	2	1	1	1	1.037	1		1.243	1		29.29	1.51	1	1	926	100.6	8.40
46397403	centrin-3 isoform 2 [Homo sapiens]	4.19	1	1	1	5	1.037	2	8.8	1.419	2	14.5	68.77	4.19	3	5	167	19.5	4.74
5902076	serine/arginine-rich splicing factor 1 isoform 1 [Homo sapiens]	8.06	3	2	2	2	1.037	3	4.4	1.291	3	8.6	309.70	8.06	9	9	248	27.7	10.36
5453760	NEDD8 precursor [Homo sapiens]	34.57	2	2	2	12	1.037	4	4.6	1.380	4	15.8	603.55	34.57	6	6	181	41.1	8.43
530386260	PREDICTED: coiled-coil domain-containing protein 146 isoform X3 [Homo sapiens]	0.97	1	1	1	3	1.037	1		1.539	1		32.07	0.97	1	1	823	97.2	9.30
578802932	PREDICTED: protein MEMO1 isoform X4 [Homo sapiens]	9.44	3	1	1	3	1.036	1		0.943	1		228.88	9.44	3	3	180	20.7	5.71
167234419	thyroid hormone receptor-associated protein 3 [Homo sapiens]	1.36	1	1	1	6	1.036	2	5.9	1.199	2	2.5	553.83	1.36	3	6	955	108.6	10.15
378744212	GTP-binding protein RIT1 isoform 3 [Homo sapiens]	4.37	3	2	1	9	1.036	4	2.5	2.848	4	9.4	71.49	4.37	3	9	183	21.6	9.09
109148542	alanine--RNA ligase, cytoplasmic [Homo sapiens]	2.89	2	2	2	5	1.036	2	4.3	1.055	2	19.6	302.18	2.89	5	5	968	106.7	5.53
378830584	PREDICTED: protein unc-13 homolog D isoform X1 [Homo sapiens]	6.44	3	5	5	18	1.036	6	3.7	1.145	6	32.9	648.83	6.44	15	18	1071	120.6	6.40
255652953	zinc finger CCH domain-containing protein 18 isoform 2 [Homo sapiens]	0.84	2	1	1	2	1.036	1		1.045	1		31.12	0.84	2	2	953	106.3	8.32
4506193	proteasome subunit beta type-1 [Homo sapiens]	51.04	1	9	9	60	1.036	22	6.9	1.235	22	18.4	2438.30	51.04	26	60	241	26.5	8.13
530372380	PREDICTED: acylglutamate-releasing enzyme isoform X1 [Homo sapiens]	9.91	3	5	5	20	1.036	7	5.7	1.124	7	3.9	1271.89	9.91	14	20	685	99.2	5.96
96304457	low molecular weight phosphotyrosine protein phosphatase isoform 1 [Homo sapiens]	16.07	2	1	1	3	1.036	1		1.318	1		339.62	16.07	3	3	112	12.2	7.74
10835067	lupus La protein [Homo sapiens]	14.22	1	5	5	20	1.035	7	9.8	1.252	7	13.6	887.33	14.22	14	20	408	46.8	7.12
38207110	probable ATP-dependent RNA helicase DDX17 isoform 1 [Homo sapiens]	10.01	6	6	7	19	1.035	7	6.0	1.155	7	32.6	663.19	10.01	17	19	729	80.2	8.27
199562283	retrotransposon-like protein 1 [Homo sapiens]	0.44	1	1	1	5	1.035	1		1.242	1		50.39	0.44	3	5	1358	154.9	5.21
47132620	keratin, type II cytoskeletal 2 epidermal [Homo sapiens]	19.87	26	4	11	47	1.0												

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
578799388	PREDICTED: ribonucleoprotein P7B-binding 2 isoform X1 [Homo sapiens]	0.77	2	1	1	2	1.032	1		1.674	1		42.08	0.77	2	2	647	70.6	7.97
189181666	beta-hexosaminidase subunit alpha preproprotein [Homo sapiens]	4.16	1	2	2	5	1.032	2	5.1	1.199	2	8.4	208.03	4.16	5	5	529	60.7	5.16
312596881	26S protease regulatory subunit 8 isoform 2 [Homo sapiens]	10.55	3	3	3	15	1.032	5	3.2	1.125	5	7.0	725.80	10.55	9	15	398	44.8	8.18
327267473	scaffold attachment factor B1 isoform 4 [Homo sapiens]	2.48	5	1	1	3	1.032	1		1.149	1		274.29	2.48	3	3	848	95.1	6.46
14656990	copper homeostasis protein catc homolog [Homo sapiens]	8.06	1	1	1	2	1.032	1		1.386	1		43.15	8.06	2	2	273	29.3	8.19
530374901	PREDICTED: protein CDV3 homolog isoform X4 [Homo sapiens]	7.62	6	2	2	4	1.032	2		0.985	2	4.4	125.09	7.62	4	4	210	21.7	5.54
15208660	E3 ubiquitin-protein ligase TRIM21 [Homo sapiens]	7.58	2	3	3	7	1.032	3	0.5	1.146	3	29.5	299.84	7.58	7	7	475	54.1	6.38
530380541	PREDICTED: bifunctional heparan sulfate N-deacetylase/N-sulfatase [Homo sapiens]	1.49	5	1	1	24	1.032	8	2.9	2.021	8	20.9	622.68	1.49	3	24	471	54.6	8.75
530395458	PREDICTED: PHD finger protein 21A isoform X9 [Homo sapiens]	1.27	6	1	1	11	1.031	4	0.8	1.093	4	1.6	145.75	1.27	3	11	629	69.0	9.74
530403927	PREDICTED: protein Z-dependent protease inhibitor isoform X1 [Homo sapiens]	3.60	2	1	1	3	1.031	1		1.074	1		198.54	3.60	3	3	444	50.7	8.27
530370277	PREDICTED: 60 kDa heat shock protein, mitochondrial isoform X1 [Homo sapiens]	5.76	1	2	2	5	1.031	2	19.8	1.253	2	12.3	232.66	5.76	5	5	573	61.0	5.87
21687129	nucC domain-containing protein 2 [Homo sapiens]	5.73	1	1	1	3	1.031	1		1.250	1		80.91	5.73	3	3	157	17.7	5.07
16105048	histone H2B type 1-K [Homo sapiens]	69.84	23	2	12	205	1.031	14	11.2	1.154	14	18.4	8249.34	69.84	34	65	293	126	10.32
530355690	PREDICTED: keratin, type II cuticular Hb3 isoform X2 [Homo sapiens]	3.13	9	1	2	10	1.031	3		1.094	3	1.8	162.70	3.13	4	10	447	49.7	5.54
578799625	PREDICTED: NAD kinase isoform X5 [Homo sapiens]	11.98	5	3	3	9	1.031	3	17.4	1.355	3	4.2	450.68	11.98	9	9	359	39.6	5.80
530385393	PREDICTED: nicotinamide phosphoribosyltransferase isoform X1 [Homo sapiens]	68.64	13	28	28	223	1.031	84	8.2	1.171	84	13.0	9194.59	68.64	79	223	491	55.5	7.15
578803933	PREDICTED: UBX domain-containing protein 4 isoform X1 [Homo sapiens]	2.80	2	1	1	3	1.031	1		1.249	1		63.02	2.80	3	3	322	36.0	5.92
578802939	PREDICTED: vacuolar protein sorting-associated protein 54 isoform 1 [Homo sapiens]	0.53	3	1	1	3	1.031	1		2.056	1		34.56	0.53	3	3	941	106.3	6.38
530428415	PREDICTED: proteasome subunit beta type-8 isoform X1 [Homo sapiens]	36.63	3	8	8	46	1.031	16	6.1	1.168	16	8.5	1874.38	36.63	24	46	243	27.0	7.18
295844834	N-acetyl-D-glucosamine kinase [Homo sapiens]	23.59	3	8	8	34	1.031	13	12.8	1.255	13	15.5	1235.54	23.59	22	34	390	42.0	6.68
578825742	PREDICTED: heterogeneous nuclear ribonucleoproteins C1/C2 isoform 1 [Homo sapiens]	33.11	7	10	10	65	1.029	29	6.2	1.229	29	11.1	2642.19	33.11	24	65	293	32.3	6.38
4825593	non-histone chromosomal protein HMG-14 [Homo sapiens]	61.00	1	6	6	31	1.031	13	5.0	1.091	13	10.6	1226.85	61.00	15	31	100	10.7	9.60
14702162	CAP-Gly domain-containing linker protein 2 isoform 2 [Homo sapiens]	0.89	1	1	1	1	1.031	1		0.971	1		29.31	0.89	1	1	1011	111.7	6.76
530416417	PREDICTED: apolipoprotein C-1 isoform X1 [Homo sapiens]	30.12	43	3	4	33	1.031	10	5.0	1.177	10	10.6	1041.02	30.12	12	33	83	9.3	8.47
401709950	ubiquitin carboxyl-terminal hydrolase lysome L3 isoform 1 [Homo sapiens]	15.98	4	3	3	10	1.031	4	2.3	1.117	4	12.7	382.74	15.98	8	10	194	21.9	4.93
54792071	small ubiquitin-related modifier 2 isoform b precursor [Homo sapiens]	30.99	7	2	2	14	1.030	5	1.5	1.200	5	7.7	569.62	30.99	6	14	71	8.1	5.41
56711324	HAUS augmin-like complex subunit 1 [Homo sapiens]	1.66	1	1	1	3	1.030	2	4.4	1.432	2	5.1	46.92	1.66	2	3	603	69.6	5.55
12667788	myosin-9 [Homo sapiens]	67.09	22	121	141	1476	1.030	478	7.8	1.188	475	16.4	68159.51	67.09	396	1476	1960	226.4	5.60
578837053	PREDICTED: calcineurin-binding protein cabin-1 isoform X11 [Homo sapiens]	0.29	9	1	1	5	1.030	2	3.1	1.090	2		69.87	0.29	3	5	2103	23.7	6.58
253970504	RNA-binding protein EN5 isoform 4 [Homo sapiens]	4.50	8	2	2	5	1.030	2	1.3	1.126	2	2.7	190.68	4.50	2	5	600	62.5	9.39
4503477	elongation factor 1-beta [Homo sapiens]	19.56	1	3	4	26	1.030	8	3.4	1.111	8	15.2	1521.80	19.56	12	26	225	24.7	4.67
41393561	cytosol aminopeptidase [Homo sapiens]	6.94	1	3	3	10	1.030	4	11.4	1.091	4	7.3	443.25	6.94	8	10	519	56.1	7.93
237681091	double-stranded RNA-specific endonuclease 1 isoform 7 [Homo sapiens]	1.34	9	1	1	12	1.030	5	9.5	1.249	3	11.7	188.05	1.34	3	12	674	73.6	9.03
190341024	SPARC-like protein 1 isoform 1 precursor [Homo sapiens]	8.28	2	2	2	5	1.029	2	10.9	0.854	2	78.0	173.28	8.28	5	5	664	75.2	4.81
94481046	metal transporter CNNM4 precursor [Homo sapiens]	0.90	5	1	1	5	1.029	2	15.5	1.290	2	24.6	97.11	0.90	3	5	775	86.6	6.07
5031595	actin-related protein 2/3 complex subunit 4 isoform a [Homo sapiens]	69.64	4	11	11	99	1.029	36	5.6	1.133	36	16.3	3825.25	69.64	33	99	168	19.7	8.43
11386183	wiskott-Aldrich syndrome protein family member 2 isoform 1 [Homo sapiens]	5.42	2	2	2	6	1.029	2	5.4	1.081	2	16.8	211.39	5.42	6	6	498	54.3	5.53
234641719	potassium voltage-gated channel subfamily KCOT member 5 isoform 1 [Homo sapiens]	0.76	4	1	1	2	1.029	1		1.180	1		31.63	0.76	2	2	923	101.2	6.50
530391071	PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X1 [Homo sapiens]	26.42	4	10	10	60	1.029	22	6.5	1.109	22	15.9	2729.64	26.42	26	60	439	48.5	5.92
4025484	receptor-interacting serine/threonine-protein kinase 3 [Homo sapiens]	0.97	1	1	1	4	1.029	1		1.137	1		68.07	0.97	3	4	518	56.9	6.47
189163485	lysosomal protective protein isoform b precursor [Homo sapiens]	8.96	3	3	4	9	1.029	3	11.4	1.188	3	9.9	368.69	8.96	9	9	480	54.4	6.61
4505753	phosphoglycerate mutase 1 [Homo sapiens]	82.28	30	19	19	322	1.029	111	7.9	1.150	110	16.1	14521.22	82.28	56	322	254	28.8	7.18
8051584	ricolin-1 precursor [Homo sapiens]	27.30	9	7	7	37	1.029	12	4.3	1.213	12	13.9	1475.65	27.30	37	326	35.1	13.86	
578815882	PREDICTED: t-SNARE domain-containing protein 1 isoform X2 [Homo sapiens]	1.14	1	1	1	1	1.029	1		1.259	1		35.09	1.14	1	1	878	94.5	8.92
9257257	WD repeat-containing protein 1 isoform 1 [Homo sapiens]	59.74	3	28	28	257	1.029	93	7.7	1.175	92	13.7	13271.42	59.74	81	257	606	66.2	6.65
19913446	neuropeptide calcium-binding protein hippocampin [Homo sapiens]	4.15	3	1	1	3	1.029	1	4.5	1.155	1		70.76	4.15	3	3	183	22.4	4.97
30181236	cognin-2 [Homo sapiens]	13.32	17	4	4	5	1.029	4	5.2	1.152	4	8.7	1137.71	13.32	15	36	548	61.2	6.07
5453567	craniofacial development protein 1 [Homo sapiens]	2.34	1	1	1	3	1.028	2	0.9	1.068	2		46.55	2.34	2	3	299	33.6	4.81
530366190	PREDICTED: lamin-B receptor isoform X1 [Homo sapiens]	9.95	2	6	6	39	1.028	15	5.8	1.118	15	6.3	1294.43	9.95	16	39	573	65.9	9.45
578827545	PREDICTED: proline-serine-threonine phosphatase-interacting protein 1 [Homo sapiens]	3.37	4	1	1	3	1.028	1		1.057	1		55.17	3.37	3	3	208	24.4	8.90
6912944	microtubule-associated protein RP/EB family member 1 [Homo sapiens]	34.33	8	8	8	30	1.028	11	6.5	1.150	11	5.0	1078.63	34.33	22	30	268	30.0	5.14
578815682	PREDICTED: phosphoglycerate kinase with glycosylphosphatidylinositol [Homo sapiens]	6.48	1	2	2	11	1.028	4	5.5	1.096	4	5.6	727.88	6.48	6	11	432	47.0	4.65
255653002	glycogen phosphorylase, liver form isoform 2 [Homo sapiens]	55.10	4	34	39	376	1.028	122	16.2	1.181	120	15.6	16285.34	55.10	114	376	813	93.1	7.63
50738462	C-reactive protein precursor [Homo sapiens]	34.38	1	7	7	70	1.028	26	10.7	1.228	26	22.0	2335.38	34.38	19	70	224	25.0	5.63
55749789	DEAF1 domain-containing protein 1A isoform 2 [Homo sapiens]	1.25	6	1	1	3	1.028	3	1.9	1.465	3	30.8	47.83	1.25	3	559	63.3	7.85	
578817902	PREDICTED: MMS19 nucleotide excision repair protein homolog isoform 1 [Homo sapiens]	1.20	7	1	1	1	1.028	1		1.164	1		28.83	1.20	1	1	666	72.9	7.30
5031839	keratin, type II cytoskeletal 6A [Homo sapiens]	24.82	16	1	16	85	1.028	1		1.073	1		2903.28	24.82	43	85	564	60.0	8.00
4759270	translin isoform 1 [Homo sapiens]	38.60	2	6	6	30	1.028	10	5.4	1.182	10	13.7	1238.88	38.60	18	30	228	26.2	6.44
530364307	PREDICTED: farnesyl pyrophosphate synthase isoform X2 [Homo sapiens]	14.45	3	4	4	12	1.028	4	5.0	1.113	4	42.3	421.93	14.45	12	12	353	40.5	5.17
332205939	ras-related protein Rab-11A isoform 2 [Homo sapiens]	20.65	3	3	3	21	1.028	7	3.0	1.210	7	11.0	856.51	20.65	9	21	155	17.6	8.85
635574580	hematopoietic lineage cell-specific protein isoform 2 [Homo sapiens]	18.26	7	8	8	34	1.028	13	6.9	1.132	13	3.4	1108.07	18.26	21	34	449	49.7	4.74
4504901	importin subunit alpha-3 [Homo sapiens]	2.69	1	2	2	2	1.028	1		1.172	1		67.44	2.69	2	2	521	57.9	4.96
578809703	PREDICTED: complement factor 1 isoform X4 [Homo sapiens]	42.00	6	22	22	164	1.028	64	6.5	1.234	64	14.9	4983.12	42.00	164	531	60.0	7.93	
5031789	inositol monophosphatase 1 isoform 1 [Homo sapiens]	20.94	3	5	5	12	1.028	5	3.4	1.144	5	33.2	631.10	20.94	12	12	277	30.2	5.26
11559925	probable Xaa-Pro aminopeptidase 3 isoform 1 [Homo sapiens]	2.76	1	1	2	6	1.028	1		1.380	1		99.40	2.76	4	6	507	57.0	6.83
217330646	activated RNA polymerase II transcriptional coactivator p15 [Homo sapiens]	28.35	3	5	5	16	1.028	6	3.8	1.093	6	8.8	329.22	28.35	13	16	127	14.4	8.60
578821284	PREDICTED: bifunctional ATP-dependent dihydroxyacetone kinase/tyrosine-binding globulin precursor [Homo sapiens]	9.50	4	3	3	12	1.028	4	2.										

Accession	Description	ZCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
23065544	glutathione S-transferase Mu 1 isoform 1 [Homo sapiens]	41.28	10	8	8	34	1,025	12	5.1	1,192	12	6.8	1425.87	41.28	22	34	218	25.7	6.70	
9966777	resistin precursor [Homo sapiens]	51.85	1	4	4	54	1,025	19	5.4	1,152	12	5.4	2533.43	51.85	12	27.6	108	11.4	6.86	
21264575	AT-rich interactive domain-containing protein 1A isoform b [Homo sapiens]	0.73	2	1	1	3	1,025	1		1,332	1		266.77	0.73	3	3	2068	218.2	6.52	
262118216	coiled-coil domain-containing protein 88B precursor [Homo sapiens]	1.29	3	2	2	7	1,025	3	6.0	1,249	2	8.1	219.91	1.29	5	7	1476	164.7	5.11	
316659409	actin, cytoplasmic 2 [Homo sapiens]	86.40	4	2	32	3749	1,025	460	10.4	1,202	40	31.6	16523.20	86.40	95	3749	375	41.8	5.48	
530415478	PREDICTED: zinc finger protein 25a isoform X1 [Homo sapiens]	1.69	2	1	1	1	1,025	1		4,713	1		32.36	1.69	1	1	474	54.8	8.98	
530417951	PREDICTED: RNA-binding protein Raly isoform X3 [Homo sapiens]	14.48	4	3	3	11	1,025	3	18.8	1,111	3	20.3	287.41	14.48	8	11	290	30.3	9.63	
10863927	peptidyl-prolyl cis-trans isomerase A [Homo sapiens]	78.79	15	12	15	329	1,025	115	7.0	1,199	113	16.8	13369.46	78.79	44	329	165	18.0	7.81	
557948119	carbonyl reductase (NADPH) 1 isoform 2 [Homo sapiens]	30.06	3	4	4	13	1,025	5	0.6	1,431	5		681.70	30.06	10	13	173	18.7	8.02	
578810123	PREDICTED: protein PRRC1 isoform X1 [Homo sapiens]	3.15	2	1	1	2	1,025	1		1,382	1		64.14	3.15	2	2	445	46.7	5.83	
375493534	casein kinase 2, alpha 1 polypeptide-like [Homo sapiens]	9.97	9	3	3	8	1,025	3	5.2	1,204	3	8.0	211.56	9.97	8	8	391	45.2	8.50	
530418095	PREDICTED: glutathione synthetase isoform X2 [Homo sapiens]	10.13	1	4	4	10	1,025	4	4.1	1,212	4	7.9	334.53	10.13	10	10	474	52.4	5.92	
110582255	ATP-binding cassette sub-family C member 8 isoform 2 [Homo sapiens]	0.32	3	1	1	5	1,025	3	6.2	1,123	3	3.4	104.38	0.32	3	5	1581	176.9	7.81	
578802915	PREDICTED: heterogeneous nuclear ribonucleoprotein A3 isoform 1 [Homo sapiens]	23.87	7	5	7	34	1,025	9	4.9	1,143	9	7.7	1267.49	23.87	20	34	331	35.4	9.17	
4506203	proteasome subunit beta type-7 precursor [Homo sapiens]	8.30	1	2	2	3	1,025	2	1.3	1,143	2	25.6	77.45	8.30	3	3	277	29.9	7.68	
578808207	PREDICTED: lateral signaling target protein 2 homolog isoform X4 [Homo sapiens]	0.85	1	1	1	4	1,025	3	2.3	1,243	3	7.3	46.47	0.85	3	4	936	101.4	5.64	
24307939	T-complex protein 1 subunit epsilon [Homo sapiens]	30.68	1	13	13	40	1,024	15	5.5	1,189	15	14.4	1387.64	30.68	35	40	541	59.6	5.66	
165905601	proline-serine-threonine phosphatase-interacting protein 2 [Homo sapiens]	9.88	1	3	3	9	1,024	3	3.7	1,020	3	12.9	284.22	9.88	9	9	334	38.8	8.48	
4506623	60S ribosomal protein L27 [Homo sapiens]	5.88	1	1	1	3	1,024	1		2,110	1		76.00	5.88	3	3	136	15.8	10.56	
530410446	PREDICTED: alpha-2-antiplasmin isoform X6 [Homo sapiens]	39.66	7	13	13	39	1,024	28	7.7	1,137	27	23.1	3459.87	39.66	39	79	464	51.7	6.29	
5821992	ras-related protein Rap-1a isoform 1 precursor [Homo sapiens]	55.43	7	8	8	27	1,049	11	14.2	1,049	11	14.2	1420.15	55.43	37	37	184	20.8	5.78	
578821773	PREDICTED: formin family homolog 3 isoform X1 [Homo sapiens]	36.65	4	18	18	80	1,024	28	5.8	1,202	28	20.5	3684.67	36.65	51	80	463	75.4	6.77	
578798632	PREDICTED: tyrosine kinase Fgr isoform X1 [Homo sapiens]	17.20	92	7	7	28	1,024	7	3.7	1,244	7	19.0	1139.47	17.20	21	28	529	59.4	5.59	
555290081	3'(2',5')-bisphosphate nucleotidase 1 isoform 2 [Homo sapiens]	6.32	6	2	2	8	1,024	3	2.5	1,121	3	1.3	166.21	6.32	5	8	253	27.5	5.33	
56699409	RNA-binding motif protein, X chromosome isoform 1 [Homo sapiens]	11.00	4	2	4	18	1,024	4	1.4	1,242	4	5.0	724.49	11.00	12	18	391	42.3	10.05	
530368014	PREDICTED: spectrin beta chain, non-erythrocytic 1 isoform X2 [Homo sapiens]	15.74	7	28	29	103	1,024	36	5.1	1,232	36	21.6	4273.44	15.74	79	103	2351	272.7	5.64	
4502161	apolipoprotein C-IV precursor [Homo sapiens]	5.51	1	1	1	2	1,024	1		0,959	1		73.89	5.51	2	2	127	14.5	8.92	
6715607	hemoglobin subunit gamma-2 [Homo sapiens]	65.31	1	1	8	240	1,024	2	2.4	1,052	2	7.4	6354.71	65.31	24	240	147	16.1	7.05	
4505891	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 precursor [Homo sapiens]	0.95	1	1	1	2	1,024	2	12.2	1			31.49	0.95	1	2	738	84.7	6.01	
7661728	regulator complex protein LMIFOR2 isoform 1 [Homo sapiens]	32.00	2	3	3	8	1,024	3	8.9	1,390	3	26.9	309.27	32.00	8	8	125	13.5	5.40	
4505701	pyridoxal kinase [Homo sapiens]	41.99	5	8	8	47	1,024	16	6.7	1,123	16	14.8	2519.26	41.99	24	47	312	35.1	6.13	
148762978	uncharacterized protein C9orf172 [Homo sapiens]	0.61	1	2	2	7	1,023	1		1,076	1		113.36	0.61	4	7	976	106.6	9.03	
530396502	PREDICTED: leucine-rich repeat transmembrane protein FLRT1 isoform 1 [Homo sapiens]	1.34	1	1	1	1	1,023	1		1,322	1		22.19	1.34	1	1	674	74.0	6.44	
4504111	growth factor receptor-bound protein 2 isoform 1 [Homo sapiens]	37.33	2	7	7	26	1,023	10	3.8	1,186	10	23.6	1019.21	37.33	20	26	217	25.2	6.32	
530418048	PREDICTED: deoxynucleoside triphosphate triphosphohydrolase SA [Homo sapiens]	6.77	2	3	3	12	1,023	4	8.5	1,028	4	10.0	517.56	6.77	9	12	591	68.1	6.90	
578818565	PREDICTED: vimentin isoform X1 [Homo sapiens]	55.79	51	33	35	345	1,023	124	7.3	1,144	124	12.2	13665.65	55.79	100	345	466	53.6	5.12	
26598323	rad GTP dissociation inhibitor beta isoform 1 [Homo sapiens]	68.76	2	19	27	201	1,023	53	6.6	1,142	53	14.0	9147.25	68.76	78	201	445	59.6	6.47	
108773810	leucine-:RNA ligase, cytoplasmic [Homo sapiens]	1.62	1	1	1	3	1,023	1		1,476	1		205.08	1.62	3	3	1176	134.4	7.30	
5031695	complement factor H-related protein 2 precursor [Homo sapiens]	25.93	3	4	6	32	1,023	9	10.1	1,225	9	18.5	1240.37	25.93	18	32	270	30.6	6.38	
295821193	serum amyloid A-1 protein preproprotein [Homo sapiens]	77.05	18	5	11	118	1,023	27	5.9	1,199	24	19.2	5803.50	77.05	28	118	122	13.5	6.79	
380837121	vesicle-trafficking protein SEC22b precursor [Homo sapiens]	12.56	1	2	2	5	1,023	2	7.2	1,320	2	26.5	124.27	12.56	5	5	215	24.7	8.51	
14210504	AP-1 complex subunit mu-1 isoform 2 [Homo sapiens]	1.89	4	1	1	3	1,023	1		1,119	1		136.78	1.89	3	3	423	48.6	7.30	
14389309	tubulin alpha-1C chain [Homo sapiens]	42.98	6	5	15	135	1,023	9	5.8	1,261	9	12.8	5383.53	42.98	42	135	449	49.9	5.10	
62926054	probable G-protein coupled receptor 179 precursor [Homo sapiens]	0.51	1	1	1	9	1,023	1	5.7	1,351	1	29.5	144.13	0.51	1	9	2367	257.2	5.71	
530391036	PREDICTED: solute carrier family 2, facilitated glucose transporter 1 isoform 1 [Homo sapiens]	2.55	4	1	1	1	1,023	1		1,277	1		0.00	2.55	1	1	314	34.3	7.36	
4504061	N-acetylglucosamine-6-sulfatase precursor [Homo sapiens]	14.37	1	6	6	10	1,023	6	5.7	1,157	6	7.9	772.42	14.37	18	18	552	62.0	8.31	
124494254	proliferation-associated protein 2G4 [Homo sapiens]	32.74	1	10	10	43	1,023	16	5.0	1,120	16	13.1	1612.97	32.74	26	43	294	43.8	6.55	
375477430	T-complex protein 1 subunit delta isoform b [Homo sapiens]	22.99	9	9	9	26	1,022	9	10.4	1,191	8	26	1019.56	22.99	26	26	509	54.7	7.83	
4502101	annexin A1 [Homo sapiens]	77.46	2	31	32	464	1,022	175	9.4	1,168	174	17.7	21807.57	77.46	89	464	346	38.7	7.02	
578807065	PREDICTED: ceruloplasmin isoform X3 [Homo sapiens]	74.93	4	1	62	811	1,022	1		1,033	1		36732.88	74.93	175	811	1065	122.1	5.72	
578826513	PREDICTED: putative V-set and immunoglobulin domain-containing protein 1 [Homo sapiens]	22.83	2	1	3	101	1,022	4	0.8	1,066	4	4.3	6300.74	22.83	9	101	127	14.1	8.84	
24430192	keratin, type I cytoskeletal 16 [Homo sapiens]	36.36	17	7	17	69	1,022	7	6.8	1,056	7	11.2	2535.41	36.36	48	69	473	51.2	5.05	
5031877	lamin-B1 isoform 1 [Homo sapiens]	29.01	2	15	15	58	1,022	21	6.1	1,135	21	14.3	2688.70	29.01	42	1	58	586	66.4	5.16
589946397	roundabout homolog 2 isoform 5 [Homo sapiens]	0.76	6	1	1	1	1,022	1		1,247	1		35.50	0.76	1	1	785	85.4	6.06	
10880979	lymphocyte-specific protein 1 isoform 1 [Homo sapiens]	48.08	6	11	11	70	1,022	28	8.5	1,131	25	15.4	374.52	48.08	10	70	339	37.2	4.74	
4507789	ubiquitin-conjugating enzyme E2 L3 isoform 1 [Homo sapiens]	64.94	3	8	8	33	1,022	12	2.0	1,149	12	12.3	1319.34	64.94	21	33	154	17.9	8.51	
7661920	eukaryotic initiation factor 4A-II [Homo sapiens]	7.79	1	2	3	11	1,022	3	0.8	1,062	3	3.3	385.79	7.79	9	11	411	46.8	6.73	
291084635	60 kDa SS-A/Ro ribonucleoprotein isoform 4 [Homo sapiens]	2.12	5	1	1	2	1,022	1		1,538	1		96.05	2.12	2	2	518	58.4	8.37	
56786155	complement C1q subcomponent subunit C precursor [Homo sapiens]	20.41	1	4	4	44	1,021	15	7.4	1,323	15	20.4	1818.42	20.41	12	44	245	25.8	8.41	
40068518	6-phosphogluconate dehydrogenase, decarboxylating [Homo sapiens]	66.46	1	30	30	419	1,021	155	8.2	1,228	153	20.0	20484.43	66.46	81	419	483	53.1	7.23	
29788785	tubulin beta chain isoform b [Homo sapiens]	64.41	8	5	20	166	1,021	10	7.2	1,240	10	21.0	6917.30	64.41	57	166	444	49.6	4.89	
530408977	PREDICTED: sulfotransferase 1A1 isoform X1 [Homo sapiens]	42.03	7	10	10	55	1,021	20	5.3	1,234	20	25.1	2053.88	42.03	29	55	295	34.1	6.62	
578814724	PREDICTED: maltase-glyucoamylase, intestinal isoform X1 [Homo sapiens]	0.73	1	1	1	3	1,021	1		1,164	1		116.44	0.73	3	3	2753	31.8	5.41	
37577157	calpain-5 [Homo sapiens]	1.09	1	1	1	4	1,021	1		1,149	1		41.12	1.09	2	4	640	73.1	7.64	
88999583	myosin light polypeptide 6 isoform 2 [Homo sapiens]	74.83	4	8	10	168	1,021	43	7.2	1,124	43	14.1	7156.22	74.83	30	168	151	17.0	4.55	
4557351	cholinesterase precursor [Homo sapiens]	1.83	2	1	1	3	1,021	1		1,004	1		191.75	1.83	3	3	602	68.4		

Accession	Description	ZCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# Asns	MW [kDa]	calc. pI
16507237	78 kDa glucose-regulated protein precursor [Homo sapien]	39.45	3	23	25	175	1.019	42	5.0	1.107	42	11.5	8015.86	39.45	71	175	654	72.3	5.16
530406263	PREDICTED: ras-related protein Rab-27A isoform X3 [Homo sapien]	25.60	4	5	20	1.019	7	20	4.6	1.192	7	13.7	904.16	25.60	14	20	168	19.2	5.38
111154090	rho GTPase-activating protein 24 isoform 3 [Homo sapien]	0.77	4	1	1	9	1.019	6	4.0	1.079	6	3.9	78.59	0.77	2	9	653	73.2	6.81
4543481	elongation factor 1-gamma [Homo sapien]	37.53	1	13	13	67	1.019	26	6.4	1.205	26	14.5	2846.89	37.53	36	67	437	50.1	6.67
5454088	acidic leucine-rich nuclear phosphoprotein 32 family member B [Hc]	28.69	13	3	9	72	1.017	11	7.2	1.107	11	15.1	2746.84	28.69	27	72	251	28.8	4.06
311771535	T-complex protein 1 subunit beta isoform 2 [Homo sapien]	11.68	2	5	5	22	1.019	7	6.1	1.057	7	6.8	916.03	11.68	14	22	488	52.7	6.44
6005942	transitional endoplasmic reticulum ATPase [Homo sapien]	57.32	54	36	37	179	1.019	65	5.6	1.144	65	15.1	6780.04	57.32	104	179	806	89.3	5.26
530368148	PREDICTED: macrophage-capping protein isoform X1 [Homo sapien]	69.25	2	14	14	123	1.019	43	8.1	1.218	42	14.0	6265.62	69.25	42	123	348	38.5	6.19
23110942	proteasome subunit alpha-type-5 isoform 1 [Homo sapien]	30.29	2	5	5	25	1.019	9	6.4	1.212	9	10.8	1174.04	30.29	15	25	241	26.4	4.79
530393330	PREDICTED: zinc finger SWIM domain-containing protein 8 isoform	0.61	10	1	1	8	1.018	3	3.0	1.376	3	1.4	139.15	0.61	3	8	1800	193.4	6.99
40385883	ribulose-phosphate 3-epimerase isoform 1 [Homo sapien]	22.81	6	4	4	14	1.018	5	1.1	1.359	5	3.8	847.65	22.81	11	14	228	24.9	5.58
20357529	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	11.47	7	3	3	7	1.018	2	0.2	1.147	2	6.8	488.69	11.47	7	7	340	37.3	6.00
24111023	Tropomyosin alpha-3 chain isoform 2 [Homo sapien]	69.76	20	19	33	246	1.018	51	7.3	1.136	49	13.1	8714.91	69.76	88	246	248	29.0	4.78
20149675	EF-hand domain-containing protein D2 [Homo sapien]	40.83	4	11	11	57	1.018	22	6.2	1.112	22	10.4	2299.16	40.83	30	57	240	26.7	5.20
5453990	proteasome activator complex subunit 1 isoform 1 [Homo sapien]	71.49	4	14	14	62	1.018	25	7.8	1.215	25	17.6	2432.81	71.49	36	62	249	28.7	6.02
530397175	PREDICTED: signal-induced proliferation-associated protein 1 isofo	2.50	1	2	2	6	1.018	2	3.4	1.100	2	14.9	341.00	2.50	6	6	1042	112.1	6.60
530387889	PREDICTED: serine/threonine-protein phosphatase 2A 55 kDa regu	7.99	15	2	2	8	1.018	3	6.7	0.990	3	15.2	325.48	7.99	6	8	288	33.5	6.61
578826102	PREDICTED: tryptophan-tRNA ligase, cytoplasmic isoform X4 [Homo sapien]	43.52	2	16	16	50	1.018	20	5.5	1.117	20	13.9	2132.99	43.52	41	50	471	53.1	6.23
57634536	alpha-related protein 4B [Homo sapien]	0.68	2	1	1	1	1.018	1	1.0	1.201	1	30.85	0.68	1	1	738	80.5	6.92	
66932947	alpha-2-macroglobulin precursor [Homo sapien]	71.71	23	78	87	2369	1.018	685	7.3	1.217	678	21.0	119449.02	71.71	247	2369	1474	163.2	6.42
341543829	dihydropyrimidinase-related protein 2 isoform 3 [Homo sapien]	12.69	11	5	5	16	1.018	6	1.6	1.293	6	6.6	769.58	12.69	13	16	536	58.1	5.81
34577063	adenylosuccinate synthetase isozyme 2 [Homo sapien]	31.80	4	12	12	49	1.018	26	8.8	1.224	26	24.2	3072.83	31.80	33	69	456	50.1	6.55
30410792	proteasome activator complex subunit 2 [Homo sapien]	38.91	4	7	7	30	1.018	11	3.8	1.118	11	10.3	1535.34	38.91	20	30	239	27.4	5.73
188536004	zinc finger protein 469 [Homo sapien]	0.23	1	1	1	1	1.018	1	0.8	1.814	1	34.37	0.23	1	1	3925	409.9	7.72	
662236841	mitogen-activated protein kinase kinase kinase 6 isoform 2 [Homo sapien]	0.47	2	1	1	6	1.018	2	6.2	1.135	2	8.0	80.00	0.47	3	6	1280	141.6	7.18
320202986	alcohol dehydrogenase NAD(P)+ [Homo sapien]	31.69	2	8	8	26	1.017	8	2.9	1.199	8	15.3	1343.90	31.69	23	26	325	36.5	6.79
578818655	PREDICTED: glycopeptide N-tetradecanoyltransferase 2 isoform X1	4.31	6	1	2	5	1.017	1	0.9	0.992	1	156.35	4.31	5	5	441	50.5	6.38	
4507903	serine/threonine-protein kinase VRK1 [Homo sapien]	3.54	3	1	1	3	1.017	1	3	1.347	1	195.33	3.54	3	3	396	45.4	8.48	
4505257	moesin [Homo sapien]	79.03	28	43	59	729	1.017	203	8.2	1.167	198	16.7	24577.23	79.03	167	729	577	67.8	6.40
10863945	X-ray repair cross-complementing protein 5 [Homo sapien]	27.46	3	13	13	81	1.017	28	6.0	1.052	28	16.0	4795.77	27.46	39	81	732	82.7	5.81
19923483	ras-related protein Rab-14 [Homo sapien]	31.63	16	3	4	15	1.017	4	6.3	1.211	4	16.4	876.50	31.63	12	15	215	23.9	6.21
530406418	PREDICTED: tropomyosin alpha-1 chain isoform X18 [Homo sapien]	40.41	29	4	16	113	1.017	5	7.4	1.113	5	11.0	3802.20	40.41	43	113	245	28.5	4.78
530403015	PREDICTED: WD repeat and HMG-box DNA-binding protein 1 isofo	1.09	1	1	1	2	1.017	1	1	1.138	1	40.99	1.09	2	2	825	92.7	5.52	
530396910	PREDICTED: synaptotagmin-like protein 2 isoform X3 [Homo sapien]	0.37	4	1	1	2	1.017	1	1.9	1.926	1	35.39	0.37	2	2	1602	178.3	5.72	
530384472	PREDICTED: chromobox protein homolog 3 isoform X1 [Homo sapien]	55.74	3	7	8	46	1.017	16	8.8	1.166	15	15.5	1539.57	55.74	23	46	183	20.8	5.33
4758638	peroxiredoxin-6 [Homo sapien]	70.98	1	15	15	105	1.017	40	5.9	1.105	39	15.5	4701.64	70.98	43	105	224	25.0	6.38
133958809	inter-alpha-trypsin inhibitor heavy chain H3 preproprotein [Homo sapien]	23.71	4	16	16	111	1.017	41	6.7	1.102	41	16.3	4969.07	23.71	47	111	890	99.8	5.74
530426021	PREDICTED: attractin isoform X2 [Homo sapien]	9.99	3	9	9	39	1.017	14	4.2	1.132	14	10.8	1546.39	9.99	39	1111	122.9	6.81	
4502133	serum amyloid P-component precursor [Homo sapien]	29.60	1	7	7	86	1.017	33	5.6	1.276	33	11.7	3352.92	29.60	27	86	223	25.4	6.54
296011003	abl interactor 1 isoform 1 [Homo sapien]	3.34	17	1	1	3	1.017	1	1	1.154	1	124.88	3.34	3	3	329	35.9	5.06	
260436922	suprabasin isoform 1 precursor [Homo sapien]	9.15	1	2	2	6	1.017	2	8.3	1.041	2	6.3	312.40	9.15	6	6	590	60.5	7.01
4506003	serine/threonine-protein phosphatase PP1-alpha catalytic subunit i	29.70	6	3	8	50	1.017	5	2.2	1.030	5	4.9	1655.83	29.70	22	50	330	37.5	6.33
10947139	arginase-1 isoform 2 [Homo sapien]	66.15	2	14	14	105	1.017	37	4.8	1.197	37	15.9	4564.48	66.15	41	105	322	34.7	7.21
362033927	astrocytic phosphoprotein PEA-15 isoform c [Homo sapien]	9.26	3	1	2	1	1.017	1	0.9	0.944	1	102.66	9.26	2	2	108	12.5	5.17	
216548487	protein-arginine desiminase type-4 [Homo sapien]	50.23	5	25	26	263	1.017	90	7.6	1.175	90	16.5	10898.00	50.23	77	263	663	74.0	6.58
635372016	endose-phosphatase E1 isoform 2 [Homo sapien]	12.32	2	1	1	3	1.017	1	1.2	1.200	1	207.12	12.32	3	3	173	19.2	5.61	
555943829	solute carrier family 2, facilitated glucose transporter member 14 isoform 1 [Homo sapien]	2.68	5	1	1	3	1.017	1	0.8	1.087	1	102.21	2.68	2	3	411	44.9	7.80	
112421122	dnal homolog subfamily C member 13 [Homo sapien]	0.85	2	2	2	5	1.016	2	3.0	1.206	2	19.9	173.85	0.85	5	5	2243	254.3	6.74
19923142	importin subunit beta-1 isoform 1 [Homo sapien]	12.21	2	9	9	39	1.016	14	5.7	1.165	14	16.0	1591.84	12.21	27	39	876	97.1	4.78
578815934	PREDICTED: triple QxxK/R motif-containing protein isoform X1 [Homo sapien]	6.98	1	1	1	3	1.016	1	1	1.231	1	101.70	6.98	3	3	86	9.7	9.36	
578815687	PREDICTED: 60S ribosomal protein L7 isoform X1 [Homo sapien]	9.13	2	1	1	5	1.016	2	2.3	1.050	2	11.2	229.23	9.13	3	5	208	24.4	10.67
4505763	phosphoglycerate kinase 1 [Homo sapien]	81.77	1	26	32	548	1.016	155	9.1	1.155	155	13.1	23325.12	81.77	92	548	417	44.6	8.10
282721079	sushi repeat-containing protein SRPK isoform 4 precursor [Homo sapien]	1.58	4	1	1	1	1.016	1	1	1.778	1	23.10	1.58	1	1	379	41.7	8.69	
578819488	PREDICTED: calcium/calmodulin-dependent protein kinase type II	2.67	22	1	1	2	1.016	1	1	1.145	1	74.44	2.67	1	2	337	36.7	9.16	
88703045	proline-rich protein 11 [Homo sapien]	1.94	1	1	1	1	1.016	1	1	2.616	1	23.44	1.94	1	1	360	40.1	10.11	
58830313	endoplasmic reticulum resident protein 29 isoform 1 precursor [Homo sapien]	31.03	2	6	6	38	1.016	14	5.3	1.159	14	13.9	1555.54	31.03	16	38	261	29.0	7.31
578822199	PREDICTED: neutrophil collagenase isoform X1 [Homo sapien]	43.24	2	15	15	186	1.016	65	4.3	1.127	64	11.2	9780.80	43.24	43	186	444	50.8	6.66
4826686	ATP-dependent RNA helicase DDX1 [Homo sapien]	2.84	1	1	1	11	1.016	4	3.7	1.184	4	16.9	678.82	2.84	3	11	740	82.4	7.23
194394158	nicotinate phosphoribosyltransferase isoform 1 [Homo sapien]	44.24	2	16	16	80	1.015	30	6.0	1.133	30	19.9	3943.08	44.24	43	80	538	57.5	5.68
5031635	cofilin-1 [Homo sapien]	80.12	20	22	22	275	1.015	99	10.2	1.157	99	12.6	10448.46	80.12	65	275	166	18.5	8.09
51873067	sulphydryl oxidase 1 isoform b precursor [Homo sapien]	22.68	2	11	11	46	1.015	16	6.2	1.176	16	18.9	1742.16	22.68	32	46	604	66.8	8.56
111496277	regulator complex protein LAMTOR3 isoform 1 [Homo sapien]	41.13	2	2	2	6	1.015	2	7.8	1.111	2	3.6	388.18	41.13	13	6	124	13.6	7.34
4506381	ras-related C3 botulinum toxin substrate 2 [Homo sapien]	53.65	6	4	9	73	1.015	18	4.9	1.647	16	21.2	2942.70	53.65	22	73	192	21.4	7.61
4501891	alpha-actinin-1 isoform b [Homo sapien]	74.89	44	38	61	592	1.015	116	16.6	1.130	112	16.6	25616.81	74.89	173	592	892	103.0	5.41
4507877	vinculin isoform VCL [Homo sapien]	59.10	4	53	53	283	1.015	103	7.5	1.192	102	15.1	14969.72	59.10	152	283	1066	116.6	6.05
6912586	6-phosphogluconolactonase [Homo sapien]	42.25	2	8	8	43	1.015	16	4.8	1.188	16	28.2	1964.01	42.25	23				

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability (%)	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability (%)	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
10835063	nucleophosmin isoform 1 [Homo sapiens]	36.73	5	9	9	58	1.014	21	6.6	1.183	21	15.4	3001.16	36.73	24	58	294	32.6	4.78
530360487	PREDICTED: protein DJ-1 isoform X1 [Homo sapiens]	77.78	1	14	14	153	1.014	53	8.4	1.148	53	10.0	7899.22	77.78	40	153	189	19.9	6.79
32313593	olfactomedin-4 precursor [Homo sapiens]	18.63	2	9	9	37	1.014	13	4.8	1.150	13	16.1	1427.38	18.63	35	37	510	57.2	5.69
4507725	anaphyretin precursor [Homo sapiens]	77.55	5	12	12	448	1.014	156	10.8	1.200	154	23.3	23290.05	77.55	26	448	147	15.9	5.76
38054324	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1 [Homo sapiens]	2.67	1	1	1	9	1.014	4	5.3	1.158	4	4.9	120.31	2.67	3	9	300	34.3	7.65
530397480	PREDICTED: phosphatidylinositol-binding clathrin assembly protein	10.79	26	5	5	18	1.014	6	6.1	1.108	6	17.2	1117.47	10.79	15	18	547	59.7	8.70
29789823	WD repeat-containing protein 75 [Homo sapiens]	1.08	1	1	1	1	1.014	1		2.470	1		40.29	1.08	1	1	830	94.4	5.96
194248072	heat shock 70 kDa protein 1A1B [Homo sapiens]	63.03	1	29	33	581	1.014	184	7.6	1.172	179	15.9	29094.94	63.03	95	581	641	70.0	5.66
4826659	F-actin-capping protein subunit beta isoform 1 [Homo sapiens]	67.65	5	18	18	165	1.014	62	6.5	1.253	61	18.3	7312.89	67.65	62	165	272	30.6	6.00
115529463	serine/threonine-protein kinase D1 [Homo sapiens]	0.55	2	1	1	5	1.014	2	6.9	1.683	2	22.4	48.32	0.55	3	5	912	101.6	6.62
87196339	collagen alpha-1(VI) chain precursor [Homo sapiens]	10.51	2	8	8	34	1.014	12	4.7	1.074	12	4.6	1277.58	10.51	24	34	1028	108.5	5.43
578813403	PREDICTED: glycine-tRNA ligase isoform X1 [Homo sapiens]	3.73	2	2	2	12	1.014	4	3.1	1.063	4	10.7	452.12	3.73	6	12	616	69.9	6.13
530434751	PREDICTED: LOW QUALITY PROTEIN: double homeobox protein 4	1.67	3	1	1	11	1.014	5	2.2	1.365	5	6	165.91	1.67	3	11	418	44.9	8.53
4885393	hemoglobin subunit epsilon [Homo sapiens]	18.37	1	3	3	218	1.013	5	7.5	1.070	5	5.4	5218.29	18.37	9	218	147	16.2	8.63
530382704	PREDICTED: serine/threonine-protein kinase RIO1 isoform X2 [Homo sapiens]	1.51	2	1	1	1	1.013	1		1.919	1		21.34	1.51	1	1	464	53.8	8.91
530380520	PREDICTED: annexin A6 isoform X2 [Homo sapiens]	67.62	11	40	41	408	1.013	146	6.5	1.148	143	12.3	16615.12	67.62	120	408	667	75.2	5.67
8393638	junctional adhesion molecule A precursor [Homo sapiens]	4.01	1	1	1	2	1.013	2	6.5				45.84	4.01	1	2	299	32.6	7.90
4557701	keratin, type I cytoskeletal 17 [Homo sapiens]	28.01	15	4	12	54	1.013	5	2.8	1.090	5	11.0	1578.61	28.01	33	54	432	48.1	5.02
38788353	regulator complex protein LIMTORS [Homo sapiens]	17.34	1	2	2	18	1.013	6	3.5	1.080	6	3.9	730.54	17.34	6	18	173	18.1	5.50
18491024	dipeptidyl peptidase 3 isoform 1 [Homo sapiens]	10.04	2	6	6	26	1.013	9	5.6	1.151	9	3.4	1557.13	10.04	16	26	737	82.5	5.10
40313626	thrombospondin-1 precursor [Homo sapiens]	2.31	2	2	2	5	1.013	2	4.8	1.121	2	10.1	352.64	2.31	2	5	170	129.3	4.94
48303549	argininosuccinate lyase isoform 3 [Homo sapiens]	6.16	4	3	3	16	1.013	6	3.4	1.166	6	9	316.94	6.16	9	16	438	48.7	6.13
578837549	PREDICTED: DEP domain-containing protein 5 isoform X10 [Homo sapiens]	0.34	8	1	1	20	1.013	19	2.9	2.373	19	31.9	142.75	0.34	1	20	1490	168.2	6.80
55749504	synectin-1 isoform 2 [Homo sapiens]	2.05	4	1	1	3	1.013	1		1.302	1		79.02	2.05	3	3	292	31.7	7.53
47132622	S-methyl-5'-thioadenosine phosphorylase [Homo sapiens]	22.61	1	4	4	18	1.013	6	7.8	1.092	6	4.5	1003.69	22.61	12	18	283	31.2	7.18
6912388	grancalcin [Homo sapiens]	44.70	6	9	9	60	1.013	20	4.7	1.140	20	17.0	2698.54	44.70	25	60	217	24.0	5.21
578838327	PREDICTED: rik-related protein kinase isoform X4 [Homo sapiens]	0.33	4	1	1	2	1.013	1		1.116	1		33.89	0.33	2	2	1526	171.9	6.34
154146191	heat shock protein HSP 90-alpha isoform 2 [Homo sapiens]	50.82	16	23	39	344	1.013	68	9.1	1.143	66	14.4	15165.21	50.82	108	344	732	84.6	5.02
4758304	protein disulfide-isomerase A4 precursor [Homo sapiens]	4.50	2	3	3	11	1.013	4	0.8	9	4	12.3	496.62	4.50	9	11	645	72.9	5.07
54632005	1-phosphatidylinositol 4,5-bisphosphate phospholipase beta-2	1.71	30	3	3	4	1.013	1		1.265	1		49.60	1.71	4	4	1170	132.4	6.29
589908406	dipeptidyl aminopeptidase-like protein 6 isoform 5 [Homo sapiens]	1.42	10	1	1	9	1.012	4	3.6	1.132	4	10.1	81.68	1.42	3	9	353	38.7	8.27
120433590	acyl-CoA-binding protein isoform 3 [Homo sapiens]	62.07	7	5	5	45	1.012	18	4.2	1.133	18	9.9	1711.91	62.07	14	45	87	10.0	6.57
530402312	PREDICTED: high mobility group protein B1 isoform X1 [Homo sapiens]	52.09	2	8	14	126	1.012	31	5.0	1.132	30	8.9	4205.85	52.09	35	126	215	24.9	5.74
530406334	PREDICTED: sorting nexin-1 isoform X2 [Homo sapiens]	2.76	7	1	1	3	1.012	1		1.065	1		221.55	2.76	3	3	399	46.4	9.19
10800140	histone H2B type 1-B [Homo sapiens]	69.84	14	2	12	186	1.012	7	4.2	1.113	7	15.4	7508.67	69.84	34	186	126	13.9	10.32
58218968	calmodulin [Homo sapiens]	52.35	4	11	11	117	1.012	44	7.9	1.152	44	32	5438.50	52.35	32	117	149	16.8	4.22
7706441	vacuolar protein sorting-associated protein 29 isoform 1 [Homo sapiens]	29.12	5	6	5	20	1.012	6	6.3	1.090	6	7.5	725.86	29.12	16	20	182	20.5	6.79
4505029	leukotrienin A-4 hydrolase isoform 1 [Homo sapiens]	46.45	6	40	40	290	1.012	105	6.3	1.161	104	11.4	12044.46	46.45	49	290	611	49.2	6.18
16418467	leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]	49.86	2	13	14	146	1.012	48	7.4	1.206	48	16.7	6171.03	49.86	41	146	347	38.2	6.95
15149476	arginine-tRNA ligase, cytoplasmic [Homo sapiens]	1.21	1	1	1	3	1.012	1		1.248	1		81.56	1.21	3	3	660	75.3	6.68
530384149	PREDICTED: ribonuclease T2 isoform X1 [Homo sapiens]	29.36	3	4	4	10	1.012	4	10.0	1.098	4	9.0	344.84	29.36	10	10	218	25.3	6.06
578823404	PREDICTED: ETS domain-containing protein Elk-3 isoform X1 [Homo sapiens]	1.47	1	1	1	3	1.012	2	3.8	1.074	2	16.2	42.66	1.47	2	3	407	44.2	8.95
5454158	valine-tRNA ligase [Homo sapiens]	2.37	3	3	3	6	1.012	3	2.7	1.247	3	7.1	220.37	2.37	6	6	1264	140.4	7.59
34577112	fructose-bisphosphate aldolase A isoform 1 [Homo sapiens]	93.96	2	26	33	518	1.012	161	8.0	1.175	160	18.5	24323.56	93.96	98	518	364	39.4	8.08
390635651	ras-related protein Rab-44 [Homo sapiens]	4.41	1	2	2	6	1.012	2	8.2	1.046	2	6.2	447.40	4.41	6	6	1021	110.8	5.09
530416279	PREDICTED: glucose-6-phosphate isomerase isoform X2 [Homo sapiens]	67.92	6	32	33	539	1.012	200	7.9	1.208	199	18.9	22373.17	67.92	95	539	558	63.1	8.32
16579888	fructose-1,6-bisphosphatase 1 [Homo sapiens]	17.16	2	4	4	19	1.012	7	9.3	1.092	7	16.3	994.38	17.16	12	19	338	36.8	6.99
4505185	macrophage migration inhibitory factor [Homo sapiens]	65.22	3	3	3	23	1.012	8	3.8	1.148	8	9.6	634.24	65.22	9	23	115	12.5	7.88
530420291	PREDICTED: gamma-parvin isoform X2 [Homo sapiens]	3.63	1	1	1	6	1.012	2	7.6	1.313	2	5.4	256.85	3.63	3	6	331	37.5	5.49
156139127	uncharacterized protein C10orf88 [Homo sapiens]	1.12	7	1	1	44	1.012	18	9.0	1.273	18	23.8	468.90	1.12	3	44	445	49.2	6.25
4505529	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	51.24	1	8	14	524	1.012	125	7.7	1.238	125	19.2	18538.23	51.24	42	524	201	23.6	5.11
13324688	WD repeat-containing protein 11 [Homo sapiens]	0.65	1	1	1	1	1.012	1		1.294	1		34.55	0.65	1	1	1224	136.6	6.92
530388884	PREDICTED: zinc finger protein ZFP62 isoform X1 [Homo sapiens]	0.46	2	1	1	1	1.012	1		1.128	1		32.83	0.46	1	1	1082	120.7	6.55
530401389	PREDICTED: 60S ribosomal protein L6 isoform X1 [Homo sapiens]	5.98	2	1	1	3	1.012	1		1.072	1		65.80	5.98	3	3	177	20.4	10.52
156937236	purpurycin-sensitive aminopeptidase [Homo sapiens]	18.39	8	13	13	52	1.011	19	5.1	1.141	19	9.4	2039.37	18.39	37	52	919	103.2	7.92
530418357	PREDICTED: serine/threonine-protein kinase 4 isoform X4 [Homo sapiens]	3.46	5	1	1	3	1.011	1		1.219	1		196.14	3.46	3	3	462	52.3	5.00
5031857	L-lactate dehydrogenase A chain isoform 1 [Homo sapiens]	78.61	10	24	26	447	1.011	141	7.8	1.219	140	16.0	17510.25	78.61	77	447	332	36.7	8.27
157649073	adenylyl cyclase-associated protein 1 [Homo sapiens]	80.42	3	32	32	470	1.011	179	8.6	1.179	171	17.7	19995.71	80.42	93	470	475	51.6	8.02
4758092	di-N-acetylcholinesterase precursor [Homo sapiens]	7.53	1	2	2	4	1.011	2	5.2	1.188	2	22.0	259.80	7.53	4	4	385	43.7	6.64
6912516	mitochondrial peptide methionine sulfoxide reductase isoform A precursor [Homo sapiens]	34.47	4	6	6	18	1.011	7	12.5	1.059	7	8.8	648.01	34.47	16	18	235	26.1	8.09
530382450	PREDICTED: dystonin isoform X17 [Homo sapiens]	0.50	1	1	2	6	1.011	1		1.259	1		68.11	0.50	4	6	3186	368.9	6.76
148596949	nucleolar and colled-body phosphoprotein 1 isoform 2 [Homo sapiens]	0.72	4	1	1	6	1.011	2	3.9	1.099	2	1.5	73.62	0.72	3	6	699	73.6	9.47
530361117	PREDICTED: heterotrimeric protein 1-binding protein 3 isoform X1 [Homo sapiens]	15.34	3	9	9	33	1.011	14	8.3	1.152	14	7.4	1249.70	15.34	33	515	57.2	9.76	
46629203	NME1-NME2 protein [Homo sapiens]	71.54	7	6	15	151	1.011	25	6.1	1.085	25	11.5	5242.34	71.54	41	151	267	30.1	8.92
4502149	apolipoprotein A-II preproprotein [Homo sapiens]	74.00	6	12	12	248	1.011	91	9.6	1.187	89	22.6	9030.19	74.00	34	248	100	11.2	6.62
578833114	PREDICTED: microtubule-associated serine/threonine-protein kinase 1 [Homo sapiens]	0.53	4	1	1	1	1.011	1		1.662	1		20.18	0.53	1	1	1314	143.4	8.06
578800587	PRED																		

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score	AB: 115/114	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
55743122	retinol-binding protein 4 precursor [Homo sapiens]	72.64	35	10	10	140	1,009	55	9.2	1.141	55	16.0	5608.45	72.64	30	140	201	23.0	6.07	
530402335	PREDICTED: plastin-2 isoform X2 [Homo sapiens]	87.40	15	50	50	867	1,009	301	8.0	1.204	301	15.3	38935.55	87.40	147	867	627	70.2	5.43	
156071465	rho GTPase-activating protein 4 isoform 2 [Homo sapiens]	12.26	2	7	7	20	1,009	7	7.3	1.161	7	2	1122.18	12.26	20	946	105.0	6.34		
94536842	ribiose-5-phosphatase isomerase [Homo sapiens]	17.36	1	4	4	12	1,009	5	0.9	1.079	5	13.9	546.15	17.36	11	12	231	33.2	8.54	
6466450	catechol O-methyltransferase isoform 5-CONT [Homo sapiens]	6.39	2	1	1	3	1,009	1	1.118	1	1	2	180.08	6.39	3	3	231	24.4	5.33	
4503011	carboxypeptidase N catalytic chain precursor [Homo sapiens]	14.41	1	4	4	23	1,009	8	6.9	1.268	8	16.8	930.09	14.41	12	23	458	52.3	7.34	
4502565	calpain small isoform 1 [Homo sapiens]	37.31	3	5	8	60	1,009	16	6.2	1.207	16	16.8	2767.69	37.31	24	60	268	28.3	5.20	
16963415	complement component C6 precursor [Homo sapiens]	32.12	5	23	23	102	1,009	36	9.4	1.225	36	23.9	4429.34	32.12	67	102	934	104.7	6.76	
578821763	PREDICTED: calpain-1 catalytic subunit isoform X1 [Homo sapiens]	24.93	1	15	15	64	1,009	23	7.2	1.214	22	64	16.0	2348.23	24.93	45	64	714	81.8	5.67
23238211	actin-related protein 2/3 complex subunit 2 [Homo sapiens]	73.00	2	21	21	248	1,009	90	7.9	1.162	90	14.9	9851.15	73.00	59	248	300	34.3	7.36	
4507521	transketolase isoform 1 [Homo sapiens]	69.50	14	39	40	654	1,009	264	8.7	1.173	232	14.7	36764.91	69.50	115	654	623	67.8	7.66	
57863257	T-complex protein 1 subunit alpha isoform a [Homo sapiens]	32.37	3	14	14	51	1,009	18	4.7	1.079	17	6.9	2069.42	32.37	3	51	556	60.3	6.11	
27544041	unconventional myosin-II [Homo sapiens]	25.87	5	19	19	101	1,009	36	6.5	1.226	36	20.7	4998.04	25.87	55	101	1098	124.8	9.11	
207029439	histone-binding protein RBBP4 isoform c [Homo sapiens]	3.85	2	2	2	2	1,009	1	0.825	1	1	39.96	3.85	2	39	39	43.5	4.96		
347582619	charged multivesicular body protein 2b isoform 5 [Homo sapiens]	5.81	2	1	1	3	1,009	1	1.149	1	1	133.27	5.81	3	3	172	19.1	6.24		
537361067	armadillo repeat-containing protein 8 isoform 5 [Homo sapiens]	1.17	7	1	1	1	1,009	1	1.291	1	1	19.79	1.17	1	1	600	67.1	6.73		
20070130	transcription factor BTF3 isoform B [Homo sapiens]	3.70	2	1	1	3	1,009	1	4.462	1	1	93.58	3.70	3	3	162	17.7	7.50		
154759259	spectrin alpha chain, non-erythrocytic 1 isoform 2 [Homo sapiens]	26.90	20	52	53	185	1,009	66	6.7	1.139	66	13.4	8511.06	26.90	147	185	2472	284.4	5.35	
530394656	PREDICTED: STE20-like serine/threonine-protein kinase isoform X1	7.23	2	6	7	16	1,009	5	9.1	1.061	5	22.7	663.89	7.23	16	1204	138.9	5.10		
6912238	peroxiredoxin-5, mitochondrial isoform a precursor [Homo sapiens]	45.79	4	10	10	135	1,008	50	9.2	1.154	50	13.7	5775.84	45.79	29	135	214	22.0	8.57	
530370030	PREDICTED: foliculin-interacting protein 2 isoform X6 [Homo sapiens]	0.58	1	1	1	1	1,008	1	1	1	1	19.45	0.58	1	1	1040	118.7	5.13		
4502511	complement component C9 precursor [Homo sapiens]	44.19	14	21	21	207	1,008	77	9.4	1.244	75	21.5	7958.91	44.19	57	207	559	63.1	5.59	
4503571	alpha-enolase isoform 1 [Homo sapiens]	78.34	14	25	30	1155	1,008	354	7.1	1.181	354	17.8	57282.38	78.34	87	1155	434	47.1	7.39	
530406429	PREDICTED: pro-cathepsin H isoform X2 [Homo sapiens]	3.70	2	1	1	3	1,008	1	1.122	1	1	114.83	3.70	3	3	297	33.2	8.19		
56682959	ferritin heavy chain [Homo sapiens]	73.22	1	9	9	71	1,008	27	9.3	1.044	27	9.6	3360.94	73.22	26	71	183	21.2	5.55	
4885375	histone H1.2 [Homo sapiens]	56.81	33	6	19	336	1,008	14	3.6	1.061	14	6.8	14857.95	56.81	52	336	213	21.4	10.93	
47132589	serine/threonine-protein kinase N1 isoform 2 [Homo sapiens]	1.59	40	1	2	5	1,008	1	1.284	1	1	80.61	1.59	5	5	942	103.9	6.37		
91208426	pre-mRNA-processing-splicing factor 8 [Homo sapiens]	1.67	1	3	3	7	1,008	3	3.2	1.191	3	3.8	395.69	1.67	7	7	2335	273.4	8.84	
122939159	protein-arginine deiminase type-2 [Homo sapiens]	22.41	1	10	11	41	1,008	11	5.2	1.188	11	16.2	1764.60	22.41	11	41	665	75.5	5.59	
255958306	perlecan 3 isoform 3 [Homo sapiens]	34.12	3	8	8	25	1,008	9	2.8	1.156	9	28.5	1380.94	34.12	21	25	422	45.8	5.43	
530410617	PREDICTED: 14-3-3 protein epsilon isoform X1 [Homo sapiens]	59.17	2	15	18	178	1,008	37	7.5	1.152	37	7.5	6883.28	59.17	53	178	240	27.4	4.89	
110611226	protein unc-13 homolog B [Homo sapiens]	0.31	2	1	1	3	1,008	1	2.274	1	1	41.63	0.31	3	3	1591	180.6	5.99		
23943880	methylthioribose-1-phosphate isomerase isoform 2 [Homo sapiens]	2.48	2	1	1	4	1,008	4	3.9	2.344	4	27.6	46.35	2.48	1	4	322	34.5	5.69	
315075331	SAAL2-SAA2 protein precursor [Homo sapiens]	40.38	3	5	9	101	1,008	24	5.0	1.180	24	26.5	3886.73	40.38	25	101	208	23.3	8.98	
530398067	PREDICTED: apolipoprotein A-I isoform X1 [Homo sapiens]	86.14	61	32	35	1250	1,008	460	8.2	1.247	454	20.5	45665.02	86.14	104	1250	267	30.8	5.76	
578813931	PREDICTED: protein CASP isoform X8 [Homo sapiens]	0.47	6	1	1	5	1,008	2	0.3	1.473	2	24.0	95.94	0.47	3	5	1494	163.1	5.81	
530362835	PREDICTED: suppressor of tumorigenicity 7 protein-like isoform X3	1.77	5	1	1	1	1,008	1	1.273	1	1	29.89	1.77	1	1	453	51.7	7.15		
578821106	PREDICTED: E11 domain-containing protein 1 isoform X1 [Homo sapiens]	35.58	4	14	14	51	1,008	18	6.3	1.207	18	25.4	2223.25	35.58	39	51	534	60.4	6.83	
4503303	neutrophil defensin 4 precursor [Homo sapiens]	1.15	1	1	1	1	1,008	1	1.199	1	1	20.15	5.15	1	1	97	10.5	8.02		
9951915	adenosylhomocysteinase isoform 1 [Homo sapiens]	38.89	9	16	16	66	1,008	22	5.5	1.133	22	4.8	2920.80	38.89	44	66	432	47.7	6.34	
22035620	apoptosis-associated speck-like protein containing a CARD isoform	61.36	3	9	9	58	1,008	20	5.5	1.157	20	25.5	2357.18	61.36	26	58	176	20.0	5.95	
543583725	prostaglandin E synthase 3 isoform f [Homo sapiens]	18.35	8	2	2	7	1,007	3	6.9	1.287	3	21.6	433.31	18.35	5	7	109	12.7	5.59	
5031749	non-histone chromosomal protein HMG-17 [Homo sapiens]	42.22	1	4	4	23	1,007	11	6.9	1.130	11	11.5	982.83	42.22	9	23	90	9.4	9.99	
578803217	PREDICTED: protein dpy-30 homolog isoform X5 [Homo sapiens]	20.20	2	1	1	3	1,007	1	1.193	1	1	204.21	20.20	3	3	99	11.2	4.88		
571026657	BRIC3 and BRCA1-A complex member 1 isoform 2 [Homo sapiens]	13.39	2	2	2	6	1,007	2	3.5	0.978	2	24.2	471.18	13.39	6	6	254	28.1	4.54	
528078313	neutrophil cytosol factor 1 [Homo sapiens]	59.74	3	21	21	190	1,007	71	6.8	1.185	71	17.6	8791.64	59.74	51	190	390	44.7	9.13	
223029410	tail-1 [Homo sapiens]	46.32	10	78	78	418	1,007	154	7.1	1.166	150	17.0	21142.13	46.32	224	418	2541	269.6	6.07	
532164704	clef1 lip and palate transmembrane protein 1 isoform 3 [Homo sapiens]	1.37	1	1	1	1	1,007	1	0.963	1	1	30.29	1.37	1	1	655	75.1	6.64		
530421543	PREDICTED: ubiquitin-like modifier-activating enzyme 1 isoform X3	40.83	3	31	32	191	1,007	68	7.0	1.141	68	12.6	9720.01	40.83	88	191	1058	117.8	5.76	
115298678	complement C3 precursor [Homo sapiens]	87.61	1	149	151	4844	1,007	1739	8.2	1.264	1679	24.6	230448.65	87.61	433	4844	1663	187.0	6.40	
530398338	PREDICTED: alpha-tectorin isoform X1 [Homo sapiens]	0.47	2	1	1	7	1,007	3	8.8	1.170	3	10.2	94.16	0.47	3	7	2150	238.8	5.39	
4506669	60S acidic ribosomal protein P1 isoform 1 [Homo sapiens]	14.04	1	1	1	3	1,007	1	1.187	1	1	165.18	14.04	3	3	114	11.5	4.32		
38455402	neutrophil gelatinase-associated lipocalin precursor [Homo sapiens]	70.21	1	16	16	443	1,007	159	8.8	1.188	155	18.9	16980.65	70.21	48	443	198	22.6	8.99	
7194597	staphylococcal nuclease domain-containing protein 1 [Homo sapiens]	11.66	1	7	7	20	1,007	7	5.7	1.139	7	6.7	792.44	11.66	6.1	20	910	101.9	7.17	
5714447	guanine nucleotide-binding protein subunit beta-2-like 1 [Homo sapiens]	16.40	1	8	8	40	1,099	8	9.5	506.72	8	16	506.72	16.40	21	317	35.1	7.99		
73858656	heparin cofactor 2 precursor [Homo sapiens]	48.10	2	21	21	173	1,007	61	4.4	1.238	60	20.7	5991.11	48.10	55	173	499	57.0	6.90	
302318952	PML-RARA-regulated adapter molecule 1 [Homo sapiens]	22.99	2	10	10	37	1,007	15	5.4	1.070	15	13.7	1180.35	22.99	26	37	670	73.9	9.67	
4506787	ras GTPase-activating-like protein IQGAP1 [Homo sapiens]	51.30	3	59	62	309	1,007	106	7.7	1.186	104	17.0	14210.01	51.30	175	309	1657	189.1	6.87	
530364093	PREDICTED: TFIIH basal transcription factor complex helicase XPB	1.67	2	1	1	4	1,007	2	12.8	1.835	2	195.1	47.34	1.67	4	4	718	81.9	7.48	
530385095	PREDICTED: src kinase-associated phosphoprotein 2 isoform X1 [Homo sapiens]	17.83	1	6	6	27	1,007	11	5.2	1.279	11	29.0	764.60	17.83	16	27	359	41.2	4.69	
530382085	PREDICTED: ribosylidihydroxycinnamide dehydrogenase [quinone]	46.32	2	8	8	35	1,007	13	7.7	1.060	13	14.1	1537.29	46.32	22	35	231	25.9	6.29	
530398960	PREDICTED: dynamin-1-like protein isoform X2 [Homo sapiens]	4.26	8	2	2	4	1,007	2	4.6	1.301	2	9.8	306.61	4.26	4	4	587	65.3	7.49	
19923106	serum paraoxonase/arylesterase 1 precursor [Homo sapiens]	44.23	6	10	10	79	1,006	27	6.7	1.304	26	20.3	3558.35	44.23	29	79	355	52.2	5.22	
459642365	dynein heavy chain 11, axonemal [Homo sapiens]	0.22	1	2	2	22	1,006	2	2.2	1.418	2	22.0	186.73	0.22	6	22	4516	520.0	6.44	
21614499	ezrin [Homo sapiens]	39.42	31	14	27	226	1,006	30	6.1	1.105	30	13.8	6927.74	39.42	79	226	586	69.4	6.27	
327315343	soritin isoform 2 [Homo sapiens]	1.73	4	1	2	7	1,006	2	0.6	1.158	2	5.5	93.00							

Accession	Description	ZCoverage	Z# Proteins	Z# Unique Peptides	Z# Peptides	Z# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
19913412	major vault protein isoform 1 [Homo sapiens]	36.95	3	22	22	94	1.005	32	7.8	1.087	30	14.7	4154.85	36.95	64	94	893	99.3	5.48	
530405396	PREDICTED: tyrosine-protein kinase CSK isoform X1 [Homo sapiens]	11.56	1	3	3	9	1.005	3	5.2	1.206	3	28.2	364.88	11.56	9	28.2	450	50.7	7.06	
47157322	protein kinase C beta type isoform 1 [Homo sapiens]	6.71	14	4	5	12	1.005	4	0.7	1.103	4	14.5	315.90	6.71	12	12	671	76.8	7.01	
4557325	apoptopogonin E precursor [Homo sapiens]	48.26	2	13	13	110	1.005	37	4.2	1.500	36	19.3	5401.50	48.26	38	110	517	36.1	5.73	
4557014	catalase [Homo sapiens]	71.73	1	36	36	478	1.009	172	7.6	1.099	172	10.4	20310.95	71.73	103	478	537	59.7	7.39	
491227401	sacsin isoform 2 [Homo sapiens]	0.45	3	2	2	2	1.005	2	4.3	1.087	2	20.2	33.77	0.45	2	2	4432	504.2	7.03	
4757900	calreticulin precursor [Homo sapiens]	58.99	1	17	17	105	1.005	42	8.7	1.146	41	12.2	4010.59	58.99	44	105	417	48.1	4.44	
11596859	39S ribosomal protein L17, mitochondrial [Homo sapiens]	4.57	1	1	1	4	1.005	2	2.9	3.057	2	10.7	50.88	4.57	3	4	175	20.0	10.11	
5803187	transaldolase [Homo sapiens]	58.16	2	26	26	335	1.005	130	6.8	1.178	130	13.5	11456.47	58.16	335	337	37.5	6.81		
4885165	cystatin-A [Homo sapiens]	30.61	1	2	2	9	1.005	3	13.6	1.156	3	7.2	634.19	30.61	6	9	98	11.0	5.50	
297206833	5-hydroxytryptamine receptor 4 isoform d [Homo sapiens]	1.67	6	1	1	2	1.005	1		1.126	1		28.67	1.67	2	2	360	40.9	8.28	
261399909	rho GTPase-activating protein 25 isoform c [Homo sapiens]	10.24	6	8	8	26	1.005	10	4.1	1.091	10	10.9	923.91	10.24	21	26	639	72.5	6.07	
5031573	actin-related protein 3 isoform 1 [Homo sapiens]	74.40	11	22	22	264	1.005	96	6.7	1.140	96	15.6	11733.98	74.40	65	264	418	47.3	5.88	
4506181	proteasome subunit alpha type-2 [Homo sapiens]	41.03	1	6	6	33	1.005	12	10	1.189	12	19.2	1724.79	41.03	17	33	234	25.9	7.43	
262206315	L-selectin precursor [Homo sapiens]	4.16	1	2	2	7	1.005	3	0.1	1.193	3	3.6	180.04	4.16	5	7	385	43.6	7.15	
530419493	PREDICTED: protein kinase C and casein kinase substrate in neuro	14.61	4	6	6	26	1.005	9	8.4	1.096	9	13.8	938.68	14.61	18	26	445	51.3	5.39	
530392494	PREDICTED: protein FAM107B isoform X3 [Homo sapiens]	32.06	2	5	5	20	1.005	8	10.5	1.212	8	15.2	568.85	32.06	13	20	131	15.5	8.20	
530393500	PREDICTED: hexokinase-1 isoform X3 [Homo sapiens]	7.65	6	5	7	24	1.005	5	1.2	1.276	5	19.9	960.08	7.65	19	24	889	99.1	6.89	
22091452	apolipoprotein M isoform 1 [Homo sapiens]	42.55	3	5	5	29	1.005	11	5.3	1.584	10	22.2	1526.66	42.55	15	29	188	21.2	6.60	
4758484	glutathione S-transferase omega-1 isoform 1 [Homo sapiens]	71.78	3	16	16	168	1.005	63	6.1	1.179	63	6.7	5488.62	71.78	46	168	241	27.5	6.01	
4502105	anexin A4 [Homo sapiens]	74.40	2	18	20	140	1.005	45	6.4	1.214	45	6.6	674.55	63.24	55	140	321	38.1	6.49	
196947407	TFIIH basal transcription factor complex helicase XPD subunit isofo	1.73	3	2	1	1	2	1.005	2	6.2	1.158	2	10.3	38.72	1.73	1	2	405	46.2	8.63
4557892	phosphatidylcholine-sterol acyltransferase precursor [Homo sapiens]	3.18	1	1	1	3	1.004	1		1.027	1		177.20	3.18	3	3	440	49.5	6.11	
18104989	tyrosine-protein phosphatase non-receptor type 6 isoform 1 [Homo	40.34	4	20	20	102	1.004	38	6.0	1.150	37	15.0	3920.00	40.34	58	102	595	67.5	7.78	
578811429	PREDICTED: mitogen-activated protein kinase 14 isoform X1 [Homo	27.92	47	6	6	21	1.004	5	2.7	1.095	5	23.7	709.51	27.92	16	21	283	32.3	4.92	
4503483	elongation factor 2 [Homo sapiens]	38.11	1	27	27	137	1.004	51	4.9	1.137	51	11.8	5258.73	38.11	74	137	858	95.3	6.83	
70906435	fibrinogen beta chain isoform 1 preproprotein [Homo sapiens]	78.00	2	39	39	1692	1.004	630	7.6	1.233	611	20.8	75900.62	78.00	108	1692	491	55.9	8.27	
153251270	calcineurin-like phosphoesterase domain-containing protein 1 isofo	47.77	2	12	12	51	1.004	18	5.2	1.110	18	14.6	2412.85	47.77	35	51	314	35.5	6.60	
4758266	flap endonuclease 1 [Homo sapiens]	4.74	1	2	2	6	1.004	2	4.8	1.207	2	8.4	211.45	4.74	6	8	380	42.6	8.62	
7657603	home-binding protein 2 [Homo sapiens]	30.73	1	5	5	26	1.004	10	6.3	1.265	10	17.8	944.69	30.73	14	26	205	22.9	4.63	
29788751	diacylglycerol kinase eta isoform 2 [Homo sapiens]	0.66	2	1	1	2	1.004	1		1.503	1		29.89	0.66	2	2	1220	134.8	6.54	
13569901	TSC22 domain family protein 4 [Homo sapiens]	7.09	1	1	1	3	1.004	1		1.143	1		344.38	7.09	3	3	395	41.0	7.21	
115387104	4-trimethylaminobutyraldehyde dehydrogenase [Homo sapiens]	6.56	1	3	3	7	1.004	3	3.8	1.134	3	1.4	315.31	6.56	7	7	518	56.3	6.57	
392307009	receptor-type tyrosine-protein phosphatase C isoform 2 precursor	16.24	6	14	14	36	1.004	15	6.8	1.135	14	9.8	1214.26	16.24	33	36	1145	131.0	6.33	
578809639	PREDICTED: MOB kinase activator 1B isoform X2 [Homo sapiens]	13.22	5	2	2	6	1.004	2	10.2	0.999	2	23.6	225.93	13.22	6	6	174	20.4	5.54	
28195394	histone H2A type 2-B [Homo sapiens]	22.31	2	1	4	28	1.004	2	0.7	1.277	2	14.1	587.90	22.31	11	28	130	14.0	10.89	
530384907	PREDICTED: GTPase IMAP family member 8 isoform X2 [Homo sap	2.85	2	2	2	7	1.004	4	4.2	1.167	4	11.7	83.24	2.85	7	7	456	51.3	8.18	
117320537	1-phosphatidylinositol 4,5-bisphosphate 3-phosphodiesterase gamma	5.06	4	1	4	10	1.004	4	5.0	1.153	4	10.2	426.26	5.06	10	1265	147.8	6.46	5.92	
117395754	keratin, type II cytoskeletal 5 [Homo sapiens]	17.12	12	2	13	68	1.004	4	4.5	1.115	4	4.5	2041.37	17.12	34	68	590	62.3	7.74	
530369318	PREDICTED: ras-related protein Ral-B isoform X4 [Homo sapiens]	6.80	2	1	1	3	1.004	1		1.191	1		241.57	6.80	3	3	206	23.4	6.62	
4503117	cystatin-B [Homo sapiens]	59.18	1	5	5	35	1.004	13	3.5	1.130	13	8.0	1099.76	59.18	15	35	98	11.1	7.56	
156616294	N-acetylmuramoyl-L-alanine amidase precursor [Homo sapiens]	30.56	2	9	9	54	1.004	19	7.4	1.204	18	17.7	2635.76	30.56	27	54	576	62.2	7.55	
290504188	hyaluronan-binding protein 2 isoform 2 [Homo sapiens]	8.43	2	4	4	9	1.003	4	5.8	1.119	4	14.7	219.92	8.43	8	9	534	59.8	6.43	
4758302	enhancer of rudimentary homolog [Homo sapiens]	16.35	1	2	2	8	1.003	3	1.7	1.085	3	4.4	163.00	16.35	6	8	104	12.3	5.92	
384229049	thymidine phosphorylase isoform 1 proprotein [Homo sapiens]	38.38	2	14	14	58	1.003	21	6.3	1.105	21	12.3	3088.16	38.38	38	58	482	49.9	5.53	
4026467	anexin A3 [Homo sapiens]	81.42	7	32	32	450	1.003	162	13.9	1.093	162	19.7	18072.92	81.42	92	450	323	36.4	5.92	
19913428	V-type proton ATPase subunit B, brain isoform [Homo sapiens]	30.53	3	10	10	48	1.003	18	8.4	1.413	16	26.4	2169.32	30.53	28	48	511	55.5	5.81	
22538442	cathepsin Z, preproprotein [Homo sapiens]	12.87	1	3	3	9	1.003	3	0.3	1.068	3	13.8	359.37	12.87	9	9	303	33.8	7.11	
23110925	proteasome subunit beta type-6 isoform 1 proprotein [Homo sapien	6.69	1	2	2	10	1.003	4	2.6	1.201	4	4.9	325.59	6.69	4	10	239	25.3	4.92	
530391028	PREDICTED: gelsolin isoform X6 [Homo sapiens]	62.24	10	35	35	742	1.003	266	16.8	1.153	264	16.8	34337.25	62.24	102	742	731	80.6	5.85	
4501987	afamin precursor [Homo sapiens]	39.90	2	19	19	177	1.003	65	4.9	1.214	63	16.4	6900.79	39.90	56	177	599	69.0	5.90	
578806141	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Homo	2.89	5	1	1	4	1.003	2	8.2	1.475	2	5.1	109.66	2.89	3	4	519	59.2	7.78	
530379128	PREDICTED: lysoM and putative peptidoglycan-binding domain-cont	1.63	13	1	1	1	1.003	1		1.154	1		23.24	1.63	1	1	306	34.5	5.79	
578823396	PREDICTED: anoxiamin-6 isoform X3 [Homo sapiens]	1.23	10	1	2	4	1.003	1		1.164	1		43.71	1.23	1	2	4	812	94.2	6.97
4006001	glutathione peroxidase 3 precursor [Homo sapiens]	28.32	1	6	6	23	1.003	9	8.1	1.254	9	10.5	413.89	28.32	16	23	236	25.5	8.13	
4557894	lysosome C precursor [Homo sapiens]	70.27	1	11	11	370	1.003	147	7.7	1.256	147	16.2	13612.48	70.27	33	370	148	16.5	9.16	
38327625	citrate synthase, mitochondrial precursor [Homo sapiens]	5.79	1	2	2	6	1.003	2	4.9	1.081	2	6	9.9	345.31	5.79	6	6	466	51.7	8.32
578811455	PREDICTED: leukocyte elastase inhibitor isoform X1 [Homo sapien	52.24	3	17	18	155	1.003	55	7.9	1.070	55	7.5	6803.54	52.24	52	155	379	42.7	6.28	
578813343	PREDICTED: thrombospondin type-1 domain-containing protein 7A	0.92	5	1	1	6	1.003	6	4.3	1.601	6	17.7	107.44	0.92	1	6	1516	169.7	7.37	
530407092	PREDICTED: aminopeptidase N isoform X1 [Homo sapiens]	4.45	1	4	4	12	1.003	4	9.0	1.105	4	3.7	498.95	4.45	12	12	967	109.5	5.48	
4506191	proteasome subunit beta type-10 precursor [Homo sapiens]	15.75	1	3	3	14	1.003	5	8.8	1.159	5	5.8	951.79	15.75	9	14	273	28.9	7.81	
29626282	protein phosphatase 1G [Homo sapiens]	4.58	1	1	1	3	1.003	1		3.331	1		138.22	4.58	3	3	546	59.2	4.36	
578811290	PREDICTED: PDZ and LIM domain protein 7 isoform X5 [Homo sap	6.38	6	1	1	6	1.003	2	7.2	1.336	2	0.2	241.40	6.38	3	6	188	21.1	9.66	
578816553	PREDICTED: cofilin isoform X2 [Homo sapiens]	0.52	3	1	1	1	1.003	1		1.104	1		27.52	0.52	1	1	1343	155.6	8.40	
21314600	carcinoembryonic antigen-related cell adhesion molecule 8 precurs	15.47	11	4	4	14	1.002	6	8.7	1.159	6	3.9	338.89	15.47	8	14	349	38.1	7.39	
192447438	vitamin K-dependent protein S preproprotein [Homo sapiens]	29.14	2	16	16	110	1.002	39	6.4	1.151	39	25.2	4692.76	29.14	45	110	676	75.1	5.67	
578831699	PREDICTED: UPF0378 protein KIAA0020 isoform X2 [H																			

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# Amino	MW [kDa]	calc. pI
348041314	cathelicidin antimicrobial peptide preproprotein [Homo sapiens]	60.12	8	13	13	94	1.001	35	5.6	1.187	35	9.8	2931.58	60.12	36	94	173	19.6	9.41
291575128	L-lactate dehydrogenase B chain [Homo sapiens]	51.50	4	15	17	132	1.001	36	7.4	1.136	50	9.7	4713.24	51.50	50	132	334	36.6	6.05
540344580	probable guanine nucleotide exchange factor MCF2L2 [Homo sapiens]	0.72	1	0	1	5	1.001	5		1.103	5	7.0	48.77	0.72	1	5	1114	126.9	6.42
45578871	serotransferrin precursor [Homo sapiens]	81.38	43	66	68	3182	1.001	1163	8.5	1.270	1149	23.8	135782.65	81.38	197	3182	698	77.0	7.12
578813718	PREDICTED: septin-7 isoform X5 [Homo sapiens]	17.10	18	5	6	26	1.001	7	2.6	1.221	7	7.7	1025.33	17.10	18	26	427	49.9	8.84
14916455	serine/threonine-protein kinase H2 [Homo sapiens]	2.34	1	1	1	1	1.001	1		0.603	1		28.83	2.34	1	1	385	43.0	9.63
299829294	neutrophil cytosol factor 2 isoform 2 [Homo sapiens]	38.46	5	16	16	61	1.001	23	5.6	1.167	23	13.2	2614.88	38.46	44	61	481	54.4	5.88
5031815	lysine-6Rase isoform 2 [Homo sapiens]	4.86	2	2	2	12	1.001	4	10.2	1.247	4	9.2	697.31	4.86	6	12	597	68.0	6.35
526118265	Golgin subfamily A member 5 [Homo sapiens]	0.82	1	1	1	11	1.001	6	23.4	2.331	6	36.2	125.22	0.82	2	11	731	82.9	5.83
70906437	fibrinogen gamma chain isoform gamma-A precursor [Homo sapiens]	82.84	4	35	36	1801	1.001	686	11.2	1.235	678	23.4	62687.08	82.84	104	1801	437	49.5	6.09
578829418	PREDICTED: p120-type mechanosensitive ion channel component	0.32	3	1	1	1	1.001	1		0.982	1		21.05	0.32	1	1	2497	283.9	7.43
7706563	ras-related protein Rab-8B [Homo sapiens]	27.05	21	2	5	37	1.001	6	7.1	1.245	6	9.6	1674.26	27.05	14	37	207	23.6	9.07
57882940	PREDICTED: protein asunder homolog isoform X4 [Homo sapiens]	1.11	2	1	1	1	1.001	1		1.189	1		0.00	1.11	1	1	631	71.9	6.62
578822409	PREDICTED: ninjurin-2 isoform X2 [Homo sapiens]	5.66	3	1	1	3	1.001	1		1.145	1		44.92	5.66	3	3	106	11.7	10.15
4557287	angiotensinogen preproprotein [Homo sapiens]	49.48	1	13	13	144	1.000	53	7.3	1.241	50	25.4	6889.06	49.48	37	144	485	53.1	6.32
14251209	chloride intracellular channel protein 1 [Homo sapiens]	82.99	8	16	16	162	1.000	60	9.1	1.203	58	20.0	5687.64	82.99	46	162	241	26.9	5.17
578824757	PREDICTED: COMM domain-containing protein 6 isoform X1 [Homo sapiens]	9.00	1	1	1	3	1.000	2	2.7	1.222	2	4.5	53.04	9.00	3	3	100	11.6	9.93
537361024	dual specificity tyrosine-phosphorylation-regulated kinase 4 isoform 1 [Homo sapiens]	2.15	1	1	1	46	1.000	17	4.1	1.276	17	12.9	545.41	2.15	3	46	233	26.3	9.01
16933542	fibronectin isoform 3 preproprotein [Homo sapiens]	49.21	28	83	83	704	1.000	255	7.9	1.181	253	17.6	32288.19	49.21	240	704	2355	259.1	5.73
5730027	KH domain-containing, RNA-binding, signal transduction-associated protein [Homo sapiens]	3.61	10	2	2	3	1.000	1		1.056	1		87.87	3.61	3	3	443	48.2	8.66
1146292750	apolipoprotein(a) precursor [Homo sapiens]	4.41	3	1	1	3	1.006	1		1.016	1		118.34	4.41	3	3	2040	228.4	6.07
58331240	retin-B precursor [Homo sapiens]	3.10	3	2	2	8	1.000	3		1.136	3	12.7	327.67	10.73	8	8	382	42.0	6.83
4503987	gamma-glutamyl hydrolase precursor [Homo sapiens]	33.96	3	8	8	40	1.000	14	4.5	1.282	14	23	1645.45	33.96	23	40	318	35.9	7.11
21735621	malate dehydrogenase, mitochondrial isoform 1 precursor [Homo sapiens]	23.96	3	6	6	23	1.000	8	5.1	1.160	8	6.7	1187.57	23.96	17	23	338	35.5	8.68
189083844	dipeptidyl peptidase 1 isoform A preproprotein [Homo sapiens]	18.36	9	6	6	26	1.000	9	8.6	1.158	9	9.7	1141.09	18.36	18	26	463	51.8	6.99
42822872	ribonuclease inhibitor [Homo sapiens]	50.11	1	14	14	93	1.000	34	5.7	1.138	33	14.6	5325.98	50.11	42	93	461	49.9	4.82
148529014	DNA damage-binding protein 1 [Homo sapiens]	3.68	1	3	3	9	1.000	3	0.8	1.384	3	12.6	517.26	3.68	9	9	1140	126.9	5.26
4506925	SH3 domain-binding glutamic acid-rich-like protein [Homo sapiens]	91.23	1	10	10	68	1.000	100	6.9	1.170	27	17.8	2753.48	91.23	28	68	114	12.8	5.25
153266841	beta-2-glycoprotein 1 precursor [Homo sapiens]	58.84	1	16	16	251	1.000	27	9.6	1.121	26	19.7	8798.46	58.84	21	251	345	38.3	7.97
530361334	PREDICTED: complement C1q subcomponent subunit B isoform X1 [Homo sapiens]	43.08	3	9	9	94	1.000	36	7.7	1.298	35	15.8	3780.59	43.08	25	94	253	26.7	6.74
70778918	inter-alpha-trypsin inhibitor heavy chain H2 precursor [Homo sapiens]	32.66	1	23	23	209	1.000	78	7.2	1.185	77	15.4	8888.92	32.66	67	209	946	106.4	6.86
48255966	UTP-glucose-1-phosphate uridylyltransferase isoform A precursor [Homo sapiens]	53.94	4	24	24	139	1.000	52	6.7	1.189	52	13.5	6625.94	53.94	63	139	508	56.9	8.15
5902134	coronin-1A [Homo sapiens]	62.91	14	30	31	375	1.000	140	9.3	1.159	134	18.6	13055.07	62.91	89	375	461	51.0	6.68
4557361	BH3-interacting domain death agonist isoform 2 [Homo sapiens]	19.49	3	3	3	24	1.000	9	5.0	1.133	9	7.4	1492.76	19.49	7	24	195	22.0	5.44
4506671	60S acidic ribosomal protein P2 [Homo sapiens]	40.87	1	3	3	10	1.000	4	7.3	1.104	4	11.1	602.09	40.87	8	10	115	11.7	4.54
550908411	uncharacterized protein KIAA1958 isoform c [Homo sapiens]	1.56	3	1	1	1	1.000	1		1.362	1		31.58	1.56	1	1	448	48.6	5.44
5013571	actin-related protein 2 isoform B [Homo sapiens]	56.09	28	15	17	177	0.999	52	5.5	1.192	50	21.5	7240.21	56.09	48	177	394	44.7	6.74
98853694	vimentin precursor [Homo sapiens]	35.36	1	11	10	110	0.999	41	19.3	1.312	41	19.3	4448.49	35.36	30	110	478	54.3	5.80
170016081	protein XBP2 [Homo sapiens]	5.00	1	5	5	16	0.999	6	10.8	1.200	6	15.8	419.08	5.00	13	16	350	39.6	5.12
53036456	PREDICTED: C4b-binding protein alpha chain isoform X2 [Homo sapiens]	47.07	1	25	25	261	0.999	101	5.4	1.199	101	15.5	9294.63	47.07	71	261	597	67.0	7.78
564473387	actin-related protein 2/3 complex subunit 3 isoform 2 [Homo sapiens]	40.11	2	8	8	55	0.999	20	7.3	1.127	20	13.7	1680.17	40.11	24	55	177	20.4	9.38
635172849	beta-hexosaminidase subunit beta isoform 2 [Homo sapiens]	11.48	2	3	3	9	0.999	3	0.2	1.093	3	10.5	456.76	11.48	9	9	331	38.2	6.44
222352168	protein ANKUB1 [Homo sapiens]	0.92	1	1	1	1	0.999	1		1.173	1		25.94	0.92	1	1	544	61.2	9.20
32483399	serine/threonine-protein kinase PAK 2 [Homo sapiens]	15.27	7	4	5	19	0.999	6	10.0	1.146	6	22.8	777.12	15.27	14	19	524	58.0	5.96
67782358	complement factor B preproprotein [Homo sapiens]	56.94	1	43	43	418	0.999	162	8.1	1.277	158	25.3	15867.40	56.94	117	418	764	85.5	7.06
289577114	eukaryotic translation initiation factor 4 gamma-2 isoform 2 [Homo sapiens]	1.73	30	1	1	6	0.999	1		1.297	1		142.81	1.73	6	6	869	98.1	6.99
108773793	glucose-4-phosphate 1-dehydrogenase isoform B [Homo sapiens]	64.08	8	33	32	296	0.999	109	6.7	1.189	108	18.5	12253.40	64.08	95	296	515	59.2	6.84
578812604	PREDICTED: nesprin-1 isoform X19 [Homo sapiens]	0.13	20	1	1	6	0.999	2		1.312	2		158.35	0.13	3	6	8721	1002.8	5.52
68509926	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DDX50 [Homo sapiens]	3.90	1	3	3	10	0.999	5	2.0	1.053	5	2.7	492.73	3.90	9	10	795	90.9	7.46
530371139	PREDICTED: N-myc-interactor isoform X1 [Homo sapiens]	32.57	1	8	8	27	0.999	11	4.8	1.278	11	30.5	1102.05	32.57	19	27	307	35.0	5.34
189458812	1,4-alpha-glucan-branching enzyme [Homo sapiens]	16.38	1	8	8	50	0.999	17	9.3	1.183	17	7.6	2670.93	16.38	24	50	702	80.4	6.32
4507149	superoxide dismutase [Cu-Zn] [Homo sapiens]	64.29	1	6	6	36	0.999	13	9.0	1.123	13	10.4	2658.11	64.29	17	36	154	15.9	6.13
58219054	bcl-2-like protein 15 [Homo sapiens]	8.59	1	1	1	2	0.999	1		1.480	1		49.75	8.59	2	2	163	17.7	4.41
4757760	adiponectin precursor [Homo sapiens]	6.15	1	1	1	3	0.992	1		0.972	1		142.42	6.15	3	3	244	26.4	5.74
71565154	alcohol dehydrogenase class-3 [Homo sapiens]	5.08	1	3	3	4	0.999	3	2.7	1.132	3	5.2	103.69	5.08	6	6	374	39.7	7.49
4502337	zinc-alpha-2-glycoprotein precursor [Homo sapiens]	59.40	1	20	20	213	0.999	77	6.0	1.255	77	17.9	8594.26	59.40	58	213	298	34.2	6.05
578810171	PREDICTED: solute carrier family 25 member 48 isoform X6 [Homo sapiens]	2.57	1	1	1	3	0.998	2	0.0	1.254	2		38.54	2.57	2	3	311	33.4	8.69
307078125	clathrin interactor 1 isoform 3 [Homo sapiens]	5.92	3	3	3	11	0.998	4	7.3	1.227	4	20.4	387.27	5.92	8	11	625	68.1	6.42
145275213	coagulation factor XII precursor [Homo sapiens]	19.35	1	8	8	36	0.998	13	5.9	1.211	13	4.1	1499.12	19.35	21	36	615	67.7	7.74
4507677	endoplasmic reticulum protein precursor [Homo sapiens]	17.68	23	12	14	52	0.998	16	8.2	1.095	16	6.4	2428.22	17.68	38	52	803	92.4	4.84
52353252	olfactory receptor 5Z4 [Homo sapiens]	3.21	1	1	1	1	0.998	1		0.908	1		20.06	3.21	1	1	312	35.5	8.53
85815829	SH3 domain-binding protein 1 [Homo sapiens]	1.28	1	1	1	3	0.998	1		1.076	1		164.23	1.28	3	3	701	75.7	6.77
48255091	glucosylase 2 subunit beta isoform 2 precursor [Homo sapiens]	11.62	6	6	6	26	0.998	9	5.9	1.109	9	12.4	987.06	11.62	26	525	59.1	4.42	
62912466	C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	27.89	3	6	6	22	0.998	8	6.1	1.203	8	8.7	672.85	27.89	8	16	22	25.1	28.3
34365783	visual system homeobox 2 [Homo sapiens]	2.49	1	1	1	6	0.998	3	1.7	1.218	3	8.4	83.42	2.49	2	6	361	39.4	7.55
578811759	PREDICTED: UHRF1-binding protein 1 isoform X3 [Homo sapiens]	0.40	17	1	1	6	0.998	2		1.130	2		53.73	0.40	3	6	1240	137.4	6.30
41393602	complement C1s subcomponent precursor [Homo sapiens]	36.19	1	18	18	103													

Accession	Description	Zcoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# Asns	MW [kDa]	calc. pI
520975489	ran-specific GTPase-activating protein isoform 4 [Homo sapiens]	22.67	6	2	2	9	0.997	3	1.0	1.150	3	1.8	532.36	22.67	6	9	150	17.5	8.24
217035154	cap2-interacting protein [Homo sapiens]	23.32	2	1	7	35	0.996	14	6.2	1.080	10	5.5	1165.10	23.32	20	35	416	44.5	5.40
530360793	PREDICTED: serine/arginine repetitive matrix protein 1 isoform X6	7.43	7	1	1	11	0.996	4	4.1	1.393	4	24.3	212.75	0.68	3	11	888	100.2	11.77
4557485	ceramidase precursor [Homo sapiens]	74.93	1	2	63	839	0.996	12	6.3	1.391	12	12.7	3786.21	74.93	178	839	1065	122.1	5.72
5174449	histone H7a [Homo sapiens]	28.17	1	7	7	35	0.996	13	6.1	1.352	13	19.3	1468.44	28.17	19	35	213	22.5	10.76
33457348	UPI055a protein C19orf10 precursor [Homo sapiens]	5.20	1	1	1	3	0.996	1		1.193	1		130.28	5.20	3	3	173	18.8	6.68
578800866	PREDICTED: gamma-interferon-inducible protein 16 isoform X2 [H]	3.69	4	2	2	5	0.996	2	1.8	1.467	2	49.6	185.54	3.69	5	5	677	76.3	9.38
530413446	PREDICTED: THO complex subunit 4 isoform X1 [Homo sapiens]	19.39	2	3	3	13	0.996	5	4.1	1.073	5	11.9	601.77	19.39	8	13	196	20.5	9.86
4506765	protein S100-A4 [Homo sapiens]	69.31	1	6	6	122	0.996	44	8.5	1.125	43	11.8	4756.62	69.31	118	122	101	11.7	6.11
205277396	dynactin subunit 1 isoform 4 [Homo sapiens]	3.78	6	3	3	9	0.996	3	4.9	1.138	3	8.2	502.17	3.78	9	9	1139	126.7	5.43
4505227	myeloid cell nuclear differentiation antigen [Homo sapiens]	77.89	59	36	37	551	0.996	194	7.4	1.174	194	13.4	23329.61	77.89	107	551	407	45.8	9.76
578813467	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isoform X1 [Homo sapiens]	38.66	11	9	14	120	0.996	32	5.5	1.138	32	10.0	4337.86	38.66	40	120	313	33.9	9.03
4503035	prothombin preproprotein [Homo sapiens]	56.59	2	27	27	222	0.996	81	7.9	1.165	81	19.3	10424.14	56.59	77	222	422	70.0	5.90
187829742	bcl-2 binding component 3 isoform 2 [Homo sapiens]	5.34	1	1	1	2	0.996	1		1.271	1		27.87	5.34	2	2	131	14.5	7.84
4757768	rho GDP-dissociation inhibitor 1 isoform a [Homo sapiens]	46.08	2	9	10	73	0.995	26	6.6	1.188	26	14.1	2904.23	46.08	26	73	204	23.2	5.11
4885379	histone H1.4 [Homo sapiens]	47.03	3	3	15	336	0.995	14	3.6	1.107	14	7.4	14918.82	47.03	44	336	219	21.9	11.03
5454052	14-3-3 protein sigma [Homo sapiens]	53.23	1	6	12	136	0.995	10	8.0	1.086	10	9.3	4063.89	53.23	34	136	248	27.8	4.74
4826898	profilin-1 [Homo sapiens]	75.00	4	12	12	738	0.995	270	8.8	1.139	268	14.2	33099.23	75.00	35	738	140	15.0	8.27
50592994	thioredoxin isoform 1 [Homo sapiens]	63.81	3	6	6	89	0.995	34	8.2	1.134	34	11.3	3886.29	63.81	18	89	105	11.7	4.92
530369184	PREDICTED: interleukin-1 receptor antagonist protein isoform X1 [Homo sapiens]	18.18	4	2	2	7	0.995	3	4.4	1.137	3	5.1	435.12	18.18	4	7	143	16.1	4.88
578823793	PREDICTED: nucleosome assembly protein 3-like 1 isoform X18 [Homo sapiens]	3.35	1	1	1	3	0.995	1		1.052	1		103.28	3.35	3	3	328	38.2	4.54
4506387	UV excision repair protein RAD23 homolog B isoform 1 [Homo sapiens]	19.80	41	6	6	26	0.995	7	7.6	1.223	7	8.3	979.35	19.80	23	26	409	43.1	4.84
4506495	40S ribosomal protein S19 [Homo sapiens]	6.21	1	1	1	3	0.995	1		1.006	1		195.92	6.21	3	3	145	16.1	10.32
209969703	protein RCC2 [Homo sapiens]	4.98	1	3	3	8	0.995	3	4.5	1.304	3	3.2	165.23	4.98	8	8	522	56.0	8.78
108796653	phosphoglycolate phosphatase [Homo sapiens]	4.05	1	1	1	3	0.995	1		1.245	1		184.22	4.05	3	3	321	34.0	6.14
4503471	elongation factor 1-alpha 1 [Homo sapiens]	56.71	2	18	18	170	0.995	61	5.9	1.119	61	15.1	6662.46	56.71	51	170	462	50.1	9.01
530383466	PREDICTED: forkhead box protein O3 isoform X1 [Homo sapiens]	1.45	1	1	1	3	0.995	3	0.0	1.319	3	12.1	31.70	1.45	1	3	484	51.7	6.30
63162572	T-complex protein 1 subunit gamma isoform a [Homo sapiens]	21.83	2	10	10	30	0.995	11	4.8	1.148	11	9.3	1193.88	21.83	27	30	545	60.5	6.49
50845386	annexin A2 isoform 2 [Homo sapiens]	70.50	2	23	24	105	0.995	38	3.9	1.105	37	8.2	4447.47	70.50	66	105	339	38.4	7.75
223890219	RNA binding motif protein, X-linked like-3 [Homo sapiens]	2.16	2	1	2	7	0.995	1		1.359	1		325.53	2.16	4	7	1067	114.9	9.10
4885399	structural maintenance of chromosomes protein 3 [Homo sapiens]	1.81	1	2	2	10	0.995	4	6.3	1.156	4	25.2	358.51	1.81	6	10	1217	141.5	7.18
300244560	cystine-rich secretory protein 3 isoform 1 precursor [Homo sapiens]	36.43	2	7	7	40	0.995	15	6.0	1.141	15	18.3	1092.23	36.43	19	40	258	29.0	7.80
258679498	carbonic anhydrase 1 isoform a [Homo sapiens]	82.76	3	13	13	449	0.995	160	10.4	1.086	160	8.6	23518.44	82.76	39	449	261	28.9	7.12
578814219	PREDICTED: inosine-5'-monophosphate dehydrogenase 1 isoform 1 [Homo sapiens]	3.05	16	1	1	5	0.995	2	0.3	1.083	2	0.2	283.22	3.05	3	5	393	42.6	9.33
4506179	proteasome subunit alpha type-1 isoform 2 [Homo sapiens]	52.85	3	12	12	58	0.995	24	7.6	1.140	24	12.0	2268.66	52.85	32	58	263	29.5	6.61
4826772	insulin-like growth factor-binding protein complex acid labile subunit	13.72	2	7	7	22	0.995	8	4.8	1.178	8	7.8	586.17	13.72	20	22	605	66.0	6.79
194097330	hexokinase-3 [Homo sapiens]	45.72	1	27	29	161	0.995	53	4.9	1.161	51	15.3	7585.22	45.72	86	161	923	99.0	5.40
4503165	calp-3 isoform 1 [Homo sapiens]	1.04	3	1	1	2	0.995	1		1.129	1		56.43	1.04	2	2	748	88.9	8.48
345197264	tumor protein D5A isoform b [Homo sapiens]	14.72	10	2	6	4	0.995	2	2.6	1.133	2	3.4	353.34	14.72	6	6	163	17.5	6.60
296179386	clathrin light chain A isoform e [Homo sapiens]	10.12	6	2	2	8	0.995	3	3.5	1.036	3	0.5	178.57	10.12	5	8	168	18.1	4.44
431822408	heat shock protein HSP 90-beta isoform c [Homo sapiens]	44.12	15	13	29	228	0.994	24	3.2	1.197	24	13.4	9905.24	44.12	81	228	714	82.3	5.06
54034555	complement C2 isoform 5 [Homo sapiens]	29.18	6	17	17	78	0.994	30	6.4	1.310	29	24.0	3013.97	29.18	50	78	723	80.1	7.46
187607300	vesican core protein isoform 2 precursor [Homo sapiens]	6.26	4	6	3	12	0.994	4	2.4	1.196	4	4.1	420.07	6.26	9	12	655	74.2	7.37
11067747	cell division cycle 5-like protein [Homo sapiens]	1.75	12	1	2	4	0.994	1		1.113	1		63.93	1.75	4	4	802	92.2	8.11
41050047	lumican precursor [Homo sapiens]	43.20	1	13	13	94	0.994	34	5.3	1.157	34	6.2	3778.36	43.20	36	94	338	38.4	6.68
4507709	GDP-L-fucose synthase [Homo sapiens]	16.20	4	4	11	4	0.994	4	5.3	1.064	4	10.5	579.86	16.20	4	11	321	35.9	6.60
20149498	ferritin light chain [Homo sapiens]	49.71	1	8	8	40	0.994	15	9.4	1.090	15	6.2	1883.52	49.71	4	40	175	20.0	5.78
195623970	alpha-2-HS-glycoprotein preproprotein [Homo sapiens]	41.69	1	11	11	327	0.994	126	13.7	1.208	125	32.1	13803.55	41.69	31	327	397	30.2	5.70
578811443	PREDICTED: dynein heavy chain 8, axonemal isoform X1 [Homo sapiens]	0.25	27	1	2	18	0.994	1		1.200	1		155.95	0.25	4	18	4707	538.3	6.13
315075311	cathepsin S isoform 2 preproprotein [Homo sapiens]	25.98	2	7	7	23	0.994	8	2.3	1.144	8	8.6	1032.39	25.98	20	23	281	31.6	8.28
19913424	V-type proton ATPase catalytic subunit A [Homo sapiens]	29.34	1	15	15	71	0.994	27	7.6	1.216	27	22.6	3108.26	29.34	44	71	617	68.3	5.52
578838337	PREDICTED: bromodomain and WD repeat-containing protein 3 isoform 1 [Homo sapiens]	0.86	8	1	2	10	0.994	1		1.004	1		165.02	0.86	4	10	1398	158.4	7.31
4502027	serum albumin preproprotein [Homo sapiens]	94.25	13	101	101	26879	0.994	10343	8.4	1.258	10216	23.3	1120981.13	94.25	291	26879	609	69.3	6.88
11956444	inorganic pyrophosphatase [Homo sapiens]	23.18	1	6	4	16	0.994	6	2.8	1.152	6	13.9	747.69	23.18	6	16	289	32.6	5.86
53032383	heterogeneous nuclear ribonucleoprotein L isoform a [Homo sapiens]	27.50	6	8	8	38	0.994	16	13.0	1.190	15	18.0	1801.05	27.50	38	158	589	44.1	8.22
53112496	janus kinase and microtubule-interacting protein 2 isoform 4 [Homo sapiens]	2.19	4	2	2	9	0.994	4	7.7	1.221	4	5.0	251.70	2.19	4	9	778	91.5	5.78
4506363	ras-related protein Rab-13 isoform 1 [Homo sapiens]	7.88	2	1	2	15	0.994	1		1.244	1		831.91	7.88	4	15	203	22.8	9.19
94538320	hydroxyacylglutathione hydrolase, mitochondrial isoform 2 [Homo sapiens]	3.85	2	1	1	3	0.994	1		1.010	1		124.19	3.85	3	3	260	28.8	7.33
262263314	cystatin-F precursor [Homo sapiens]	4.83	1	1	1	9	0.994	3	3.1	1.573	3	9.6	273.94	4.83	3	9	145	16.4	8.48
530412093	PREDICTED: interferon-induced 35 kDa protein isoform X1 [Homo sapiens]	22.73	2	7	7	21	0.994	8	4.8	1.217	8	25.7	704.69	22.73	18	21	286	31.5	6.09
11641247	Golgi-associated plant pathogenesis-related protein 1 isoform a [Homo sapiens]	31.82	5	4	4	23	0.994	8	4.3	1.183	8	22.7	1442.67	31.82	12	23	154	17.2	6.91
530418509	PREDICTED: eukaryotic translation initiation factor 2 subunit 2 isoform 1 [Homo sapiens]	17.20	2	4	4	12	0.994	4	8.6	1.092	4	7.4	593.72	17.20	12	12	314	36.2	5.48
571019457	pipecolin-4-alpha-carboxamide hydratase isoform 3 [Homo sapiens]	29.09	1	1	1	3	0.994	1		0.964	1		132.87	29.09	3	3	55	49.7	6.09
11559929	costarmer subunit gamma-1 [Homo sapiens]	1.26	1	1	1	2	0.994	1		0.908	1		106.80	1.26	2	2	874	97.7	5.47
5902072	serpin B3 [Homo sapiens]	22.31	2	8	8	27	0.994	10	7.4	1.091	10	4.0	1085.04	22.31	23	27	390	44.5	6.81
4758112	spliceosome RNA helicase DDX39B [Homo sapiens]	17.52	3	13	7	37	0.994	13	6.3	1.195	13	14.5	1063.32	17.52	19	37	428	49.0	5.67
150170699	kinesin-like protein KIF26A [Homo sapiens]	0.74	1	2</															

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
7661862	protein phosphatase 1F [Homo sapiens]	2.64	1	1	1	15	0.992	5	2.3	1.094	5	9.3	623.72	2.64	3	15	454	49.8	5.10
195976754	lysferlin isoform 9 [Homo sapiens]	0.73	16	1	1	6	0.992	2	1.2	1.043	2	21.8	266.34	0.73	3	6	2066	235.8	5.67
578813682	PREDICTED: caspase recruitment domain-containing protein 11 iso	0.94	4	1	1	2	0.992	1					33.71	0.94	2	2	854	98.6	5.50
578846043	PREDICTED: uncharacterized protein LOC102725101 [Homo sapie	7.52	2	1	1	202	0.992	9					5642.45	7.52	9	202	359	39.1	6.47
5453710	LIM and SH3 domain protein 1 isoform a [Homo sapiens]	32.96	5	9	9	40	0.992	17		1.140	17	7.8	1230.88	32.96	20	40	261	29.7	7.05
315434251	voltage-gated potassium channel subunit beta-2 isoform 4 [Homo	30.33	12	7	7	20	0.992	9		1.094	9	7.3	627.20	30.33	15	20	300	33.6	8.35
62739186	complement factor H isoform a precursor [Homo sapiens]	57.51	5	54	60	853	0.992	291		1.250	289	18.5	34483.01	57.51	171	853	1231	139.0	6.62
40254823	phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 isoform t	5.30	2	4	4	11	0.992	4		1.241	4	13.4	440.71	5.30	11	11	1188	133.1	7.59
13129110	methylcosome protein 50 [Homo sapiens]	4.39	1	1	1	3	0.991	1		1.198	1		186.44	4.39	3	3	342	36.7	5.17
530380257	PREDICTED: core histone macro-H2A.1 isoform X3 [Homo sapiens]	36.96	6	11	11	75	0.991	27		1.246	27	21.5	3605.72	36.96	32	75	368	39.0	9.80
45580688	complement component C7 precursor [Homo sapiens]	46.62	1	25	25	143	0.991	52		1.164	52	7.3	6666.60	46.62	74	143	843	93.5	6.48
530397289	PREDICTED: neuroblast differentiation-associated protein AHNAK t	7.41	9	7	7	17	0.991	6		1.073	6	10.0	552.69	7.41	15	17	5438	580.3	6.14
45343507	eosinophil cationic protein precursor [Homo sapiens]	46.25	1	8	8	80	0.991	31		1.208	31	12.2	3181.19	46.25	23	80	160	18.4	10.02
578808568	PREDICTED: NEDD4-binding protein 2 isoform X2 [Homo sapiens]	0.65	14	2	2	22	0.991	9		1.331	9	5.9	287.90	0.65	6	22	1690	189.7	5.25
89191868	von Willebrand factor preproprotein [Homo sapiens]	1.74	1	3	4	14	0.991	4		1.073	3	3.4	370.95	1.74	11	14	2813	309.1	5.49
4056663	60S ribosomal protein L8 [Homo sapiens]	4.28	1	1	1	3	0.991	1		1.053	1		104.16	4.28	3	3	257	28.0	11.03
4557323	apolipoprotein C-III precursor [Homo sapiens]	34.34	1	3	3	26	0.991	9		1.261	9	17.5	1531.35	34.34	9	26	99	10.8	5.51
530369466	PREDICTED: solute carrier family 35 member F5 isoform X2 [Homo	0.97	3	1	1	9	0.991	3		1.179	3	17.7	145.14	0.97	3	9	515	58.1	9.40
4503529	eukaryotic initiation factor 4A-1 isoform 3 [Homo sapiens]	22.91	5	9	10	43	0.991	14		1.091	14	8.2	1378.23	22.91	28	43	406	46.1	5.48
530381201	PREDICTED: docking protein 3 isoform X5 [Homo sapiens]	8.18	5	2	2	6	0.991	2		1.329	2	15.7	319.82	8.18	6	6	330	35.7	5.60
4836360	heterogeneous nuclear ribonucleoprotein F [Homo sapiens]	21.45	3	4	4	29	0.991	7		1.124	7	15.5	1116.37	21.45	29	415	45.6	5.59	
25777615	26S proteasome non-ATPase regulatory subunit 7 [Homo sapiens]	7.41	1	1	1	6	0.991	2		1.361	2	2.2	548.66	7.41	3	6	324	37.0	6.77
156231037	kininogen-1 isoform 1 precursor [Homo sapiens]	38.82	1	3	30	337	0.991	5		1.198	5	20.1	14965.49	38.82	82	337	644	71.9	6.81
15431288	60S ribosomal protein L10a [Homo sapiens]	10.14	1	2	2	6	0.991	2		0.939	2	39.0	146.92	10.14	6	6	217	24.8	9.94
21264355	SWI/SNF-related matrix-associated actin-dependent regulator of ch	2.43	1	1	1	2	0.991	1		1.232	1		85.19	2.43	2	2	411	46.6	4.88
578828247	PREDICTED: SUMO-conjugating enzyme UBC9 isoform X4 [Homo s	6.96	2	2	2	7	0.991	3		1.199	3	3.3	253.50	6.96	4	7	158	18.0	8.66
98986457	host cell factor 1 [Homo sapiens]	0.54	4	1	1	3	0.991	1		1.211	1		111.19	0.54	3	3	2035	208.6	7.46
5174663	protein S100-P [Homo sapiens]	86.32	1	8	8	130	0.990	46		1.218	46	22.4	8587.20	86.32	22	130	95	10.4	4.88
4885381	histone H1.5 [Homo sapiens]	43.81	1	11	16	294	0.990	75		1.196	75	15.1	12374.37	43.81	47	294	226	10.22	5.92
169636428	calcin [Homo sapiens]	1.36	1	1	1	4	0.990	2		1.029	2		76.03	1.36	2	4	588	46.5	8.18
586798140	bridging integrator 2 isoform 2 [Homo sapiens]	21.71	6	8	8	46	0.990	16		0.975	16	15.5	2055.32	21.71	23	46	539	59.2	5.00
158138507	mitogen-activated protein kinase 3 isoform 3 [Homo sapiens]	17.01	21	1	4	14	0.990	1		1.352	1		574.71	17.01	9	14	335	38.3	6.20
530373067	PREDICTED: tetranectin isoform X1 [Homo sapiens]	41.88	2	5	5	16	0.990	6		1.162	6	11.8	887.96	41.88	13	16	160	17.8	5.05
157502193	26S proteasome non-ATPase regulatory subunit 13 isoform 1 [Homo	2.13	2	1	1	3	0.990	1		1.021	1		90.93	2.13	3	3	376	42.9	5.81
289547631	leukocyte immunoglobulin-like receptor subfamily A member 3 isofo	24.37	78	7	7	35	0.990	11		1.155	11	45.6	1457.34	24.37	20	35	439	47.4	8.09
193083114	poly(C)-binding protein 2 isoform g [Homo sapiens]	11.95	11	1	4	15	0.990	1		1.231	1		263.44	11.95	9	15	318	33.5	8.24
578810779	PREDICTED: ras GTPase-activating protein-binding protein 1 isofo	4.94	1	1	1	3	0.990	2		1.090	2	23.1	177.31	4.94	2	3	466	52.1	5.52
530426780	PREDICTED: TNF receptor-associated factor 2 isoform X2 [Homo s	2.81	3	2	2	11	0.990	4		1.062	4	5.4	176.70	2.81	2	11	533	59.1	7.52
578819493	PREDICTED: antigen KI-67 isoform X1 [Homo sapiens]	0.29	3	1	1	2	0.990	1		1.388	1		31.07	0.29	2	2	2406	264.8	9.88
19482158	desert hedgehog protein preproprotein [Homo sapiens]	1.26	1	1	1	2	0.990	2		1.317	2	9.8	16.49	1.26	1	2	396	43.5	9.28
530402464	PREDICTED: M-phase phosphoprotein 8 isoform X2 [Homo sapiens]	1.01	3	1	1	3	0.990	1		1.127	1		83.64	1.01	3	3	597	68.4	5.54
6912286	caspase-14 precursor [Homo sapiens]	12.81	1	3	3	9	0.990	3		1.107	3	16.9	383.10	12.81	9	9	242	27.7	5.58
5729850	guanine nucleotide-binding protein G(k) subunit alpha [Homo sapie	13.28	13	1	4	20	0.990	1		0.978	1		904.43	13.28	12	20	354	40.5	5.69
530389385	PREDICTED: copine-3 isoform X1 [Homo sapiens]	44.69	17	15	16	97	0.990	28		1.204	28	21.2	4296.38	44.69	41	97	537	60.1	5.85
4826902	serpin B10 [Homo sapiens]	63.73	1	20	20	103	0.990	37		1.115	37	19.2	4399.44	63.73	56	103	397	45.4	6.16
73858570	pleiotrophin protease C1 inhibitor precursor [Homo sapiens]	40.60	5	20	20	281	0.990	103		1.213	101	16.8	10921.88	40.60	58	281	580	55.1	4.55
88702793	vasorin precursor [Homo sapiens]	2.38	1	1	1	3	0.990	1		0.952	1		240.79	2.38	2	3	673	71.7	7.39
530424154	PREDICTED: zinc finger protein 319 isoform X1 [Homo sapiens]	1.03	1	1	1	23	0.990	9		1.806	8	28.3	237.82	1.03	3	3	283	62.5	8.37
73858564	corticosteroid-binding globulin precursor [Homo sapiens]	34.32	1	10	10	57	0.990	21		1.209	21	15.5	2610.70	34.32	28	57	405	45.1	6.94
118601081	heterogeneous nuclear ribonucleoprotein U-like protein 2 [Homo s	10.28	8	10	11	39	0.990	10		1.082	10	6.0	1262.82	10.28	30	39	747	85.1	6.01
530415598	PREDICTED: heterogeneous nuclear ribonucleoprotein U-like protei	6.61	7	4	5	10	0.989	4		1.136	4	13.9	392.22	6.61	10	10	756	84.7	8.78
37594464	ADP-sugar pyrophosphatase [Homo sapiens]	4.11	1	1	1	3	0.989	1		1.008	1		129.49	4.11	3	3	219	24.3	4.94
22209001	tigger transposable element-derived protein 1 [Homo sapiens]	0.85	1	1	1	1	0.989	1		1.274	1		24.60	0.85	1	1	591	67.3	8.46
343867374	glutaredoxin-1 [Homo sapiens]	74.53	3	5	5	55	0.989	20		1.199	19	13.2	1201.17	74.53	15	55	106	11.8	8.09
22208975	high mobility group protein HMGB-1/HMG-Y isoform b [Homo sapie	37.50	1	3	3	10	0.989	2		1.136	2	9.8	143.15	37.50	2	7	96	10.7	10.32
547234776	RBP12-like protein isoform 3 [Homo sapiens]	0.58	3	1	1	118	0.989	62		1.415	61	31.6	1147.47	0.58	3	118	1197	132.6	8.68
7661878	kinasin-like protein KIF14 [Homo sapiens]	0.55	1	1	1	6	0.989	2		1.809	2	24.5	95.05	0.55	3	6	1648	186.4	7.91
161169015	neuron navigator 2 isoform 3 [Homo sapiens]	0.30	7	1	1	1	0.989	1		1.200	1		22.26	0.30	1	1	2365	254.8	8.94
395132436	60S ribosomal protein L18 isoform 2 [Homo sapiens]	8.18	2	1	1	2	0.989	1		1.261	1		137.33	8.18	2	2	159	18.1	11.84
324021743	vitamin D-binding protein isoform 1 precursor [Homo sapiens]	79.75	5	35	37	705	0.989	249		1.214	248	20.4	28821.92	79.75	106	705	474	52.9	5.45
224028248	non-POU domain-containing octamer-binding protein isoform 2 [Homo	11.78	2	2	3	17	0.989	5		1.143	5	8.7	925.38	11.78	8	17	382	43.8	8.63
45031143	cathespin D preproprotein [Homo sapiens]	20.63	1	7	7	31	0.989	12		1.151	12	13.7	1345.00	20.63	17	31	412	44.5	6.54
495528154	collagen alpha-1(V) chain isoform 2 preproprotein [Homo sapiens]	1.74	2	5	5	5	0.989	2		1.204	2	13.8	337.33	1.74	5	5	1838	183.5	5.07
12569962	ras-related protein Rab-18 [Homo sapiens]	45.77	23	5	8	54	0.989	13		1.163	13	24.5	2644.36	45.77	24	54	201	22.2	5.73
4504489	histidine-rich glycoprotein precursor [Homo sapiens]	35.05	7	15	16	198	0.989	73		1.215	72	17.4	6920.55	35.05	47	198	525	59.5	7.50
530417632	PREDICTED: glyca maturation factor gamma isoform X1 [Homo sapo	60.40	6	3	5	59	0.989	14		1.135	14	8.9	2258.87	60.40	15	59	101	12.0	5.03
221316614	extracellular matrix protein 1 isoform 1 precursor [Homo sapiens]	10.74	3	4	4	15	0.988	5		1.102	4	16.1	687.27	10.74	12	15	540	60.6	6.71
530356822	PREDICTED: uncharacterized protein LOC101929393 [Homo sapie	3.24	2	1	1	13	0.988	7		1.112	6	60.8	118.07	3.24	2	13	185	20.3	8.87

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# As	MW [kDa]	calc. pI
4502063	arachidonate 12-lipoxygenase, 12R-type [Homo sapiens]	0.71	4	1	1	1	0.987	1		1.127	1		32.89	0.71	1	1	701	80.3	7.64
451172106	coronin-1C isoform b [Homo sapiens]	23.42	7	10	11	44	0.987	14		1.147	14		1549.48	23.42	28	44	474	53.2	7.08
578837685	PREDICTED: plectin-B2 isoform X5 [Homo sapiens]	0.54	2	1	1	1	0.987	1		0.962	1		32.83	0.54	1	1	1838	205.0	6.24
197927454	protein DEX2 isoform 2 [Homo sapiens]	12.32	3	4	4	21	0.987	9	3.6	1.191	9	19.6	765.62	12.32	10	21	241	38.7	8.15
533631160	PREDICTED: flamm-binding LIM protein 1 isoform X1 [Homo sapiens]	3.21	1	1	1	1	0.987	1		1.371	1		0.00	3.21	1	1	374	40.3	6.43
219842236	tyrosine-protein kinase Fes/Fps isoform 4 [Homo sapiens]	4.61	4	2	2	6	0.987	2	8.3	1.252	2	1.2	389.45	4.61	6	6	694	78.6	6.80
530379292	PREDICTED: transportin-1 isoform X2 [Homo sapiens]	1.39	12	2	2	12	0.987	1		1.444	1		130.66	1.39	5	12	866	98.6	4.97
32189394	ATP synthase subunit beta, mitochondrial precursor [Homo sapiens]	10.59	1	4	4	18	0.986	6	3.7	1.274	6	5.0	1263.63	10.59	12	18	529	56.5	5.40
20357559	galectin-10 [Homo sapiens]	43.66	3	6	6	69	0.986	26	6	1.089	26	6	5	2123.75	43.66	69	142	16.4	9.37
14149680	extended synaptotagmin-1 isoform 2 [Homo sapiens]	2.54	2	2	2	6	0.986	2	4.5	1.138	2	5.9	314.19	2.54	6	6	1104	122.8	5.83
5031569	alpha-centractin [Homo sapiens]	33.78	6	4	8	44	0.986	6	3.8	1.295	6	22.0	1235.14	33.78	23	44	376	42.6	6.64
530375309	PREDICTED: polyhomocytic-like protein 3 isoform X3 [Homo sapiens]	0.56	6	1	1	3	0.986	1		1.262	1		54.98	0.56	3	3	897	96.5	7.27
578833911	PREDICTED: tubulin-folding cofactor B isoform X1 [Homo sapiens]	9.33	1	1	1	3	0.986	1		1.442	1		208.33	9.33	3	3	193	27.8	4.94
7664942	glyoxaldehyde-3-phosphate dehydrogenase isoform 1 [Homo sapiens]	90.45	3	3	27	1785	0.986	34	10.8	1.451	34	31.7	94183.39	90.45	79	1785	335	36.0	8.46
4504351	hemoglobin subunit delta [Homo sapiens]	92.52	1	8	15	2318	0.985	79	8.5	1.073	79	7.3	120925.19	92.52	43	2318	147	16.0	8.05
110624781	myosin-13 [Homo sapiens]	0.98	36	1	3	23	0.985	1		1.406	1		476.32	0.98	8	23	1938	223.5	5.68
126362971	serine/threonine-protein kinase 10 [Homo sapiens]	10.85	1	7	8	23	0.985	7	7.2	1.301	7	22.8	893.32	10.85	23	23	968	112.1	6.95
19923231	ras-related protein Rab-6A isoform a [Homo sapiens]	14.90	21	2	3	9	0.985	2	2.5	1.010	2	3.9	368.41	14.90	9	9	208	23.5	5.54
4506597	60S ribosomal protein L12 [Homo sapiens]	14.55	1	2	2	6	0.985	2	0.3	1.205	2	14.4	402.27	14.55	6	6	165	17.8	9.42
530420952	PREDICTED: male-specific lethal 3 homolog isoform X2 [Homo sapiens]	1.69	5	1	1	2	0.985	1		0.806	1		69.83	1.69	2	2	355	40.6	8.85
578806618	PREDICTED: TPR and arkyn repeat-containing protein 1 isoform 1 [Homo sapiens]	0.30	1	1	1	1	0.985	1		0.30	1		24.08	0.30	1	1	269	341.0	5.97
19923973	BTB/POZ domain-containing protein KCTD12 [Homo sapiens]	26.77	4	6	6	28	0.985	9	3.3	1.219	9	13.2	880.56	26.77	20	28	325	35.7	5.64
45027909	wiskott-Aldrich syndrome protein [Homo sapiens]	11.95	1	4	4	17	0.985	6	14.1	1.177	6	16.8	805.10	11.95	12	17	502	52.9	6.64
4506017	serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform 1 [Homo sapiens]	12.94	2	3	3	17	0.985	6	3.2	1.150	6	12.0	914.16	12.94	9	17	309	35.6	5.54
530383948	PREDICTED: DNA polymerase zeta catalytic subunit isoform X4 [Homo sapiens]	0.19	4	1	1	1	0.985	1		1.244	1		15.58	0.19	1	1	2679	301.0	8.00
52487191	endoplasmic reticulum resident protein 44 precursor [Homo sapiens]	7.88	1	2	3	14	0.985	3	0.3	1.248	3	11.5	436.94	7.88	9	14	406	46.9	5.26
578814066	PREDICTED: flamm-C isoform X1 [Homo sapiens]	2.39	3	1	9	64	0.984	6	9.0	1.085	6	2.2	1441.85	2.39	25	64	2632	281.4	6.04
11339298	immunoglobulin lambda-like polypeptide 1 isoform a precursor [Homo sapiens]	14.08	1	2	2	34	0.984	12	7.1	1.042	12	12.0	603.49	14.08	6	34	213	22.9	10.07
530369689	PREDICTED: striated muscle preferentially expressed protein kinase epidermal secretory protein E1 precursor [Homo sapiens]	0.21	23	1	5	5	0.984	3	3.3	1.145	3	5.6	34.47	0.21	3	5	2418	263.4	6.09
5453678	immunoglobulin lambda-like polypeptide 5 isoform 1 [Homo sapiens]	31.79	2	3	11	5	0.984	5	10.7	1.357	5	3.3	279.41	31.79	7	11	151	16.6	7.65
295986608	immunoglobulin lambda-like polypeptide 5 isoform 1 [Homo sapiens]	47.66	2	9	9	1880	0.984	678	9.5	1.271	670	24.6	79472.07	47.66	27	1880	214	23.0	8.84
578839125	PREDICTED: putative V-set and immunoglobulin domain-containing protein [Homo sapiens]	21.29	1	2	4	190	0.984	38	2.9	1.293	38	21.2	10249.28	21.29	12	190	155	17.4	9.91
530412286	PREDICTED: ATP-citrate synthase isoform X3 [Homo sapiens]	28.34	21	23	24	119	0.984	42	5.2	1.181	42	14.1	5339.78	28.34	71	119	1101	120.8	7.33
530379158	PREDICTED: centrosomal protein PCO5 isoform X2 [Homo sapiens]	1.28	4	1	1	1	0.984	1		0.956	1		29.02	1.28	1	1	547	60.3	7.92
34541817	kinesin-like protein KIF2A isoform 3 [Homo sapiens]	1.60	4	1	1	3	0.984	1		1.244	1		206.66	1.60	3	3	686	77.7	6.58
556695469	mRNA-capping enzyme isoform b [Homo sapiens]	1.22	2	1	1	1	0.983	1		1.136	1		15.16	1.22	1	1	574	66.0	8.38
4557587	fumarylacetoacetate [Homo sapiens]	4.77	1	2	2	5	0.983	2	0.1	1.313	2	18.7	165.65	4.77	5	5	419	46.3	6.95
4480052	cathepsin isoform a [Homo sapiens]	33.56	9	6	26	9	0.983	5	1.9	1.174	5	9	935.28	33.56	17	26	149	56.4	5.97
4504041	guanine nucleotide-binding protein (G(i)) subunit alpha-2 isoform 1 [Homo sapiens]	43.10	21	8	12	52	0.983	12	5.5	1.171	12	17.8	2371.85	43.10	33	52	355	40.4	5.54
583966148	isocitrate dehydrogenase [NADP], mitochondrial isoform 2 [Homo sapiens]	25.75	3	9	10	35	0.983	12	2.5	1.139	12	13.7	1298.22	25.75	25	35	400	45.2	7.75
10835240	high mobility group nucleosome-binding domain-containing protein [Homo sapiens]	26.67	1	2	2	7	0.983	3	5.1	1.160	3	2.1	181.18	26.67	5	7	90	9.5	10.48
578810775	PREDICTED: glucosamine-6-phosphate isomerase 1 isoform X2 [Homo sapiens]	22.15	7	6	6	24	0.983	9	3.5	1.137	9	22.0	892.48	22.15	16	24	289	32.6	6.92
578828075	PREDICTED: pyrin isoform X1 [Homo sapiens]	3.33	2	2	2	5	0.983	2		0.959	2	25.0	171.14	3.33	5	5	780	86.3	7.94
578819639	PREDICTED: tumor domain-containing protein 1 isoform X3 [Homo sapiens]	0.72	3	1	1	8	0.983	3	11.0	2.113	3	20.9	78.53	0.72	3	8	1104	123.7	6.19
6912396	glyoxylate reductase/hydroxyglutarate reductase [Homo sapiens]	23.17	2	4	4	12	0.983	4	8.2	1.387	4	22.7	623.85	23.17	12	12	328	35.6	7.39
530390765	PREDICTED: ferritin-binding protein 1 isoform X20 [Homo sapiens]	6.35	23	5	15	5	0.983	5	3.1	1.047	5	25.9	481.17	6.35	15	551	64.0	5.24	
32130518	apolipoprotein C-II precursor [Homo sapiens]	34.45	1	2	2	10	0.982	4	14.9	1.268	4	28.8	393.13	34.45	6	10	101	11.3	4.72
58761500	obg-like ATPase 1 isoform 1 [Homo sapiens]	10.61	2	3	3	7	0.982	3	7.8	1.112	3	0.4	308.62	10.61	7	7	396	44.7	7.81
530364287	PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sapiens]	14.24	3	7	7	23	0.982	8	8.8	1.113	8	14.8	929.12	14.24	20	23	660	75.3	6.48
578812388	PREDICTED: collagen alpha-1(XII) chain isoform X1 [Homo sapiens]	2.81	2	2	2	6	0.982	2	4.6	1.172	2	6.6	290.04	0.81	6	6	2972	323.4	5.54
648216372	aspartate--tRNA ligase, cytoplasmic isoform 2 [Homo sapiens]	9.23	2	3	3	9	0.982	3	2.9	1.027	3	2.5	335.62	9.23	9	9	401	45.7	5.71
325652048	transcription elongation factor B polypeptide 1 isoform b [Homo sapiens]	21.88	2	2	2	4	0.982	2	4.0	1.098	2	11.3	75.07	21.88	4	4	96	10.8	5.36
62198235	drebrin-like protein isoform b [Homo sapiens]	25.81	5	10	10	52	0.982	19	7.2	1.123	19	14.4	2282.30	25.81	27	52	430	48.2	5.05
54568992	regulator of telomere elongation helicase 1 isoform 4 [Homo sapiens]	0.80	4	1	1	1	0.982	1		0.549	1		22.49	0.80	1	1	996	108.4	8.15
578812959	PREDICTED: utrophin isoform X6 [Homo sapiens]	0.32	6	2	2	28	0.982	10	10.2	1.272	10	5.8	576.42	0.32	6	28	2499	287.1	5.47
38504669	serpin B8 isoform a [Homo sapiens]	9.89	6	2	3	14	0.982	2	1.8	1.021	2	9.4	637.81	9.89	8	14	374	47.2	5.57
539845980	protein phosphatase 1 regulatory subunit 7 isoform 6 [Homo sapiens]	12.96	7	3	3	20	0.982	7	5.9	1.066	7	9.9	1034.23	12.96	9	20	301	35.1	5.31
578834355	PREDICTED: glutamate receptor ionotropic, kainate 5 isoform X5 [Homo sapiens]	1.10	4	1	1	2	0.982	1		1.072	1		32.02	1.10	2	2	912	101.9	8.75
32483377	thioredoxin-dependent peroxide reductase, mitochondrial isoform 1 [Homo sapiens]	17.23	2	4	4	12	0.982	4	3.2	1.069	4	5.2	456.24	17.23	12	12	238	25.8	7.46
5803076	chromobox protein homolog 1 [Homo sapiens]	19.46	1	2	3	8	0.982	2	1.6	1.129	2	14.7	222.72	19.46	8	8	185	21.4	4.93
4504067	aspartate aminotransferase, cytoplasmic [Homo sapiens]	20.10	56	6	7	25	0.981	8	9.8	1.144	8	10.2	1089.47	20.10	19	25	413	46.2	7.01
578813854	PREDICTED: A-kinase anchor protein 9 isoform X3 [Homo sapiens]	0.91	66	3	5	18	0.981	3	4.5	1.320	3	9.0	200.84	0.91	11	18	3860	447.3	4.98
385157974	dynactin subunit 2 isoform 3 [Homo sapiens]	12.72	3	3	3	7	0.981	3	11.9	1.050	3	6.8	242.87	12.72	7	7	401	44.2	5.21
11386147	proasparaginase a precursor [Homo sapiens]	25.95	3	12	12	106	0.981	40	6.9	1.155	39	12.4	4338.69	25.95	35	106	524	58.1	5.17
18375644	tyrosine-protein phosphatase non-receptor type 11 isoform 2 [Homo sapiens]	2.39	4	1	1	2	0.981	1		1.078	1		112.29	2.39	2	2	460	52.8	7.44
17149836	peptidyl-prolyl cis-trans isomerase FKBP1A isoform a [Homo sapiens]	82.41	4	9	9	84	0.981	31	6.3	1.201	30	22.3	4030.17	82.41	25	84	108	11.9	8.16
195222722	U6 snRNA-associated Sm-like protein LSM5 isoform b [Homo sapiens]	37.10	2	1	1	3	0.												

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score	AB: 115/114	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
28302131	hemoglobin subunit gamma-1 [Homo sapiens]	65.99	1	8	246	0.979	4	6.3	1.028	4	4.8	6619.35	65.99	24	246	147	16.1	7.20		
4503149	cathepsin G preproprotein [Homo sapiens]	47.06	1	14	18	0.979	65	6.8	1.160	65	12.6	6837.08	47.06	36	175	255	28.8	11.19		
295332611	tyrosine-protein kinase SYK isoform c [Homo sapiens]	8.50	8	5	5	16	0.978	6	3.1	1.094	5	4.6	502.70	8.50	14	16	612	69.5	7.56	
31563514	N-alpha-acetyltransferase 20 isoform c [Homo sapiens]	6.31	3	1	1	20	0.978	12	5.3	1.307	12	13.4	177.96	6.31	2	20	111	12.7	4.67	
4885413	histidine triad nucleotide-binding protein 1 [Homo sapiens]	39.48	1	4	4	14	0.978	5	3.6	1.126	5	5.2	507.65	39.48	11	14	126	13.8	6.95	
319918857	coronin-7 isoform 3 [Homo sapiens]	6.19	4	5	5	17	0.978	6	10.9	1.143	6	39.2	556.34	6.19	14	17	840	91.6	6.14	
305410789	glutathione reductase, mitochondrial isoform 2 precursor [Homo sapiens]	44.22	4	15	15	88	0.978	32	4.9	1.129	32	39.9	4392.00	44.22	44	88	493	53.0	8.84	
4503299	class E basic helix-loop-helix protein 40 [Homo sapiens]	1.21	1	1	1	2	0.978	2	16.1	1.207	2	0.3	26.29	1.21	1	2	412	45.5	8.10	
31652249	lipopolysaccharide-binding protein [Homo sapiens]	9.98	1	4	4	26	0.978	9	6.7	1.228	9	17.9	1507.61	9.98	12	26	481	53.3	6.70	
162809334	pregnancy zone protein precursor [Homo sapiens]	25.44	1	18	27	554	0.978	25	6.4	1.161	24	20.8	35163.24	25.44	76	554	1482	163.8	6.38	
32171249	prostaglandin-H2 D-isomerase precursor [Homo sapiens]	17.37	1	2	2	6	0.978	2	5.9	0.990	2	6	11.2	6	6	190	21.0	7.80		
291575165	monocyte differentiation antigen CD14 precursor [Homo sapiens]	20.00	1	5	5	18	0.978	7	5.4	1.307	7	9.1	760.85	20.00	14	18	375	40.1	6.23	
210147567	glutamate-rich protein 4B [Homo sapiens]	1.01	1	1	1	2	0.978	2	4.5	1.163	2	23.2	48.10	1.01	1	2	696	81.6	4.75	
25121972	copine-8 [Homo sapiens]	2.48	18	1	2	25	0.978	1	1.112	1.112	1	4	610.86	2.48	1	2	564	63.1	5.96	
222144309	prenylated Rab acceptor protein 1 [Homo sapiens]	4.32	1	1	1	2	0.978	2	3.0	14.549	2	145.1	31.25	4.32	1	2	185	20.6	7.34	
530367946	PREDICTED: serine/arginine-rich splicing factor 1 isoform X2 [Homo sapiens]	13.00	5	2	2	3	0.978	2	22.8	1.279	2	22.0	57.94	13.00	3	3	223	25.6	11.80	
60097902	flaggrin [Homo sapiens]	6.45	1	8	8	41	0.978	15	7.9	1.037	15	8.5	1793.99	6.45	21	41	4061	434.9	9.25	
15431310	keratin, type I cytoskeletal 14 [Homo sapiens]	44.49	18	8	21	95	0.978	10	6.7	1.094	10	4.0	3343.80	44.49	59	95	472	51.6	5.16	
40353764	biphosphoglycerate mutase [Homo sapiens]	0.96	1	5	5	25	0.978	9	10.0	1.125	9	6.2	945.92	0.96	14	25	259	30.0	6.54	
29789445	desmoglein-4 isoform 2 preproprotein [Homo sapiens]	29.54	5	1	2	27	0.977	1	1.375	1.375	1	35.21	0.96	5	27	1040	113.8	4.56		
530381587	PREDICTED: FYVE, RhoGEF and PH domain-containing protein 2 [Homo sapiens]	0.97	2	1	1	1	0.977	1	0.97	0.97	1	31.03	0.97	1	1	620	70.0	7.90		
530421227	PREDICTED: ribosomal protein S6 kinase alpha-1 isoform X5 [Homo sapiens]	2.96	18	2	2	8	0.977	3	1.1	1.249	3	12.9	329.73	2.96	5	8	710	80.6	6.29	
4507645	triosephosphate isomerase isoform 1 [Homo sapiens]	78.71	3	14	14	208	0.977	75	6.7	1.136	75	11.3	10311.34	78.71	42	208	249	26.7	8.98	
254692833	NHS-like protein 2 [Homo sapiens]	1.06	2	1	1	3	0.977	1	0.948	0.948	1	7.9	129.96	1.06	3	3	1225	133.2	7.77	
567315950	THAP domain-containing protein 5 isoform 3 [Homo sapiens]	3.00	3	1	1	3	0.977	1	1.065	1.065	1	80.12	3.00	3	3	233	26.5	4.92		
127139033	NADPH-cytochrome P450 reductase [Homo sapiens]	6.76	1	3	3	8	0.977	3	9.0	1.102	3	7.9	461.43	6.76	8	8	680	77.0	5.58	
4502067	protein AMBP preproprotein [Homo sapiens]	46.88	2	14	14	140	0.977	52	8.1	1.171	51	12.8	5420.14	46.88	38	140	352	39.0	6.25	
126012562	prolow-density lipoprotein receptor-related protein 1 precursor [Homo sapiens]	0.11	1	1	1	7	0.977	3	8.4	1.375	3	26.7	68.27	0.11	3	7	4544	504.3	5.39	
530389740	PREDICTED: uncharacterized protein KIAA0205 isoform X1 [Homo sapiens]	0.58	1	1	1	2	0.977	2	1.8	1.169	2	3.3	232.37	0.58	14	2073	224.4	9.09		
530399442	PREDICTED: R3H domain-containing protein 2 isoform X1S [Homo sapiens]	0.61	16	1	1	30	0.976	11	4.0	1.151	11	17.4	298.01	0.61	3	30	976	106.9	8.85	
530381599	PREDICTED: peptidase inhibitor 16 isoform X3 [Homo sapiens]	3.70	1	1	1	3	0.976	1	1.018	1.018	1	158.53	3.70	3	3	270	29.7	5.71		
4505811	serine/threonine-protein kinase pim-1 isoform 2 [Homo sapiens]	1.60	14	1	1	3	0.976	1	0.956	0.956	1	70.90	1.60	3	3	313	35.7	6.11		
530377342	PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	3.75	7	2	2	6	0.976	2	5.1	1.397	2	17.7	166.08	3.75	6	6	534	59.5	7.91	
62243068	insulin-like growth factor-binding protein 3 isoform b precursor [Homo sapiens]	11.68	57	4	4	23	0.976	4	2.5	1.046	4	4.2	473.25	11.68	11	23	291	31.7	8.69	
41322910	plectin isoform 1d [Homo sapiens]	2.99	21	11	11	33	0.976	13	8.6	1.131	13	8.5	926.07	2.99	29	33	4515	512.3	5.77	
18104982	tyrosine-protein phosphatase non-receptor type 2 isoform 3 [Homo sapiens]	1.98	8	1	1	4	0.976	4	3.8	1.398	4	18.1	78.02	1.98	2	4	353	41.0	6.40	
24308273	costars family protein ABRA1 [Homo sapiens]	54.32	1	3	3	26	0.976	10	8.4	1.215	10	13.2	984.57	54.32	8	26	10	9.1	6.29	
156231067	TBC1 domain family member 8 [Homo sapiens]	1.08	7	1	2	3	0.975	1	3	1.233	1	39.52	1.08	3	3	1140	130.0	5.52		
24025535	collagen alpha-1(VI) chain isoform 4 precursor [Homo sapiens]	7.70	8	14	14	59	0.975	21	7.3	1.122	21	12.9	2813.56	7.70	40	59	2570	278.0	8.15	
295424842	signal recognition particle receptor subunit alpha isoform 2 [Homo sapiens]	3.93	2	1	2	5	0.975	1	0.944	0.944	1	114.83	3.93	5	5	610	66.5	9.04		
222136639	C-1-tetrahydrofolate synthase, cytoplasmic [Homo sapiens]	8.66	1	8	8	20	0.975	8	8.7	1.072	8	20.7	566.86	8.66	20	20	935	101.5	7.30	
4757804	copper transport protein ATOX1 [Homo sapiens]	20.59	8	2	2	11	0.975	4	2.5	1.136	4	4.7	142.12	20.59	5	11	68	7.4	7.24	
228008398	heterogeneous nuclear ribonucleoprotein Q isoform 3 [Homo sapiens]	15.04	9	5	7	25	0.975	5	2.0	1.334	5	7.6	951.53	15.04	19	25	527	58.7	7.56	
325652118	probable aminopeptidase NPEPL1 isoform 3 [Homo sapiens]	2.53	3	1	1	3	0.974	1	1.102	1.102	1	100.48	2.53	3	3	475	50.5	6.55		
13124873	core-binding factor subunit beta isoform 2 [Homo sapiens]	7.69	4	2	2	6	0.974	2	3.0	1.341	2	8.3	108.17	7.69	6	6	182	21.5	6.60	
31408161	rpe-related protein Rab-18 isoform 4 [Homo sapiens]	7.69	4	1	2	6	0.974	2	3.0	1.353	2	68.10	7.69	2	2	182	20.4	5.90		
4557395	carbonic anhydrase 2 isoform 1 [Homo sapiens]	55.00	2	11	11	131	0.974	46	8.5	1.077	46	6.8	6862.67	55.00	32	131	260	29.2	7.40	
14861860	testicular acid phosphatase precursor [Homo sapiens]	1.41	2	2	2	2	0.974	2	2.6	1.200	2	5.7	49.97	1.41	1	2	426	46.1	8.21	
4826952	26S proteasome non-ATPase regulatory subunit 5 isoform 1 [Homo sapiens]	5.95	2	2	2	6	0.974	2	6.1	1.203	2	13.9	356.71	5.95	6	6	504	56.2	5.48	
30089926	F-box only protein 11 isoform 1 [Homo sapiens]	1.07	5	1	1	5	0.974	2	5.7	1.292	2	15.6	76.40	1.07	2	5	843	94.0	6.84	
34222391	zinc finger protein 605 isoform 1 [Homo sapiens]	2.65	36	2	3	9	0.974	3	0.5	1.123	3	3.0	113.46	2.65	7	9	641	74.3	9.11	
50428938	ATPase ASNA1 [Homo sapiens]	5.46	1	2	2	6	0.974	2	6.4	1.141	2	10.1	162.16	5.46	6	6	348	38.8	4.91	
207442677	uncharacterized protein C19orf7 [Homo sapiens]	3.83	4	1	1	4	0.974	1	2.065	2.065	1	35.14	3.83	2	4	209	24.2	8.75		
41349456	prolyl endopeptidase [Homo sapiens]	6.06	2	3	3	16	0.974	6	4.5	1.258	6	9.5	885.53	6.06	7	16	710	80.6	5.86	
19913416	AP-2 complex subunit alpha-1 isoform 2 [Homo sapiens]	1.57	2	1	1	3	0.974	1	1.57	1.247	1	187.23	1.57	2	3	965	105.3	7.66		
57879051	PREDICTED: uncharacterized protein LOC100293211 [Homo sapiens]	25.93	2	6	8	318	0.974	50	5.7	1.312	50	19.2	9597.86	25.93	24	318	270	29.5	8.59	
306922420	trophoblast glycoprotein-like precursor [Homo sapiens]	2.36	1	1	1	1	0.974	1	28.83	2.36	1	1	28.83	2.36	1	1	382	40.4	8.27	
4502171	adenine phosphoribosyltransferase isoform a [Homo sapiens]	45.56	2	6	6	44	0.974	15	6.5	1.310	15	18.1	1690.71	45.56	18	44	180	19.6	6.02	
578826850	PREDICTED: tropomodulin-3 isoform X1 [Homo sapiens]	15.34	2	5	5	22	0.974	8	11.2	1.192	8	10.1	636.46	15.34	14	22	352	39.6	5.19	
4503625	coagulation factor X preproprotein [Homo sapiens]	8.61	3	3	3	18	0.973	6	8.5	1.364	6	15.8	747.03	8.61	9	18	488	54.7	5.94	
4503107	cystatin-C precursor [Homo sapiens]	19.18	1	2	2	6	0.973	2	8.0	1.078	2	4.7	382.90	19.18	6	6	146	15.8	8.75	
291045225	titin isoform N2-A [Homo sapiens]	0.11	33	4	7	23	0.973	3	0.7	1.253	3	247.65	0.11	15	23	33423	3711.3	6.52		
530403364	PREDICTED: nesprin-2 isoform X7 [Homo sapiens]	0.16	46	1	2	3	0.973	1	1.174	1.174	1	35.56	0.16	3	3	6883	795.9	5.39		
21735417	protein bicaudal D homolog 2 isoform 1 [Homo sapiens]	0.97	2	1	1	2	0.973	1	1.465	1.465	1	26.39	0.97	2	2	824	93.5	5.44		
45580723	haptoglobin-related protein precursor [Homo sapiens]	50.00	2	5	21	1913	0.973	13	2.8	1.192	13	12.3	67245.04	50.00	61	1913	348	39.0	7.09	
334724455	acetyl-coenzyme A synthetase, cytoplasmic isoform 3 [Homo sapiens]	1.82	9	2	2	32	0.973	2	2.7	0.747	2	54.0	482.66	1.82	5	32	606	67.6	6.15	
4506631	60S ribosomal protein L30 [Homo sapiens]	13.91	1	1	1	6	0.973	2	0.6	1.154	2	20.4	316.51	13.91	3	6	115	12.8	9.63	
239049591	glycogen [starch																			

Accession	Description	Zcoverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI	
530381903	PREDICTED: high mobility group protein HMG-I/HMG-Y isoform X3	35.51	1	1	3	8	0.970	1	1.292	1	1		219.62	35.51	7	8	107	11.7	10.32	
52317237	olfactory receptor 4C6 [Homo sapiens]	2.27		1	1	2	0.970	2	4.4	1.619	2		33.08	2.27	1	2	309	34.5	8.13	
5902102	small nuclear ribonucleoprotein Sm D1 isoform 1 [Homo sapiens]	36.97	2	3	3	26	0.970	9	5.9	1.131	9		13.6	981.97	36.97	9	26	119	13.3	11.56
591979295	PREDICTED: forms-binding protein 1-like isoform X1 [Homo sapiens]	1.13	4	1	1	15	0.970	7	7.3	1.315	7		14.7	156.56	1.13	3	15	533	61.8	5.94
4552419	flavin reductase (MDPR) [Homo sapiens]	59.71	1	8	8	74	0.970	27	8.9	1.034	27		5.5	3541.53	59.71	74	206	22.1	7.65	
4553771	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit	3.69	1	2	2	6	0.970	2	0.4	1.208	2		9.0	95.56	3.69	6	4	379	44.4	5.08
33286420	pyruvate kinase PKM isoform b [Homo sapiens]	76.65	36	2	47	853	0.970	4	9.4	1.337	4		23.6	37814.24	76.65	133	853	531	58.0	7.71
383872515	ubiquitin-conjugating enzyme E2 variant 1 isoform g [Homo sapiens]	48.57	31	6	7	23	0.969	7	2.3	1.040	7		9.2	651.46	48.57	18	23	105	12.0	9.72
22550104	ubiquitin carboxyl-terminal hydrolase 32 [Homo sapiens]	0.37	1	1	1	2	0.969	1	0.37	1.769	1		33.94	0.37	2	2	1604	181.5	6.44	
578838500	PREDICTED: putative bifunctional UDP-N-acetylglucosamine transferase	1.53	11	1	1	1	0.969	1	1.046		1		22.82	1.53	1	1	652	71.4	6.79	
34147630	elongation factor Tu, mitochondrial precursor [Homo sapiens]	3.74	1	1	1	6	0.969	2	3.8	1.032	2		14.4	291.94	3.74	3	6	455	49.8	7.61
54186040	protein disulfide-isomerase A6 isoform c precursor [Homo sapiens]	16.25	8	6	6	21	0.969	8	3.7	1.101	8		16.3	1081.34	16.25	17	21	437	47.8	5.08
9288645	ubiquitin carboxyl-terminal hydrolase 14 isoform b [Homo sapiens]	10.48	1	4	4	21	0.969	8	9.0	1.054	8		7.8	894.84	10.48	12	21	459	52.4	5.78
4550549	non-secretory ribonuclease precursor [Homo sapiens]	19.88	1	3	3	24	0.969	8	8.9	1.244	8		19.5	1021.40	19.88	9	24	161	18.3	8.73
4506127	ribose-phosphate pyrophosphokinase 1 isoform 1 [Homo sapiens]	18.24	5	4	4	17	0.969	5	8.7	1.115	5		12.0	811.31	18.24	11	17	318	34.8	6.98
315221152	60S ribosomal protein L11 isoform 2 [Homo sapiens]	10.73	2	1	2	8	0.968	1	1.266		1		156.44	10.73	6	8	177	20.1	9.60	
578802657	PREDICTED: SET and MYND domain-containing protein 5 isoform X1	1.91	4	1	1	2	0.968	1	1.256		1		33.42	1.91	2	2	366	41.7	4.83	
217416409	transmembrane protein 17 [Homo sapiens]	4.55	1	1	1	1	0.968	1	28.32	4.55	1		28.32	4.55	1	1	198	23.0	6.79	
115527662	collagen alpha-2(VI) chain isoform 2C2 precursor [Homo sapiens]	2.16	3	2	2	5	0.968	2	5.8	1.054	2		10.8	128.77	2.16	5	5	1019	108.5	6.21
530421640	PREDICTED: mediator of RNA polymerase II transcription subunit 1	0.67	4	1	1	1	0.968	1	1.156		1		28.83	0.67	1	1	1338	148.5	8.60	
530386607	PREDICTED: leucine-rich repeat and WD repeat-containing protein 1	2.22	1	1	1	1	0.968	1	1.519		1		35.72	2.22	1	1	495	53.7	6.93	
17158041	40S ribosomal protein S6 [Homo sapiens]	6.83	32	1	2	6	0.968	1	1.442		1		148.00	6.83	6	6	249	28.7	10.84	
530423350	PREDICTED: importin-5 isoform X2 [Homo sapiens]	3.59	1	2	2	6	0.968	2	1.4	1.234	2		18.5	392.39	3.59	6	6	1115	125.5	4.92
336391093	ras-related protein Rab-2A isoform b [Homo sapiens]	19.15	4	3	3	9	0.968	3	3.5	1.099	3		9.1	486.74	19.15	9	9	188	20.8	6.11
4503513	eukaryotic translation initiation factor 3 subunit 1 [Homo sapiens]	2.77	1	1	1	3	0.968	1	0.930		1		96.14	2.77	3	3	325	36.5	5.64	
4885153	crk-like protein [Homo sapiens]	9.57	1	2	2	6	0.968	2	1.5	1.293	2		14.1	265.31	9.57	6	6	303	33.8	6.74
530416665	PREDICTED: inactive serine/threonine-protein kinase VRK3 isoform	1.46	3	1	1	2	0.968	2	1.9	1.145	2		4.9	24.55	1.46	1	2	412	45.9	9.09
126032350	DNA-dependent protein kinase catalytic subunit isoform 2 [Homo sapiens]	2.56	25	9	9	34	0.967	10	5.2	1.169	10		13.7	737.69	2.56	24	34	4097	465.2	7.17
578767738	PREDICTED: putative UPF069 protein ENSP0000383144 [Homo sapiens]	1.92	2	1	1	2	0.967	1	1.120		1		25.48	1.92	2	2	416	46.1	10.85	
301171475	ATP-dependent RNA helicase DDX33 isoform 3 [Homo sapiens]	3.87	6	1	2	4	0.967	1	1.096		1		330.34	3.87	6	6	445	71.3	6.62	
13124875	myosin-11 isoform SMA2 [Homo sapiens]	9.03	17	1	19	165	0.967	1	0.911		1		6515.52	9.03	53	165	1938	223.4	5.53	
222352151	poly(rC)-binding protein 1 [Homo sapiens]	19.38	1	3	5	14	0.966	4	2.0	1.134	4		5.5	476.74	19.38	11	14	356	37.5	7.09
578805786	PREDICTED: bis(5'-adenosyl)-triphosphatase isoform X4 [Homo sapiens]	6.12	2	1	1	3	0.966	1	1.120		1		110.06	6.12	3	3	147	16.8	7.08	
324120908	doublecortin domain-containing protein 5 [Homo sapiens]	0.67	1	1	1	2	0.965	1	1.090		1		28.34	0.67	2	2	890	100.3	8.95	
4506221	26S proteasome non-ATPase regulatory subunit 12 isoform 1 [Homo sapiens]	12.06	2	4	4	14	0.965	5	5.2	1.438	5		17.3	664.56	12.06	11	14	456	52.9	7.65
530391261	PREDICTED: TBC1 domain family member 13 isoform X1 [Homo sapiens]	2.47	1	1	1	4	0.965	2	13.8	1.160	2		6.0	55.43	2.47	2	4	324	37.7	4.97
237649049	small nuclear ribonucleoprotein Sm D2 isoform 2 [Homo sapiens]	43.52	2	4	4	16	0.965	6	0.4	1.240	6		7.5	535.03	43.52	11	16	108	12.4	9.89
31377468	dedicator of cytokinesis protein 2 [Homo sapiens]	2.19	4	4	4	10	0.965	4	0.8	1.221	4		33.7	214.60	2.19	10	1830	211.8	6.87	
4507231	single-stranded DNA-binding protein, mitochondrial precursor [Homo sapiens]	4.05	2	1	1	2	0.964	1	1.193		1		27.48	4.05	2	2	148	17.2	9.60	
7657015	RNA-splicing ligase RttB homolog [Homo sapiens]	1.98	1	1	1	4	0.964	2	4.9	1.143	2		8.7	102.01	1.98	3	4	505	55.2	7.23
578823733	PREDICTED: matrix metalloproteinase-19 isoform X1 [Homo sapiens]	3.58	4	1	2	10	0.964	2	3.8	1.127	2		16.9	164.61	3.58	6	10	279	31.7	7.94
530374793	PREDICTED: DCN1-like protein 1 isoform X1 [Homo sapiens]	9.84	2	2	2	7	0.964	3	9.8	1.220	3		18.8	315.42	9.84	5	7	244	28.3	4.94
530392249	PREDICTED: FERM domain-containing protein 4A isoform X7 [Homo sapiens]	0.86	13	1	1	1	0.964	1	1.143		1		0.00	0.86	1	1	701	76.9	8.98	
4507467	transforming growth factor-beta-induced protein ig-h3 precursor [Homo sapiens]	35.87	1	16	17	102	0.964	35	7.3	1.177	34		17.9	4142.41	35.87	47	102	683	74.6	7.71
530363595	PREDICTED: zinc finger MYM-type protein 4 isoform X4 [Homo sapiens]	1.06	6	2	2	2	0.964	1	2.168		1		19.93	1.06	2	2	1224	136.2	8.13	
48164934	collagen alpha-1(I) chain precursor [Homo sapiens]	1.83	6	2	2	6	0.964	6	2.1	1.179	6		3.7	380.56	1.83	6	1366	129.2	8.95	
42794779	unconventional myosin-XVIIa isoform b [Homo sapiens]	1.86	5	3	3	7	0.963	3	4.5	1.110	3		14.0	387.95	1.86	7	7	2039	231.1	6.20
14141159	heterogeneous nuclear ribonucleoprotein H3 isoform b [Homo sapiens]	7.55	4	1	2	6	0.963	1	1.174		1		346.74	7.55	6	6	331	35.2	6.87	
118918435	von Willebrand factor A domain-containing protein 3B [Homo sapiens]	0.54	3	1	1	4	0.963	2	20.0	1.188	2		19.4	105.97	0.54	2	4	1294	145.7	7.33
149999611	signal recognition particle 14 kDa protein [Homo sapiens]	25.74	1	4	4	14	0.963	5	13.1	1.117	5		10.2	646.37	25.74	11	14	136	14.6	10.04
4557795	merlin isoform 1 [Homo sapiens]	2.02	25	1	2	9	0.963	3	1.1	1.041	3		7.6	87.25	2.02	5	9	595	69.6	6.47
7705753	complement C1q subcomponent subunit A precursor [Homo sapiens]	17.55	1	3	3	26	0.962	9	2.4	1.264	8		5.1	1105.73	17.55	9	26	245	26.0	9.11
19913408	DNA topoisomerase 2-beta [Homo sapiens]	0.68	2	1	1	2	0.962	1	1.190		1		62.09	0.68	2	2	1621	182.5	8.06	
530414990	PREDICTED: alpha-protein kinase 2 isoform X1 [Homo sapiens]	0.53	2	1	1	8	0.962	2	20.9	1.132	2		6.6	122.14	0.53	3	8	1501	163.7	5.44
578811811	PREDICTED: transcriptional-regulating factor 1 isoform X8 [Homo sapiens]	1.08	7	1	1	8	0.962	1	1.347		1		28.58	1.08	8	8	741	80.8	6.51	
379698844	coiled-coil domain-containing protein 51 isoform 2 [Homo sapiens]	2.32	2	1	1	2	0.962	1	1.215		1		42.34	2.32	2	2	302	33.6	6.96	
530413435	PREDICTED: myb-related transcription factor, partner of profilin-like	1.61	6	1	1	1	0.962	1	1.075		1		29.57	1.61	1	1	311	33.9	12.12	
341604768	60S ribosomal protein L13 isoform 2 [Homo sapiens]	5.73	2	1	1	3	0.962	1	1.095		1		186.15	5.73	3	3	192	22.2	11.65	
257900451	piezo-type mechanosensitive ion channel component 2 [Homo sapiens]	0.18	1	1	1	2	0.961	2	3.6	1.633	2		80.4	28.95	0.18	2	2	2752	317.9	6.15
578816096	PREDICTED: zinc finger protein ZFAT isoform X1 [Homo sapiens]	0.83	5	1	1	1	0.961	1	1.228		1		19.24	0.83	1	1	845	94.3	7.53	
530365604	PREDICTED: rho guanine nucleotide exchange factor 2 isoform X9	1.22	11	1	1	3	0.961	1	1.082		1		123.10	1.22	3	3	817	92.8	5.71	
5031981	26S proteasome non-ATPase regulatory subunit 14 [Homo sapiens]	20.32	1	1	2	17	0.961	7	10.5	1.283	6		34.5	672.14	20.32	7	17	310	34.6	6.52
530378067	PREDICTED: hedgehog-interacting protein isoform X1 [Homo sapiens]	1.03	3	1	1	2	0.961	1	1.553		1		27.88	1.03	2	2	682	76.8	6.02	
578810348	PREDICTED: microtubule-associated serine/threonine-protein kinase	0.26	11	1	1	2	0.960	1	1.483		1		25.60	0.26	2	2	2275	247.6	8.54	
27754778	ficollin-3 isoform 2 precursor [Homo sapiens]	7.99	2	2	2	11	0.960	4	0.9	1.257	4		14.0	302.20	7.99	6	11	288	31.7	6.84
46094009	melanoma inhibitory activity protein 2 precursor [Homo sapiens]	1.53	1	1	1	7	0.960	3	3.2	1.834	3		25.8	112.44	1.53	3	7	654	74.0	4.34
619328949	cytoplasmic FMRI-interacting protein 2 isoform b [Homo sapiens]	3.83	5	4	4	20	0.960	7	8.6	1.103	7		6.8	903.06	3.83	12	20	1227	142.5	7.17
1064																				

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
3359854	billiverdin reductase A precursor [Homo sapiens]	25.00	1	5	5	17	0.955	6	12.5	1.201	6	12.8	562.77	25.00	14	17	296	33.4	6.44
530413726	PREDICTED: trafficking protein particle complex subunit 8 isoform	0.69	5	1	1	1	0.955	1			1		27.20	0.69	1	1	1161	130.1	7.52
167900484	pentraxin-related protein PTX3 precursor [Homo sapiens]	10.50	1	3	3	9	0.955	3	17.2	1.212	3	19.9	549.74	10.50	9	9	381	41.9	5.01
4536907	serine/arginine-rich splicing factor 3 [Homo sapiens]	26.83	1	4	4	10	0.955	4	4.2	1.255	4	1.7	317.86	26.83	10	10	164	19.3	11.65
49472823	eukaryotic translation initiation factor 3 subunit G [Homo sapiens]	2.50	1	1	1	1	0.955	1	1.122	1.122	1	2.50	30.48	2.50	1	1	320	35.6	6.13
195972866	keratin, type I cytoskeletal 10 [Homo sapiens]	31.16	15	12	14	72	0.954	20	10.6	1.077	20	7.5	3690.33	31.16	42	72	584	58.8	5.21
4759224	programmed cell death protein 6 [Homo sapiens]	8.80	2	1	1	3	0.954	1		1.282	1		97.41	8.80	3	3	125	14.3	6.04
530382158	PREDICTED: serpin B9 isoform X1 [Homo sapiens]	5.32	3	1	2	12	0.954	1		0.897	1		472.77	5.32	6	12	376	42.4	5.86
530397198	PREDICTED: syntaxin-3 isoform X6 [Homo sapiens]	3.57	6	1	1	3	0.954	1		1.140	1		109.78	3.57	3	3	252	28.8	5.22
530410472	PREDICTED: vacuolar protein sorting-associated protein 53 homolog	1.25	4	1	1	1	0.953	1		1.110	1		30.07	1.25	1	1	641	72.4	7.83
283806699	zinc finger BED domain-containing protein 1 [Homo sapiens]	1.44	1	1	1	2	0.953	1		1.255	1		36.43	1.44	2	2	694	78.1	6.10
88501734	integrin alpha-M isoform 2 precursor [Homo sapiens]	14.67	3	14	14	47	0.953	16	9.4	1.131	16	11.8	1974.80	14.67	41	47	1152	127.1	7.23
66933016	inosine 5'-monophosphate dehydrogenase 2 [Homo sapiens]	3.70	2	1	1	2	0.953	1		1.297	1		129.29	3.70	2	2	514	55.8	4.90
530409856	PREDICTED: chromodomain-helicase-DNA-binding protein 3 isoform	0.59	15	1	1	1	0.953	1		1.267	1		23.14	0.59	1	1	1185	134.9	6.67
531990811	ubiquitin-conjugating enzyme E2 A isoform 4 [Homo sapiens]	10.08	3	1	1	1	0.953	1		1.024	1		22.45	10.08	1	1	119	13.6	4.75
12965178	taste receptor type 2 member 13 [Homo sapiens]	2.64	1	1	1	4	0.953	2	2.2	1.140	2	31.2	60.83	2.64	2	4	303	35.1	9.66
64762445	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 isoform b	7.01	17	3	3	8	0.952	3	3.2	1.172	3	7.9	282.48	7.01	8	8	471	54.4	7.56
118402586	lactoylglutathione lyase [Homo sapiens]	41.85	1	7	7	22	0.952	8	6.9	1.029	8	8.4	707.51	41.85	19	22	184	20.8	5.31
34249321	interleukin-18 isoform 2 precursor [Homo sapiens]	4.23	2	1	1	6	0.952	2	5.1	1.143	2	19.7	93.70	4.23	3	6	189	21.9	4.78
4507509	metalloproteinase inhibitor 1 precursor [Homo sapiens]	5.80	1	1	1	3	0.952	1		1.043	1		173.10	5.80	3	3	207	23.2	8.10
7170145	methyl-CpG-binding domain protein 2 isoform-specific isoform [Homo	1.99	4	1	1	1	0.952	1		1.067	1		29.50	1.99	1	1	302	31.7	10.78
4502643	T-complex protein 1 subunit zeta isoform A [Homo sapiens]	29.94	6	12	12	71	0.952	26	9.8	1.200	26	14.5	2789.40	29.94	34	71	531	58.0	6.68
100913206	ATP-dependent RNA helicase A [Homo sapiens]	3.15	4	4	4	12	0.951	4	2.7	1.255	4	8.3	380.72	3.15	10	12	1270	140.9	6.84
17978485	vacuolar protein sorting-associated protein 18 homolog [Homo sap	1.13	1	1	1	3	0.951	1		1.541	1		121.98	1.13	3	3	973	110.1	6.07
16306548	serine--tRNA ligase, cytoplasmic [Homo sapiens]	2.72	2	1	1	2	0.951	1		0.837	1		57.40	2.72	2	2	514	58.7	6.43
31742501	sorting nexin-27 [Homo sapiens]	1.89	2	1	1	3	0.950	1		1.245	1		125.91	1.89	3	3	528	59.8	6.32
154146216	pleckstrin homology domain-containing family A member 2 [Homo	1.65	1	1	1	2	0.950	1		1.892	1		33.04	1.65	2	2	425	47.2	8.66
91105767	tyrosine-protein phosphatase non-receptor type substrate 1 precu	7.94	4	3	3	8	0.950	3	3.2	1.298	3	4.0	345.37	7.94	8	8	504	54.9	6.98
3993641	uncharacterized protein C1orf142 [Homo sapiens]	13.24	1	1	1	2	0.950	1		1.060	1		44.22	13.24	2	2	204	21.6	5.48
530365342	PREDICTED: protein S100-A7 isoform X1 [Homo sapiens]	55.45	1	5	8	115	0.950	26	6.0	1.110	26	12.5	6246.67	55.45	24	115	101	11.5	6.77
21361176	retinal dehydrogenase 1 [Homo sapiens]	7.98	2	4	4	4	0.950	4	3.4	1.088	4	8.0	430.77	7.98	10	10	501	54.8	6.73
4505711	metalloproteinase inhibitor 2 precursor [Homo sapiens]	11.82	1	2	2	4	0.950	2	7.8	2.171	2	129.6	82.41	11.82	4	4	220	24.4	7.49
578824944	PREDICTED: paraspeckle component 1 isoform X2 [Homo sapiens]	5.39	2	1	1	3	0.950	1		1.008	1		79.57	5.39	3	3	427	49.2	6.43
371877525	arachidonate 5-lipoxygenase isoform 2 [Homo sapiens]	4.21	3	2	2	6	0.950	2	10.5	1.094	2	15.8	348.95	4.21	6	6	642	74.6	5.63
5174613	nucleosome assembly protein 1-like 4 [Homo sapiens]	2.93	1	1	1	3	0.949	1		1.440	1		93.96	2.93	3	3	375	42.8	4.69
530379765	PREDICTED: eukaryotic peptide chain release factor subunit 1 iso	11.88	3	3	3	6	0.949	3	10.9	0.921	3	29.3	251.41	11.88	6	6	404	45.4	5.57
19923821	hydroxyprolyl-4-hydroxylase-related protein 5 [Homo sapiens]	1.24	1	1	1	6	0.949	3	1.1	1.116	3	18.4	74.65	1.24	2	6	564	61.4	7.20
50735768	B-cell CLL/lymphoma 7 protein family member C isoform 1 [Homo	4.85	1	2	2	6	0.949	1		2.577	1	4.5	80.81	4.85	6	6	242	26.4	10.74
388990228	chitinotriase-1 isoform 2 precursor [Homo sapiens]	9.17	3	3	3	11	0.949	4	28.5	1.486	4	28.5	578.85	9.17	6	11	447	49.6	6.19
4505981	platelet basic protein preproprotein [Homo sapiens]	14.84	1	2	2	2	0.949	2	5.6	1.086	2	8.0	267.25	14.84	6	6	128	13.9	8.79
578798461	PREDICTED: WD repeat-containing protein 65 isoform X4 [Homo s	0.59	4	1	1	2	0.948	2	0.5	2.132	2	47.6	30.31	0.59	1	2	1192	138.4	5.64
392513662	interleukin enhancer-binding factor 2 isoform 2 [Homo sapiens]	2.84	2	1	1	6	0.948	2	3.2	1.098	2	5.0	245.41	2.84	3	6	352	38.9	4.94
4506691	40S ribosomal protein S16 [Homo sapiens]	14.38	2	2	2	6	0.948	2	1.0	1.105	2	15.9	272.24	14.38	6	6	146	16.4	10.21
530386628	PREDICTED: myosin regulatory light chain 10 isoform X1 [Homo s	6.80	1	1	1	2	0.947	1		1.204	1		105.21	6.80	2	2	147	16.9	4.70
11225266	transient receptor potential cation channel subfamily M member 5	0.77	2	1	1	2	0.947	1		1.088	1		33.43	0.77	1	2	1165	131.4	6.77
57880587	PREDICTED: fibronin-B isoform X7 [Homo sapiens]	3.84	6	1	1	3	0.946	1		1.247	1		1402.01	3.84	25	43	2109	225.9	6.00
530372374	PREDICTED: histone-lysine N-methyltransferase SETD2 isoform X1	0.29	4	1	1	2	0.946	1		1.215	1		37.27	0.29	2	2	2058	230.7	5.80
578802374	PREDICTED: obscurin isoform X32 [Homo sapiens]	3.01	43	3	4	15	0.946	3	0.0	1.441	3	41.5	218.16	3.01	7	15	7297	796.4	5.83
530424129	PREDICTED: COX assembly mitochondrial protein 2 homolog isofo	4.97	1	1	1	1	0.946	1		1.248	1		30.11	4.97	1	1	181	19.7	8.97
530397403	PREDICTED: cleavage and polyadenylation specificity factor subun	6.56	6	1	1	3	0.946	1		0.813	1		156.88	6.56	3	3	381	41.9	9.57
41393614	ras-related protein Rab-5C isoform A [Homo sapiens]	16.20	4	3	3	11	0.945	1		1.000	1		344.58	16.20	8	11	216	23.5	8.41
530400175	PREDICTED: amphoterin-induced protein isoform X1 [Homo sapi	1.72	1	1	1	2	0.945	2	11.4	1.054	2	3.6	28.22	1.72	1	2	522	57.9	8.40
39753957	torin-1A-interacting protein 1 isoform 2 [Homo sapiens]	2.40	1	1	1	3	0.945	1		1.068	1		217.09	2.40	3	3	583	66.2	8.18
387596071	thoredoxin reductase 1, cytoplasmic isoform 5 [Homo sapiens]	14.97	9	4	5	11	0.945	4	9.9	1.253	4	8.6	424.83	14.97	11	11	461	50.8	6.62
22538465	proteasome subunit beta type 3 [Homo sapiens]	31.71	1	5	5	21	0.945	9	4.5	1.047	9	7.4	796.63	31.71	13	21	205	22.9	6.55
115334675	ubiquitin thioesterase otulin [Homo sapiens]	1.99	1	1	1	2	0.945	1		2.387	1		36.14	1.99	2	2	352	40.2	5.47
66932916	mitogen-activated protein kinase 1 [Homo sapiens]	24.44	19	4	7	29	0.944	6	14.4	1.161	6	17.2	956.26	24.44	18	29	360	41.4	6.98
124028517	transcription factor PU.1 isoform 2 [Homo sapiens]	3.70	2	1	1	3	0.944	1		1.408	1		114.84	3.70	3	3	270	31.1	6.80
38201714	ELAV-like protein 1 [Homo sapiens]	3.37	1	1	1	3	0.944	1		1.159	1		103.89	3.37	3	3	326	36.1	9.17
8923541	UPF0587 protein C1orf123 [Homo sapiens]	10.63	1	1	1	1	0.944	1		1.121	1		25.18	10.63	1	1	160	18.0	5.01
154240671	maestro heat-like repeat-containing protein family member 2B [Ho	0.50	1	1	1	1	0.943	1		1.576	1		33.71	0.50	1	1	1585	180.7	6.28
530418502	PREDICTED: dolichol-phosphate mannosyltransferase isoform X3 (l	4.23	4	1	1	2	0.943	1		1.247	1		19.60	4.23	2	2	189	21.9	9.41
238908495	pleckstrin homology domain-containing family D member 1 [Homo	1.38	1	1	1	4	0.943	1	1.0	1.125	4	0.8	52.44	1.38	1	4	506	59.2	6.44
33356148	fornin-like protein 1 [Homo sapiens]	3.27	10	3	3	9	0.943	3	14.2	1.320	3	8.6	177.94	3.27	9	9	1100	121.8	5.72
195539356	proteasome subunit beta type-5 isoform 2 [Homo sapiens]	7.50	2	1	1	3	0.943	1		0.986	1		128.71	7.50	3	3	160	17.8	7.24
578808222	PREDICTED: actin filament-associated protein 1 isoform X3 [Homo	0.90	3	1	1	1	0.942	1		0.918	1		24.78	0.90	1	1	558	62.1	6.71
209863034	perostin isoform 4 precursor [Homo sapiens]	47.67	5	1	26	159	0.942	1		1.040	1		7396.91	47.67	76	159	751	83.8	8.18
578832623	PREDICTED: Ish1 domain and HEAT repeat-containing protein KIAA	0.70	7	1	1	2	0.942	1		2.564	1		30.64	0.70	2	2	860	96.9	6.43
40806221	thymocyte nuclear protein 1 isoform 1 [Homo sapiens]	12.44	4	3	3	8	0.942	3	6.5	1.069	3	13.9	227.90						

Accession	Description	Zcoverage	Z# Proteins	Z# Unique Peptides	Z# Peptides	Z# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
530394395	PREDICTED: WD repeat-containing protein 96 isoform X5 [Homo sapiens]	0.52	6	1	1	1	0.934	1		1.064	1		24.80	0.52	1	1	1535	176.8	5.76
526253088	endothelial differentiation-related factor 1 isoform 4 [Homo sapiens]	11.81	5	1	1	8	0.934	3	7.8	1.145	3	37.9	270.63	11.81	3	8	127	14.1	9.80
22027655	AP-1 complex subunit sigma-2 isoform 2 [Homo sapiens]	5.73	4	1	2	0.933		1		0.929	1		44.81	5.73	1	2	157	18.6	5.47
14150496	transmembrane protein 79 [Homo sapiens]	2.03	1	1	1	0.933		1		5.752	1		39.51	2.03	1	2	394	43.5	4.93
269841098	phosphotyrosine phosphatidylserine inorganic pyrophosphate phosphatase	9.63	2	2	2	12	0.933	5	5.7	1.082	5	5.3	291.95	9.63	6	12	270	29.1	6.15
320461689	ankyrin repeat and SOCS box protein 12 [Homo sapiens]	2.20	1	1	1	1	0.932	1		1.173	1		28.63	2.20	1	1	318	35.0	6.21
226530313	protein-methionine sulfatase oxidase MICALL1 isoform 2 [Homo sapiens]	2.36	2	2	2	5	0.932	2	12.8	1.274	2	17.4	240.62	3.36	5	5	981	108.5	6.48
578804605	PREDICTED: UDP-glucose:glycoprotein glucosyltransferase 1 isoform 1 [Homo sapiens]	0.71	4	1	1	1	0.931	1		1.137	1		134.56	0.71	3	3	1544	176.2	5.63
530383030	PREDICTED: Lebercilin isoform X2 [Homo sapiens]	2.15	1	1	1	1	0.931	1		1.064	1		25.09	2.15	1	1	697	80.5	7.68
7019439	ATP-sensitive inward rectifier potassium channel 14 [Homo sapiens]	2.06	1	1	1	1	0.931	1		1.255	1		21.27	2.06	1	1	436	47.8	5.41
375298720	gamma-tubulin complex component 2 isoform 3 [Homo sapiens]	0.78	3	1	1	1	0.930	1		1.085	1		41.53	0.78	1	1	772	88.0	6.76
223278387	calmodulin-like protein 5 [Homo sapiens]	21.23	1	2	2	8	0.930	3		1.149	3		681.93	21.23	5	8	146	15.9	4.44
578825543	PREDICTED: centrosomal protein of 126 kDa isoform X2 [Homo sapiens]	0.47	2	1	1	1	0.930	1		1.195	1		0.00	0.47	1	1	1055	123.1	6.60
4502315	V-type proton ATPase subunit C 1 [Homo sapiens]	6.54	1	2	2	4	0.929	2	3.9	1.062	2	29.6	292.40	6.54	4	4	382	43.9	7.46
42544239	complement factor D preproprotein [Homo sapiens]	34.39	1	6	6	13	0.928	5	7.5	1.096	5	13.9	299.08	34.39	13	13	253	27.0	7.71
530397411	PREDICTED: isospartyl peptidase/asparginase isoform X3 [Homo sapiens]	5.56	2	1	1	3	0.928	1		1.154	1		120.80	5.56	3	3	180	19.0	7.88
566559963	phosphopantothenate-cysteine ligase isoform C [Homo sapiens]	10.48	3	1	1	2	0.928	1		1.004	1		96.75	10.48	2	2	105	12.0	6.57
11342680	beta-centractin [Homo sapiens]	14.36	2	1	4	14	0.928	2	0.3	2.070	2	27.6	460.45	14.36	10	14	376	42.3	6.40
9507239	immunoglobulin Iota chain precursor [Homo sapiens]	3.45	2	1	1	10	0.927	4	6.9	1.080	4	3.4	172.71	3.45	3	10	145	16.6	6.76
578822447	PREDICTED: centrosomal protein KIAA1731 isoform X7 [Homo sapiens]	0.42	7	1	1	3	0.927	1		1.249	1		66.38	0.42	3	3	2382	268.9	5.71
4507137	small nuclear ribonucleoprotein C [Homo sapiens]	11.11	1	1	1	3	0.927	1		1.407	1		188.56	11.11	3	3	76	8.5	8.88
4504523	10 kDa heat shock protein, mitochondrial [Homo sapiens]	6.86	2	1	1	1	0.927	1		1.077	1		31.18	6.86	1	1	102	10.9	8.92
530407962	PREDICTED: zinc finger CCHC domain-containing protein 7A isoform 1 [Homo sapiens]	0.73	2	1	1	1	0.926	1		1.228	1		24.30	0.73	1	1	958	109.2	7.24
48717372	mediator of RNA polymerase II transcription subunit 11 [Homo sapiens]	8.55	1	1	1	8	0.925	5	4.0	3.673	5	64.3	92.88	8.55	3	8	117	13.1	5.96
392996949	UV excision repair protein RAD23 homolog A isoform 2 [Homo sapiens]	8.01	41	2	4	11	0.923	2	13.5	1.171	11	11.1	302.07	8.01	11	11	362	39.5	4.58
313102999	diacylglycerol kinase zeta isoform 7 [Homo sapiens]	0.66	1	1	1	1	0.923	1		1.193	1		32.92	0.66	1	1	906	101.2	7.61
4503727	peptidyl-prolyl cis-trans isomerase FKBP1 [Homo sapiens]	6.25	1	2	2	5	0.923	1	5.2	1.167	2	3.2	120.41	6.25	5	5	224	25.2	9.28
52370487	ubiquitin-like-conjugating enzyme ATG3 isoform 2 [Homo sapiens]	3.22	2	1	1	3	0.923	1		1.090	1		81.52	3.22	3	3	311	35.4	4.79
262116263	55 kDa erythrocyte membrane protein isoform 4 [Homo sapiens]	1.15	4	1	1	1	0.923	1		1.029	1		26.67	1.15	1	1	436	49.0	7.31
530404921	PREDICTED: serine/threonine-protein kinase IkkB isoform X2 [Homo sapiens]	1.49	1	1	1	1	0.923	1		1.181	1		27.71	1.49	1	1	873	95.4	6.30
578838049	PREDICTED: protein-cysteine N-palmitoyltransferase porcupine isoform 1 [Homo sapiens]	4.33	14	1	2	2	0.922	1		1.205	1		44.57	4.33	2	2	323	36.3	7.99
114431246	keratin, type I cytoskeletal 28 [Homo sapiens]	3.02	15	1	2	7	0.922	1		1.303	1		105.47	3.02	5	7	464	50.5	5.47
578837230	PREDICTED: 3-mercaptopyruvate sulfurtransferase isoform X2 [Homo sapiens]	9.28	3	2	2	6	0.922	2	4.8	1.395	2	30.9	230.46	9.28	6	6	237	26.4	8.06
530422114	PREDICTED: RNA-binding protein 41 isoform X4 [Homo sapiens]	2.50	7	1	1	3	0.921	3	7.6	1.436	3	21.2	38.42	2.50	3	3	240	28.1	8.82
530414204	PREDICTED: asparagine-tRNA ligase, cytoplasmic isoform X1 [Homo sapiens]	1.46	2	1	1	2	0.921	1		1.272	1		42.62	1.46	2	2	547	62.8	6.25
530384257	PREDICTED: bcl-2-associated transcription factor 1 isoform X3 [Homo sapiens]	1.40	6	1	1	3	0.921	1		1.242	1		77.54	1.40	3	3	642	73.2	10.17
578828512	PREDICTED: PDI domain-containing protein 9 isoform X1 [Homo sapiens]	2.73	5	1	1	2	0.920	1		1.020	1		32.40	2.73	2	2	220	25.4	7.23
13559861	ras-related protein Rab-31 [Homo sapiens]	9.23	3	2	2	5	0.920	3	2.0	1.378	2	17.4	108.27	9.23	5	195	192	21.7	7.04
530399725	ras-related protein Rab-31 [Homo sapiens]	9.23	3	2	2	5	0.920	3	2.0	1.378	2	17.4	108.27	9.23	5	195	192	21.7	7.04
271398277	cytosolic non-specific dipeptidase isoform 2 [Homo sapiens]	5.37	2	1	1	3	0.919	1		0.988	1		222.42	5.37	3	3	391	43.8	6.48
51477708	heterogeneous nuclear ribonucleoprotein D0 isoform d [Homo sapiens]	29.27	9	1	9	36	0.918	1		1.001	1		1515.28	29.27	19	36	287	30.7	8.41
530364444	PREDICTED: protein PRRC2C isoform X16 [Homo sapiens]	0.41	18	1	1	1	0.918	1		1.133	1		27.31	0.41	1	1	2708	296.8	8.79
151301228	pre-mRNA-processing factor 40 homolog A [Homo sapiens]	0.97	4	1	1	3	0.918	1		1.017	1		123.97	0.97	3	3	930	105.9	7.99
14281429	basic leucine zipper and W2 domain-containing protein 1 isoform 4 [Homo sapiens]	9.35	4	2	2	11	0.918	4		1.282	3	4.5	459.63	9.35	6	11	353	40.5	6.46
122939149	rho GTPase-activating protein 9 isoform 3 [Homo sapiens]	6.95	8	2	2	5	0.917	2	8.5	1.025	2	1.7	299.69	6.95	5	5	547	61.1	8.19
525362616	acyl-coenzyme A oxidase 1 isoform 6 [Homo sapiens]	15.06	7	2	2	5	0.917	2	0.1	1.241	2	8.8	260.71	15.06	5	166	18.0	6.94	
42476083	interferon alpha-8 precursor [Homo sapiens]	4.16	1	1	1	1	0.917	1		1.348	1		28.83	4.16	1	1	189	22.0	5.43
530409873	PREDICTED: SET and MYND domain-containing protein 4 isoform 1 [Homo sapiens]	2.68	3	2	2	7	0.917	2		1.597	2	39.8	106.62	2.68	5	7	635	70.6	7.30
530393909	PREDICTED: uncharacterized protein C10orf118 isoform X2 [Homo sapiens]	1.34	17	1	2	10	0.917	3	0.0	1.760	1		158.08	1.34	6	10	898	103.6	6.27
4504297	histone H3.1 [Homo sapiens]	61.03	3	1	9	73	0.916	6	19.4	1.988	4	94.2	1809.12	61.03	26	73	136	15.4	11.12
528524494	dynein light chain roadblock-type 1 isoform b [Homo sapiens]	19.05	7	1	1	3	0.916	1		1.137	1		160.14	19.05	3	3	63	7.3	7.25
339895853	RAC-beta serine/threonine-protein kinase isoform 2 [Homo sapiens]	1.91	3	1	1	1	0.916	1		1.047	1		23.75	1.91	1	1	419	48.5	6.15
206597509	arf-GAP domain and FG repeat-containing protein 1 isoform 4 [Homo sapiens]	4.02	8	2	2	6	0.916	2		1.348	2	13.4	225.96	4.02	6	6	522	54.1	8.92
14150155	vacuolar protein sorting-associated protein 25 [Homo sapiens]	5.68	1	1	1	3	0.915	1		1.323	1	8.6	133.36	5.68	3	3	176	20.7	6.34
53078329	centrosomal protein of 65 kDa isoform 2 [Homo sapiens]	1.83	4	2	4	4	0.914	2	7.2	1.187	2		64.21	1.83	4	7	111	80.3	6.23
31542319	coatamer subunit epsilon isoform a [Homo sapiens]	18.51	3	4	4	9	0.914	3	11.9	1.274	3	8.6	384.96	18.51	9	9	308	34.5	5.12
10863889	U4/U6.U5 tri-snRNP-associated protein 1 [Homo sapiens]	2.50	1	1	1	3	0.913	1		1.562	1		154.81	2.50	3	3	800	90.2	6.13
214832050	dual specificity protein phosphatase 19 isoform 2 [Homo sapiens]	4.82	2	1	1	2	0.911	1		1.434	1		35.72	4.82	2	2	166	18.3	8.07
20330805	guanine nucleotide-binding protein G(i) subunit alpha-2 [Homo sapiens]	6.50	13	1	3	10	0.911	1		2.354	1		399.36	6.50	7	10	354	40.2	5.24
118572606	hemicentin-1 precursor [Homo sapiens]	0.25	1	1	1	8	0.910	2	7.5	1.420	2	29.1	61.23	0.25	3	8	5635	613.0	6.49
530393088	PREDICTED: adenosine kinase isoform X1 [Homo sapiens]	13.27	5	2	2	9	0.910	3	0.4	1.128	3	7.5	771.38	13.27	6	9	294	33.1	8.03
55650347	vacuolar protein sorting-associated protein VTA1 homolog isoform 1 [Homo sapiens]	3.60	3	1	2	2	0.910	1		1.240	1		49.51	3.60	2	2	222	24.5	5.29
4505469	adenophag-3 isoform 2 preproprotein [Homo sapiens]	2.72	2	1	1	3	0.909	3	29.7	1.342	3	35.8	42.63	2.72	3	257	29.3	9.39	
4503535	eukaryotic translation initiation factor 4E isoform 1 [Homo sapiens]	14.75	6	3	3	9	0.908	4	0.3	1.158	4		300.47	14.75	7	9	217	25.1	6.15
5174735	tubulin beta-4B chain [Homo sapiens]	64.27	5	2	20	161	0.907	1		1.279	1		6449.98	64.27	55	161	445	49.8	4.89
530360520	PREDICTED: serine/threonine-protein kinase mTOR isoform X2 [Homo sapiens]	0.34	2	1	1	3	0.907	3	10.0	1.258	3	143.9	33.95	0.34	1	3	2322	263.7	7.21
116235474	serine/threonine-protein kinase 11-interacting protein [Homo sapiens]	0.55	1	1	1	2	0.907	1		4.975	1		33.08	0.55	2	2	1099	121.3	5.39
14165466	poly(pyrimidine tract-binding protein 1 isoform C [Homo sapiens]	13.56	37	4	5	31	0.907	5	4.1	1.372	5	1.1	1250.78	13.56	15	31	531	57.2	9.17
314233960	NLR family CARD domain-containing protein 4 [Homo sapiens]	1.07	1	1	1	3	0.906	1		1.025	1</								

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
115298659	spectrin alpha chain, erythrocytic 1 [Homo sapiens]	1.32	1	2	2	5	0.888	2	18.2	1.047	2	38.3	171.96	1.32	5	5	2419	279.8	5.05
568384725	BRO1 domain-containing protein BROX isoform c [Homo sapiens]	7.40	7	1	1	2	0.887	1		1.354			64.53	7.40	2	2	338	38.2	8.60
578807020	PREDICTED: programmed cell death protein 10 isoform X4 [Homo sapiens]	4.72	1	1	1	3	0.886	1		0.648	1		72.36	4.72	3	3	212	24.7	8.19
70788355	ankyrin-1 isoform 2 [Homo sapiens]	0.47	6	1	1	2	0.884	1		1.085	1		31.67	0.47	2	2	1719	188.9	6.62
145309300	cyclin-dependent kinase 13 isoform 2 [Homo sapiens]	0.96	93	1	2	12	0.883	2	8.8	1.392	2	70.3	222.87	0.96	6	12	1452	158.3	9.70
530436491	PREDICTED: uncharacterized protein LOC101930119 [Homo sapiens]	4.09	2	1	1	1	0.883	1		1.238	1		28.41	4.09	1	1	220	24.5	9.17
530406392	PREDICTED: E3 ubiquitin-protein ligase TRIM69 isoform X2 [Homo sapiens]	6.08	53	1	3	8	0.882	2		1.257	1		43.97	6.08	4	8	296	34.0	6.73
578824474	PREDICTED: probable ATP-dependent RNA helicase DDX23 isoform 1 [Homo sapiens]	1.00	9	1	1	2	0.882	1		1.372	1		27.35	1.00	2	2	602	71.4	9.66
287326622	tyrosine-protein kinase HCK isoform d [Homo sapiens]	11.11	102	2	5	18	0.881	2	8.6	1.167	2	0.3	519.92	11.11	11	18	504	57.2	6.86
4506629	60S ribosomal protein L29 [Homo sapiens]	9.43	1	1	1	3	0.880	1		1.065	1		185.41	9.43	3	3	159	17.7	11.66
530407865	PREDICTED: calcium-regulated heat stable protein 1 isoform X2 [Homo sapiens]	10.88	2	1	1	2	0.873	1		1.347	1		52.02	10.88	2	2	147	15.9	8.21
9951923	carbonic anhydrase-related protein 11 precursor [Homo sapiens]	1.83	1	1	1	1	0.873	1		1.335	1		16.88	1.83	1	1	328	36.2	9.74
530402038	PREDICTED: NEDD4-binding protein 2-like 1 isoform X1 [Homo sapiens]	1.23	6	1	1	1	0.873	1		0.976	1		29.27	1.23	1	1	568	65.8	6.15
578800828	PREDICTED: glutamine synthetase isoform X1 [Homo sapiens]	2.14	1	1	1	3	0.872	1		0.815	1		96.09	2.14	3	3	373	42.0	6.89
315113860	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit 1 [Homo sapiens]	3.03	2	1	1	2	0.870	1		1.751	1		132.98	3.03	2	2	429	50.2	5.78
66346685	plasmalogen activator inhibitor 1 RNA-binding protein isoform 4 [Homo sapiens]	7.49	4	2	2	4	0.869	2	16.0	0.989	2	18.4	78.86	7.49	4	4	387	42.4	8.44
209862791	zinc finger protein 90 [Homo sapiens]	2.00	1	1	1	1	0.869	1		1.240	1		24.26	2.00	1	1	601	69.0	9.22
578821102	PREDICTED: NADP-dependent malic enzyme, mitochondrial isoform 1 [Homo sapiens]	2.88	4	1	1	3	0.868	1		0.853	1		91.35	2.88	3	3	313	35.2	7.87
4506505	regulator of G-protein signaling 10 isoform b [Homo sapiens]	7.19	2	1	1	3	0.868	1		1.323	1		165.80	7.19	3	3	167	19.6	5.87
211971072	FEIM and POZ domain-containing protein 4 [Homo sapiens]	0.45	3	1	1	2	0.867	1		2.879	1		34.99	0.45	2	2	1322	144.3	5.25
578825986	PREDICTED: kctd-like protein 28 isoform X3 [Homo sapiens]	1.51	4	1	1	1	0.867	1		1.097	1		42.10	1.51	1	1	332	38.0	6.45
217222894	116 kDa US small nuclear ribonucleoprotein component isoform b [Homo sapiens]	2.67	4	1	2	12	0.865	1		1.984	1		462.62	2.67	6	12	937	105.3	5.22
63055057	beta-actin-like protein 2 [Homo sapiens]	30.85	1	14	975	0.864	1	1		1.283	1		31378.87	30.85	42	975	376	42.0	5.59
39995109	ganglioside GM2 activator isoform 1 precursor [Homo sapiens]	10.36	1	1	1	3	0.863	1		0.972	1		183.40	10.36	3	3	193	20.8	5.31
157266317	serine/threonine-protein kinase ATR [Homo sapiens]	0.38	7	1	2	3	0.862	1		0.989	1		47.20	0.38	3	3	2644	301.2	7.43
618466461	dynein heavy chain 12, axonemal isoform 3 [Homo sapiens]	0.38	27	1	2	18	0.861	1		1.659	1		159.13	0.38	4	18	3964	454.9	5.85
530411988	PREDICTED: granulins isoform X1 [Homo sapiens]	14.33	1	6	6	43	0.860	16	8.3	1.186	15	20.1	1206.02	14.33	16	43	593	63.5	6.83
530412114	PREDICTED: integrin beta-4 isoform X4 [Homo sapiens]	0.63	9	1	1	1	0.860	1		1.205	1		0.00	0.63	1	1	1752	194.9	6.10
578816585	PREDICTED: DENN domain-containing protein 4C isoform X4 [Homo sapiens]	0.82	5	1	1	9	0.859	4	12.1	1.106	4	9.6	178.79	0.82	3	9	1556	162.1	6.57
116063554	putative deoxyribose-phosphate aldolase isoform 1 [Homo sapiens]	3.14	1	1	2	0.858	1	1		1.136	1		56.03	3.14	2	2	318	35.2	8.94
510785746	ankyrin repeat and LEM domain-containing protein 1 isoform 2 [Homo sapiens]	1.11	1	1	1	2	0.858	1		1.531	1		46.15	1.11	2	2	632	68.0	6.98
166362713	cadherin-5 preproprotein [Homo sapiens]	0.64	1	1	11	0.858	1	6	3.4	2.154	6	74.5	99.89	0.64	2	11	784	87.5	5.43
24638446	histone H2A type 2-C [Homo sapiens]	59.69	10	1	6	52	0.857	6	20.6	1.924	4	183.7	1607.21	59.69	18	52	129	14.0	10.90
339895886	prospero homeobox protein 2 isoform 2 [Homo sapiens]	3.84	3	1	2	0.853	1	1		2.325	1		50.15	3.84	2	2	365	40.5	8.69
578821054	PREDICTED: protein argonaute 12-like [Homo sapiens]	3.00	1	1	1	2	0.852	1		2.881	1		25.74	3.00	2	2	233	24.2	11.09
530410543	PREDICTED: 60S ribosomal protein L26 isoform X1 [Homo sapiens]	9.66	3	1	1	6	0.851	2	7.6	1.144	2	9.6	194.68	9.66	3	6	145	17.2	10.55
67782319	spectrin beta chain, erythrocytic isoform b [Homo sapiens]	0.66	5	1	2	4	0.850	1		1.607	1		123.17	0.66	4	4	2137	246.3	5.27
62912474	leucine-rich repeat-containing G-protein coupled receptor 6 isoform 1 [Homo sapiens]	1.45	1	1	1	0.845	1	1		27.26	1		27.26	1.45	1	1	828	89.2	5.99
112791063	metal regulatory transcription factor 1 [Homo sapiens]	1.20	1	1	1	0.845	1	1		20.27	1.20	1	20.27	1.20	1	1	753	80.9	5.30
4505585	platelet-activating factor acetylhydrolase IB subunit beta isoform a [Homo sapiens]	14.41	4	2	2	14	0.843	5	17.2	1.232	4	5.1	551.75	14.41	6	14	229	25.6	5.92
530423607	PREDICTED: leucine-rich repeat-containing protein 16C isoform X1 [Homo sapiens]	0.51	7	1	1	1	0.842	1		1.542	1		28.72	0.51	1	1	1372	148.1	6.55
13676857	heat shock-related 70 kDa protein 2 [Homo sapiens]	18.15	1	1	10	146	0.840	1		1.042	1		6906.01	18.15	29	146	639	70.0	5.74
108350815	metallothionein-1H [Homo sapiens]	13.11	5	1	1	3	0.840	1		1.011	1		92.86	13.11	3	3	61	6.0	8.06
32171238	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 [Homo sapiens]	1.96	1	1	1	2	0.839	1		1.097	1		39.33	1.96	2	2	511	56.8	8.68
578816120	PREDICTED: sperm-associated antigen 1 isoform X2 [Homo sapiens]	0.57	2	1	1	8	0.839	3	33.6	1.082	3	2.4	133.36	0.57	3	8	884	98.8	6.87
530407244	PREDICTED: protein argonaute-45 homolog A isoform X3 [Homo sapiens]	3.13	45	1	2	13	0.845	1		0.765	1		216.09	3.13	6	11	799	87.2	6.90
93252551	CWIF9-like protein 1 [Homo sapiens]	2.60	1	1	1	9	0.836	3	21.1	1.434	3	13.4	351.58	2.60	3	9	538	60.6	7.24
530414991	PREDICTED: transmembrane protein 161A isoform X1 [Homo sapiens]	2.26	3	1	4	0.833	1	1	0.1	6.831	1		66.02	2.26	2	4	354	39.2	8.38
7706244	protein CutA isoform 2 precursor [Homo sapiens]	8.97	3	1	1	3	0.831	1		0.987	1		196.28	8.97	3	3	156	16.8	5.51
578824503	PREDICTED: ARF GTPase-activating protein G1T2 isoform X12 [Homo sapiens]	4.70	12	1	1	2	0.831	1		1.018	1		44.16	4.70	2	2	596	66.3	6.20
4822891	migration and invasion enhancer 1 [Homo sapiens]	20.00	2	1	1	3	0.830	1		1.736	1		131.29	20.00	3	3	115	12.4	4.37
166235186	methylthioribulose-1-phosphate dehydratase [Homo sapiens]	4.55	1	1	1	2	0.826	1		0.801	1		36.50	4.55	2	2	242	27.1	7.12
578816292	PREDICTED: metastasis suppressor protein 1 isoform X15 [Homo sapiens]	1.03	13	1	1	1	0.819	1		1.065	1		19.52	1.03	1	1	677	73.7	6.58
586798161	general vesicular transport factor p115 isoform 2 [Homo sapiens]	1.87	4	1	1	2	0.818	1		1.218	1		62.93	1.87	2	2	962	107.8	4.91
530391772	PREDICTED: protein FAM189A2 isoform X2 [Homo sapiens]	1.15	1	1	1	0.816	1	1		1.133	1		28.81	1.15	1	1	522	57.7	6.10
5453690	dnaj homolog subfamily B member 1 [Homo sapiens]	2.94	1	1	1	2	0.813	1		1.181	1		49.00	2.94	2	2	340	38.0	8.63
91208418	transcription elongation regulator 1 isoform 2 [Homo sapiens]	1.49	4	2	2	2	0.812	2	21.5	1.144	2		31.08	1.49	2	2	1077	121.6	8.54
289547636	complement C1r subcomponent-like protein isoform 1 precursor [Homo sapiens]	10.06	1	2	3	11	0.811	2	21.8	1.959	1		497.75	10.06	8	11	487	53.5	7.20
4505501	oxidized low-density lipoprotein receptor 1 isoform 1 [Homo sapiens]	6.23	1	1	1	3	0.810	1		1.254	3		232.24	6.23	3	3	273	30.9	7.28
34966527	active regulator of SIRT1 [Homo sapiens]	4.41	1	1	1	2	0.807	1		1.439	1		49.56	4.41	2	2	136	15.4	10.74
222144324	myosin regulatory light chain 12B [Homo sapiens]	72.09	6	1	12	123	0.798	1		0.976	1		5256.33	72.09	36	123	172	19.8	4.84
16933567	ras-related protein Rab-8A [Homo sapiens]	20.29	20	1	4	22	0.795	1		1.713	1		1092.19	20.29	11	22	207	23.7	9.07
60498978	EMILIN 2 precursor [Homo sapiens]	0.66	1	1	1	2	0.795	1		1.237	1		33.26	0.66	2	2	1053	115.6	6.46
530367595	PREDICTED: latent-transforming growth factor beta-binding protein 1 [Homo sapiens]	0.72	11	3	3	0.769	1	1		1.424	1		60.05	0.72	3	3	1247	134.0	7.50
221136814	coiled-coil domain-containing protein 154 [Homo sapiens]	0.90	1	1	1	2	0.764	1		1.166	1		33.74	0.90	2	2	667	75.4	8.24
216548056	cardiotrophin-1 isoform 2 [Homo sapiens]	5.50	2	1	1	1	0.756	1		1.160	1		23.03	5.50	1	1	200	21.1	9.41
475808427	POTE ankyrin domain family member 1 [Homo sapiens]	10.14	2	1	9	407	0.749	1		1.397	1		1321.09	10.14	26	407	1075	121.2	6.21
153791352	POTE ankyrin domain family member F [Homo sapiens]	11.63	2	1	10	700	0.732	14	6.3	1.474	14	25.9	26363.09	11.63	30	700	1075	121.4	6.20
168480800	BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 [Homo sapiens]	1.61	2	1	1	1	0.705	1		1.848	1		18.48	1.61	1	1	435	48	

Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs	AB: 115/114	AB: 115/114 Count	AB: 115/114 Variability [%]	AB: 117/116	AB: 117/116 Count	AB: 117/116 Variability [%]	Score A(3,6,7)	Coverage A(3,6,7)	# Peptides A(3,6,7)	# PSM A(3,6,7)	# AAs	MW [kDa]	calc. pI
130499472	PIH1 domain-containing protein 2 isoform 2 [Homo sapiens]	2.43	2	1	1	1							28.14	2.43	1	1	288	32.7	6.24
397138098	PREDICTED: uncharacterized protein LOC10096598 [Homo sapiens]	2.40	2	1	1	12							118.94	2.40	3	12	208	23.2	7.93
216548152	RNA pseudouridylylase domain-containing protein 3 isoform 1 [Homo sapiens]	2.38	2	1	1	1							31.62	2.38	1	1	336	36.9	10.29
578830445	PREDICTED: ubiquinol-cytochrome-c reductase complex assembly factor 1 [Homo sapiens]	2.27	10	1	1	15							214.19	2.27	3	15	220	25.0	9.77
14150564	trichoplein keratin filament-binding protein [Homo sapiens]	2.21	50	1	2	5							61.05	2.21	5	5	498	61.0	6.54
348605285	TNFAIP3-interacting protein 3 isoform 2 [Homo sapiens]	2.17	2	1	1	1							21.69	2.17	1	1	369	44.1	7.61
82617626	paralemnin-2 isoform b [Homo sapiens]	2.11	4	1	1	1							32.42	2.11	1	1	379	42.2	5.10
578837535	PREDICTED: PRKCA-binding protein isoform X3 [Homo sapiens]	2.09	4	1	1	1							25.87	2.09	1	1	287	32.8	5.17
578805484	PREDICTED: arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1 [Homo sapiens]	2.01	4	1	1	1							33.88	2.01	1	1	298	31.5	11.87
578820417	PREDICTED: dickkopf-related protein 3 isoform X3 [Homo sapiens]	1.94	19	1	1	1							20.85	1.94	1	1	258	27.9	7.20
40788007	FYN-binding protein 2 [Homo sapiens]	1.79	3	1	1	3							59.69	1.79	2	3	783	85.3	6.48
5174647	protein-tyrosine kinase 6 isoform 1 [Homo sapiens]	1.77	1	1	1	1							28.83	1.77	1	1	451	51.8	7.03
530370501	PREDICTED: polykain isoform X4 [Homo sapiens]	1.72	1	1	1	1							29.41	1.72	1	1	349	39.8	8.92
530370275	PREDICTED: long-chain specific acyl-CoA dehydrogenase, mitochondrial isoform 1 [Homo sapiens]	1.71	2	1	1	1							41.11	1.71	1	1	409	45.3	6.83
530399245	PREDICTED: coiled-coil domain-containing protein 91 isoform X4 [Homo sapiens]	1.70	3	1	1	1							0.00	1.70	1	1	411	47.0	5.43
7019569	vacuolar protein sorting-associated protein 4A [Homo sapiens]	1.60	1	1	1	1							41.10	1.60	1	1	437	48.9	7.80
530361936	PREDICTED: coiled-coil domain-containing protein 17 isoform X10 [Homo sapiens]	1.58	5	1	1	1							29.41	1.58	1	1	443	47.8	6.04
320461728	DNA replication ATP-dependent helicase/nuclease DNA2 [Homo sapiens]	1.51	30	2	2	2							34.29	1.51	2	2	1060	120.3	7.74
358679303	mucopolip-3 isoform 2 [Homo sapiens]	1.41	3	1	1	2							61.02	1.41	2	2	497	57.7	6.46
661903019	hyaluronan synthase 1 isoform 2 [Homo sapiens]	1.39	2	1	1	1							29.41	1.39	1	1	577	64.7	9.19
578830763	PREDICTED: sodium-independent sulfate anion transporter isoform 1 [Homo sapiens]	1.36	52	1	2	2							46.78	1.36	2	2	441	47.5	6.71
574957162	major facilitator superfamily domain-containing protein 1 isoform 3 [Homo sapiens]	1.36	4	1	1	1							30.85	1.36	1	1	368	40.5	8.00
75627567	dyslexia susceptibility 1 candidate gene 1 protein isoform b [Homo sapiens]	1.33	24	1	1	2							40.21	1.33	2	2	376	44.0	9.36
5729812	RNA polymerase II elongation factor ELL [Homo sapiens]	1.29	1	1	1	1							28.90	1.29	1	1	621	68.2	9.33
578817063	PREDICTED: protein tyrosine phosphatase domain-containing protein 1 [Homo sapiens]	1.27	6	1	1	1							35.99	1.27	1	1	630	70.6	7.66
115496169	myosin-7 [Homo sapiens]	1.24	15	1	4	19							463.22	1.24	9	19	1935	223.0	5.80
296080691	TCDD-inducible poly (ADP-ribose) polymerase [Homo sapiens]	1.22	1	1	1	2							46.03	1.22	1	2	657	76.2	6.65
221625538	MORC family CW-type zinc finger protein 1 [Homo sapiens]	1.22	17	2	2	3							57.66	1.22	3	3	984	112.8	7.85
62945417	dystrophia myotonia WD repeat-containing protein [Homo sapiens]	1.19	4	1	2	26							362.92	1.19	4	26	674	70.4	7.24
530424037	PREDICTED: HEAT repeat-containing protein 3 isoform X1 [Homo sapiens]	1.18	2	1	1	1							32.18	1.18	1	1	594	65.8	5.11
530405894	PREDICTED: unconventional myosin-Va isoform X7 [Homo sapiens]	1.15	9	1	3	23							214.34	1.15	8	23	1481	172.8	8.48
14277682	protocadherin gamma-C4 isoform 2 precursor [Homo sapiens]	1.15	2	1	1	2							28.32	1.15	1	2	871	94.4	5.12
530386281	PREDICTED: RAD50-interacting protein 1 isoform X1 [Homo sapiens]	1.11	4	1	1	1							24.93	1.11	1	1	451	51.9	5.53
530415807	PREDICTED: zinc finger protein 599 isoform X1 [Homo sapiens]	1.09	2	1	1	1							29.41	1.09	1	1	551	63.4	8.56
21361749	ubiquitin carboxyl-terminal hydrolase 49 isoform b [Homo sapiens]	1.09	2	1	1	1							24.53	1.09	1	1	640	73.4	9.25
530401776	PREDICTED: tectonic-2 isoform X1 [Homo sapiens]	1.07	4	1	1	1							33.21	1.07	1	1	652	71.6	5.11
4508029	zinc finger protein 45 [Homo sapiens]	1.03	1	1	1	1							28.16	1.03	1	1	682	78.2	8.66
148612825	ras-associating and dilute domain-containing protein [Homo sapiens]	1.02	39	1	2	3							24.11	1.02	3	3	1075	117.4	7.09
578806453	PREDICTED: semaphorin-3F isoform X4 [Homo sapiens]	1.02	3	1	1	2							39.62	1.02	2	2	588	66.0	8.07
578813371	PREDICTED: NAC-alpha domain-containing protein 1 isoform X1 [Homo sapiens]	0.96	2	1	1	1							37.59	0.96	1	1	1349	139.8	4.22
54792092	ATM interactor isoform 1 [Homo sapiens]	0.85	1	1	1	1							32.33	0.85	1	1	823	88.3	5.16
530390312	PREDICTED: ankyrin repeat domain-containing protein 20A2 isoform 1 [Homo sapiens]	0.85	7	1	1	1							28.84	0.85	1	1	822	93.9	7.94
4758650	kinesin heavy chain isoform 5C [Homo sapiens]	0.84	1	1	1	1							28.16	0.84	1	1	957	109.4	6.19
578802241	PREDICTED: nuclear valosin-containing protein-like isoform X7 [Homo sapiens]	0.84	8	1	1	2							31.50	0.84	2	2	592	65.2	6.55
578830435	PREDICTED: alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminidase 1 [Homo sapiens]	0.82	5	1	1	1							26.46	0.82	1	1	729	82.1	8.13
530421602	PREDICTED: RNA-binding protein 10 isoform X3 [Homo sapiens]	0.76	4	1	1	7							51.88	0.76	7	7	917	101.1	7.17
530366183	PREDICTED: melanoma inhibitory activity protein 3 isoform X2 [Homo sapiens]	0.76	4	1	1	1							36.49	0.76	1	1	785	87.4	6.83
342307096	huntingtin-interacting protein 1 isoform 2 [Homo sapiens]	0.71	4	1	1	3							37.87	0.71	1	3	986	110.6	5.27
6912446	potassium voltage-gated channel subfamily H member 4 [Homo sapiens]	0.69	1	1	1	1							15.66	0.69	1	1	1017	111.6	8.54
145580626	transcription factor E2F7 [Homo sapiens]	0.66	3	1	1	1							27.01	0.66	1	1	911	99.8	8.16
578833657	PREDICTED: uncharacterized protein KIAA1683 isoform X2 [Homo sapiens]	0.65	4	1	1	1							29.41	0.65	1	1	1085	115.7	9.77
411147433	F-box only protein 38 isoform c [Homo sapiens]	0.64	4	1	1	2							36.87	0.64	2	2	943	107.6	6.18
118421089	chromodomain-helicase-DNA-binding protein 2 isoform 1 [Homo sapiens]	0.60	5	1	2	5							57.00	0.60	5	5	1828	211.2	8.10
229692308	thugonin-like 2 isoform 2 [Homo sapiens]	0.56	5	1	1	1							24.42	0.56	1	1	1260	143.9	7.68
578810444	PREDICTED: protein LAP2 isoform X4 [Homo sapiens]	0.56	1	1	1	1							19.02	0.56	1	1	1246	139.9	5.33
291621660	dmX-like protein 2 isoform 3 [Homo sapiens]	0.54	8	1	2	5							123.08	0.54	5	5	2400	270.0	6.60
464402377	WD repeat-containing protein 72 isoform a [Homo sapiens]	0.54	1	1	1	1							35.36	0.54	1	1	1102	123.3	6.67
132566536	voltage-dependent calcium channel subunit alpha-2/delta-4 [Homo sapiens]	0.53	1	1	1	1							24.39	0.53	1	1	1137	127.9	5.35
578812608	PREDICTED: PHD finger protein 3 isoform X5 [Homo sapiens]	0.51	4	1	1	1							24.54	0.51	1	1	1181	133.5	8.31
46488921	astrotactin-1 isoform 2 precursor [Homo sapiens]	0.49	3	1	1	1							26.63	0.49	1	1	1216	135.0	5.15
578810445	PREDICTED: ATP-dependent RNA helicase DHX29 isoform X2 [Homo sapiens]	0.46	2	1	1	1							21.21	0.46	1	1	1318	149.5	8.29
116534990	transient receptor potential cation channel subfamily A member 1 [Homo sapiens]	0.45	9	1	1	5							51.72	0.45	3	5	1119	127.4	7.12
37452823	Golgin subfamily B member 1 isoform 4 [Homo sapiens]	0.44	11	1	2	3							35.27	0.44	3	3	3184	367.2	5.02
183583553	collagen alpha-5(VI) chain isoform 2 precursor [Homo sapiens]	0.44	2	1	1	1							28.74	0.44	1	1	2526	279.8	7.36
578838883	PREDICTED: plexin-A3 isoform X4 [Homo sapiens]	0.41	5	1	1	2							30.64	0.41	1	2	1719	190.1	7.25
578837337	PREDICTED: EF-hand calcium-binding domain-containing protein 6 [Homo sapiens]	0.35	3	1	1	2							30.88	0.35	1	2	1424	163.8	8.46
578825656	PREDICTED: zinc finger FYVE domain-containing protein 26 isoform 1 [Homo sapiens]	0.32	2	1	1	2							23.13	0.32	2	2	2497	279.9	6.28
578811634	PREDICTED: zinc finger protein 40 isoform X2 [Homo sapiens]	0.30	2	1	1	1							30.94	0.30	1	1	2026	222.1	8.31
88501738	TRIO and F-actin-binding protein isoform 6 [Homo sapiens]	0.25	1	1	1	2							34.52	0.25	2	2	2365	261.2	8.48
222144249	dynein heavy chain domain-containing protein 1 isoform 1 [Homo sapiens]	0.21	60	1	2	6							57.32	0.21	4	6	4753	533.3	6.71

Appendix C

Cytokine

Antibody Array Assay Results		Assay Data		
Cytokine Profiling Antibody Array		Median Signal	681	378
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots	
			Bigger Sample	Smaller Sample
Beta actin	2.62	Beta actin	14532	21117
TGF beta Receptor III	2.27	TGF beta Receptor III	1459	1841
Total PSA	2.18	Total PSA	2236	2701
Catenin-alpha1	2.02	Catenin-alpha1	9018	10087
CEA	2.01	CEA	4750	5298
MMP-2	1.98	MMP-2	5091	5584
FSH	1.88	FSH	1146	1199
IL-12	1.88	IL-12	7715	8054
Catenin-gamma	1.87	Catenin-gamma	2756	2866
TYRO3	1.86	TYRO3	1093	1130
LEC	1.85	LEC	772	792
FGFR1 Oncogene Partner	1.83	FGFR1 Oncogene Partner	1356	1380
C-Kit	1.82	C-Kit	2664	2685
VEGFB	1.77	VEGFB	6366	6259
BCL-10	1.77	BCL-10	6891	6770
TGF-beta1	1.77	TGF-beta1	3778	3708
MMP-10	1.76	MMP-10	8395	8192
gAcrp30/Adipolean	1.75	gAcrp30/Adipolean	1304	1265
CD14	1.67	CD14	1048	970
TGF beta2	1.59	TGF beta2	1365	1204
NGF beta	1.56	NGF beta	1590	1380
FGF-5	1.56	FGF-5	1466	1272
MCP-2	1.54	MCP-2	419	358
AKT1	1.54	AKT1	351	300
IL-1 beta	1.52	IL-1 beta	404	340
STAT6	1.51	STAT6	387	325
GAPDH	1.49	GAPDH	432	358
Myeloperoxidase (MPO)	1.49	Myeloperoxidase (MPO)	684	566
Prolactin	1.49	Prolactin	341	281
MDC	1.48	MDC	382	313
HER3	1.48	HER3	399	327
E-Selectin	1.47	E-Selectin	389	318
sFas Ligand/Apo1L	1.47	sFas Ligand/Apo1L	416	340
Leptin	1.46	Leptin	865	700
sRANKL	1.45	sRANKL	13558	10914
SCGF-beta	1.45	SCGF-beta	458	368
GSK3 beta	1.45	GSK3 beta	796	639
EGR1	1.45	EGR1	477	383
PDGFB	1.45	PDGFB	759	609
SCF	1.44	SCF	471	377
Hepatocyte Growth Factor (HGF)	1.44	Hepatocyte Growth Factor (HGF)	392	313
IL-6	1.44	IL-6	404	322
Adiponectin	1.44	Adiponectin	452	360
MCP-4	1.43	MCP-4	378	300
L-Selectin	1.42	L-Selectin	461	365
4E-BP1	1.42	4E-BP1	347	274
TSH	1.42	TSH	371	293
HGH	1.42	HGH	330	261
IL-7	1.42	IL-7	346	273
BMP-7/OP-1	1.42	BMP-7/OP-1	379	298
EGF	1.42	EGF	540	426

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.04	0.04
0.07	0.05
0.10	0.07
0.20	0.23
0.06	0.08
0.35	0.66
0.05	0.08
0.08	0.12
0.07	0.11
0.03	0.10
0.07	0.11
0.06	0.04
0.04	0.06
0.10	0.07
0.09	0.11
0.15	0.16
0.08	0.05
0.12	0.02
0.15	0.13
0.03	0.04
0.03	0.07
0.05	0.10
0.03	0.13
0.03	0.02
0.01	0.03
0.02	0.05
0.02	0.05
0.11	0.06
0.03	0.03
0.03	0.09
0.02	0.02
0.02	0.05
0.02	0.01
0.02	0.03
0.08	0.06
0.04	0.04
0.09	0.07
0.02	0.02
0.11	0.04
0.02	0.02
0.03	0.02
0.02	0.01
0.04	0.02
0.02	0.07
0.02	0.02
0.03	0.03
0.02	0.02
0.02	0.01
0.01	0.04
0.02	0.02
0.03	0.03

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
21.34	55.87
2.14	4.87
3.28	7.15
13.24	26.69
6.98	14.01
7.48	14.77
1.68	3.17
11.33	21.31
4.05	7.58
1.61	2.99
1.13	2.09
1.99	3.65
3.91	7.10
9.35	16.56
10.12	17.91
5.55	9.81
12.33	21.67
1.92	3.35
1.54	2.57
2.00	3.18
2.33	3.65
2.15	3.36
0.61	0.95
0.51	0.79
0.59	0.90
0.57	0.86
0.63	0.95
1.00	1.50
0.50	0.74
0.56	0.83
0.59	0.86
0.57	0.84
0.61	0.90
1.27	1.85
19.91	28.87
0.67	0.97
1.17	1.69
0.70	1.01
1.11	1.61
0.69	1.00
0.58	0.83
0.59	0.85
0.66	0.95
0.56	0.79
0.68	0.96
0.51	0.72
0.55	0.78
0.49	0.69
0.51	0.72
0.56	0.79
0.79	1.13

Antibody Array Assay Results		Assay Data							
Cytokine Profiling Antibody Array									
		Median Signal		681		378			
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal		
			Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	
MCP-1/MCAF	1.42	MCP-1/MCAF	402	317	0.02	0.03	0.59	0.84	
hCG	1.42	hCG	339	266	0.01	0.02	0.50	0.70	
NAP-2	1.42	NAP-2	374	294	0.02	0.02	0.55	0.78	
Myostatin (GDF-8)	1.41	Myostatin (GDF-8)	3265	2560	0.14	0.21	4.79	6.77	
RANTES	1.40	RANTES	462	359	0.02	0.03	0.68	0.95	
beta hCG	1.40	beta hCG	431	334	0.01	0.04	0.63	0.88	
LH (Human Luteinizing Hormone)	1.39	LH (Human Luteinizing Hormone)	339	263	0.02	0.01	0.50	0.69	
FGF-basic	1.39	FGF-basic	368	285	0.01	0.03	0.54	0.75	
IFN-gamma	1.39	IFN-gamma	388	299	0.03	0.03	0.57	0.79	
VEGF	1.39	VEGF	14260	10992	0.14	0.08	20.94	29.08	
sIL-2R alpha	1.39	sIL-2R alpha	509	391	0.03	0.01	0.75	1.03	
MIP-3beta	1.38	MIP-3beta	984	752	0.11	0.13	1.44	1.99	
TECK	1.37	TECK	515	391	0.07	0.02	0.76	1.04	
PTK6	1.37	PTK6	408	310	0.03	0.02	0.60	0.82	
IL-15	1.36	IL-15	2094	1585	0.03	0.04	3.08	4.19	
MCP-3	1.36	MCP-3	740	558	0.02	0.03	1.09	1.48	
ICAM-1	1.36	ICAM-1	428	323	0.02	0.04	0.63	0.85	
MMP-23	1.36	MMP-23	465	350	0.03	0.05	0.68	0.93	
EPCAM	1.35	EPCAM	467	350	0.02	0.03	0.69	0.93	
PSA-ACT	1.35	PSA-ACT	839	629	0.16	0.09	1.23	1.66	
Thyroglobulin	1.35	Thyroglobulin	481	360	0.02	0.06	0.71	0.95	
IL-20	1.35	IL-20	437	327	0.02	0.03	0.64	0.87	
Insulin	1.35	Insulin	468	350	0.02	0.03	0.69	0.92	
Free PSA	1.35	Free PSA	325	243	0.03	0.03	0.48	0.64	
MIP-5	1.34	MIP-5	372	277	0.01	0.02	0.55	0.73	
GATA1	1.34	GATA1	478	356	0.04	0.04	0.70	0.94	
BMP-4	1.34	BMP-4	494	367	0.02	0.03	0.73	0.97	
BAFF	1.33	BAFF	618	458	0.02	0.05	0.91	1.21	
S 100A10/P11	1.33	S 100A10/P11	459	340	0.01	0.06	0.67	0.90	
TIMP2	1.33	TIMP2	808	598	0.04	0.08	1.19	1.58	
Neurturin	1.33	Neurturin	418	308	0.02	0.05	0.61	0.82	
HDAC5	1.33	HDAC5	1718	1267	0.09	0.09	2.52	3.35	
TPO	1.33	TPO	367	271	0.02	0.04	0.54	0.72	
alpha hCG	1.32	alpha hCG	404	297	0.06	0.04	0.59	0.79	
FAK	1.32	FAK	605	445	0.02	0.01	0.89	1.18	
MIP-3alpha	1.32	MIP-3alpha	383	282	0.01	0.02	0.56	0.75	
Osteopontin	1.32	Osteopontin	663	487	0.05	0.03	0.97	1.29	
ALCAM	1.32	ALCAM	1433	1052	0.07	0.10	2.10	2.78	
4-1BB Receptor	1.32	4-1BB Receptor	392	287	0.02	0.02	0.57	0.76	
IP-10	1.32	IP-10	385	282	0.01	0.01	0.56	0.75	
FGF-16	1.32	FGF-16	474	348	0.05	0.03	0.70	0.92	
Angiopoietin-1	1.31	Angiopoietin-1	441	321	0.02	0.03	0.65	0.85	
LYN	1.31	LYN	472	344	0.02	0.08	0.69	0.91	
BD-2	1.31	BD-2	425	309	0.02	0.00	0.62	0.82	
Androgen receptor	1.31	Androgen receptor	2888	2097	0.10	0.13	4.24	5.55	
TNF-alpha	1.30	TNF-alpha	423	306	0.02	0.03	0.62	0.81	
MMP-9	1.30	MMP-9	399	289	0.02	0.02	0.59	0.76	
EG-VEGF	1.30	EG-VEGF	462	334	0.03	0.02	0.68	0.88	
ApoE3	1.30	ApoE3	1204	870	0.05	0.07	1.77	2.30	
C-reactive Protein (CRP)	1.30	C-reactive Protein (CRP)	344	249	0.02	0.03	0.51	0.66	
Eotaxin-3	1.30	Eotaxin-3	471	340	0.03	0.03	0.69	0.90	
ITGA5	1.30	ITGA5	493	355	0.02	0.06	0.72	0.94	

Antibody Array Assay Results		Assay Data									
Cytokine Profiling Antibody Array											
		Median Signal		681		378					
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots				Coefficient of Variation for Replicates		Data Normalized to Median Signal		
			Bigger Sample		Smaller Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	
IL-11	1.29	IL-11	413	296	0.02	0.02	0.61	0.78			
Eotaxin	1.29	Eotaxin	405	291	0.03	0.01	0.59	0.77			
AKT2	1.29	AKT2	599	430	0.03	0.04	0.88	1.14			
NT-3	1.29	NT-3	402	288	0.05	0.02	0.59	0.76			
GSK3 alpha	1.29	GSK3 alpha	532	381	0.02	0.04	0.78	1.01			
TWEAK	1.29	TWEAK	438	313	0.01	0.04	0.64	0.83			
CA125	1.28	CA125	373	264	0.02	0.02	0.55	0.70			
FGFR2	1.28	FGFR2	585	414	0.05	0.05	0.86	1.10			
CIB1	1.27	CIB1	549	389	0.06	0.02	0.81	1.03			
PDGFR beta	1.27	PDGFR beta	446	315	0.04	0.03	0.65	0.83			
TACI	1.27	TACI	998	702	0.06	0.04	1.47	1.86			
CD40	1.27	CD40	2920	2053	0.02	0.08	4.29	5.43			
IGF-BP5	1.27	IGF-BP5	1216	855	0.10	0.06	1.79	2.26			
NGFR	1.26	NGFR	475	333	0.02	0.03	0.70	0.88			
IGF 1R	1.26	IGF 1R	603	421	0.02	0.01	0.89	1.11			
Angiopoietin-2	1.26	Angiopoietin-2	483	337	0.03	0.03	0.71	0.89			
TGF beta3	1.26	TGF beta3	542	378	0.01	0.08	0.80	1.00			
Beta-2-Microglobulin	1.25	Beta-2-Microglobulin	6782	4723	0.02	0.05	9.96	12.49			
FLI1	1.25	FLI1	661	460	0.08	0.03	0.97	1.22			
BRAK	1.25	BRAK	515	358	0.02	0.04	0.76	0.95			
Artemin	1.25	Artemin	446	309	0.04	0.03	0.66	0.82			
KDR (VEGFR2)	1.25	KDR (VEGFR2)	414	286	0.02	0.02	0.61	0.76			
LD78beta	1.24	LD78beta	655	450	0.03	0.10	0.96	1.19			
MLL	1.23	MLL	1244	849	0.08	0.05	1.83	2.25			
sCD40 Ligand	1.23	sCD40 Ligand	469	320	0.03	0.03	0.69	0.85			
CA19-9	1.22	CA19-9	526	356	0.01	0.00	0.77	0.94			
Flt-1	1.21	Flt-1	489	330	0.04	0.03	0.72	0.87			
TGF beta Receptor II	1.21	TGF beta Receptor II	680	457	0.07	0.08	1.00	1.21			
PDGFR alpha	1.20	PDGFR alpha	891	594	0.05	0.06	1.31	1.57			
HCC-1	1.20	HCC-1	653	435	0.05	0.04	0.96	1.15			
VCAM-1	1.20	VCAM-1	576	383	0.03	0.02	0.85	1.01			
NP-1	1.20	NP-1	743	494	0.07	0.07	1.09	1.31			
CTGF	1.20	CTGF	1394	926	0.07	0.10	2.05	2.45			
AXL	1.19	AXL	454	301	0.04	0.03	0.67	0.79			
PlGF	1.19	PlGF	717	473	0.10	0.07	1.05	1.25			
MMP-16	1.19	MMP-16	469	309	0.04	0.04	0.69	0.82			
TIMP3	1.19	TIMP3	618	407	0.02	0.02	0.91	1.08			
Eotaxin-2	1.19	Eotaxin-2	480	316	0.05	0.03	0.70	0.84			
MMP-14	1.19	MMP-14	463	305	0.06	0.04	0.68	0.81			
MMP-8	1.18	MMP-8	652	428	0.04	0.22	0.96	1.13			
FGF-10	1.18	FGF-10	506	331	0.02	0.02	0.74	0.88			
CA15-3	1.18	CA15-3	471	308	0.03	0.02	0.69	0.82			
NT-4	1.17	NT-4	514	335	0.03	0.02	0.76	0.89			
Galectin-3	1.17	Galectin-3	2016	1314	0.04	0.04	2.96	3.48			
HDAC1	1.17	HDAC1	701	455	0.07	0.05	1.03	1.20			
CD44	1.16	CD44	515	333	0.02	0.02	0.76	0.88			
Vaspin	1.16	Vaspin	698	450	0.06	0.07	1.03	1.19			
MMP-7	1.16	MMP-7	725	467	0.15	0.09	1.07	1.24			
RON	1.16	RON	438	281	0.02	0.03	0.64	0.74			
MMP-3	1.15	MMP-3	508	326	0.19	0.06	0.75	0.86			
SOX2	1.15	SOX2	537	343	0.02	0.11	0.79	0.91			
AFP	1.15	AFP	2387	1521	0.12	0.09	3.51	4.02			
HDAC7	1.15	HDAC7	466	297	0.05	0.02	0.68	0.79			
PROZ	1.14	PROZ	2063	1302	0.06	0.06	3.03	3.44			
YES 1	1.14	YES 1	491	310	0.02	0.04	0.72	0.82			
MEC	1.13	MEC	713	448	0.07	0.18	1.05	1.19			
IGF-BP3	1.13	IGF-BP3	964	603	0.05	0.07	1.41	1.60			
S 100B	1.13	S 100B	485	303	0.01	0.03	0.71	0.80			

Antibody Array Assay Results		Assay Data		
Cytokine Profiling Antibody Array		Median Signal	681	378
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots	
			Bigger Sample	Smaller Sample
Lymphotoctin	1.13	Lymphotoctin	504	315
STAT5A	1.12	STAT5A	481	299
WNT-1	1.12	WNT-1	599	372
Granzyme B	1.11	Granzyme B	846	523
MIG	1.11	MIG	564	349
MMP-11	1.11	MMP-11	715	440
S100 A1	1.11	S100 A1	651	401
MMP-19	1.11	MMP-19	820	504
IL-2	1.10	IL-2	527	322
Heregulin	1.10	Heregulin	885	539
sCD22	1.10	sCD22	768	467
STAT1	1.09	STAT1	544	330
FGFR3	1.09	FGFR3	741	449
IGF-BP2	1.09	IGF-BP2	673	407
CTGFL/WISP-2	1.09	CTGFL/WISP-2	745	450
IL-16	1.08	IL-16	522	311
HDAC6	1.07	HDAC6	659	393
SRC	1.07	SRC	522	311
sTNF-receptor	1.07	sTNF-receptor	628	374
IGF-BP7	1.06	IGF-BP7	911	539
Apolipoprotein L1 (APOL1)	1.06	Apolipoprotein L1 (APOL1)	557	329
SDF-1alpha	1.06	SDF-1alpha	1605	945
IL-8	1.05	IL-8	682	399
SDF-1beta	1.05	SDF-1beta	557	326
RELM beta	1.05	RELM beta	647	378
IL-19	1.05	IL-19	1172	680
WNT-3a	1.04	WNT-3a	572	332
GATA3	1.04	GATA3	613	354
sTRAIL/APO2L	1.04	sTRAIL/APO2L	561	324
HDAC9	1.04	HDAC9	548	315
Tyrosinase	1.03	Tyrosinase	605	347
MMP-1	1.03	MMP-1	717	410
IFN-lambda2	1.03	IFN-lambda2	1230	704
BD-3	1.03	BD-3	548	312
IL-10	1.02	IL-10	796	453
HDAC10	1.02	HDAC10	603	340
Apolipoprotein F (APOF)	1.01	Apolipoprotein F (APOF)	675	380
FGF-17	1.01	FGF-17	552	309
GDNF	1.00	GDNF	553	309
CTACK	1.00	CTACK	631	352
Maspin	1.00	Maspin	706	393
MMP-15	1.00	MMP-15	553	308
GCP-2	1.00	GCP-2	534	297
M-CSF	1.00	M-CSF	623	345
IL-4	0.99	IL-4	641	353
TSLP	0.99	TSLP	619	340
Integrin beta5	0.99	Integrin beta5	599	328
GDF-3	0.98	GDF-3	874	478
BD-4	0.98	BD-4	594	324
BMP-2	0.98	BMP-2	766	416
STAT3	0.98	STAT3	568	308
Ubiquitin	0.97	Ubiquitin	841	454
IL-17D	0.97	IL-17D	604	325
MIP-1beta	0.97	MIP-1beta	588	316
ERCC6	0.97	ERCC6	931	500
Cardiotrophin-1	0.96	Cardiotrophin-1	947	504
FGF-acidic	0.96	FGF-acidic	748	398
TL-1A	0.96	TL-1A	597	317

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.03	0.03
0.04	0.04
0.06	0.04
0.05	0.07
0.03	0.04
0.07	0.04
0.05	0.06
0.17	0.09
0.01	0.02
0.09	0.06
0.08	0.04
0.03	0.02
0.14	0.05
0.04	0.05
0.04	0.02
0.05	0.02
0.09	0.06
0.01	0.03
0.03	0.02
0.08	0.02
0.07	0.02
0.14	0.11
0.05	0.04
0.03	0.04
0.05	0.04
0.04	0.03
0.05	0.02
0.03	0.02
0.03	0.02
0.05	0.03
0.04	0.02
0.08	0.04
0.07	0.07
0.02	0.01
0.05	0.05
0.08	0.04
0.05	0.02
0.04	0.02
0.04	0.02
0.04	0.03
0.04	0.02
0.01	0.02
0.05	0.02
0.04	0.04
0.03	0.03
0.03	0.03
0.05	0.04
0.05	0.04
0.05	0.01
0.03	0.03
0.03	0.00
0.07	0.01
0.06	0.03
0.07	0.04
0.07	0.04
0.03	0.02

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.74	0.83
0.71	0.79
0.88	0.98
1.24	1.38
0.83	0.92
1.05	1.16
0.96	1.06
1.20	1.33
0.77	0.85
1.30	1.42
1.13	1.24
0.80	0.87
1.09	1.19
0.99	1.08
1.09	1.19
0.77	0.82
0.97	1.04
0.77	0.82
0.92	0.99
1.34	1.43
0.82	0.87
2.36	2.50
1.00	1.06
0.82	0.86
0.95	1.00
1.72	1.80
0.84	0.88
0.90	0.94
0.82	0.86
0.80	0.83
0.89	0.92
1.05	1.09
1.81	1.86
0.80	0.83
1.17	1.20
0.89	0.90
0.99	1.01
0.81	0.82
0.81	0.82
0.93	0.93
1.04	1.04
0.81	0.81
0.78	0.78
0.92	0.91
0.94	0.93
0.91	0.90
0.88	0.87
1.28	1.26
0.87	0.86
1.12	1.10
0.83	0.82
1.24	1.20
0.89	0.86
0.86	0.84
1.37	1.32
1.39	1.33
1.10	1.05
0.88	0.84

Antibody Array Assay Results		Assay Data							
Cytokine Profiling Antibody Array									
		Median Signal		681		378			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal		
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	
MIP-1alpha	0.95	MIP-1alpha	606	320	0.02	0.02	0.89	0.85	
BDNF	0.95	BDNF	610	321	0.05	0.05	0.90	0.85	
IGF-I	0.95	IGF-I	747	393	0.05	0.03	1.10	1.04	
Oncostatin M	0.94	Oncostatin M	568	298	0.02	0.04	0.83	0.79	
Persephin	0.94	Persephin	695	363	0.04	0.04	1.02	0.96	
IL-33	0.94	IL-33	685	358	0.06	0.03	1.01	0.95	
sDLL-4	0.94	sDLL-4	975	509	0.04	0.02	1.43	1.35	
MIP-3	0.94	MIP-3	562	292	0.03	0.03	0.82	0.77	
PDGF-AA	0.93	PDGF-AA	642	333	0.02	0.03	0.94	0.88	
Apolipoprotein L2 (APOL2)	0.93	Apolipoprotein L2 (APOL2)	657	338	0.07	0.04	0.96	0.89	
GRO-gamma	0.93	GRO-gamma	627	322	0.09	0.01	0.92	0.85	
LIGHT	0.92	LIGHT	776	397	0.02	0.05	1.14	1.05	
HER2	0.92	HER2	683	350	0.02	0.03	1.00	0.93	
OPG	0.92	OPG	757	386	0.06	0.05	1.11	1.02	
GM-CSF	0.91	GM-CSF	647	328	0.05	0.01	0.95	0.87	
Resistin	0.91	Resistin	16635	8370	0.11	0.09	24.43	22.14	
Follistatin	0.90	Follistatin	829	415	0.06	0.09	1.22	1.10	
TARC	0.90	TARC	595	298	0.03	0.02	0.87	0.79	
STAT5A/B	0.90	STAT5A/B	783	391	0.02	0.07	1.15	1.03	
PDGF-BB	0.90	PDGF-BB	666	332	0.03	0.02	0.98	0.88	
Neuroserpin	0.89	Neuroserpin	820	407	0.03	0.03	1.20	1.08	
Endostatin	0.89	Endostatin	967	479	0.04	0.06	1.42	1.27	
NCoR1	0.89	NCoR1	778	383	0.04	0.03	1.14	1.01	
IL-17B	0.88	IL-17B	765	375	0.12	0.02	1.12	0.99	
CXCL16	0.88	CXCL16	782	383	0.03	0.03	1.15	1.01	
IGF-BP1	0.87	IGF-BP1	1073	518	0.02	0.04	1.58	1.37	
MIA-2	0.87	MIA-2	902	434	0.16	0.04	1.32	1.15	
sTRAIL Receptor-2	0.86	sTRAIL Receptor-2	804	385	0.05	0.02	1.18	1.02	
APC	0.86	APC	1047	500	0.10	0.10	1.54	1.32	
IL-9	0.86	IL-9	687	328	0.02	0.03	1.01	0.87	
MMP-13	0.86	MMP-13	712	339	0.06	0.03	1.05	0.90	
APRIL	0.86	APRIL	703	334	0.01	0.03	1.03	0.88	
I-TAC	0.85	I-TAC	629	298	0.02	0.02	0.92	0.79	
IL-17E	0.85	IL-17E	745	353	0.06	0.02	1.09	0.93	
Fractalkine	0.85	Fractalkine	651	307	0.03	0.02	0.96	0.81	
E-cadherin	0.85	E-cadherin	1001	473	0.03	0.07	1.47	1.25	
IL-17F	0.85	IL-17F	729	343	0.05	0.02	1.07	0.91	
Catenin-beta 1	0.85	Catenin-beta 1	687	323	0.04	0.03	1.01	0.86	
FGF-4	0.85	FGF-4	1047	492	0.07	0.04	1.54	1.30	
FAS	0.84	FAS	1395	653	0.06	0.05	2.05	1.73	
PF-4	0.84	PF-4	1366	637	0.09	0.08	2.01	1.69	
BCA-1	0.84	BCA-1	663	309	0.08	0.03	0.97	0.82	
EMAP-II	0.84	EMAP-II	894	417	0.11	0.02	1.31	1.10	
TRADD	0.84	TRADD	901	420	0.06	0.04	1.32	1.11	
PAI-1	0.83	PAI-1	1019	472	0.08	0.03	1.50	1.25	
I-309	0.83	I-309	728	337	0.04	0.01	1.07	0.89	
CNTF	0.83	CNTF	1052	486	0.06	0.07	1.54	1.29	
MIA	0.83	MIA	1055	487	0.04	0.03	1.55	1.29	
NNT-1/BCSF-3	0.83	NNT-1/BCSF-3	747	344	0.10	0.02	1.10	0.91	
NOV	0.83	NOV	843	388	0.08	0.05	1.24	1.03	
TFF-2	0.83	TFF-2	773	355	0.10	0.05	1.14	0.94	
4-1BBL	0.82	4-1BBL	939	428	0.07	0.03	1.38	1.13	
AITRL	0.82	AITRL	1020	463	0.07	0.03	1.50	1.22	
FER	0.82	FER	793	360	0.06	0.03	1.16	0.95	
IL-31	0.82	IL-31	965	437	0.08	0.08	1.42	1.16	
MIP-4	0.81	MIP-4	686	309	0.04	0.04	1.01	0.82	
Nanog	0.81	Nanog	1004	451	0.07	0.07	1.47	1.19	
TIMP4	0.80	TIMP4	857	382	0.05	0.04	1.26	1.01	

Antibody Array Assay Results		Assay Data						
Cytokine Profiling Antibody Array		Median Signal		681	378			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
TGF-alpha	0.80	TGF-alpha	1039	463	0.03	0.04	1.53	1.22
Visfatin	0.79	Visfatin	1456	640	0.07	0.06	2.14	1.69
Betacellulin	0.79	Betacellulin	907	398	0.10	0.03	1.33	1.05
IL-17 (IL-17A)	0.78	IL-17 (IL-17A)	801	348	0.13	0.02	1.18	0.92
BLK	0.77	BLK	1084	466	0.09	0.06	1.59	1.23
IL-1alpha	0.76	IL-1alpha	747	317	0.03	0.03	1.10	0.84
Exodus-2	0.76	Exodus-2	931	394	0.03	0.02	1.37	1.04
Galectin-1	0.76	Galectin-1	1304	551	0.04	0.05	1.91	1.46
Cadherin-pan	0.76	Cadherin-pan	1206	508	0.08	0.06	1.77	1.34
TIMP-1	0.75	TIMP-1	2690	1127	0.09	0.08	3.95	2.98
GRO/MGSA	0.75	GRO/MGSA	1114	466	0.08	0.02	1.64	1.23
Midkine	0.75	Midkine	959	401	0.10	0.02	1.41	1.06
GRO-beta	0.75	GRO-beta	811	338	0.03	0.01	1.19	0.89
IL-21	0.75	IL-21	919	382	0.09	0.05	1.35	1.01
IL-5	0.74	IL-5	897	370	0.03	0.08	1.32	0.98
Ferritin	0.73	Ferritin	13829	5575	0.05	0.16	20.31	14.75
IL-3	0.72	IL-3	836	334	0.16	0.04	1.23	0.88
IL-22	0.72	IL-22	1008	401	0.04	0.03	1.48	1.06
Adipolean Variant	0.71	Adipolean Variant	1093	429	0.02	0.03	1.60	1.13
HDAC3	0.71	HDAC3	1067	418	0.08	0.04	1.57	1.11
IL-1RA	0.70	IL-1RA	1380	535	0.05	0.05	2.03	1.42
G-CSF	0.70	G-CSF	952	369	0.11	0.03	1.40	0.98
KGF	0.68	KGF	843	320	0.03	0.04	1.24	0.85
TNF-beta	0.68	TNF-beta	1090	412	0.04	0.03	1.60	1.09
IL-13	0.68	IL-13	971	365	0.14	0.03	1.43	0.97
sRANK Receptor	0.68	sRANK Receptor	1132	425	0.07	0.03	1.66	1.12
Flt3-Ligand	0.67	Flt3-Ligand	791	293	0.05	0.07	1.16	0.77
BD-1	0.66	BD-1	1145	420	0.05	0.04	1.68	1.11
IGF-II	0.66	IGF-II	1393	511	0.05	0.04	2.05	1.35
sTNF-receptor II	0.66	sTNF-receptor II	1234	451	0.05	0.02	1.81	1.19
ENA-78	0.65	ENA-78	1100	395	0.03	0.02	1.62	1.05
IFN-beta	0.65	IFN-beta	1294	464	0.06	0.05	1.90	1.23
EGFR	0.61	EGFR	1308	441	0.04	0.04	1.92	1.17
Heregulin-beta1	0.58	Heregulin-beta1	1689	547	0.06	0.05	2.48	1.45
PTHrP	0.10	PTHrP	7919	421	0.11	0.06	11.63	1.11
Min	1.18	Average of Empty Spots	383	274	0.03	0.02		
Max	2.62	Average of Negative Controls	356	295	0.02	0.02		
Mean	1.42	Average of Positive Makers	33394	27966	0.08	0.07		

Appendix D

Explorer

Antibody Array Assay Results		Assay Data			
Explorer Antibody Array		Median Signal		128	83
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	Bigger Sample
Vascular Endothelial Growth Factor(VEGF)	4.59	Vascular Endothelial Growth Factor(VEGF)	222	663	0.07
Actin beta	3.40	Actin beta	136	299	0.14
Survivin	2.78	Survivin	426	768	0.18
CD57	2.47	CD57	263	422	0.08
CD2	2.33	CD2	2757	4179	0.47
ADP-ribosylation Factor (ARF-6)	2.28	ADP-ribosylation Factor (ARF-6)	1063	1575	0.24
HPV 16-E7	2.23	HPV 16-E7	2467	3571	0.03
FSH	2.20	FSH	382	547	0.19
Golgi Complex	2.20	Golgi Complex	554	791	0.20
CD1	2.12	CD1	5802	8008	0.30
Laminin-s	2.11	Laminin-s	1225	1680	0.86
MHC I (HLA25 and HLA-Aw32)	2.01	MHC I (HLA25 and HLA-Aw32)	804	1050	0.24
Thymidylate Synthase	2.00	Thymidylate Synthase	162	211	0.10
CEA / CD66e	1.92	CEA / CD66e	695	868	0.53
IgG	1.91	IgG	24504	30440	0.01
Keratin, Multi	1.85	Keratin, Multi	529	637	0.07
CD45/T200/LCA	1.85	CD45/T200/LCA	1020	1227	0.76
Kappa Light Chain	1.81	Kappa Light Chain	1489	1752	0.16
Plasminogen	1.80	Plasminogen	234	274	0.02
Glucagon	1.80	Glucagon	399	466	0.10
Calmodulin	1.80	Calmodulin	658	769	0.03
B-cell Linker Protein (BLNK)	1.79	B-cell Linker Protein (BLNK)	104	121	0.03
NGF-Receptor (p75NGFR)	1.79	NGF-Receptor (p75NGFR)	81	94	0.00
HPV 16	1.66	HPV 16	687	742	0.25
L1 Cell Adhesion Molecule	1.65	L1 Cell Adhesion Molecule	140	151	0.43
c-erbB-4/HER-4	1.65	c-erbB-4/HER-4	176	189	0.22
CD43	1.63	CD43	1682	1777	0.33
Retinoid X Receptor (hRXR)	1.62	Retinoid X Receptor (hRXR)	418	441	0.10
Parathyroid Hormone Receptor Type 1	1.62	Parathyroid Hormone Receptor Type 1	186	196	0.14
MHC II (HLA-DP and DR)	1.60	MHC II (HLA-DP and DR)	1362	1417	0.02
c-Abl	1.60	c-Abl	684	711	0.04
DR3	1.59	DR3	303	312	0.19
Biotin	1.58	Biotin	63691	65535	0.04
Oct-2/	1.58	Oct-2/	63	64	0.17
CD1b	1.57	CD1b	269	275	0.11
CD53	1.57	CD53	96	98	0.00
XRCC1	1.57	XRCC1	106	108	0.05
Int-2 Oncoprotein	1.56	Int-2 Oncoprotein	145	147	0.03
Lambda Light Chain	1.54	Lambda Light Chain	65535	65535	0.00
XPG	1.53	XPG	123	123	0.11
Streptavidin	1.53	Streptavidin	6876	6848	0.13
CD29	1.52	CD29	124	123	0.03
Alpha Lactalbumin	1.51	Alpha Lactalbumin	259	254	0.02
Retinoic Acid Receptor (b)	1.51	Retinoic Acid Receptor (b)	336	329	0.13
alpha-1-antitrypsin	1.51	alpha-1-antitrypsin	13221	12929	0.01
CA19-9	1.50	CA19-9	111	108	0.04
CD105	1.50	CD105	127	124	0.17
IgM (m-Heavy Chain)	1.50	IgM (m-Heavy Chain)	579	565	0.16
BrdU	1.50	BrdU	159	154	0.08
Keratin 15	1.49	Keratin 15	1599	1545	0.18
Synuclein pan	1.49	Synuclein pan	57	55	0.07

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
1.74	7.98
1.06	3.60
3.33	9.25
2.05	5.08
21.58	50.35
8.32	18.97
19.31	43.02
2.99	6.58
4.33	9.52
45.42	96.48
9.59	20.23
6.29	12.64
1.27	2.54
5.44	10.45
191.81	366.75
4.14	7.67
7.98	14.78
11.65	21.11
1.83	3.30
3.12	5.61
5.15	9.26
0.81	1.46
0.63	1.13
5.38	8.94
1.10	1.81
1.37	2.27
13.16	21.40
3.27	5.31
1.46	2.36
10.66	17.07
5.35	8.56
2.37	3.76
498.56	789.58
0.49	0.77
2.10	3.31
0.75	1.18
0.83	1.30
1.14	1.77
512.99	789.58
0.96	1.48
53.82	82.51
0.97	1.48
2.02	3.06
2.63	3.96
103.49	155.77
0.86	1.30
0.99	1.49
4.53	6.81
1.24	1.86
12.52	18.61
0.45	0.66

Antibody Array Assay Results		Assay Data							
Explorer Antibody Array		Median Signal				83			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Protein List	Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
MGMT	1.48	MGMT	61	59		0.19	0.30	0.48	0.70
PDGFR, beta	1.47	PDGFR, beta	967	923		0.29	0.09	7.57	11.11
Microphthalmia	1.47	Microphthalmia	98	93		0.34	0.03	0.76	1.12
bcl-XL	1.47	bcl-XL	4442	4236		0.16	0.04	34.77	51.03
PLC gamma 1	1.47	PLC gamma 1	2132	2033		0.22	0.14	16.69	24.49
Bovine Serum Albumin	1.47	Bovine Serum Albumin	118	112		0.02	0.06	0.92	1.35
Gamma Glutamyl Transferase (gGT)	1.46	Gamma Glutamyl Transferase (gGT)	80	76		0.13	0.25	0.62	0.91
F.VIII/VWF	1.46	F.VIII/VWF	70	66		0.03	0.04	0.54	0.80
c-erbB-2/HER-2/neu Ab-1 (21N)	1.46	c-erbB-2/HER-2/neu Ab-1 (21N)	176	167		0.05	0.04	1.38	2.01
Androgen Receptor	1.45	Androgen Receptor	72	68		0.02	0.04	0.56	0.82
p170	1.45	p170	54	51		0.01	0.01	0.42	0.61
Integrin beta5	1.45	Integrin beta5	231	218		0.08	0.13	1.81	2.62
Laminin B1/b1	1.45	Laminin B1/b1	13478	12663		0.21	0.02	105.50	152.56
Adenovirus	1.45	Adenovirus	476	447		0.08	0.12	3.72	5.38
CA125	1.44	CA125	73	68		0.07	0.12	0.57	0.82
E2F-4	1.44	E2F-4	125	117		0.17	0.19	0.98	1.41
Dysferlin	1.44	Dysferlin	75	70		0.09	0.21	0.58	0.84
Superoxide Dismutase	1.44	Superoxide Dismutase	67	63		0.00	0.01	0.52	0.75
Thymine Glycols	1.43	Thymine Glycols	57	53		0.19	0.01	0.44	0.63
Cryptococcus neoformans	1.43	Cryptococcus neoformans	49	46		0.03	0.05	0.38	0.55
Cdk7	1.43	Cdk7	324	301		0.04	0.01	2.54	3.62
Moesin	1.43	Moesin	444	411		0.46	0.44	3.47	4.95
p300 / CBP	1.42	p300 / CBP	73	68		0.08	0.05	0.57	0.81
E3-binding protein (ARM1)	1.41	E3-binding protein (ARM1)	66	61		0.06	0.13	0.52	0.73
Bonzo / STRL33 / TYMSTR	1.41	Bonzo / STRL33 / TYMSTR	2024	1849		0.26	0.21	15.84	22.28
Interferon-a(II)	1.41	Interferon-a(II)	64	58		0.06	0.02	0.50	0.70
CD56/NCAM-1	1.41	CD56/NCAM-1	1625	1483		0.06	0.05	12.72	17.87
14.3.3, Pan	1.40	14.3.3, Pan	107	98		0.01	0.05	0.84	1.17
Epithelial Specific Antigen	1.40	Epithelial Specific Antigen	680	617		0.11	0.04	5.32	7.43
Prohibitin	1.39	Prohibitin	5922	5350		0.07	0.20	46.36	64.46
CD59 / MACIF / M1RL / Protectin	1.39	CD59 / MACIF / M1RL / Protectin	61	55		0.00	0.00	0.48	0.66
LRP / MVP	1.39	LRP / MVP	61	55		0.06	0.04	0.47	0.66
Interferon-g	1.39	Interferon-g	85	77		0.05	0.18	0.67	0.92
p35nck5a	1.38	p35nck5a	144	130		0.09	0.09	1.13	1.56
IPO-38 Proliferation Marker	1.38	IPO-38 Proliferation Marker	151	135		0.00	0.02	1.18	1.63
Notch	1.38	Notch	498	446		0.02	0.04	3.89	5.37
Axonal Growth Cones	1.38	Axonal Growth Cones	429	385		0.01	0.02	3.36	4.63
MHC I (HLA-B)	1.38	MHC I (HLA-B)	212	190		0.12	0.05	1.66	2.28
Perforin	1.38	Perforin	120	108		0.05	0.01	0.94	1.30
Cystic Fibrosis Transmembrane Regulator	1.38	Cystic Fibrosis Transmembrane Regulator	173	155		0.09	0.12	1.35	1.86
IL-1 beta	1.38	IL-1 beta	58	52		0.04	0.01	0.45	0.62
CD3zeta	1.38	CD3zeta	206	185		0.03	0.16	1.61	2.22
Glycophorin A	1.38	Glycophorin A	53	47		0.01	0.03	0.41	0.57
Thrombospondin	1.38	Thrombospondin	100	90		0.11	0.17	0.78	1.08
Ruv C	1.38	Ruv C	199	178		0.07	0.03	1.55	2.14
IL-3	1.38	IL-3	47	42		0.00	0.03	0.37	0.51
XPF	1.37	XPF	186	165		0.23	0.24	1.45	1.99
FGF-1	1.37	FGF-1	50	44		0.07	0.03	0.39	0.53
Progesterone Receptor (phospho-specific)	1.37	Progesterone Receptor (phospho-specific) - Serine 19	1052	934		0.22	0.23	8.23	11.25
Fascin	1.37	Fascin	67	59		0.03	0.02	0.52	0.71
Cytochrome c	1.37	Cytochrome c	84	75		0.08	0.01	0.66	0.90
mGluR1	1.36	mGluR1	53	47		0.04	0.02	0.41	0.56

Antibody Array Assay Results		Assay Data			
Explorer Antibody Array					
		Median Signal		128	83
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	
Cullin-3 (CUL-3)	1.36	Cullin-3 (CUL-3)	2588	2289	
TNF alpha	1.36	TNF alpha	43	38	
CD155/PVR (Polio Virus Receptor)	1.36	CD155/PVR (Polio Virus Receptor)	90	80	
CDw17	1.36	CDw17	56	49	
Heat Shock Protein 90a/hsp86	1.36	Heat Shock Protein 90a/hsp86	629	554	
IL-10	1.35	IL-10	54	48	
Thyroid Hormone Receptor, Human	1.35	Thyroid Hormone Receptor, Human	1032	906	
Fyn	1.35	Fyn	94	83	
Milk Fat Globule Membrane Protein	1.35	Milk Fat Globule Membrane Protein	1413	1240	
PGP9.5	1.35	PGP9.5	61	54	
TIMP-1	1.35	TIMP-1	69	61	
Human Sodium Iodide Symporter (hNIS)	1.35	Human Sodium Iodide Symporter (hNIS)	170	149	
IL-10R	1.35	IL-10R	52	46	
tau	1.34	tau	103	90	
Hepatocyte Growth Factor	1.34	Hepatocyte Growth Factor	95	83	
Ret Oncoprotein	1.34	Ret Oncoprotein	75	66	
Collagen IV	1.34	Collagen IV	95	83	
Casein	1.34	Casein	213	186	
SIM Ag (SIMA-4D3)	1.34	SIM Ag (SIMA-4D3)	59	52	
IL-6	1.34	IL-6	67	58	
Keratin 14	1.34	Keratin 14	51	44	
TR2	1.34	TR2	897	781	
IL-30	1.34	IL-30	43	37	
Neurofilament	1.34	Neurofilament	54	47	
Gamma Glutamylcysteine Synthetase(GC	1.34	Gamma Glutamylcysteine Synthetase(GCS)/Glutamat	1494	1300	
Insulin Receptor Substrate-1	1.34	Insulin Receptor Substrate-1	61	53	
Cdk1/p34cdc2	1.34	Cdk1/p34cdc2	570	495	
Amyloid A	1.34	Amyloid A	65	56	
Adrenocorticotrophic Hormone	1.34	Adrenocorticotrophic Hormone	72	63	
SHP-1	1.34	SHP-1	212	184	
Thomsen-Friedenreich Antigen	1.34	Thomsen-Friedenreich Antigen	61	53	
CD94	1.34	CD94	117	102	
TGF-beta 2	1.34	TGF-beta 2	83	72	
TIMP-2	1.33	TIMP-2	49	43	
Caspase 9	1.33	Caspase 9	53	46	
Mcl-1	1.33	Mcl-1	71	62	
Negative Control for Mouse IgG2a	1.33	Negative Control for Mouse IgG2a	90	78	
SRF (Serum Response Factor)	1.33	SRF (Serum Response Factor)	104	90	
Surfactant Protein A	1.33	Surfactant Protein A	45	39	
CD68	1.33	CD68	63	55	
CDw78	1.33	CDw78	67	58	
Prolactin	1.33	Prolactin	77	67	
Retinol Binding Protein	1.33	Retinol Binding Protein	909	785	
Ku (p80)	1.33	Ku (p80)	77	66	
G-CSF	1.33	G-CSF	44	38	
Tyrosinase	1.33	Tyrosinase	76	66	
Pneumocystis jiroveci	1.33	Pneumocystis jiroveci	51	44	
ER Ca+2 ATPase2	1.32	ER Ca+2 ATPase2	68	59	
GCDFP-15	1.32	GCDFP-15	47	40	
Bcl-6	1.32	Bcl-6	72	62	
Synaptophysin	1.32	Synaptophysin	118	101	
CD42b	1.32	CD42b	442	380	
Activin Receptor Type II	1.32	Activin Receptor Type II	71	61	
CD54/ICAM-1	1.32	CD54/ICAM-1	71	61	
mGluR5	1.32	mGluR5	212	182	
TdT	1.32	TdT	67	58	
Hepatocyte	1.32	Hepatocyte	46	39	

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.10	0.12
0.03	0.00
0.24	0.13
0.01	0.00
0.49	0.20
0.10	0.01
0.06	0.03
0.11	0.04
0.02	0.03
0.02	0.07
0.08	0.06
0.12	0.06
0.03	0.02
0.01	0.17
0.07	0.09
0.00	0.05
0.11	0.01
0.01	0.01
0.00	0.01
0.03	0.10
0.01	0.00
0.18	0.01
0.02	0.00
0.03	0.00
0.17	0.19
0.00	0.05
0.04	0.11
0.01	0.00
0.00	0.06
0.08	0.05
0.01	0.01
0.06	0.03
0.02	0.14
0.00	0.05
0.01	0.02
0.06	0.01
0.12	0.14
0.08	0.09
0.02	0.02
0.02	0.06
0.20	0.01
0.04	0.01
0.35	0.13
0.03	0.02
0.02	0.02
0.00	0.08
0.01	0.05
0.02	0.01
0.05	0.00
0.01	0.06
0.04	0.01
0.12	0.22
0.08	0.07
0.02	0.02
0.01	0.07
0.00	0.06
0.02	0.00

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
20.25	27.58
0.34	0.46
0.70	0.96
0.43	0.59
4.92	6.67
0.42	0.57
8.07	10.92
0.74	0.99
11.06	14.94
0.48	0.64
0.54	0.73
1.33	1.79
0.41	0.55
0.81	1.08
0.74	1.00
0.59	0.79
0.74	0.99
1.66	2.23
0.46	0.62
0.52	0.70
0.40	0.53
7.02	9.41
0.33	0.45
0.42	0.57
11.69	15.66
0.48	0.64
4.46	5.96
0.50	0.67
0.56	0.75
1.66	2.22
0.47	0.63
0.92	1.22
0.65	0.87
0.38	0.51
0.41	0.55
0.56	0.74
0.70	0.93
0.81	1.08
0.35	0.46
0.49	0.66
0.52	0.69
0.60	0.80
7.12	9.45
0.60	0.80
0.34	0.45
0.59	0.79
0.40	0.52
0.53	0.70
0.36	0.48
0.56	0.74
0.92	1.22
3.46	4.57
0.56	0.73
0.56	0.73
1.66	2.19
0.52	0.69
0.36	0.47

Antibody Array Assay Results		Assay Data	
Explorer Antibody Array		Median Signal12883	
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots Bigger SampleSmaller Sample
Mucin 2	1.32	Mucin 2	8169
DNA Ligase I	1.32	DNA Ligase I	7060
GSK-3	1.32	GSK-3	5648
TNFA	1.32	TNFA	4942
Ku (p70/p80)	1.32	Ku (p70/p80)	159136
Tubulin-b	1.32	Tubulin-b	7665
CNPase	1.32	CNPase	2309719750
CD32/Fcg Receptor II	1.32	CD32/Fcg Receptor II	10791
CD84	1.31	CD84	406346
RPA/p32	1.31	RPA/p32	10993
TRAP	1.31	TRAP	4438
CD21	1.31	CD21	6455
SRC1 (Steroid Receptor Coactivator-1)	1.31	SRC1 (Steroid Receptor Coactivator-1)	9883
Lck	1.31	Lck	11094
DNA-PKcs	1.31	DNA-PKcs	10791
Glycogen Synthase Kinase 3b (GSK3b)	1.31	Glycogen Synthase Kinase 3b (GSK3b)	12191034
CD15	1.31	CD15	7967
CD9	1.31	CD9	6353
Glicentin	1.30	Glicentin	6959
Apolipoprotein D	1.30	Apolipoprotein D	8572
CD5	1.30	CD5	5244
Bromodeoxyuridine (BrdU)	1.30	Bromodeoxyuridine (BrdU)	140118
Prostate Specific Antigen	1.30	Prostate Specific Antigen	162137
IFN gamma	1.30	IFN gamma	5547
MMP-15 / MT2-MMP	1.30	MMP-15 / MT2-MMP	4941
PCTAIRE2	1.30	PCTAIRE2	120101
Estriol	1.30	Estriol	2015517032
p21WAF1	1.30	p21WAF1	10992
mRANKL	1.30	mRANKL	6151
Dystrophin	1.29	Dystrophin	8874
DNA Polymerase Beta	1.29	DNA Polymerase Beta	7261
Cyclin D3	1.29	Cyclin D3	9176
Keratin 16	1.29	Keratin 16	5949
CITED1	1.29	CITED1	231193
Neurofilament (200kDa)	1.29	Neurofilament (200kDa)	6857
Xanthine Oxidase	1.29	Xanthine Oxidase	6857
FGF-2	1.29	FGF-2	5244
Laminin B2/g1	1.29	Laminin B2/g1	5244
Amyloid Beta (APP)	1.29	Amyloid Beta (APP)	50124191
Collagen II	1.29	Collagen II	156130
Mucin 5AC	1.29	Mucin 5AC	9176
uPA	1.28	uPA	5848
TID-1	1.28	TID-1	6151
ER beta	1.28	ER beta	7058
Ruv A	1.28	Ruv A	10386
p130	1.28	p130	10588
CCK-8	1.28	CCK-8	7260
CD50/ICAM-3	1.28	CD50/ICAM-3	436363
Granulocyte	1.28	Granulocyte	1486212370
CD26/DPP IV	1.28	CD26/DPP IV	525437
Ubiquitin	1.28	Ubiquitin	4840
CD10	1.28	CD10	460383
Prostate Specific Acid Phosphatase	1.28	Prostate Specific Acid Phosphatase	210175
NuMA	1.28	NuMA	9276
Progesterone Receptor	1.28	Progesterone Receptor	120100
IL-4	1.27	IL-4	5848
Acinus	1.27	Acinus	1121928

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.04	0.06
0.10	0.05
0.05	0.00
0.07	0.02
0.00	0.03
0.00	0.00
0.03	0.07
0.11	0.03
0.01	0.20
0.08	0.01
0.00	0.02
0.04	0.01
0.01	0.05
0.08	0.17
0.03	0.04
0.00	0.16
0.04	0.04
0.06	0.08
0.14	0.01
0.02	0.04
0.03	0.06
0.04	0.06
0.15	0.07
0.08	0.05
0.07	0.07
0.03	0.08
0.05	0.05
0.01	0.02
0.04	0.03
0.02	0.08
0.06	0.06
0.04	0.11
0.06	0.00
0.09	0.11
0.05	0.01
0.03	0.01
0.05	0.02
0.08	0.05
0.12	0.17
0.11	0.08
0.05	0.04
0.06	0.03
0.04	0.01
0.05	0.05
0.01	0.04
0.01	0.06
0.00	0.07
0.04	0.05
0.02	0.01
0.14	0.01
0.04	0.02
0.01	0.09
0.43	0.13
0.04	0.02
0.13	0.11
0.02	0.00
0.35	0.30

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.63	0.83
0.55	0.72
0.44	0.58
0.38	0.50
1.24	1.64
0.59	0.78
180.80	237.95
0.83	1.10
3.17	4.17
0.85	1.11
0.34	0.45
0.50	0.66
0.76	1.00
0.86	1.13
0.83	1.09
9.54	12.46
0.62	0.81
0.49	0.64
0.54	0.70
0.67	0.87
0.41	0.53
1.09	1.42
1.27	1.65
0.43	0.56
0.38	0.49
0.94	1.22
157.77	205.20
0.85	1.11
0.47	0.61
0.69	0.89
0.56	0.73
0.71	0.92
0.46	0.59
1.80	2.33
0.53	0.68
0.53	0.68
0.41	0.52
0.41	0.52
39.23	50.49
1.22	1.57
0.71	0.92
0.45	0.58
0.47	0.61
0.54	0.70
0.80	1.03
0.82	1.05
0.56	0.72
3.41	4.37
116.34	149.04
4.11	5.26
0.37	0.48
3.60	4.61
1.64	2.10
0.72	0.92
0.94	1.20
0.45	0.58
8.77	11.17

Antibody Array Assay Results		Assay Data		
Explorer Antibody Array				
		Median Signal	128	83
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
Fibrillin-1	1.27	Fibrillin-1	93	77
Heparan Sulfate Proteoglycan	1.27	Heparan Sulfate Proteoglycan	64	53
Factor VIII Related Antigen	1.27	Factor VIII Related Antigen	186	153
MAGE-1	1.27	MAGE-1	117	97
CD79b	1.27	CD79b	74	61
IRAK	1.27	IRAK	2954	2435
IL-5	1.27	IL-5	60	49
Fibronectin	1.27	Fibronectin	170	140
Inhibin alpha	1.27	Inhibin alpha	48	40
Thyroglobulin	1.27	Thyroglobulin	68	56
Transglutaminase II	1.27	Transglutaminase II	186	153
CD100/Leukocyte Semaphorin	1.26	CD100/Leukocyte Semaphorin	70	58
Synuclein	1.26	Synuclein	146	120
CLAUDIN 7	1.26	CLAUDIN 7	53	44
Keratin 10	1.26	Keratin 10	198	163
Medroxyprogesterone Acetate (MPA)	1.26	Medroxyprogesterone Acetate (MPA)	136	112
EMA/CA15-3/MUC-1	1.26	EMA/CA15-3/MUC-1	78	64
IL17	1.26	IL17	64	52
Phospho-Ser/Thr/Tyr	1.26	Phospho-Ser/Thr/Tyr	77	63
CD98	1.26	CD98	58	47
Ruv B	1.26	Ruv B	112	92
Negative Control for Mouse IgG1	1.26	Negative Control for Mouse IgG1	169	138
Heat Shock Factor 2	1.26	Heat Shock Factor 2	63	51
Keratin 18	1.26	Keratin 18	65	53
MDM2	1.25	MDM2	79	64
LewisB	1.25	LewisB	203	165
ZAP-70	1.25	ZAP-70	92	75
Hepatocyte Factor Homologue-4	1.25	Hepatocyte Factor Homologue-4	75	61
MHC I (HLA-A)	1.25	MHC I (HLA-A)	83	68
Tubulin-a	1.25	Tubulin-a	193	157
Maltose Binding Protein	1.25	Maltose Binding Protein	70	57
Caspase 3	1.25	Caspase 3	67	54
Stat5	1.25	Stat5	59	48
bcl-2a	1.25	bcl-2a	177	144
Negative Control for Mouse IgM	1.25	Negative Control for Mouse IgM	66	53
Retinoblastoma	1.25	Retinoblastoma	66	53
Toxoplasma Gondii	1.25	Toxoplasma Gondii	66	53
Urocortin	1.24	Urocortin	71	57
Actin, Muscle Specific	1.24	Actin, Muscle Specific	65	53
Nitric Oxide Synthase, brain (bNOS)	1.24	Nitric Oxide Synthase, brain (bNOS)	3136	2531
DR5	1.24	DR5	57	46
CD46	1.24	CD46	215	174
IL-1 alpha	1.24	IL-1 alpha	47	38
Synuclein beta	1.24	Synuclein beta	65	52
Insulin Receptor	1.24	Insulin Receptor	69	56
CDw75	1.24	CDw75	97	78
CD24	1.24	CD24	230	185
Rad18	1.24	Rad18	3367	2706
TRP75 / gp75	1.23	TRP75 / gp75	61	49
Cadherin-E	1.23	Cadherin-E	73	59
TTF-1	1.23	TTF-1	81	65
FITC	1.23	FITC	153	123
CDC25C	1.23	CDC25C	60	48
GluR4	1.23	GluR4	60	48
p130cas	1.23	p130cas	75	60
Cyclin B1	1.23	Cyclin B1	1284	1026
Thyroid Stimulating Hormone (TSH)	1.23	Thyroid Stimulating Hormone (TSH)	202	161

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.01	0.08
0.14	0.04
0.10	0.01
0.19	0.11
0.04	0.05
0.10	0.02
0.04	0.03
0.02	0.04
0.00	0.02
0.05	0.01
0.10	0.09
0.04	0.01
0.03	0.05
0.03	0.02
0.03	0.04
0.07	0.07
0.03	0.08
0.03	0.00
0.04	0.09
0.04	0.03
0.08	0.01
0.02	0.02
0.06	0.03
0.04	0.03
0.03	0.07
0.14	0.15
0.04	0.05
0.08	0.07
0.09	0.07
0.08	0.02
0.05	0.04
0.03	0.03
0.04	0.01
0.05	0.03
0.08	0.03
0.05	0.03
0.05	0.13
0.09	0.12
0.04	0.04
0.19	0.16
0.00	0.03
0.00	0.10
0.05	0.06
0.03	0.03
0.00	0.06
0.01	0.07
0.22	0.09
0.13	0.13
0.04	0.07
0.06	0.04
0.10	0.05
0.02	0.16
0.05	0.06
0.02	0.03
0.04	0.09
0.19	0.02
0.17	0.14

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.72	0.92
0.50	0.63
1.45	1.84
0.92	1.16
0.58	0.73
23.12	29.33
0.47	0.59
1.33	1.68
0.38	0.48
0.53	0.67
1.45	1.84
0.55	0.69
1.14	1.44
0.41	0.52
1.55	1.96
1.06	1.34
0.61	0.77
0.50	0.63
0.60	0.76
0.45	0.57
0.88	1.10
1.32	1.66
0.49	0.61
0.51	0.64
0.61	0.77
1.59	1.99
0.72	0.90
0.59	0.73
0.65	0.81
1.51	1.89
0.54	0.68
0.52	0.65
0.46	0.57
1.39	1.73
0.51	0.64
0.51	0.64
0.55	0.69
0.51	0.63
24.54	30.49
0.45	0.55
1.68	2.09
0.36	0.45
0.50	0.63
0.54	0.67
0.76	0.94
1.80	2.22
26.35	32.60
0.47	0.58
0.57	0.70
0.63	0.78
1.20	1.48
0.47	0.58
0.47	0.58
0.59	0.72
10.05	12.36
1.58	1.94

Antibody Array Assay Results		Assay Data		
Explorer Antibody Array				
		Median Signal	128	83
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots	
			Bigger Sample	Smaller Sample
Leukotriene (C4, D4, E4)	1.23	Leukotriene (C4, D4, E4)	70	56
Claudin 3	1.23	Claudin 3	72	57
Rhodopsin (Opsin)	1.23	Rhodopsin (Opsin)	488	389
Adenovirus Fiber	1.23	Adenovirus Fiber	3326	2648
CD106 / VCAM	1.22	CD106 / VCAM	71	57
XPA	1.22	XPA	179	142
MMP-10 (Stromilysin-2)	1.22	MMP-10 (Stromilysin-2)	456	362
TrxR2	1.22	TrxR2	63	50
Adenovirus Type 5 E1A	1.22	Adenovirus Type 5 E1A	179	142
MMP-9 (92kDa Collagenase IV)	1.22	MMP-9 (92kDa Collagenase IV)	97	77
Ezrin/p81/80K/Cytovillin	1.22	Ezrin/p81/80K/Cytovillin	68	54
GnRH Receptor	1.22	GnRH Receptor	169	134
Plasma Cell Marker	1.22	Plasma Cell Marker	1947	1543
Cdk5	1.22	Cdk5	63	50
Alpha Fetoprotein (AFP)	1.22	Alpha Fetoprotein (AFP)	108	86
CD165	1.22	CD165	98	78
GSTmu	1.22	GSTmu	53	42
pS2	1.22	pS2	141	111
14.3.3 gamma	1.22	14.3.3 gamma	150	119
p19ARF	1.22	p19ARF	2067	1632
CD61 / Platelet Glycoprotein IIIA	1.21	CD61 / Platelet Glycoprotein IIIA	64	50
CD25/IL-2 Receptor a	1.21	CD25/IL-2 Receptor a	132	104
FHIT	1.21	FHIT	68	54
CD4	1.21	CD4	70	55
CD30 (Reed-Sternberg Cell Marker)	1.21	CD30 (Reed-Sternberg Cell Marker)	89	70
Pax-5	1.21	Pax-5	63	49
MART-1/Melan-A	1.21	MART-1/Melan-A	81	64
LewisA	1.21	LewisA	74	58
IGF-1R	1.21	IGF-1R	102	80
SODD (Silencer of Death Domain)	1.20	SODD (Silencer of Death Domain)	561	439
Catenin gamma	1.20	Catenin gamma	108	85
Vimentin	1.20	Vimentin	62	48
p15INK4b	1.20	p15INK4b	66	52
Ras	1.20	Ras	744	580
Presenillin	1.20	Presenillin	75	59
6-Histidine	1.20	6-Histidine	89	69
IGF-I	1.20	IGF-I	66	51
Neutrophil Elastase	1.20	Neutrophil Elastase	4223	3287
sm	1.20	sm	428	333
HIF-1a	1.20	HIF-1a	77	60
MHC II (HLA-DP)	1.20	MHC II (HLA-DP)	101	79
Amylin Peptide	1.20	Amylin Peptide	65	51
MMP-7 (Matrilysin)	1.19	MMP-7 (Matrilysin)	121	94
CD40	1.19	CD40	116	90
Parkin	1.19	Parkin	203	158
Collagen VII	1.19	Collagen VII	71	55
p170 / MDR-1	1.19	p170 / MDR-1	87	67
EGFR	1.19	EGFR	184	143
Hepatic Nuclear Factor-3B	1.19	Hepatic Nuclear Factor-3B	162	125
MMP-2 (72kDa Collagenase IV)	1.19	MMP-2 (72kDa Collagenase IV)	93	72
hPL	1.19	hPL	66	51
Neurofilament (160kDa)	1.19	Neurofilament (160kDa)	95	73
AIF (Apoptosis Inducing Factor)	1.19	AIF (Apoptosis Inducing Factor)	5419	4184
IP10/CRG2	1.19	IP10/CRG2	75	58
Heat Shock Factor 1	1.19	Heat Shock Factor 1	66	51
CDC6	1.18	CDC6	113	87
Collagen IX	1.18	Collagen IX	87	67

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.03	0.01
0.05	0.05
0.08	0.34
0.24	0.06
0.02	0.09
0.05	0.00
0.10	0.16
0.00	0.03
0.22	0.08
0.17	0.01
0.03	0.01
0.02	0.10
0.19	0.02
0.03	0.04
0.08	0.12
0.07	0.01
0.09	0.02
0.06	0.01
0.01	0.07
0.13	0.09
0.10	0.00
0.08	0.02
0.02	0.09
0.08	0.08
0.01	0.01
0.03	0.09
0.14	0.03
0.08	0.15
0.09	0.03
0.18	0.06
0.09	0.14
0.08	0.06
0.11	0.04
0.05	0.22
0.08	0.08
0.01	0.04
0.05	0.08
0.06	0.11
0.05	0.05
0.12	0.01
0.06	0.10
0.09	0.01
0.03	0.13
0.01	0.00
0.08	0.15
0.08	0.03
0.16	0.08
0.12	0.06
0.09	0.07
0.04	0.03
0.02	0.00
0.11	0.04
0.02	0.07
0.07	0.09
0.03	0.01
0.02	0.04
0.11	0.03

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.54	0.67
0.56	0.69
3.82	4.68
26.04	31.90
0.56	0.68
1.40	1.71
3.57	4.36
0.49	0.60
1.40	1.71
0.76	0.92
0.53	0.64
1.32	1.61
15.24	18.58
0.49	0.60
0.85	1.03
0.77	0.93
0.41	0.50
1.10	1.34
1.17	1.43
16.18	19.66
0.50	0.60
1.03	1.25
0.53	0.64
0.55	0.66
0.69	0.84
0.49	0.59
0.63	0.77
0.58	0.70
0.79	0.96
4.39	5.29
0.85	1.02
0.48	0.58
0.52	0.62
5.82	6.99
0.59	0.70
0.69	0.83
0.51	0.61
33.06	39.60
3.35	4.01
0.60	0.72
0.79	0.95
0.51	0.61
0.94	1.13
0.91	1.08
1.59	1.90
0.56	0.66
0.68	0.81
1.44	1.72
1.26	1.51
0.72	0.86
0.52	0.61
0.74	0.88
42.41	50.40
0.58	0.69
0.51	0.61
0.88	1.04
0.68	0.80

Antibody Array Assay Results		Assay Data						
Explorer Antibody Array			Median Signal	128	83			
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
			Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
Claudin 2	1.18	Claudin 2	67	52	0.11	0.01	0.52	0.62
Keratin 10/13	1.18	Keratin 10/13	61	47	0.06	0.02	0.47	0.56
BAG-1	1.18	BAG-1	84	65	0.03	0.03	0.66	0.78
MMP-1 (Collagenase-I)	1.18	MMP-1 (Collagenase-I)	65	50	0.03	0.04	0.50	0.60
B-Cell	1.18	B-Cell	339	260	0.14	0.08	2.65	3.13
E2F-3	1.18	E2F-3	69	53	0.05	0.01	0.54	0.63
MADD	1.18	MADD	682	522	0.18	0.22	5.33	6.29
Chromogranin A	1.18	Chromogranin A	162	124	0.12	0.08	1.27	1.49
CD18	1.18	CD18	102	78	0.08	0.02	0.80	0.94
CDw60	1.18	CDw60	70	54	0.08	0.01	0.55	0.64
Clathrin	1.18	Clathrin	261	199	0.10	0.08	2.04	2.40
Thyroid Hormone Receptor beta, human	1.18	Thyroid Hormone Receptor beta, human	146	112	0.17	0.07	1.14	1.34
Heat Shock Protein 75/hsp75	1.17	Heat Shock Protein 75/hsp75	95	73	0.19	0.03	0.74	0.87
Cadherin-P	1.17	Cadherin-P	51	39	0.13	0.06	0.40	0.46
SV40 Large T Antigen	1.17	SV40 Large T Antigen	135	103	0.07	0.05	1.05	1.23
FSH-b	1.17	FSH-b	147	112	0.02	0.02	1.15	1.34
Renal Cell Carcinoma	1.17	Renal Cell Carcinoma	69	53	0.16	0.01	0.54	0.63
Testosterone	1.17	Testosterone	82	62	0.04	0.02	0.64	0.75
von Hippel-Lindau Protein	1.17	von Hippel-Lindau Protein	107	81	0.05	0.02	0.83	0.98
JNK Activating kinase (JNK1)	1.17	JNK Activating kinase (JNK1)	653	496	0.20	0.19	5.11	5.98
CD95 / Fas	1.17	CD95 / Fas	121	92	0.02	0.07	0.94	1.10
O ct-1	1.17	O ct-1	98	74	0.08	0.08	0.76	0.89
Insulin	1.17	Insulin	79	60	0.12	0.06	0.61	0.72
alpha-1-antichymotrypsin	1.17	alpha-1-antichymotrypsin	3160	2394	0.02	0.05	24.73	28.84
MMP-19	1.17	MMP-19	68	52	0.02	0.01	0.53	0.62
Keratin 20	1.16	Keratin 20	109	83	0.08	0.11	0.85	0.99
Myelin / Oligodendrocyte	1.16	Myelin / Oligodendrocyte	74	56	0.00	0.03	0.58	0.67
Nucleophosmin (NPM)	1.16	Nucleophosmin (NPM)	80	61	0.07	0.08	0.63	0.73
Exo1	1.16	Exo1	645	487	0.15	0.03	5.05	5.87
ATM	1.16	ATM	80	60	0.17	0.05	0.62	0.72
Growth Hormone (hGH)	1.16	Growth Hormone (hGH)	116	88	0.06	0.09	0.91	1.05
IL-8	1.16	IL-8	388	293	0.09	0.08	3.04	3.52
b Galactosidase	1.16	b Galactosidase	108	81	0.27	0.02	0.84	0.98
Heat Shock Protein 70/hsp70	1.16	Heat Shock Protein 70/hsp70	77	58	0.06	0.02	0.60	0.70
Parathyroid Hormone	1.16	Parathyroid Hormone	77	58	0.00	0.10	0.60	0.70
TAG-72	1.16	TAG-72	69	52	0.05	0.01	0.54	0.62
Calretinin	1.16	Calretinin	71	53	0.05	0.03	0.55	0.64
Calponin	1.16	Calponin	4826	3628	0.04	0.20	37.77	43.70
MCM5	1.16	MCM5	113	85	0.18	0.11	0.88	1.02
CD23	1.15	CD23	70	53	0.02	0.12	0.55	0.63
Cdk2	1.15	Cdk2	80	60	0.04	0.05	0.63	0.72
Claudin 5	1.15	Claudin 5	64	48	0.02	0.12	0.50	0.58
GFAP	1.15	GFAP	62	47	0.11	0.08	0.49	0.56
UCP3	1.15	UCP3	76	57	0.13	0.10	0.59	0.69
Ang-1	1.15	Ang-1	70	52	0.05	0.03	0.54	0.63
CD6	1.15	CD6	1173	876	0.19	0.04	9.18	10.55
MCM2	1.15	MCM2	79	59	0.02	0.10	0.62	0.71
Actin, skeletal muscle	1.15	Actin, skeletal muscle	71	53	0.06	0.00	0.56	0.64
Progesterone Receptor (phospho-specific)	1.15	Progesterone Receptor (phospho-specific) - Serine 29	99	74	0.27	0.11	0.77	0.89
MyoD1	1.15	MyoD1	5791	4316	0.13	0.15	45.33	52.00
Rabies Virus	1.15	Rabies Virus	139	104	0.23	0.06	1.09	1.25
PPAR-gamma	1.15	PPAR-gamma	65	48	0.05	0.03	0.50	0.58
PCNA	1.14	PCNA	113	84	0.01	0.03	0.88	1.01
IL-2	1.14	IL-2	76	56	0.14	0.05	0.59	0.67
HRP	1.14	HRP	89	66	0.05	0.04	0.70	0.80
Ang-2	1.14	Ang-2	68	50	0.03	0.00	0.53	0.60

Antibody Array Assay Results		Assay Data		
Explorer Antibody Array		Median Signal	128	83
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots	
			Bigger Sample	Smaller Sample
ITK	1.14	ITK	165	122
S100A4	1.14	S100A4	126	93
PSCA	1.14	PSCA	71	52
Topo II beta	1.13	Topo II beta	70	52
CD138	1.13	CD138	104	77
Keratin, LMW	1.13	Keratin, LMW	95	70
Prostate Apoptosis Response Protein-4	1.13	Prostate Apoptosis Response Protein-4	66	49
IgA	1.13	IgA	16036	11781
Caspase 1	1.13	Caspase 1	1082	794
GAPDH	1.13	GAPDH	166	122
Surfactant Protein B	1.13	Surfactant Protein B	77	57
CD14	1.13	CD14	137	101
Caldesmon	1.13	Caldesmon	113	83
CD79a mb-1	1.13	CD79a mb-1	114	84
Retinoblastoma (Rb) (Phospho-specific Serine 608)	1.13	Retinoblastoma (Rb) (Phospho-specific Serine 608)	69	51
Osteopontin	1.13	Osteopontin	82	60
PMP-22	1.12	PMP-22	76	56
a-B-Crystallin	1.12	a-B-Crystallin	74	54
CXCR4 / Fusin	1.12	CXCR4 / Fusin	305	222
Gastrin 1	1.12	Gastrin 1	134	97
Ornithine Decarboxylase	1.12	Ornithine Decarboxylase	101	73
CD20	1.12	CD20	148	108
PDGF	1.12	PDGF	79	57
Transforming Growth Factor a	1.12	Transforming Growth Factor a	146	106
CD45RB	1.12	CD45RB	118	86
Mek6	1.11	Mek6	639	462
MHC II (HLA-DQ)	1.11	MHC II (HLA-DQ)	163	118
MMP-11 (Stromelysin-3)	1.11	MMP-11 (Stromelysin-3)	88	63
Caspase 7 (Mch 3)	1.11	Caspase 7 (Mch 3)	1128	812
Fli-1	1.11	Fli-1	79	57
MAP2a,b	1.11	MAP2a,b	123	88
CD16	1.10	CD16	223	160
HDAC1	1.10	HDAC1	73	52
CIDE-A	1.10	CIDE-A	691	496
MLH1	1.10	MLH1	80	57
GM-CSF	1.10	GM-CSF	51	37
ERCC1	1.10	ERCC1	677	484
Prolactin Receptor	1.10	Prolactin Receptor	4449	3179
CD115/c-fms/CSF-1R/M-CSFR	1.10	CD115/c-fms/CSF-1R/M-CSFR	212	152
c-jun	1.10	c-jun	154	110
Mucin 3 (MUC3)	1.10	Mucin 3 (MUC3)	202	144
Raf-1 (Phospho-specific)	1.10	Raf-1 (Phospho-specific)	152	108
Neurofilament (68kDa)	1.10	Neurofilament (68kDa)	162	115
Alkaline Phosphatase (AP)	1.10	Alkaline Phosphatase (AP)	655	466
CD36GPIIb/GPIV	1.09	CD36GPIIb/GPIV	220	157
HDJ-2/DNAJ	1.09	HDJ-2/DNAJ	120	85
S100A6	1.09	S100A6	154	110
Vitamin D Receptor (VDR)	1.09	Vitamin D Receptor (VDR)	738	525
p95VAV	1.09	p95VAV	80	57
PLAP	1.09	PLAP	93	66
Myosin Smooth Muscle Heavy Chain	1.09	Myosin Smooth Muscle Heavy Chain	93	66
Cdk4	1.09	Cdk4	154	109
p63 (p53 Family Member)	1.09	p63 (p53 Family Member)	115	81
Rad51	1.09	Rad51	229	162
MHC II (HLA-DR)	1.09	MHC II (HLA-DR)	190	134
E2F-1	1.09	E2F-1	758	535

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.13	0.09
0.07	0.09
0.13	0.05
0.04	0.04
0.16	0.01
0.04	0.01
0.00	0.04
0.04	0.02
0.32	0.14
0.01	0.04
0.09	0.06
0.03	0.04
0.18	0.13
0.04	0.31
0.08	0.01
0.00	0.12
0.07	0.01
0.01	0.12
0.05	0.09
0.11	0.03
0.02	0.04
0.21	0.16
0.10	0.07
0.02	0.11
0.11	0.11
0.16	0.22
0.13	0.04
0.02	0.11
0.21	0.10
0.10	0.04
0.02	0.03
0.08	0.00
0.03	0.00
0.43	0.29
0.06	0.07
0.22	0.02
0.11	0.00
0.24	0.34
0.23	0.08
0.00	0.10
0.08	0.01
0.06	0.03
0.03	0.06
0.25	0.01
0.03	0.06
0.11	0.22
0.27	0.10
0.08	0.08
0.13	0.06
0.11	0.09
0.07	0.12
0.08	0.00
0.02	0.07
0.04	0.00
0.02	0.12
0.15	0.19

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
1.29	1.46
0.99	1.12
0.55	0.63
0.55	0.62
0.81	0.92
0.74	0.84
0.52	0.58
125.52	141.93
8.47	9.57
1.30	1.46
0.60	0.68
1.07	1.21
0.88	0.99
0.89	1.01
0.54	0.61
0.64	0.72
0.59	0.67
0.58	0.64
2.38	2.67
1.05	1.17
0.79	0.88
1.16	1.30
0.61	0.69
1.14	1.27
0.92	1.03
5.00	5.57
1.27	1.42
0.68	0.76
8.83	9.78
0.61	0.68
0.96	1.06
1.75	1.93
0.57	0.63
5.41	5.97
0.62	0.69
0.40	0.44
5.30	5.83
34.82	38.30
1.66	1.83
1.20	1.32
1.58	1.73
1.19	1.30
1.26	1.39
5.13	5.61
1.72	1.89
0.94	1.02
1.21	1.32
5.78	6.32
0.62	0.68
0.73	0.80
0.72	0.79
1.21	1.31
0.90	0.98
1.79	1.95
1.48	1.61
5.93	6.45

Antibody Array Assay Results		Assay Data		
Explorer Antibody Array				
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
PR3 (Proteinase 3)	1.09	PR3 (Proteinase 3)	7675	5416
GRIP1	1.09	GRIP1	95	67
CDC14A Phosphatase	1.09	CDC14A Phosphatase	78	55
bcl-X	1.08	bcl-X	71	50
b-2-Microglobulin	1.08	b-2-Microglobulin	73	51
Phosphotyrosine	1.08	Phosphotyrosine	204	144
Erk1	1.08	Erk1	228	160
GLUT-3	1.08	GLUT-3	101	71
Claudin 4	1.08	Claudin 4	64	45
14-3-3 beta	1.08	14-3-3 beta	107	75
p16INK4a	1.08	p16INK4a	68	48
Chorionic Gonadotropin beta (hCG-beta)	1.07	Chorionic Gonadotropin beta (hCG-beta)	123	86
CD1a	1.07	CD1a	113	79
Surfactant Protein B (Pro)	1.07	Surfactant Protein B (Pro)	141	98
Progesterone	1.07	Progesterone	1623	1130
Epithelial Membrane Antigen (EMA / CA15-MUC-1)	1.07	Epithelial Membrane Antigen (EMA / CA15-MUC-1)	179	125
GST	1.07	GST	133	93
Calcium Pump ATPase	1.07	Calcium Pump ATPase	148	103
Cyclin E	1.07	Cyclin E	3647	2532
CD81/TAPA-1	1.06	CD81/TAPA-1	94	65
MHC I (HLA-A,B,C)	1.06	MHC I (HLA-A,B,C)	159	110
Tubulin	1.06	Tubulin	443	305
p53	1.06	p53	87	60
TGF beta 3	1.05	TGF beta 3	186	127
Heregulin	1.05	Heregulin	117	80
Myeloid Specific Marker	1.05	Myeloid Specific Marker	177	121
Oct-3/	1.05	Oct-3/	79	54
CD71 / Transferrin Receptor	1.05	CD71 / Transferrin Receptor	111	76
CD231	1.05	CD231	166	113
MHC II (HLA-DR) Ia	1.05	MHC II (HLA-DR) Ia	155	106
L-Plastin	1.05	L-Plastin	348	237
MMP-13 (Collagenase-3)	1.04	MMP-13 (Collagenase-3)	120	81
Flt-4	1.04	Flt-4	76	52
Chk1	1.04	Chk1	1520	1029
RPA/p70	1.04	RPA/p70	176	119
COX2	1.04	COX2	83	56
GLUT-1	1.03	GLUT-1	79	53
p73a/b	1.03	p73a/b	81	54
Connexin 43	1.03	Connexin 43	93	62
Mitochondria	1.03	Mitochondria	80	53
Fas-ligand	1.02	Fas-ligand	81	54
Bax	1.02	Bax	107	71
Tropomyosin	1.02	Tropomyosin	167	111
Ga0	1.02	Ga0	92	61
Glucose-Regulated Protein 94	1.02	Glucose-Regulated Protein 94	86	57
P504S	1.02	P504S	74	49
Filaggrin	1.02	Filaggrin	96	63
E2F-2	1.01	E2F-2	9241	6087
Cathepsin D	1.01	Cathepsin D	81	53
Laminin Receptor	1.01	Laminin Receptor	305	200
Muc-1	1.01	Muc-1	97	64
Keratin 8 (phospho-specific Ser73)	1.00	Keratin 8 (phospho-specific Ser73)	178	116
APC11	1.00	APC11	551	359
NF kappa B / p65 (Rel A)	1.00	NF kappa B / p65 (Rel A)	675	439
RAD1	1.00	RAD1	174	113
Actin, Pan	1.00	Actin, Pan	115	75

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.02	0.05
0.07	0.04
0.07	0.05
0.04	0.03
0.20	0.03
0.12	0.06
0.04	0.04
0.05	0.11
0.08	0.05
0.14	0.07
0.04	0.13
0.01	0.01
0.06	0.14
0.02	0.06
0.04	0.08
0.05	0.03
0.15	0.07
0.11	0.03
0.21	0.06
0.00	0.02
0.06	0.01
0.17	0.31
0.14	0.08
0.11	0.11
0.00	0.14
0.00	0.06
0.09	0.03
0.10	0.05
0.13	0.08
0.16	0.09
0.10	0.16
0.16	0.16
0.17	0.01
0.09	0.04
0.03	0.05
0.03	0.06
0.18	0.08
0.11	0.00
0.04	0.07
0.29	0.05
0.13	0.01
0.09	0.03
0.02	0.11
0.10	0.08
0.14	0.04
0.09	0.04
0.08	0.00
0.07	0.13
0.24	0.03
0.03	0.03
0.10	0.03
0.06	0.12
0.21	0.05
0.08	0.17
0.46	0.09
0.31	0.09

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
60.08	65.25
0.74	0.81
0.61	0.66
0.56	0.60
0.57	0.61
1.60	1.73
1.78	1.93
0.79	0.85
0.50	0.54
0.83	0.90
0.53	0.57
0.96	1.03
0.88	0.95
1.10	1.18
12.70	13.61
1.40	1.50
1.04	1.11
1.15	1.23
28.54	30.50
0.74	0.78
1.24	1.32
3.46	3.67
0.68	0.72
1.45	1.53
0.92	0.96
1.39	1.46
0.62	0.65
0.86	0.91
1.30	1.36
1.21	1.27
2.72	2.85
0.94	0.98
0.59	0.62
11.90	12.39
1.38	1.43
0.65	0.67
0.62	0.64
0.63	0.65
0.72	0.75
0.62	0.64
0.63	0.64
0.83	0.85
1.31	1.33
0.72	0.73
0.67	0.68
0.58	0.58
0.75	0.76
72.33	73.34
0.63	0.64
2.39	2.41
0.76	0.77
1.39	1.40
4.31	4.32
5.28	5.29
1.36	1.36
0.90	0.90

Antibody Array Assay Results		Assay Data		
Explorer Antibody Array				
		Median Signal	128	83
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots	
			Bigger Sample	Smaller Sample
Heat Shock Protein 60/hsp60	0.99	Heat Shock Protein 60/hsp60	120	77
Estradiol	0.99	Estradiol	194	125
CD45RO	0.99	CD45RO	8930	5753
Mast Cell Chymase	0.99	Mast Cell Chymase	8147	5239
Tenascin	0.99	Tenascin	91	59
Gai1	0.99	Gai1	6158	3943
Luciferase	0.97	Luciferase	90	57
GABA a Receptor 1	0.97	GABA a Receptor 1	94	60
Estrogen Receptor	0.97	Estrogen Receptor	96	61
CD8	0.97	CD8	110	69
SIRP a1	0.97	SIRP a1	949	598
LH	0.97	LH	166	104
S100	0.96	S100	101	63
MMP-16 / MT3-MMP	0.96	MMP-16 / MT3-MMP	384	240
DcR1	0.95	DcR1	121	75
Macrophage	0.95	Macrophage	27363	16885
Keratin 8/18	0.95	Keratin 8/18	3273	2018
CD137 (4-1BB)	0.95	CD137 (4-1BB)	94	58
Keratin 5/6/18	0.95	Keratin 5/6/18	367	226
cdh1	0.95	cdh1	118	73
PHAS-II	0.94	PHAS-II	152	93
Neuron Specific Enolase	0.94	Neuron Specific Enolase	3636	2230
I-Kappa-B Kinase b (IKKb)	0.94	I-Kappa-B Kinase b (IKKb)	171	104
p73a	0.94	p73a	160	98
Myogenin	0.94	Myogenin	189	115
GluR6/7	0.94	GluR6/7	93	57
Keratin 8	0.93	Keratin 8	4890	2969
Caspase 5	0.93	Caspase 5	101	61
Keratin 5/8	0.93	Keratin 5/8	150	91
c-fos	0.93	c-fos	98	59
Desmin	0.93	Desmin	102	61
Ki67	0.92	Ki67	244	146
Melanoma (gp100)	0.92	Melanoma (gp100)	4679	2795
GluR 2/3	0.92	GluR 2/3	91	54
CREB	0.91	CREB	607	360
Green Fluorescent Protein (GFP)	0.91	Green Fluorescent Protein (GFP)	131	78
Pds1	0.91	Pds1	418	247
claudin 11	0.91	claudin 11	103	61
Keratin 19	0.91	Keratin 19	313	184
MAP1B	0.90	MAP1B	4433	2604
CD35/CR1	0.89	CD35/CR1	269	156
DJ-1	0.89	DJ-1	103	59
Grb2	0.88	Grb2	695	400
GluR1	0.88	GluR1	102	58
CREB-Binding Protein	0.88	CREB-Binding Protein	124	71
Cdk8	0.88	Cdk8	814	463
Paxillin	0.88	Paxillin	146	83
Keratin, Pan	0.87	Keratin, Pan	114	65
Bcl10 / CIPER / CLAP / mE10	0.87	Bcl10 / CIPER / CLAP / mE10	352	199
APC	0.87	APC	107	60
Negative Control for Mouse IgG3	0.87	Negative Control for Mouse IgG3	254	143
SREBP-1 (Sterol Regulatory Element Bind	0.86	SREBP-1 (Sterol Regulatory Element Binding Protein-1	127	71
Catenin alpha	0.84	Catenin alpha	88	48
Myeloperoxidase	0.84	Myeloperoxidase	4854	2654
Adenovirus Type 2 E1A	0.84	Adenovirus Type 2 E1A	5639	3080
NF kappa B / p50	0.83	NF kappa B / p50	1080	584

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.15	0.06
0.13	0.18
0.04	0.01
0.11	0.09
0.11	0.01
0.19	0.11
0.27	0.10
0.21	0.04
0.10	0.43
0.03	0.08
0.00	0.02
0.15	0.07
0.20	0.20
0.40	0.01
0.22	0.10
0.08	0.07
0.16	0.13
0.04	0.06
0.28	0.01
0.06	0.01
0.03	0.02
0.01	0.01
0.02	0.20
0.19	0.12
0.07	0.04
0.05	0.01
0.01	0.05
0.08	0.00
0.14	0.10
0.16	0.02
0.01	0.05
0.06	0.09
0.06	0.09
0.16	0.05
0.34	0.30
0.18	0.12
0.06	0.00
0.06	0.08
0.05	0.07
0.17	0.24
0.00	0.10
0.19	0.02
0.01	0.08
0.03	0.15
0.03	0.01
0.16	0.03
0.10	0.03
0.12	0.03
0.05	0.15
0.05	0.07
0.01	0.09
0.01	0.11
0.09	0.03
0.03	0.00
0.15	0.17
0.31	0.15

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.94	0.93
1.52	1.51
69.90	69.31
63.77	63.12
0.71	0.70
48.20	47.51
0.70	0.69
0.74	0.72
0.75	0.73
0.86	0.83
7.42	7.20
1.30	1.25
0.79	0.76
3.00	2.89
0.94	0.90
214.19	203.43
25.62	24.31
0.73	0.69
2.87	2.72
0.92	0.87
1.19	1.12
28.46	26.86
1.33	1.25
1.25	1.17
1.48	1.39
0.73	0.68
38.27	35.77
0.79	0.73
1.17	1.09
0.77	0.71
0.79	0.73
1.91	1.76
36.63	33.67
0.71	0.65
4.75	4.33
1.03	0.93
3.27	2.97
0.80	0.73
2.45	2.22
34.70	31.37
2.10	1.88
0.80	0.71
5.44	4.81
0.79	0.70
0.97	0.85
6.37	5.58
1.14	1.00
0.89	0.78
2.76	2.39
0.83	0.72
1.99	1.72
0.99	0.85
0.68	0.58
37.99	31.97
44.14	37.11
8.45	7.04

Antibody Array Assay Results		Assay Data	
Explorer Antibody Array		Median Signal	12883
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots Bigger SampleSmaller Sample
Wnt-1	0.83	Wnt-1	9451
Cyclin C	0.82	Cyclin C	247132
Heat Shock Protein 27/hsp27	0.81	Heat Shock Protein 27/hsp27	40582135
Mekk-1	0.79	Mekk-1	14876
Stat6	0.79	Stat6	10353
Fra2	0.79	Fra2	212109
Granzyme B	0.78	Granzyme B	198101
Raf1	0.78	Raf1	492249
Vinculin	0.78	Vinculin	200101
p27Kip1	0.77	p27Kip1	17989
Syk	0.76	Syk	480238
B7-H2	0.76	B7-H2	35271741
nm23	0.76	nm23	14672
Topoisomerase IIa	0.76	Topoisomerase IIa	17285
Myoglobin	0.75	Myoglobin	12159
Thymidine Phosphorylase	0.75	Thymidine Phosphorylase	12461
ERK2	0.75	ERK2	18992
Caspase 8 (FLICE)	0.74	Caspase 8 (FLICE)	13967
Ferritin	0.74	Ferritin	1686815
Heat Shock Protein 90b/hsp84	0.74	Heat Shock Protein 90b/hsp84	13967
Zip kinase	0.73	Zip kinase	260124
Helicobacter pylori	0.73	Helicobacter pylori	265125
Claudin-1	0.71	Claudin-1	18485
Cyclin E2	0.71	Cyclin E2	14869
ROC	0.71	ROC	11955
I-FLICE / CASPER	0.71	I-FLICE / CASPER	18685
CD63	0.70	CD63	22801038
D4-GDI	0.69	D4-GDI	20191
DNA Polymerase Gamma	0.68	DNA Polymerase Gamma	14163
Bim (BOD)	0.68	Bim (BOD)	385170
Filamin	0.67	Filamin	2149939
MMP-14 / MT1-MMP	0.67	MMP-14 / MT1-MMP	18380
DP-2	0.67	DP-2	21292
Caspase 6 (Mch 2)	0.67	Caspase 6 (Mch 2)	16371
DFF45 / ICAD	0.65	DFF45 / ICAD	583247
CDC37	0.65	CDC37	1435605
NOS-i	0.64	NOS-i	20285
Histone H1	0.64	Histone H1	1208503
TNF-R2	0.64	TNF-R2	17673
E2F-5	0.63	E2F-5	374154
Flk-1 / KDR / VEGFR2	0.63	Flk-1 / KDR / VEGFR2	14660
Amphiregulin	0.63	Amphiregulin	17069
DcR2 / TRAIL-R4 / TRUNDD	0.62	DcR2 / TRAIL-R4 / TRUNDD	13053
Negative Control for Rabbit IgG	0.62	Negative Control for Rabbit IgG	16065
Somatostatin Receptor-I	0.62	Somatostatin Receptor-I	24398
Mek2	0.62	Mek2	308124
Daxx	0.62	Daxx	16265
APC2	0.61	APC2	12951
A-Raf	0.60	A-Raf	19878
Ask1 / MAPKKK5	0.60	Ask1 / MAPKKK5	22789
Calcitonin	0.60	Calcitonin	17468
Caspase 2	0.60	Caspase 2	18070
Bak	0.59	Bak	299116
Involucrin	0.59	Involucrin	852328
TACE (TNF-alpha converting enzyme) / ADAM17	0.59	TACE (TNF-alpha converting enzyme) / ADAM17	24695
Gab-1	0.59	Gab-1	316121

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.37	0.13
0.26	0.04
0.20	0.01
0.18	0.13
0.02	0.04
0.02	0.15
0.30	0.13
0.45	0.29
0.19	0.06
0.02	0.06
0.03	0.01
0.14	0.18
0.15	0.00
0.12	0.01
0.06	0.05
0.05	0.04
0.45	0.04
0.14	0.08
0.08	0.09
0.10	0.07
0.04	0.01
0.16	0.09
0.20	0.15
0.68	0.09
0.23	0.05
0.01	0.13
0.03	0.06
0.06	0.20
0.23	0.03
0.16	0.01
0.09	0.10
0.03	0.08
0.08	0.06
0.03	0.09
0.19	0.06
0.24	0.19
0.01	0.18
0.18	0.01
0.11	0.07
0.06	0.08
0.16	0.08
0.02	0.08
0.07	0.12
0.03	0.05
0.15	0.14
0.00	0.09
0.07	0.07
0.05	0.03
0.03	0.10
0.11	0.14
0.21	0.12
0.01	0.17
0.16	0.14
0.04	0.07
0.01	0.07
0.17	0.10

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.73	0.61
1.93	1.58
31.77	25.72
1.16	0.92
0.80	0.63
1.66	1.31
1.55	1.21
3.85	2.99
1.57	1.22
1.40	1.07
3.75	2.86
27.61	20.98
1.14	0.87
1.35	1.02
0.94	0.71
0.97	0.73
1.48	1.10
1.08	0.81
13.20	9.82
1.08	0.80
2.03	1.49
2.07	1.51
1.44	1.02
1.16	0.83
0.93	0.66
1.45	1.02
17.85	12.50
1.57	1.09
1.10	0.75
3.01	2.05
16.82	11.31
1.43	0.96
1.66	1.11
1.28	0.85
4.56	2.97
11.23	7.28
1.58	1.02
9.46	6.06
1.37	0.87
2.92	1.86
1.14	0.72
1.33	0.83
1.01	0.63
1.25	0.78
1.90	1.18
2.41	1.49
1.26	0.78
1.01	0.61
1.55	0.93
1.78	1.07
1.36	0.81
1.41	0.84
2.34	1.39
6.67	3.95
1.93	1.14
2.47	1.45

Antibody Array Assay Results		Assay Data			
Explorer Antibody Array					
		Median Signal		128	83
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	
Amyloid A4 Protein Precursor	0.58	Amyloid A4 Protein Precursor	214	80	
PHAS-I	0.58	PHAS-I	420	157	
Lck (p56lck)	0.57	Lck (p56lck)	270	101	
CIDE-B	0.57	CIDE-B	321	120	
ARC	0.57	ARC	380	142	
Nck	0.57	Nck	208	77	
p73	0.56	p73	420	153	
FLIP	0.56	FLIP	218	79	
FADD (FAS-Associated death domain-con	0.55	FADD (FAS-Associated death domain-containing Prote	188	67	
Cyclin D1	0.55	Cyclin D1	244	87	
p57Kip2 Ab-7	0.54	p57Kip2 Ab-7	309	109	
CDC47	0.54	CDC47	279	98	
Flt-1 / VEGFR1	0.54	Flt-1 / VEGFR1	230	81	
GAD65	0.54	GAD65	272	95	
Catenin beta	0.54	Catenin beta	178	62	
Mek1	0.54	Mek1	241	84	
H.Pylori	0.53	H.Pylori	185	64	
p14ARF	0.53	p14ARF	167	58	
Cadherin, (Pan)	0.53	Cadherin, (Pan)	231	80	
Nitric Oxide Synthase, endothelial (eNOS)	0.53	Nitric Oxide Synthase, endothelial (eNOS)	276	95	
Stat3	0.53	Stat3	226	78	
Stat5b	0.53	Stat5b	172	59	
RAIDD	0.52	RAIDD	224	76	
DNA Primase (p49)	0.52	DNA Primase (p49)	195	66	
p19Skp1	0.52	p19Skp1	207	70	
Stat5a	0.51	Stat5a	225	75	
TRADD	0.51	TRADD	225	75	
NOS-u	0.51	NOS-u	354	118	
DNA Primase (p58)	0.51	DNA Primase (p58)	210	69	
PDGFR, alpha	0.51	PDGFR, alpha	265	87	
p18INK4c	0.50	p18INK4c	257	84	
DFF40 (DNA Fragmentation Factor 40) / C	0.50	DFF40 (DNA Fragmentation Factor 40) / CAD	258	84	
c-Src	0.50	c-Src	233	76	
PARP	0.50	PARP	231	75	
Endostatin	0.49	Endostatin	174	56	
Cullin-1 (CUL-1)	0.49	Cullin-1 (CUL-1)	160	51	
PARP (Poly ADP-Ribose Polymerase)	0.49	PARP (Poly ADP-Ribose Polymerase)	314	99	
XRCC2	0.48	XRCC2	211	66	
MyD88	0.48	MyD88	218	68	
Cdk3	0.44	Cdk3	357	103	
MMP-23	0.44	MMP-23	301	86	
Cullin-2 (CUL-2)	0.42	Cullin-2 (CUL-2)	213	58	
Stat-1	0.42	Stat-1	414	112	
CDC34	0.41	CDC34	254	68	
BRCA2 (aa 1323-1346)	0.35	BRCA2 (aa 1323-1346)	275	62	
Min	1.33				
Max	4.59				
Mean	1.55				

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.31	0.12
0.20	0.05
0.19	0.11
0.44	0.29
0.34	0.16
0.15	0.01
0.38	0.13
0.43	0.12
0.34	0.14
0.13	0.17
0.31	0.08
0.32	0.01
0.18	0.17
0.32	0.18
0.03	0.00
0.06	0.03
0.38	0.20
0.37	0.01
0.24	0.13
0.45	0.16
0.59	0.05
0.06	0.06
0.40	0.11
0.06	0.04
0.27	0.04
0.27	0.02
0.19	0.13
0.08	0.04
0.08	0.06
0.17	0.03
0.07	0.03
0.11	0.17
0.29	0.10
0.06	0.02
0.09	0.01
0.30	0.04
0.48	0.20
0.25	0.06
0.10	0.10
0.37	0.08
0.15	0.11
0.48	0.02
0.20	0.14
0.41	0.03
0.31	0.07

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
1.67	0.96
3.28	1.89
2.11	1.21
2.51	1.44
2.97	1.70
1.63	0.92
3.28	1.84
1.70	0.95
1.47	0.80
1.91	1.04
2.41	1.31
2.18	1.18
1.80	0.97
2.13	1.14
1.39	0.75
1.88	1.01
1.44	0.77
1.30	0.69
1.81	0.96
2.16	1.14
1.77	0.93
1.34	0.70
1.75	0.92
1.52	0.80
1.62	0.84
1.76	0.90
1.76	0.90
2.77	1.42
1.64	0.83
2.07	1.05
2.01	1.01
2.02	1.01
1.82	0.91
1.81	0.90
1.36	0.67
1.25	0.61
2.46	1.19
1.65	0.80
1.70	0.82
2.79	1.23
2.35	1.03
1.67	0.70
3.24	1.35
1.99	0.81
2.15	0.75

Appendix E

Signaling

Antibody Array Assay Results		Assay Data			
Signaling Explorer Antibody Array					
			Median Signal	283	225
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots		
			Bigger Sample	Smaller Sample	
Tubulin alpha	4.41	Tubulin alpha	2453	8594	
BAD	2.15	BAD	1315	2247	
GAD1	1.91	GAD1	1756	2666	
MAP4K4	1.88	MAP4K4	849	1268	
p42 MAPK	1.87	p42 MAPK	5165	7674	
Caveolin-1	1.73	Caveolin-1	2848	3910	
CDH9	1.67	CDH9	4784	6330	
TNFA	1.63	TNFA	2503	3249	
SND1/P100	1.63	SND1/P100	2801	3633	
CA 15-3	1.58	CA 15-3	516	648	
Keratin 15	1.58	Keratin 15	2304	2884	
NYREN18	1.57	NYREN18	203	253	
SP3/4	1.57	SP3/4	1299	1622	
KCNMB2	1.56	KCNMB2	4242	5261	
CDH24	1.55	CDH24	9045	11150	
CEA	1.55	CEA	328	403	
CMC1	1.53	CMC1	1311	1596	
Retinoic Acid Receptor beta	1.53	Retinoic Acid Receptor beta	1367	1662	
Claudin 5	1.53	Claudin 5	5219	6339	
Cytochrome b561 D1	1.52	Cytochrome b561 D1	17291	20861	
MMP-10	1.52	MMP-10	2050	2468	
mGluR2/3	1.51	mGluR2/3	2648	3184	
IgG	1.51	IgG	53652	64397	
GRB14	1.51	GRB14	13254	15852	
G RTP1	1.50	G RTP1	1155	1372	
mGluR4	1.49	mGluR4	1387	1637	
Actin-alpha-1	1.47	Actin-alpha-1	10264	11984	
STAT3	1.47	STAT3	263	307	
LPA	1.47	LPA	267	311	
GAD1/2	1.46	GAD1/2	2230	2578	
TNF Receptor II	1.45	TNF Receptor II	1461	1680	
iNOS	1.44	iNOS	1275	1456	
RIT1	1.43	RIT1	1861	2117	
Actin-gamma2	1.43	Actin-gamma2	839	954	
KIF4A	1.42	KIF4A	1486	1675	
ARSI	1.41	ARSI	7206	8095	
Desmin	1.41	Desmin	13560	15175	
Beta-Actin	1.40	Beta-Actin	2110	2342	
UBR1	1.40	UBR1	1665	1847	
Thrombin Receptor	1.39	Thrombin Receptor	2550	2825	
CD40	1.39	CD40	785	870	
TP53INP1	1.39	TP53INP1	2418	2664	
AKT2	1.39	AKT2	188	207	
CDYL2	1.38	CDYL2	1128	1238	
MAGE-1	1.38	MAGE-1	1021	1118	
BCL-10	1.37	BCL-10	765	834	
ABCD1	1.37	ABCD1	3413	3719	
PIP5K1C	1.37	PIP5K1C	647	704	
Heregulin	1.37	Heregulin	396	430	
HDAC5	1.37	HDAC5	567	616	
		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
		0.04	0.47	8.67	38.24
		0.21	0.50	4.65	10.00
		0.13	0.04	6.20	11.86
		0.45	0.01	3.00	5.64
		0.41	0.32	18.25	34.14
		0.08	0.25	10.06	17.39
		0.58	0.75	16.90	28.16
		0.01	0.06	8.84	14.46
		0.01	0.17	9.90	16.16
		0.27	0.02	1.82	2.88
		0.01	0.04	8.14	12.83
		0.41	0.08	0.72	1.13
		0.15	0.01	4.59	7.22
		0.05	0.04	14.99	23.41
		0.08	0.12	31.96	49.61
		0.05	0.08	1.16	1.79
		0.06	0.04	4.63	7.10
		0.01	0.05	4.83	7.39
		0.00	0.12	18.44	28.20
		0.04	0.06	61.10	92.82
		0.04	0.08	7.24	10.98
		0.07	0.05	9.36	14.16
		0.10	0.02	189.58	286.53
		0.05	0.02	46.83	70.53
		0.05	0.01	4.08	6.10
		0.07	0.10	4.90	7.28
		0.09	0.05	36.27	53.32
		0.41	0.22	0.93	1.36
		0.05	0.04	0.94	1.38
		0.05	0.03	7.88	11.47
		0.08	0.07	5.16	7.47
		0.14	0.08	4.50	6.48
		0.13	0.10	6.57	9.42
		0.07	0.10	2.96	4.24
		0.09	0.08	5.25	7.45
		0.03	0.16	25.46	36.02
		0.26	0.42	47.92	67.52
		0.05	0.06	7.46	10.42
		0.03	0.05	5.88	8.22
		0.07	0.02	9.01	12.57
		0.02	0.00	2.77	3.87
		0.08	0.13	8.54	11.85
		0.16	0.11	0.66	0.92
		0.05	0.01	3.99	5.51
		0.05	0.11	3.61	4.97
		0.20	0.20	2.70	3.71
		0.08	0.07	12.06	16.55
		0.03	0.03	2.28	3.13
		0.13	0.12	1.40	1.91
		0.13	0.11	2.00	2.74

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array								
			Median Signal	283	225			
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots			Coefficient of Variation for Replicates		Data Normalized to Median Signal
			Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample	Bigger Sample
RCBTB1	1.36	RCBTB1	1117	1209		0.11	0.04	3.95
Claudin 3	1.36	Claudin 3	2312	2495		0.07	0.04	8.17
HSP105	1.35	HSP105	857	918		0.08	0.03	3.03
GLUT1	1.35	GLUT1	1375	1473		0.04	0.10	4.86
ACTR-1C	1.34	ACTR-1C	1701	1811		0.11	0.28	6.01
VEGFB	1.34	VEGFB	1088	1155		0.11	0.18	3.84
MYLIP	1.34	MYLIP	2509	2663		0.15	0.12	8.87
GADD45 beta	1.33	GADD45 beta	1310	1388		0.10	0.10	4.63
MTA1	1.33	MTA1	940	994		0.08	0.09	3.32
ARC	1.33	ARC	5210	5498		0.06	0.05	18.41
ARFIP1	1.32	ARFIP1	6420	6754		0.14	0.01	22.69
CSF2 (GM-CSF)	1.32	CSF2 (GM-CSF)	265	278		0.08	0.36	0.93
BAGE2	1.32	BAGE2	773	810		0.06	0.22	2.73
ORAV1	1.32	ORAV1	2248	2353		0.03	0.04	7.94
GRP75	1.31	GRP75	275	287		0.15	0.22	0.97
GPRIN2	1.31	GPRIN2	1367	1424		0.08	0.05	4.83
Thyroid Hormone Receptor alpha	1.31	Thyroid Hormone Receptor alpha	526	547		0.07	0.05	1.86
DP-1	1.31	DP-1	1807	1877		0.01	0.06	6.38
GNPAT	1.31	GNPAT	1053	1092		0.10	0.26	3.72
CDK7	1.30	CDK7	314	325		0.03	0.06	1.11
Actin-pan	1.30	Actin-pan	3203	3312		0.05	0.03	11.32
Angiopoietin-2	1.30	Angiopoietin-2	116	120		0.26	0.05	0.41
CAGE1	1.30	CAGE1	187	192		0.00	0.01	0.66
Galectin 3	1.30	Galectin 3	673	692		0.01	0.06	2.38
HSP90A	1.29	HSP90A	9403	9642		0.28	0.11	33.23
MMP-9	1.29	MMP-9	198	203		0.10	0.08	0.70
Testosterone	1.29	Testosterone	63928	65535		0.04	0.00	225.89
KITH	1.29	KITH	184	189		0.10	0.06	0.65
FGFR1 Oncogene Partner	1.29	FGFR1 Oncogene Partner	441	452		0.07	0.08	1.56
Ik3-2	1.29	Ik3-2	364	372		0.00	0.05	1.29
SRPK1	1.28	SRPK1	622	634		0.07	0.08	2.20
Lamin A (Cleaved-Asp230)	1.28	Lamin A (Cleaved-Asp230)	960	978		0.01	0.08	3.39
CREB-BP	1.28	CREB-BP	641	650		0.02	0.28	2.26
KCNJ2	1.27	KCNJ2	411	416		0.07	0.01	1.45
CATD (heavy chain,Cleaved-Leu169)	1.27	CATD (heavy chain,Cleaved-Leu169)	2159	2184		0.07	0.21	7.63
IP3KC	1.27	IP3KC	1023	1033		0.11	0.00	3.61
CD80	1.27	CD80	1448	1462		0.12	0.02	5.11
COX1	1.27	COX1	1366	1379		0.01	0.03	4.83
MASP1 (heavy chain,Cleaved-Arg448)	1.27	MASP1 (heavy chain,Cleaved-Arg448)	330	333		0.04	0.01	1.16
Collagen alpha1 XVIII	1.27	Collagen alpha1 XVIII	1610	1623		0.01	0.09	5.69
TGF beta Receptor III	1.26	TGF beta Receptor III	496	498		0.01	0.14	1.75
RAB11FIP4	1.26	RAB11FIP4	1126	1130		0.12	0.04	3.98
Catenin-alpha1	1.26	Catenin-alpha1	756	759		0.10	0.04	2.67
Pax-5	1.26	Pax-5	2647	2658		0.06	0.15	9.35
Patched	1.26	Patched	2038	2046		0.02	0.07	7.20
UBE1L	1.26	UBE1L	442	442		0.16	0.07	1.56
INSL4	1.26	INSL4	265	265		0.03	0.12	0.93
REN	1.26	REN	1108	1107		0.05	0.01	3.91
MAP3K10	1.26	MAP3K10	208	207		0.09	0.02	0.73
PLD4	1.26	PLD4	395	394		0.02	0.06	1.39

Antibody Array Assay Results

Assay Data

Signaling Explorer Antibody Array

		Median Signal		283	225				
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots			Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
Catenin-beta 1	1.25	Catenin-beta 1	242	241		0.06	0.16	0.85	1.07
MAPK 11	1.25	MAPK 11	5705	5669		0.05	0.07	20.16	25.22
NFYC	1.25	NFYC	835	829		0.02	0.00	2.95	3.69
C-Kit	1.25	C-Kit	575	570		0.05	0.05	2.03	2.53
KCNA1	1.25	KCNA1	668	661		0.06	0.00	2.36	2.94
TUBGCP3	1.24	TUBGCP3	631	624		0.17	0.02	2.23	2.77
AIRE	1.24	AIRE	736	725		0.03	0.08	2.60	3.23
Tubulin beta	1.24	Tubulin beta	474	465		0.08	0.18	1.67	2.07
SLC27A5	1.23	SLC27A5	370	363		0.05	0.01	1.31	1.61
XRCC6	1.23	XRCC6	247	242		0.17	0.08	0.87	1.07
TGF beta2	1.23	TGF beta2	443	433		0.03	0.02	1.56	1.92
SERPINB9	1.23	SERPINB9	199	195		0.06	0.03	0.70	0.87
MAT1	1.23	MAT1	461	450		0.06	0.08	1.63	2.00
TRXR2	1.23	TRXR2	702	685		0.07	0.06	2.48	3.05
Tubulin gamma	1.23	Tubulin gamma	454	442		0.02	0.08	1.60	1.97
EMR3	1.23	EMR3	1221	1189		0.03	0.10	4.31	5.29
MAP3K4	1.23	MAP3K4	188	183		0.04	0.06	0.66	0.81
ACAD10	1.23	ACAD10	317	308		0.06	0.19	1.12	1.37
Notch 1 (Cleaved-Val1754)	1.23	Notch 1 (Cleaved-Val1754)	408	397		0.05	0.01	1.44	1.77
FAS	1.22	FAS	306	297		0.12	0.03	1.08	1.32
APC6	1.22	APC6	410	399		0.01	0.09	1.45	1.77
p73	1.22	p73	327	317		0.09	0.12	1.16	1.41
NKX3.1	1.22	NKX3.1	419	405		0.06	0.02	1.48	1.80
GAS6	1.22	GAS6	371	359		0.06	0.01	1.31	1.60
NCoR1	1.22	NCoR1	288	279		0.16	0.13	1.02	1.24
14-3-3 theta	1.22	14-3-3 theta	398	384		0.03	0.05	1.40	1.71
IgA	1.21	IgA	1040	1003		0.42	0.44	3.67	4.46
Survivin	1.21	Survivin	169	163		0.01	0.06	0.60	0.72
NM23	1.21	NM23	600	578		0.02	0.00	2.12	2.57
CD302	1.21	CD302	337	324		0.01	0.03	1.19	1.44
GPR151	1.21	GPR151	2754	2651		0.07	0.07	9.73	11.80
TIMP3	1.21	TIMP3	261	251		0.06	0.17	0.92	1.11
CSF-1 (MCSF)	1.21	CSF-1 (MCSF)	180	173		0.06	0.05	0.63	0.77
GFR alpha-1	1.21	GFR alpha-1	221	212		0.04	0.16	0.78	0.94
IRF4	1.21	IRF4	312	299		0.11	0.04	1.10	1.33
CIDEB	1.21	CIDEB	351	336		0.02	0.07	1.24	1.49
TIMP4	1.20	TIMP4	254	243		0.08	0.08	0.90	1.08
PLK5	1.20	PLK5	655	627		0.01	0.11	2.31	2.79
Tyrosinase	1.20	Tyrosinase	207	198		0.00	0.10	0.73	0.88
JAB1	1.20	JAB1	387	370		0.12	0.09	1.37	1.64
TUBGCP6	1.20	TUBGCP6	371	354		0.01	0.09	1.31	1.57
SLC27A4	1.20	SLC27A4	203	194		0.03	0.05	0.72	0.86
ADCK2	1.20	ADCK2	661	630		0.03	0.12	2.34	2.80
Fibronectin	1.20	Fibronectin	964	918		0.14	0.16	3.40	4.08
FAS ligand	1.20	FAS ligand	533	508		0.06	0.13	1.88	2.26
Histone H2B (Acetyl-Lys15)	1.20	Histone H2B (Acetyl-Lys15)	209	199		0.04	0.14	0.74	0.88
FGF22	1.20	FGF22	1111	1058		0.11	0.20	3.93	4.71
IKB alpha	1.20	IKB alpha	770	731		0.14	0.08	2.72	3.25
SLC6A16	1.20	SLC6A16	698	662		0.06	0.08	2.46	2.95
CHKB	1.19	CHKB	302	287		0.25	0.09	1.07	1.27
Cytochrome P450 2B6	1.19	Cytochrome P450 2B6	778	738		0.09	0.17	2.75	3.28
PKCB1	1.19	PKCB1	399	378		0.09	0.01	1.41	1.68
GRP78	1.19	GRP78	520	493		0.11	0.21	1.84	2.19
Mammaglobin	1.19	Mammaglobin	245	232		0.06	0.09	0.87	1.03
NCK2	1.19	NCK2	290	275		0.03	0.11	1.02	1.22

Antibody Array Assay Results		Assay Data							
Signaling Explorer Antibody Array									
		Median Signal		283		225			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal		
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	
Claudin 2	1.19	Claudin 2	516	488	0.02	0.37	1.82	2.17	
FGFR2	1.19	FGFR2	278	263	0.09	0.05	0.98	1.17	
mGluR6	1.19	mGluR6	250	236	0.09	0.06	0.88	1.05	
Keratin 5	1.19	Keratin 5	285	269	0.08	0.08	1.01	1.19	
PSA-ACT	1.19	PSA-ACT	628	592	0.00	0.18	2.22	2.63	
human Albumin	1.19	human Albumin	5646	5317	0.27	0.28	19.95	23.66	
DMGDH	1.19	DMGDH	729	687	0.05	0.04	2.58	3.05	
TLE2	1.19	TLE2	299	281	0.16	0.26	1.05	1.25	
NSE	1.18	NSE	270	254	0.02	0.04	0.95	1.13	
SENP2	1.18	SENP2	388	365	0.01	0.01	1.37	1.62	
Fibrillin-1	1.18	Fibrillin-1	327	308	0.05	0.08	1.16	1.37	
Synuclein gamma	1.18	Synuclein gamma	400	376	0.01	0.01	1.41	1.67	
CIB3	1.18	CIB3	194	182	0.10	0.02	0.69	0.81	
Bax	1.18	Bax	751	705	0.09	0.06	2.65	3.13	
TIMP1	1.18	TIMP1	742	696	0.05	0.02	2.62	3.09	
INHA (Inhibin alpha)	1.18	INHA (Inhibin alpha)	168	157	0.07	0.18	0.59	0.70	
SYK	1.18	SYK	355	333	0.07	0.01	1.25	1.48	
IGFBP2	1.18	IGFBP2	213	199	0.14	0.05	0.75	0.89	
mGluR8	1.18	mGluR8	301	281	0.13	0.13	1.06	1.25	
ALCAM	1.18	ALCAM	225	210	0.06	0.06	0.79	0.93	
CLIP1	1.17	CLIP1	1264	1180	0.03	0.05	4.47	5.25	
XRCC5	1.17	XRCC5	287	268	0.10	0.07	1.01	1.19	
Cullin 2	1.17	Cullin 2	791	737	0.02	0.06	2.80	3.28	
GLUT3	1.17	GLUT3	290	270	0.06	0.07	1.02	1.20	
RAB3GAP2	1.17	RAB3GAP2	216	201	0.04	0.17	0.76	0.89	
MMP-11	1.17	MMP-11	494	460	0.00	0.12	1.75	2.04	
Prolactin	1.17	Prolactin	299	278	0.06	0.02	1.05	1.23	
CLDN6	1.17	CLDN6	837	778	0.02	0.01	2.96	3.46	
CNTROB	1.17	CNTROB	253	235	0.10	0.08	0.89	1.05	
XRCC3	1.17	XRCC3	316	294	0.11	0.07	1.12	1.31	
Potassium Channel Kv3.2b	1.17	Potassium Channel Kv3.2b	644	598	0.14	0.01	2.27	2.66	
ST5	1.17	ST5	286	265	0.02	0.02	1.01	1.18	
TP53I11	1.17	TP53I11	341	317	0.02	0.06	1.20	1.41	
PDGFB	1.17	PDGFB	333	309	0.00	0.03	1.17	1.37	
EFNA3	1.17	EFNA3	745	691	0.15	0.09	2.63	3.07	
MLH3	1.17	MLH3	275	255	0.14	0.03	0.97	1.13	
CD37	1.17	CD37	1388	1287	0.36	0.11	4.90	5.72	
TNF Receptor I	1.17	TNF Receptor I	253	234	0.06	0.06	0.89	1.04	
ADCK5	1.17	ADCK5	195	181	0.06	0.29	0.69	0.80	
GAS1	1.17	GAS1	443	410	0.02	0.04	1.57	1.82	
JM4	1.16	JM4	326	301	0.12	0.11	1.15	1.34	
WNT 10B	1.16	WNT 10B	138	128	0.04	0.08	0.49	0.57	
ZP4	1.16	ZP4	656	606	0.01	0.02	2.32	2.69	
MMP-2	1.16	MMP-2	1154	1066	0.09	0.07	4.08	4.74	
TUSC5	1.16	TUSC5	193	178	0.07	0.06	0.68	0.79	
GRK7	1.16	GRK7	424	391	0.07	0.02	1.50	1.74	
FKBP1	1.16	FKBP1	867	800	0.10	0.05	3.06	3.56	
RASSF4	1.16	RASSF4	218	201	0.03	0.14	0.77	0.89	
Catenin-gamma	1.16	Catenin-gamma	1099	1012	0.01	0.08	3.88	4.50	
beta-2-Microglobulin	1.16	beta-2-Microglobulin	3715	3419	0.07	0.15	13.13	15.21	
CDH18	1.16	CDH18	251	231	0.04	0.08	0.89	1.03	
AOS1	1.16	AOS1	406	374	0.02	0.03	1.43	1.66	
MMP-7	1.16	MMP-7	381	350	0.12	0.11	1.34	1.56	
GRP94	1.16	GRP94	281	258	0.03	0.09	0.99	1.15	
Myostatin	1.16	Myostatin	261	240	0.04	0.07	0.92	1.07	

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array			Median Signal	283	225			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
Synaptophysin	1.16	Synaptophysin	267	245	0.13	0.04	0.94	1.09
KCNK17	1.16	KCNK17	490	450	0.02	0.01	1.73	2.00
USP30	1.16	USP30	173	159	0.34	0.32	0.61	0.71
RAB6C	1.16	RAB6C	195	179	0.11	0.16	0.69	0.79
SENP5	1.16	SENP5	237	217	0.07	0.04	0.84	0.97
TOP2B	1.16	TOP2B	255	234	0.05	0.08	0.90	1.04
MMP23 (Cleaved-Tyr79)	1.15	MMP23 (Cleaved-Tyr79)	2300	2109	0.02	0.01	8.13	9.38
RAB40B	1.15	RAB40B	403	370	0.16	0.20	1.42	1.64
FOXN4	1.15	FOXN4	304	279	0.01	0.02	1.07	1.24
HSPB2	1.15	HSPB2	262	240	0.04	0.21	0.93	1.07
Pirh2 (RCHY1)	1.15	Pirh2 (RCHY1)	154	141	0.03	0.03	0.54	0.63
Mammaglobin B	1.15	Mammaglobin B	484	443	0.07	0.14	1.71	1.97
TUBB3 (Tubulin beta 3)	1.15	TUBB3 (Tubulin beta 3)	444	406	0.06	0.08	1.57	1.80
Sodium Channel-pan	1.15	Sodium Channel-pan	260	238	0.11	0.01	0.92	1.06
cAMP	1.15	cAMP	293	267	0.01	0.22	1.03	1.19
GPR132	1.15	GPR132	338	309	0.03	0.22	1.19	1.37
MMP-19	1.15	MMP-19	463	423	0.13	0.02	1.64	1.88
GANP	1.15	GANP	229	209	0.02	0.06	0.81	0.93
CHP2	1.15	CHP2	227	207	0.06	0.05	0.80	0.92
Cyclin L1	1.15	Cyclin L1	182	166	0.10	0.06	0.64	0.74
Collagen II	1.15	Collagen II	400	364	0.07	0.04	1.41	1.62
MAP2K6	1.14	MAP2K6	303	276	0.08	0.09	1.07	1.23
MPS1	1.14	MPS1	1014	922	0.05	0.03	3.58	4.10
SENP7	1.14	SENP7	290	264	0.03	0.08	1.02	1.17
SRY	1.14	SRY	312	283	0.06	0.14	1.10	1.26
DGKD	1.14	DGKD	224	204	0.03	0.09	0.79	0.91
ACOT2	1.14	ACOT2	136	124	0.04	0.05	0.48	0.55
XRCC2	1.14	XRCC2	256	232	0.07	0.13	0.90	1.03
Claudin 11	1.14	Claudin 11	1240	1125	0.03	0.07	4.38	5.01
ERAS	1.14	ERAS	375	340	0.17	0.11	1.33	1.51
MMP-14	1.14	MMP-14	236	214	0.05	0.04	0.83	0.95
Sirp alpha1	1.14	Sirp alpha1	214	194	0.07	0.03	0.76	0.86
S6K	1.14	S6K	428	388	0.06	0.21	1.51	1.72
Nrf2	1.14	Nrf2	255	231	0.03	0.09	0.90	1.03
FOXRI	1.14	FOXRI	217	197	0.09	0.04	0.77	0.87
TPD54	1.14	TPD54	281	254	0.06	0.07	0.99	1.13
p50 CDC37	1.14	p50 CDC37	206	187	0.01	0.03	0.73	0.83
ATP5S	1.14	ATP5S	248	225	0.19	0.01	0.88	1.00
GluR5	1.14	GluR5	311	282	0.03	0.12	1.10	1.25
ERF	1.14	ERF	257	233	0.13	0.00	0.91	1.03
Vimentin	1.14	Vimentin	236	213	0.15	0.09	0.83	0.95
LDLRAD1	1.14	LDLRAD1	173	156	0.06	0.05	0.61	0.69
IP6K2	1.14	IP6K2	172	155	0.04	0.06	0.61	0.69
FAKD2	1.14	FAKD2	166	150	0.06	0.03	0.59	0.67
p44/42 MAPK	1.14	p44/42 MAPK	448	404	0.16	0.01	1.58	1.80
MAP3K1	1.14	MAP3K1	226	204	0.07	0.01	0.80	0.91
60S Ribosomal Protein L10	1.14	60S Ribosomal Protein L10	281	254	0.00	0.10	0.99	1.13
WNT1	1.13	WNT1	339	305	0.07	0.11	1.20	1.36
MARK	1.13	MARK	229	206	0.10	0.05	0.81	0.92
PARL	1.13	PARL	214	192	0.07	0.07	0.75	0.85
p44 MAPK	1.13	p44 MAPK	343	308	0.25	0.07	1.21	1.37
Lys-acetylated proteins	1.13	Lys-acetylated proteins	243	218	0.04	0.12	0.86	0.97
Cyclosome 1	1.13	Cyclosome 1	495	445	0.08	0.02	1.75	1.98
Sumo1	1.13	Sumo1	333	299	0.10	0.10	1.18	1.33
Ki67	1.13	Ki67	273	245	0.14	0.00	0.96	1.09

Antibody Array Assay Results		Assay Data		
Signaling Explorer Antibody Array				
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
Glucagon	1.13	Glucagon	281	252
SERC1	1.13	SERC1	164	147
Proteinase 3	1.13	Proteinase 3	120	108
Septin-7	1.13	Septin-7	206	185
XPA	1.13	XPA	302	270
EKI2	1.13	EKI2	162	145
AP-2	1.13	AP-2	398	356
Tyk2	1.13	Tyk2	289	259
SENP6	1.13	SENP6	260	233
SLC25A31	1.13	SLC25A31	231	206
Granzyme B	1.13	Granzyme B	343	307
Cytochrome P450 17A1	1.12	Cytochrome P450 17A1	314	280
TGF alpha	1.12	TGF alpha	453	405
Peripherin	1.12	Peripherin	7395	6598
HSP60	1.12	HSP60	273	244
HNF4alpha/gamma	1.12	HNF4alpha/gamma	577	514
LRP11	1.12	LRP11	410	365
CLN6	1.12	CLN6	244	217
HDAC1	1.12	HDAC1	266	237
TGF beta3	1.12	TGF beta3	259	231
BRSK1	1.12	BRSK1	418	372
CCT6A	1.12	CCT6A	182	162
STEA2	1.12	STEA2	191	170
CDK5R2	1.12	CDK5R2	313	278
HDAC7	1.12	HDAC7	258	230
Somatostatin	1.12	Somatostatin	317	282
ERCC1	1.12	ERCC1	528	470
MMP-23	1.12	MMP-23	223	198
LDLRAD3	1.12	LDLRAD3	250	222
Bak	1.12	Bak	418	371
Prostate-specific Antigen	1.12	Prostate-specific Antigen	244	217
5-HT-5A	1.12	5-HT-5A	384	341
FSH	1.12	FSH	247	219
IL20RB	1.12	IL20RB	198	176
Cytochrome P450 2C8	1.12	Cytochrome P450 2C8	202	179
KPB1/2	1.11	KPB1/2	192	170
PML	1.11	PML	355	314
USF2	1.11	USF2	220	195
SENP3	1.11	SENP3	203	179
PBOV1	1.11	PBOV1	215	190
Cytochrome P450 26C1	1.11	Cytochrome P450 26C1	291	257
Synuclein beta	1.11	Synuclein beta	298	263
PIAS2	1.11	PIAS2	217	191
IPKB	1.11	IPKB	238	210
p300/CBP	1.11	p300/CBP	305	269
CYB5R1	1.11	CYB5R1	448	395
Kallikrein-11 (Cleaved-Ile54)	1.11	Kallikrein-11 (Cleaved-Ile54)	215	190
PPHLN	1.11	PPHLN	207	182
HER3	1.11	HER3	2370	2089
Cytochrome P450 26A1	1.11	Cytochrome P450 26A1	825	727
CNGA2	1.11	CNGA2	508	448
STK24	1.11	STK24	214	189
LIMK2	1.11	LIMK2	633	557
FLI1	1.11	FLI1	256	225
FGFR3	1.11	FGFR3	323	284

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.11	0.07
0.07	0.04
0.01	0.01
0.16	0.03
0.03	0.05
0.01	0.00
0.07	0.03
0.01	0.13
0.00	0.06
0.05	0.01
0.10	0.05
0.02	0.21
0.03	0.01
0.46	0.06
0.10	0.14
0.06	0.14
0.03	0.07
0.03	0.17
0.01	0.09
0.10	0.02
0.05	0.06
0.04	0.00
0.10	0.03
0.01	0.05
0.03	0.05
0.09	0.01
0.06	0.01
0.09	0.02
0.10	0.17
0.06	0.06
0.08	0.07
0.01	0.05
0.07	0.06
0.03	0.08
0.05	0.01
0.09	0.00
0.11	0.00
0.01	0.19
0.07	0.06
0.11	0.07
0.03	0.01
0.05	0.03
0.06	0.12
0.06	0.02
0.09	0.03
0.12	0.13
0.01	0.19
0.01	0.05
0.10	0.03
0.01	0.05
0.11	0.03
0.09	0.07
0.05	0.02
0.09	0.03
0.00	0.02

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.99	1.12
0.58	0.65
0.42	0.48
0.73	0.82
1.07	1.20
0.57	0.64
1.41	1.58
1.02	1.15
0.92	1.03
0.81	0.92
1.21	1.36
1.11	1.25
1.60	1.80
26.13	29.35
0.96	1.08
2.04	2.29
1.45	1.62
0.86	0.97
0.94	1.05
0.92	1.03
1.48	1.65
0.64	0.72
0.67	0.75
1.10	1.24
0.91	1.02
1.12	1.25
1.87	2.09
0.79	0.88
0.88	0.99
1.48	1.65
0.86	0.96
1.36	1.52
0.87	0.97
0.70	0.78
0.71	0.79
0.68	0.75
1.25	1.39
0.78	0.87
0.72	0.80
0.76	0.84
1.03	1.14
1.05	1.17
0.77	0.85
0.84	0.93
1.08	1.19
1.58	1.76
0.76	0.84
0.73	0.81
8.37	9.29
2.92	3.23
1.80	1.99
0.76	0.84
2.23	2.48
0.90	1.00
1.14	1.26

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array			Median Signal	283	225			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots			Coefficient of Variation for Replicates		
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample	
PLK3	1.11	PLK3	205	180		0.01	0.02	0.72
PLA1A	1.11	PLA1A	187	165		0.00	0.00	0.66
Claudin 1	1.11	Claudin 1	652	574		0.05	0.05	2.30
Cytochrome c	1.11	Cytochrome c	401	353		0.22	0.03	1.42
TSH2	1.11	TSH2	165	145		0.05	0.01	0.58
XRCC1	1.11	XRCC1	252	221		0.11	0.11	0.89
MLL	1.11	MLL	235	207		0.02	0.16	0.83
UBA2	1.11	UBA2	243	214		0.05	0.01	0.86
CDK5R1	1.11	CDK5R1	205	180		0.06	0.06	0.72
USP13	1.11	USP13	172	151		0.08	0.01	0.61
MMP1 (Cleaved-Phe100)	1.11	MMP1 (Cleaved-Phe100)	156	137		0.03	0.09	0.55
IP6K3	1.11	IP6K3	426	374		0.05	0.01	1.50
APOL2	1.10	APOL2	208	183		0.12	0.05	0.73
ATP5H	1.10	ATP5H	771	676		0.00	0.15	2.72
GABRG1	1.10	GABRG1	226	198		0.08	0.08	0.80
VCAM1	1.10	VCAM1	145	127		0.04	0.00	0.51
PROZ	1.10	PROZ	322	282		0.07	0.05	1.14
TIMP2	1.10	TIMP2	266	233		0.10	0.14	0.94
NPTN	1.10	NPTN	482	422		0.01	0.06	1.70
CREBZF	1.10	CREBZF	157	137		0.10	0.04	0.55
MGMT	1.10	MGMT	452	395		0.08	0.09	1.60
MAP3K6	1.10	MAP3K6	205	179		0.06	0.04	0.72
SLC4A11	1.10	SLC4A11	424	370		0.05	0.08	1.50
ASC	1.10	ASC	414	361		0.04	0.06	1.46
CBLN4	1.10	CBLN4	234	204		0.10	0.02	0.83
Presenilin 1	1.10	Presenilin 1	238	207		0.13	0.01	0.84
FAK	1.10	FAK	164	143		0.00	0.12	0.58
CNTN4	1.10	CNTN4	190	166		0.02	0.01	0.67
Ezrin	1.10	Ezrin	299	260		0.02	0.05	1.05
Octamer-binding transcription factor 1	1.10	Octamer-binding transcription factor 1	368	320		0.01	0.06	1.30
SKP1A/p19	1.10	SKP1A/p19	316	275		0.00	0.03	1.12
Cytochrome P450 19A1	1.10	Cytochrome P450 19A1	405	352		0.02	0.08	1.43
ATF5	1.10	ATF5	243	211		0.06	0.07	0.86
TrkA	1.10	TrkA	196	171		0.05	0.12	0.69
MAP3K3	1.10	MAP3K3	338	294		0.06	0.04	1.19
IL-1beta (Cleaved-Asp210)	1.10	IL-1beta (Cleaved-Asp210)	238	207		0.13	0.13	0.84
CASP2 (p18,Cleaved-Thr325)	1.09	CASP2 (p18,Cleaved-Thr325)	345	300		0.43	0.05	1.22
Keratin 17	1.09	Keratin 17	437	380		0.05	0.08	1.54
Notch 2 (Cleaved-Asp1733)	1.09	Notch 2 (Cleaved-Asp1733)	271	236		0.05	0.01	0.96
HDAC6	1.09	HDAC6	282	245		0.04	0.03	1.00
MAPK10	1.09	MAPK10	492	427		0.06	0.09	1.74
MRC2	1.09	MRC2	179	156		0.06	0.02	0.63
SORL1	1.09	SORL1	247	214		0.14	0.09	0.87
CDC2	1.09	CDC2	292	254		0.08	0.03	1.03
HDAC10	1.09	HDAC10	262	227		0.03	0.09	0.92
Collagen I alpha2	1.09	Collagen I alpha2	235	204		0.04	0.08	0.83
MUC13	1.09	MUC13	151	131		0.01	0.05	0.53
TRADD	1.09	TRADD	316	274		0.03	0.10	1.12
MMP-3	1.09	MMP-3	278	241		0.10	0.08	0.98
Cytochrome P450 1A2	1.09	Cytochrome P450 1A2	237	205		0.06	0.19	0.84
Prostate Apoptosis Response protein-4	1.09	Prostate Apoptosis Response protein-4	263	228		0.02	0.00	0.93
NT	1.09	NT	229	198		0.06	0.11	0.81
COX11	1.09	COX11	307	266		0.03	0.14	1.08
CDH10	1.09	CDH10	378	327		0.11	0.10	1.33

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array			Median Signal	283	225			
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
			Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
BIM	1.09	BIM	348	301	0.01	0.06	1.23	1.34
DNA Polymerase lambda	1.09	DNA Polymerase lambda	178	154	0.01	0.07	0.63	0.68
Keratin 7	1.09	Keratin 7	240	208	0.05	0.09	0.85	0.92
TNK1	1.09	TNK1	203	176	0.03	0.04	0.72	0.78
CA6	1.09	CA6	236	204	0.09	0.08	0.83	0.91
EFNA2	1.09	EFNA2	221	191	0.04	0.12	0.78	0.85
RABEP2	1.09	RABEP2	463	400	0.02	0.01	1.63	1.78
HCK	1.09	HCK	158	136	0.00	0.07	0.56	0.61
TUSC2	1.09	TUSC2	234	202	0.20	0.02	0.83	0.90
CHK2	1.09	CHK2	165	142	0.00	0.12	0.58	0.63
KAP0	1.09	KAP0	362	312	0.08	0.02	1.28	1.39
BARD1	1.09	BARD1	196	169	0.04	0.01	0.69	0.75
MER	1.09	MER	138	119	0.01	0.13	0.49	0.53
SIRPG	1.09	SIRPG	297	256	0.12	0.07	1.05	1.14
CA13	1.08	CA13	322	277	0.03	0.03	1.14	1.23
PIAS3	1.08	PIAS3	256	220	0.01	0.10	0.90	0.98
SLC9A9	1.08	SLC9A9	319	275	0.09	0.10	1.13	1.22
GADD45GIP1	1.08	GADD45GIP1	308	265	0.06	0.10	1.09	1.18
14-3-3 epsilon	1.08	14-3-3 epsilon	204	176	0.03	0.08	0.72	0.78
GABA-B Receptor	1.08	GABA-B Receptor	279	240	0.12	0.06	0.99	1.07
XRCC4	1.08	XRCC4	329	283	0.11	0.11	1.16	1.26
LAMC3	1.08	LAMC3	236	203	0.08	0.08	0.83	0.90
BST2	1.08	BST2	186	160	0.09	0.06	0.66	0.71
CD18 (ITGB2)	1.08	CD18 (ITGB2)	203	174	0.02	0.15	0.72	0.77
WASF3	1.08	WASF3	464	399	0.14	0.13	1.64	1.77
CD97beta (Cleaved-Ser531)	1.08	CD97beta (Cleaved-Ser531)	230	197	0.03	0.07	0.81	0.88
Histone H3 (Acetyl-Lys23)	1.08	Histone H3 (Acetyl-Lys23)	297	255	0.17	0.20	1.05	1.13
Guanylate Cyclase beta	1.08	Guanylate Cyclase beta	293	251	0.06	0.00	1.03	1.12
Octamer-binding transcription factor 6	1.08	Octamer-binding transcription factor 6	309	265	0.01	0.06	1.09	1.18
PRKX	1.08	PRKX	270	231	0.06	0.07	0.95	1.03
ATBP3	1.08	ATBP3	574	492	0.15	0.02	2.03	2.19
Parathyroid Hormone	1.08	Parathyroid Hormone	315	270	0.01	0.06	1.11	1.20
ABHD4	1.08	ABHD4	206	176	0.13	0.07	0.73	0.78
TNF14	1.08	TNF14	223	191	0.07	0.06	0.79	0.85
ARSK	1.08	ARSK	435	372	0.10	0.25	1.54	1.66
TGF beta Receptor II	1.08	TGF beta Receptor II	354	303	0.05	0.08	1.25	1.35
Dynamin-2	1.08	Dynamin-2	132	113	0.11	0.01	0.46	0.50
Keratin 8	1.08	Keratin 8	294	251	0.00	0.07	1.04	1.12
PHLA1	1.08	PHLA1	218	186	0.03	0.05	0.77	0.83
NEDD8	1.08	NEDD8	251	215	0.06	0.06	0.89	0.95
Caspase 10	1.08	Caspase 10	450	385	0.00	0.06	1.59	1.71
DAK	1.08	DAK	254	217	0.02	0.01	0.90	0.97
MYC	1.08	MYC	192	164	0.07	0.01	0.68	0.73
Influenza B virus Nucleoprotein	1.08	Influenza B virus Nucleoprotein	141	120	0.01	0.04	0.50	0.53
MART-1	1.08	MART-1	383	327	0.00	0.13	1.35	1.45
Ubiquitin	1.07	Ubiquitin	304	260	0.08	0.10	1.07	1.15
MOK	1.07	MOK	202	172	0.00	0.07	0.71	0.77
ADH7	1.07	ADH7	178	152	0.08	0.07	0.63	0.67
POLE1	1.07	POLE1	229	195	0.05	0.15	0.81	0.87
Cytochrome P450 24A1	1.07	Cytochrome P450 24A1	338	288	0.16	0.10	1.19	1.28
alpha hCG	1.07	alpha hCG	126	108	0.06	0.10	0.45	0.48
CDCP1	1.07	CDCP1	160	137	0.02	0.02	0.57	0.61
FRK	1.07	FRK	218	186	0.00	0.05	0.77	0.83
ATG4B	1.07	ATG4B	289	246	0.07	0.02	1.02	1.09

Antibody Array Assay Results		Assay Data		
Signaling Explorer Antibody Array				
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
EDD	1.07	EDD	316	269
FRS3	1.07	FRS3	265	226
SERC2	1.07	SERC2	288	245
CPM	1.07	CPM	253	215
SLC25A6	1.07	SLC25A6	192	163
PPRC1	1.07	PPRC1	249	212
SENP8	1.07	SENP8	366	312
DNA Polymerase zeta	1.07	DNA Polymerase zeta	292	249
USP24	1.07	USP24	181	154
Keratin 18	1.07	Keratin 18	388	330
PAK2	1.07	PAK2	167	142
CPN1	1.07	CPN1	234	199
MDM2	1.07	MDM2	330	281
SPINK6	1.07	SPINK6	220	187
SERC3	1.07	SERC3	249	212
PRPF19	1.07	PRPF19	189	161
CHST10	1.07	CHST10	216	183
LH	1.07	LH	186	158
RAB5C	1.07	RAB5C	199	169
NF1	1.07	NF1	347	295
RET	1.07	RET	142	121
Cytochrome P450 4F2	1.07	Cytochrome P450 4F2	225	191
MCM2	1.07	MCM2	225	191
ILKAP	1.07	ILKAP	258	219
CDC40	1.07	CDC40	205	174
Fra-2	1.07	Fra-2	399	339
Claudin 7	1.07	Claudin 7	464	394
CA125	1.07	CA125	112	95
AMACR	1.07	AMACR	226	191
p300	1.07	p300	324	274
TACC1	1.07	TACC1	248	210
5-HT-1F	1.07	5-HT-1F	206	174
Cytochrome P450 3A43	1.07	Cytochrome P450 3A43	209	177
Myeloperoxidase	1.07	Myeloperoxidase	228	193
NGFR	1.07	NGFR	182	154
ADD2	1.07	ADD2	234	198
LILRA1	1.06	LILRA1	172	145
14-3-3 gamma	1.06	14-3-3 gamma	214	181
YAP	1.06	YAP	201	170
GGH	1.06	GGH	249	211
EIF4G2	1.06	EIF4G2	291	246
FMN2	1.06	FMN2	226	191
TAF4	1.06	TAF4	187	158
HGH	1.06	HGH	158	133
MMP-16	1.06	MMP-16	264	223
5-HT-3A	1.06	5-HT-3A	196	165
RAD50	1.06	RAD50	196	165
ITIH1 (Cleaved-Asp672)	1.06	ITIH1 (Cleaved-Asp672)	141	119
LYN	1.06	LYN	135	114
TNXB	1.06	TNXB	163	138
Octamer-binding transcription factor 3	1.06	Octamer-binding transcription factor 3	272	229
Cullin 1	1.06	Cullin 1	3968	3346
Lck	1.06	Lck	150	127
EEF1G	1.06	EEF1G	185	156

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.07	0.02
0.07	0.05
0.06	0.07
0.03	0.01
0.01	0.00
0.01	0.00
0.02	0.14
0.03	0.19
0.02	0.06
0.00	0.13
0.07	0.00
0.05	0.01
0.04	0.08
0.12	0.05
0.09	0.06
0.08	0.03
0.11	0.05
0.07	0.00
0.12	0.14
0.01	0.11
0.01	0.03
0.05	0.12
0.05	0.29
0.02	0.07
0.04	0.05
0.11	0.16
0.03	0.00
0.04	0.07
0.02	0.07
0.13	0.02
0.02	0.05
0.04	0.11
0.17	0.12
0.01	0.06
0.08	0.04
0.00	0.03
0.05	0.06
0.02	0.00
0.00	0.10
0.12	0.08
0.01	0.14
0.02	0.05
0.04	0.05
0.06	0.05
0.15	0.05
0.00	0.12
0.11	0.03
0.05	0.00
0.01	0.01
0.04	0.01
0.01	0.01
0.10	0.06
0.04	0.07
0.05	0.04

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
1.11	1.20
0.93	1.00
1.02	1.09
0.89	0.96
0.68	0.73
0.88	0.94
1.29	1.39
1.03	1.11
0.64	0.69
1.37	1.47
0.59	0.63
0.83	0.88
1.17	1.25
0.78	0.83
0.88	0.94
0.67	0.71
0.76	0.81
0.66	0.70
0.70	0.75
1.23	1.31
0.50	0.54
0.79	0.85
0.79	0.85
0.91	0.97
0.72	0.77
1.41	1.51
1.64	1.75
0.39	0.42
0.80	0.85
1.14	1.22
0.88	0.93
0.73	0.77
0.74	0.79
0.80	0.86
0.64	0.69
0.83	0.88
0.61	0.65
0.75	0.80
0.71	0.75
0.88	0.94
1.03	1.09
0.80	0.85
0.66	0.70
0.56	0.59
0.93	0.99
0.69	0.73
0.69	0.73
0.50	0.53
0.48	0.51
0.58	0.61
0.96	1.02
14.02	14.89
0.53	0.56
0.65	0.69

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array			Median Signal	283	225			
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
			Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
ABHD11	1.06	ABHD11	169	143	0.09	0.01	0.60	0.63
Involucrin	1.06	Involucrin	388	327	0.14	0.04	1.37	1.45
ALDH3B1	1.06	ALDH3B1	169	142	0.09	0.05	0.60	0.63
PKM2	1.06	PKM2	172	145	0.09	0.00	0.61	0.64
CKI-gamma1	1.06	CKI-gamma1	165	139	0.02	0.01	0.58	0.62
RAD51L1	1.06	RAD51L1	165	139	0.09	0.02	0.58	0.62
COX15	1.06	COX15	222	187	0.07	0.19	0.78	0.83
SLCO1A2	1.06	SLCO1A2	178	150	0.02	0.05	0.63	0.67
SLC39A7	1.06	SLC39A7	168	141	0.02	0.01	0.59	0.63
CARKL	1.06	CARKL	183	154	0.11	0.06	0.65	0.69
MUSK	1.06	MUSK	148	125	0.00	0.02	0.52	0.55
Collagen XX alpha1	1.06	Collagen XX alpha1	252	212	0.09	0.07	0.89	0.94
HAT	1.06	HAT	308	259	0.11	0.07	1.09	1.15
beta hCG	1.06	beta hCG	242	203	0.08	0.17	0.85	0.90
KCNK4	1.06	KCNK4	241	203	0.04	0.09	0.85	0.90
ADCY7	1.06	ADCY7	175	147	0.11	0.02	0.62	0.65
CD2 Tail-binding	1.06	CD2 Tail-binding	216	181	0.02	0.02	0.76	0.81
SLC5A2	1.06	SLC5A2	281	236	0.02	0.10	0.99	1.05
RHOBTB3	1.06	RHOBTB3	234	197	0.02	0.03	0.83	0.87
PYK2 (FAK2)	1.06	PYK2 (FAK2)	159	134	0.04	0.12	0.56	0.59
RASH/RASK	1.06	RASH/RASK	332	279	0.26	0.10	1.17	1.24
DNAJB4	1.06	DNAJB4	245	206	0.03	0.02	0.87	0.91
MAP2K4	1.06	MAP2K4	292	245	0.26	0.00	1.03	1.09
JAK1	1.06	JAK1	202	169	0.00	0.03	0.71	0.75
TUSC3	1.06	TUSC3	257	216	0.01	0.04	0.91	0.96
BUB1B	1.06	BUB1B	211	177	0.01	0.06	0.74	0.79
Dysferlin	1.06	Dysferlin	443	371	0.03	0.08	1.56	1.65
MUTYH	1.06	MUTYH	513	430	0.01	0.00	1.81	1.91
BCA3	1.06	BCA3	155	130	0.05	0.01	0.55	0.58
DNA Polymerase beta	1.06	DNA Polymerase beta	297	249	0.04	0.03	1.05	1.11
PAR4	1.06	PAR4	124	104	0.04	0.03	0.44	0.46
ELOVL4	1.06	ELOVL4	216	181	0.09	0.02	0.76	0.81
E2F4	1.06	E2F4	343	287	0.10	0.05	1.21	1.28
PPGB (32k,Cleaved-Arg326)	1.05	PPGB (32k,Cleaved-Arg326)	207	173	0.02	0.20	0.73	0.77
SPTBN1	1.05	SPTBN1	216	181	0.02	0.04	0.76	0.80
RAB37	1.05	RAB37	339	284	0.04	0.13	1.20	1.26
ERCC5	1.05	ERCC5	252	211	0.07	0.06	0.89	0.94
Thyroid Hormone Receptor beta	1.05	Thyroid Hormone Receptor beta	295	247	0.03	0.01	1.04	1.10
COX19	1.05	COX19	285	239	0.06	0.10	1.01	1.06
Cyclin A	1.05	Cyclin A	401	336	0.01	0.02	1.42	1.49
RAN	1.05	RAN	309	259	0.08	0.01	1.09	1.15
CD55	1.05	CD55	554	463	0.03	0.08	1.96	2.06
ABHD14A	1.05	ABHD14A	186	156	0.08	0.02	0.66	0.69
CFAB Bb (Cleaved-Lys260)	1.05	CFAB Bb (Cleaved-Lys260)	195	163	0.04	0.12	0.69	0.73
p63	1.05	p63	280	234	0.08	0.02	0.99	1.04
HSP40	1.05	HSP40	453	379	0.02	0.04	1.60	1.68
GAPDH	1.05	GAPDH	386	322	0.05	0.05	1.36	1.43
Laminin	1.05	Laminin	173	145	0.02	0.05	0.61	0.64
MRCKB	1.05	MRCKB	215	180	0.09	0.03	0.76	0.80
BAD (Cleaved-Asp71)	1.05	BAD (Cleaved-Asp71)	242	202	0.03	0.24	0.86	0.90
TGF beta1	1.05	TGF beta1	251	210	0.00	0.12	0.89	0.93
MADD	1.05	MADD	197	164	0.10	0.14	0.69	0.73
Keratin 16	1.05	Keratin 16	266	222	0.01	0.11	0.94	0.99
SAA4	1.05	SAA4	145	121	0.03	0.02	0.51	0.54

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array			Median Signal	283	225			
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
			Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
BMP8A	1.05	BMP8A	220	183	0.17	0.08	0.78	0.81
TUBGCP5	1.05	TUBGCP5	277	231	0.05	0.06	0.98	1.03
CD247 (CD32)	1.05	CD247 (CD32)	132	110	0.04	0.06	0.47	0.49
CD31	1.05	CD31	144	120	0.03	0.06	0.51	0.53
MMP-13	1.05	MMP-13	384	320	0.02	0.09	1.36	1.42
MMP-8	1.05	MMP-8	399	333	0.02	0.10	1.41	1.48
Collagen XXIII alpha1	1.05	Collagen XXIII alpha1	294	245	0.04	0.07	1.04	1.09
KIAA1967	1.05	KIAA1967	219	182	0.04	0.09	0.77	0.81
NKX26	1.05	NKX26	189	157	0.06	0.02	0.67	0.70
Collagen III	1.05	Collagen III	820	683	0.10	0.04	2.90	3.04
RAB38	1.05	RAB38	259	216	0.02	0.24	0.92	0.96
CD253	1.05	CD253	310	258	0.05	0.01	1.09	1.15
Octamer-binding transcription factor 2	1.05	Octamer-binding transcription factor 2	301	250	0.04	0.01	1.06	1.11
GADD153	1.05	GADD153	390	324	0.06	0.01	1.38	1.44
GPR120	1.05	GPR120	443	368	0.09	0.03	1.56	1.64
LRRK1	1.05	LRRK1	235	195	0.04	0.04	0.83	0.87
POLDIP3	1.05	POLDIP3	327	272	0.00	0.01	1.15	1.21
Collagen IV alpha4	1.05	Collagen IV alpha4	229	190	0.06	0.09	0.81	0.85
DOK7	1.05	DOK7	297	247	0.10	0.13	1.05	1.10
PPP1R8	1.05	PPP1R8	225	187	0.06	0.02	0.80	0.83
CA14	1.05	CA14	240	199	0.01	0.09	0.85	0.89
DDR2	1.05	DDR2	157	130	0.06	0.05	0.55	0.58
Cytochrome P450 3A7	1.05	Cytochrome P450 3A7	186	155	0.08	0.09	0.66	0.69
TPD52	1.05	TPD52	298	248	0.01	0.01	1.05	1.10
FA13A (Cleaved-Gly39)	1.05	FA13A (Cleaved-Gly39)	207	172	0.12	0.02	0.73	0.76
GPR174	1.05	GPR174	159	132	0.00	0.04	0.56	0.59
CDKL1	1.05	CDKL1	209	174	0.06	0.00	0.74	0.77
PARP	1.05	PARP	127	105	0.01	0.04	0.45	0.47
STEAP4	1.04	STEAP4	252	209	0.02	0.05	0.89	0.93
Collagen IX alpha3	1.04	Collagen IX alpha3	278	230	0.02	0.04	0.98	1.02
Gastrin	1.04	Gastrin	245	203	0.01	0.02	0.86	0.90
POLD3	1.04	POLD3	201	166	0.05	0.04	0.71	0.74
EPN3	1.04	EPN3	230	190	0.09	0.07	0.81	0.85
ITGA7 (light chain,Cleaved-Glu959)	1.04	ITGA7 (light chain,Cleaved-Glu959)	288	238	0.02	0.15	1.02	1.06
CST9L	1.04	CST9L	180	149	0.06	0.09	0.64	0.66
MAP4K6	1.04	MAP4K6	215	178	0.03	0.00	0.76	0.79
PIAS4	1.04	PIAS4	324	268	0.00	0.02	1.14	1.19
TENS3	1.04	TENS3	269	223	0.04	0.01	0.95	0.99
hCG	1.04	hCG	185	153	0.04	0.07	0.65	0.68
CDH2	1.04	CDH2	304	251	0.02	0.03	1.07	1.12
APOL1	1.04	APOL1	211	175	0.11	0.04	0.75	0.78
Mlx	1.04	Mlx	220	182	0.00	0.01	0.78	0.81
IGF 1R	1.04	IGF 1R	159	131	0.00	0.02	0.56	0.58
Insulin	1.04	Insulin	265	219	0.06	0.13	0.93	0.97
NCOA7	1.04	NCOA7	215	178	0.09	0.02	0.76	0.79
SHC3	1.04	SHC3	204	168	0.09	0.00	0.72	0.75
ABHD12	1.04	ABHD12	206	170	0.14	0.05	0.73	0.76
SKP2/p45	1.04	SKP2/p45	328	271	0.03	0.01	1.16	1.20
XRCC3	1.04	XRCC3	200	165	0.15	0.01	0.70	0.73
ARHGEF9	1.04	ARHGEF9	194	160	0.10	0.10	0.68	0.71
SENP1	1.04	SENP1	544	448	0.05	0.04	1.92	1.99
THRB (AP2,Cleaved-Arg327)	1.04	THRB (AP2,Cleaved-Arg327)	341	281	0.09	0.03	1.20	1.25
SPTBN5	1.04	SPTBN5	168	138	0.09	0.07	0.59	0.61
B-RAF	1.04	B-RAF	224	185	0.06	0.11	0.79	0.82

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array								
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
p50 Dynaminin	1.04	p50 Dynaminin	360	297	0.00	0.01	1.27	1.32
XPF	1.04	XPF	325	268	0.07	0.10	1.15	1.19
HDAC3	1.04	HDAC3	379	312	0.01	0.13	1.34	1.39
ACTR3	1.04	ACTR3	184	151	0.04	0.00	0.65	0.67
CD14	1.04	CD14	198	163	0.08	0.12	0.70	0.72
EPCAM	1.04	EPCAM	119	98	0.03	0.07	0.42	0.43
EPHA1	1.04	EPHA1	338	278	0.02	0.08	1.19	1.24
STMN4	1.04	STMN4	183	151	0.02	0.01	0.65	0.67
CIB1	1.04	CIB1	152	125	0.07	0.08	0.54	0.56
HDAC9	1.04	HDAC9	296	243	0.01	0.10	1.04	1.08
FABP4	1.04	FABP4	135	111	0.04	0.18	0.48	0.49
DNA Polymerase alpha	1.04	DNA Polymerase alpha	222	183	0.03	0.02	0.78	0.81
LATH	1.03	LATH	416	342	0.29	0.21	1.47	1.52
GPR152	1.03	GPR152	261	215	0.13	0.08	0.92	0.95
Cyclin F	1.03	Cyclin F	691	567	0.06	0.02	2.44	2.52
PIK3R5	1.03	PIK3R5	201	165	0.06	0.10	0.71	0.73
p14 ARF	1.03	p14 ARF	366	300	0.08	0.04	1.29	1.33
14-3-3 eta	1.03	14-3-3 eta	229	188	0.02	0.08	0.81	0.83
DOK4	1.03	DOK4	192	158	0.02	0.05	0.68	0.70
PDGFR alpha	1.03	PDGFR alpha	405	332	0.02	0.02	1.43	1.47
ZADH1	1.03	ZADH1	169	139	0.02	0.07	0.60	0.62
Ku70	1.03	Ku70	272	223	0.05	0.06	0.96	0.99
R-spondin 1	1.03	R-spondin 1	130	107	0.03	0.02	0.46	0.47
PDGFR beta	1.03	PDGFR beta	141	116	0.02	0.07	0.50	0.51
CDKA2	1.03	CDKA2	227	186	0.00	0.01	0.80	0.83
MAP2K2 (MEK2)	1.03	MAP2K2 (MEK2)	133	109	0.03	0.06	0.47	0.48
LHR2A	1.03	LHR2A	271	222	0.02	0.04	0.96	0.99
PDK2	1.03	PDK2	284	233	0.07	0.07	1.00	1.03
DNAJB11	1.03	DNAJB11	256	210	0.17	0.03	0.90	0.93
NCOA3	1.03	NCOA3	206	169	0.08	0.01	0.73	0.75
BAGE4	1.03	BAGE4	236	193	0.02	0.06	0.83	0.86
CNN2	1.03	CNN2	252	206	0.04	0.11	0.89	0.92
LILRA2	1.03	LILRA2	192	157	0.11	0.00	0.68	0.70
BUB3	1.03	BUB3	235	192	0.07	0.07	0.83	0.85
CPB2	1.03	CPB2	235	192	0.05	0.05	0.83	0.85
ELOVL1	1.03	ELOVL1	210	172	0.11	0.05	0.74	0.76
KLHL3	1.03	KLHL3	207	169	0.05	0.00	0.73	0.75
APAF-1-ALT	1.03	APAF-1-ALT	343	280	0.02	0.00	1.21	1.25
MAP3KL4	1.03	MAP3KL4	708	578	0.07	0.05	2.50	2.57
DGKH	1.03	DGKH	261	213	0.13	0.13	0.92	0.95
COX7S/A2	1.03	COX7S/A2	283	231	0.02	0.12	1.00	1.03
CAMK5	1.03	CAMK5	228	186	0.06	0.03	0.80	0.83
TBP	1.03	TBP	227	185	0.07	0.05	0.80	0.82
S100 A1	1.03	S100 A1	437	356	0.03	0.01	1.54	1.58
CHST6	1.03	CHST6	270	220	0.03	0.04	0.95	0.98
GSK3 alpha	1.03	GSK3 alpha	135	110	0.01	0.03	0.48	0.49
IL-10	1.02	IL-10	175	142	0.05	0.01	0.62	0.63
Keratin 20	1.02	Keratin 20	298	242	0.10	0.04	1.05	1.08
LDOC1L	1.02	LDOC1L	300	244	0.02	0.02	1.06	1.09
GCNT7	1.02	GCNT7	279	227	0.05	0.02	0.98	1.01
CDCA7	1.02	CDCA7	305	248	0.10	0.07	1.08	1.10
mGluR7	1.02	mGluR7	375	305	0.08	0.07	1.32	1.35
BUB1	1.02	BUB1	270	220	0.10	0.04	0.95	0.98
PLA2G4D	1.02	PLA2G4D	289	235	0.00	0.06	1.02	1.04

Antibody Array Assay Results		Assay Data		
Signaling Explorer Antibody Array				
		Median Signal	283	225
Protein List	Fold Change between Samples Smaller Sample/Bigger Sample	Protein List	Average Signal of Replicate Spots Bigger SampleSmaller Sample	
ARHGEF12	1.02	ARHGEF12	267	217
RASSF6	1.02	RASSF6	221	180
MMP-1	1.02	MMP-1	421	342
GPRIN1	1.02	GPRIN1	298	242
TNF11	1.02	TNF11	298	242
Hepatitis B Surface Antigen	1.02	Hepatitis B Surface Antigen	168	136
SVOP	1.02	SVOP	168	136
PAR1	1.02	PAR1	593	481
ACVL1	1.02	ACVL1	178	145
Cytochrome P450 27A1	1.02	Cytochrome P450 27A1	332	270
KDR (VEGFR2)	1.02	KDR (VEGFR2)	120	97
SLU7	1.02	SLU7	258	209
MMP-15	1.02	MMP-15	292	237
SHIP1	1.02	SHIP1	528	429
DOK3	1.02	DOK3	252	205
CEBPE	1.02	CEBPE	533	433
EMR2	1.02	EMR2	188	153
GRK5	1.02	GRK5	207	168
Calcyclin (S100A6)	1.02	Calcyclin (S100A6)	238	193
NSG2	1.02	NSG2	230	186
USP53	1.02	USP53	203	165
FAKD1	1.02	FAKD1	216	175
AP2C	1.02	AP2C	248	201
GPR18	1.02	GPR18	205	166
PARP3	1.02	PARP3	155	126
C9	1.02	C9	533	432
Stefin B	1.02	Stefin B	286	232
NFRKB	1.02	NFRKB	255	206
LW-1	1.02	LW-1	181	147
CRP	1.02	CRP	171	138
HOXB2	1.02	HOXB2	186	151
S100B	1.02	S100B	134	108
SLC4A8/10	1.02	SLC4A8/10	181	146
RSK1 (p90 RSK)	1.02	RSK1 (p90 RSK)	139	112
Collagen VI alpha3	1.02	Collagen VI alpha3	243	197
PLK2	1.02	PLK2	350	283
ZHX2	1.02	ZHX2	248	201
Calnexin	1.02	Calnexin	180	146
IPKA	1.02	IPKA	282	228
ROR1	1.02	ROR1	209	169
Angiopoietin-1	1.02	Angiopoietin-1	151	122
CD154 (sCD40-Ligand)	1.02	CD154 (sCD40-Ligand)	115	93
ATPAF2	1.02	ATPAF2	273	220
CST1	1.02	CST1	197	159
Akt	1.02	Akt	311	251
Septin-2	1.02	Septin-2	253	204
KLKB1 (heavy chain,Cleaved-Arg390)	1.02	KLKB1 (heavy chain,Cleaved-Arg390)	635	512
4-Mar	1.01	4-Mar	201	162
TSH1	1.01	TSH1	278	224
5-HT-2C	1.01	5-HT-2C	226	182
ELOVL3	1.01	ELOVL3	249	201

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.06	0.08
0.04	0.21
0.02	0.13
0.02	0.05
0.05	0.11
0.01	0.00
0.06	0.01
0.17	0.29
0.01	0.06
0.03	0.11
0.01	0.09
0.02	0.08
0.22	0.08
0.01	0.02
0.12	0.07
0.03	0.09
0.01	0.02
0.03	0.07
0.07	0.02
0.08	0.13
0.08	0.04
0.03	0.12
0.05	0.07
0.05	0.07
0.06	0.02
0.13	0.00
0.06	0.10
0.03	0.02
0.18	0.04
0.08	0.18
0.11	0.03
0.04	0.03
0.04	0.05
0.07	0.04
0.02	0.04
0.03	0.06
0.03	0.08
0.09	0.05
0.02	0.00
0.02	0.13
0.23	0.01
0.04	0.04
0.03	0.01
0.08	0.20
0.02	0.05
0.04	0.03
0.20	0.06
0.04	0.05
0.04	0.05
0.03	0.01
0.08	0.10

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.94	0.97
0.78	0.80
1.49	1.52
1.05	1.08
1.05	1.08
0.59	0.61
0.59	0.61
2.09	2.14
0.63	0.64
1.17	1.20
0.42	0.43
0.91	0.93
1.03	1.05
1.87	1.91
0.89	0.91
1.88	1.92
0.66	0.68
0.73	0.75
0.84	0.86
0.81	0.83
0.72	0.73
0.76	0.78
0.87	0.89
0.72	0.74
0.55	0.56
1.88	1.92
1.01	1.03
0.90	0.92
0.64	0.65
0.60	0.61
0.66	0.67
0.47	0.48
0.64	0.65
0.49	0.50
0.86	0.87
1.24	1.26
0.88	0.89
0.64	0.65
0.99	1.01
0.74	0.75
0.53	0.54
0.40	0.41
0.96	0.98
0.70	0.71
1.10	1.12
0.89	0.91
2.24	2.28
0.71	0.72
0.98	1.00
0.80	0.81
0.88	0.89

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array								
			Median Signal	283	225			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots			Coefficient of Variation for Replicates		Data Normalized to Median Signal
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample	Bigger Sample
Urocortin	1.01	Urocortin	270	217		0.01	0.06	0.95
FAM84B	1.01	FAM84B	257	207		0.14	0.05	0.91
PLA2G4C	1.01	PLA2G4C	259	209		0.04	0.21	0.92
HLA-DOA	1.01	HLA-DOA	180	145		0.05	0.03	0.93
Histone 1F0	1.01	Histone 1F0	485	390		0.02	0.09	0.63
CBR3	1.01	CBR3	228	184		0.06	0.03	1.71
C1S (heavy chain,Cleaved-Arg437)	1.01	C1S (heavy chain,Cleaved-Arg437)	354	285		0.06	0.07	0.81
AIFM2	1.01	AIFM2	256	206		0.09	0.05	1.25
GNL3L	1.01	GNL3L	159	128		0.07	0.03	0.90
PTK6 (breast tumor kinase)	1.01	PTK6 (breast tumor kinase)	118	95		0.02	0.08	0.56
ZAP70	1.01	ZAP70	120	97		0.02	0.05	0.42
RFPL4A	1.01	RFPL4A	225	181		0.09	0.14	0.42
LPL	1.01	LPL	151	121		0.03	0.14	0.42
FOXB1/2	1.01	FOXB1/2	265	213		0.00	0.10	0.79
DJ-1	1.01	DJ-1	436	350		0.00	0.03	0.53
Cytochrome P450 2W1	1.01	Cytochrome P450 2W1	499	401		0.07	0.08	0.94
SIAH1	1.01	SIAH1	247	198		0.01	0.01	1.54
6-Phosphofructo-2-Kinase	1.01	6-Phosphofructo-2-Kinase	310	249		0.04	0.11	1.76
HER2	1.01	HER2	310	249		0.05	0.09	0.87
DCC	1.01	DCC	219	176		0.18	0.00	1.10
DOK6	1.01	DOK6	290	233		0.00	0.03	1.10
A26C2/3	1.01	A26C2/3	267	214		0.05	0.11	1.11
LIMK1	1.01	LIMK1	236	190		0.02	0.05	1.10
EPN2	1.01	EPN2	264	212		0.07	0.02	1.11
PIGH	1.01	PIGH	264	212		0.19	0.05	0.77
Gamma-glutamyltransferase 4 (heavy chain, Cleaved)	1.01	Gamma-glutamyltransferase 4 (heavy chain, Cleaved)	251	201		0.02	0.06	1.02
NEGR1	1.01	NEGR1	251	201		0.04	0.02	0.94
CLDN19	1.01	CLDN19	294	236		0.05	0.00	0.93
MYH14	1.01	MYH14	177	142		0.13	0.09	0.89
HMG20B	1.01	HMG20B	190	152		0.06	0.01	0.89
STEA3	1.01	STEA3	270	217		0.06	0.05	1.04
Synuclein-pan	1.01	Synuclein-pan	356	285		0.01	0.05	0.63
Cytochrome P450 7B1	1.01	Cytochrome P450 7B1	182	146		0.00	0.06	0.67
S100Z	1.01	S100Z	398	319		0.08	0.01	0.95
CD44	1.01	CD44	134	107		0.01	0.01	1.26
Mevalonate Kinase	1.01	Mevalonate Kinase	277	222		0.04	0.06	0.64
Histone H3 (Acetyl-Lys27)	1.01	Histone H3 (Acetyl-Lys27)	257	206		0.07	0.14	1.41
CYB5R3	1.01	CYB5R3	304	244		0.05	0.20	0.47
IL-1 alpha	1.01	IL-1 alpha	108	87		0.04	0.06	0.98
BCLW	1.01	BCLW	354	284		0.06	0.00	0.91
PTEN	1.01	PTEN	128	103		0.01	0.06	1.07
CBLN2	1.01	CBLN2	261	209		0.04	0.07	0.38
GSK3 beta	1.01	GSK3 beta	161	129		0.02	0.07	1.25
DNAL1	1.01	DNAL1	238	191		0.04	0.09	0.45
CATL1 (heavy chain,Cleaved-Thr288)	1.01	CATL1 (heavy chain,Cleaved-Thr288)	246	197		0.08	0.10	0.92
TAF6L	1.01	TAF6L	251	201		0.00	0.11	0.57
DCT	1.01	DCT	193	154		0.07	0.02	0.84
EPHB6	1.01	EPHB6	220	176		0.05	0.04	0.87
RABEP1	1.01	RABEP1	240	192		0.08	0.04	0.89
ITGA5 (heavy chain,Cleaved-Phe42)	1.01	ITGA5 (heavy chain,Cleaved-Phe42)	148	118		0.02	0.01	0.68

Antibody Array Assay Results		Assay Data			
Signaling Explorer Antibody Array					
		Median Signal			
		283225			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	
ULK3	1.01	ULK3	250	200	0.00
5-Mar	1.01	5-Mar	235	188	0.02
ACTN 1/2/3/4	1.01	ACTN 1/2/3/4	235	188	0.02
G3BP2	1.01	G3BP2	319	255	0.02
A1BG	1.01	A1BG	159	127	0.04
JNKK	1.01	JNKK	241	192	0.01
CDCA2	1.01	CDCA2	298	238	0.03
Flt3 ligand	1.01	Flt3 ligand	278	222	0.00
TOP2A	1.00	TOP2A	302	241	0.05
MATK (CTK)	1.00	MATK (CTK)	121	97	0.05
Mucin-14	1.00	Mucin-14	249	199	0.05
TALL-2	1.00	TALL-2	311	248	0.13
HPRT	1.00	HPRT	131	104	0.01
CLK2	1.00	CLK2	187	149	0.02
LEG9	1.00	LEG9	246	196	0.14
MUM1	1.00	MUM1	271	216	0.05
SLC24A4	1.00	SLC24A4	180	143	0.04
AFP	1.00	AFP	1365	1087	0.07
CD10	1.00	CD10	128	102	0.03
2-Mar	1.00	2-Mar	451	359	0.08
RAB7L1	1.00	RAB7L1	284	226	0.07
STAT5A/B	1.00	STAT5A/B	396	315	0.02
CD3EAP	1.00	CD3EAP	456	363	0.11
EPHB2	1.00	EPHB2	290	231	0.07
ATP6V1H	1.00	ATP6V1H	229	182	0.21
Keratin 19	1.00	Keratin 19	305	242	0.01
CHD4	1.00	CHD4	246	196	0.02
Collagen V alpha2	1.00	Collagen V alpha2	239	190	0.05
p19 INK4d	1.00	p19 INK4d	270	215	0.04
ERAB	1.00	ERAB	501	398	0.13
ENDOGL1	1.00	ENDOGL1	241	191	0.04
SLC5A3	1.00	SLC5A3	192	152	0.08
EFNA5	1.00	EFNA5	221	175	0.06
LAMA3	1.00	LAMA3	264	210	0.04
cTnI (TNNI3)	1.00	cTnI (TNNI3)	145	115	0.01
PGP9.5	1.00	PGP9.5	290	230	0.05
IL-8	1.00	IL-8	138	109	0.04
RHG17	1.00	RHG17	287	228	0.13
DFFA	1.00	DFFA	388	308	0.04
Myoglobin	1.00	Myoglobin	154	122	0.01
STAT5A	1.00	STAT5A	229	181	0.03
LDLRAD2	1.00	LDLRAD2	178	141	0.09
Osteopontin	1.00	Osteopontin	350	277	0.07
PCNA	1.00	PCNA	312	247	0.01
DNA-PK	1.00	DNA-PK	436	345	0.05
TUBGCP4	1.00	TUBGCP4	268	212	0.13
CHST2	1.00	CHST2	323	256	0.01
PTTG1	1.00	PTTG1	325	257	0.12
AURKB	1.00	AURKB	127	100	0.04
IKK-gamma	1.00	IKK-gamma	315	249	0.10
PLA2G4E	1.00	PLA2G4E	263	208	0.03
ABHD14B	1.00	ABHD14B	186	147	0.10
ADCY8	1.00	ADCY8	248	196	0.03
Free PSA (KLK3)	1.00	Free PSA (KLK3)	124	98	0.06
				Bigger SampleSmaller Sample	
				0.000.08	
				0.020.07	
				0.020.09	
				0.020.12	
				0.040.04	
				0.010.07	
				0.030.04	
				0.000.02	
				0.050.04	
				0.050.04	
				0.050.00	
				0.130.02	
				0.010.03	
				0.020.03	
				0.140.01	
				0.050.15	
				0.040.00	
				0.070.02	
				0.030.12	
				0.080.15	
				0.070.08	
				0.020.04	
				0.110.08	
				0.070.01	
				0.210.02	
				0.010.08	
				0.020.04	
				0.050.13	
				0.040.04	
				0.130.07	
				0.040.01	
				0.080.11	
				0.060.10	
				0.040.03	
				0.010.04	
				0.050.01	
				0.040.06	
				0.130.05	
				0.040.03	
				0.010.05	
				0.030.01	
				0.090.07	
				0.070.01	
				0.010.04	
				0.050.09	
				0.130.05	
				0.010.04	
				0.120.07	
				0.040.03	
				0.100.03	
				0.030.19	
				0.100.08	
				0.030.01	
				0.060.12	
				Bigger SampleSmaller Sample	
				0.880.89	
				0.830.83	
				0.830.83	
				1.131.13	
				0.560.57	
				0.850.85	
				1.051.06	
				0.980.99	
				1.071.07	
				0.430.43	
				0.880.88	
				1.101.10	
				0.460.46	
				0.660.66	
				0.870.87	
				0.960.96	
				0.630.64	
				4.824.84	
				0.450.45	
				1.591.60	
				1.001.01	
				1.401.40	
				1.611.61	
				1.021.03	
				0.810.81	
				1.081.08	
				0.870.87	
				0.840.84	
				0.950.95	
				1.771.77	
				0.850.85	
				0.680.68	
				0.780.78	
				0.930.93	
				0.510.51	
				1.021.02	
				0.490.48	
				1.011.01	
				1.371.37	
				0.540.54	
				0.810.81	
				0.630.63	
				1.241.23	
				1.101.10	
				1.541.53	
				0.950.94	
				1.141.14	
				1.151.14	
				0.450.44	
				1.111.11	
				0.930.92	
				0.660.65	
				0.880.87	
				0.440.44	

Antibody Array Assay Results

Assay Data

Signaling Explorer Antibody Array

		Median Signal								
		283					225			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots			Coefficient of Variation for Replicates			Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample
ADK	0.99	ADK	391	309		0.00	0.14		1.38	1.37
Serpin A5	0.99	Serpin A5	238	188		0.07	0.05		0.84	0.84
RASSF2	0.99	RASSF2	923	729		0.03	0.03		3.26	3.24
MSH6	0.99	MSH6	281	222		0.00	0.05		0.99	0.99
FGF-1	0.99	FGF-1	105	83		0.01	0.04		0.37	0.37
Integrin beta5	0.99	Integrin beta5	282	223		0.24	0.12		1.00	0.99
Collagen XXV alpha1	0.99	Collagen XXV alpha1	197	155		0.01	0.16		0.69	0.69
EFEMP1	0.99	EFEMP1	258	204		0.00	0.02		0.91	0.91
NRBF2	0.99	NRBF2	239	189		0.00	0.03		0.84	0.84
CER1	0.99	CER1	133	105		0.03	0.07		0.47	0.46
SRC	0.99	SRC	130	103		0.02	0.02		0.46	0.46
FHIT	0.99	FHIT	397	313		0.04	0.10		1.40	1.39
Amylin	0.99	Amylin	376	296		0.08	0.02		1.33	1.32
Histone H2B	0.99	Histone H2B	279	220		0.01	0.02		0.98	0.98
Cytochrome P450 2A6	0.99	Cytochrome P450 2A6	271	214		0.09	0.08		0.96	0.95
SLK	0.99	SLK	219	173		0.06	0.02		0.77	0.77
LAMA5	0.99	LAMA5	217	171		0.06	0.07		0.77	0.76
CBLN1	0.99	CBLN1	301	237		0.04	0.07		1.06	1.05
Collagen XVIII alpha1	0.99	Collagen XVIII alpha1	245	193		0.03	0.07		0.86	0.86
CBP (Acetyl-Lys1535)	0.99	CBP (Acetyl-Lys1535)	186	146		0.07	0.03		0.66	0.65
MAST3	0.99	MAST3	314	247		0.02	0.02		1.11	1.10
RPC8	0.99	RPC8	284	223		0.17	0.07		1.00	0.99
MSH2	0.99	MSH2	544	428		0.21	0.09		1.92	1.90
Elk1	0.99	Elk1	269	212		0.06	0.08		0.95	0.94
CNKR2	0.99	CNKR2	206	162		0.05	0.00		0.73	0.72
Collagen IV alpha3 (Cleaved-Pro1426)	0.99	Collagen IV alpha3 (Cleaved-Pro1426)	220	173		0.08	0.09		0.78	0.77
GABRA6	0.99	GABRA6	236	185		0.12	0.04		0.83	0.82
Caspase 6 (Cleaved-Asp162)	0.99	Caspase 6 (Cleaved-Asp162)	310	244		0.04	0.07		1.10	1.08
EGF	0.99	EGF	138	108		0.10	0.01		0.49	0.48
HSF2	0.99	HSF2	399	313		0.13	0.08		1.41	1.39
Keratin 1 (CK1)	0.99	Keratin 1 (CK1)	124	97		0.01	0.15		0.44	0.43
SH-PTP2	0.99	SH-PTP2	394	309		0.02	0.04		1.39	1.37
Collagen XIX alpha1	0.99	Collagen XIX alpha1	270	212		0.05	0.09		0.95	0.94
SLC17A2	0.99	SLC17A2	175	137		0.08	0.01		0.62	0.61
FES	0.99	FES	305	239		0.01	0.07		1.08	1.06
SIRPB1	0.99	SIRPB1	384	301		0.18	0.01		1.36	1.34
HOXA11/D11	0.99	HOXA11/D11	232	182		0.07	0.01		0.82	0.81
Smad4	0.99	Smad4	200	157		0.05	0.00		0.70	0.70
DNA Polymerase theta	0.99	DNA Polymerase theta	378	297		0.02	0.02		1.34	1.32
Annexin A6	0.99	Annexin A6	404	317		0.04	0.05		1.43	1.41
CATD (light chain,Cleaved-Gly65)	0.99	CATD (light chain,Cleaved-Gly65)	230	180		0.02	0.07		0.81	0.80
MMP15 (Cleaved-Tyr132)	0.99	MMP15 (Cleaved-Tyr132)	197	155		0.10	0.05		0.70	0.69
Collagen IV alpha3	0.99	Collagen IV alpha3	271	213		0.01	0.01		0.96	0.95
CDC25C	0.99	CDC25C	162	127		0.12	0.14		0.57	0.57
CHST8	0.99	CHST8	236	185		0.04	0.02		0.83	0.82
POTE8	0.99	POTE8	317	248		0.04	0.07		1.12	1.10
PTH (Parathyroid Hormone)	0.99	PTH (Parathyroid Hormone)	127	100		0.01	0.11		0.45	0.44
ERK2	0.99	ERK2	139	109		0.04	0.03		0.49	0.48
GATA1	0.99	GATA1	139	109		0.04	0.08		0.49	0.48
MARK2	0.99	MARK2	259	203		0.10	0.09		0.91	0.90
BRI3B	0.99	BRI3B	305	239		0.03	0.06		1.08	1.06
CKI-gamma2	0.99	CKI-gamma2	277	217		0.05	0.00		0.98	0.96
PARP (Cleaved-Asp214)	0.99	PARP (Cleaved-Asp214)	417	327		0.03	0.01		1.47	1.45
IL-6	0.99	IL-6	129	101		0.03	0.06		0.46	0.45
KCNK15	0.99	KCNK15	226	177		0.08	0.07		0.80	0.79

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array			Median Signal	283	225			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
SIX5	0.99	SIX5	184	144	0.12	0.11	0.65	0.64
C3AR1	0.99	C3AR1	246	193	0.02	0.09	0.87	0.86
CHK1	0.99	CHK1	124	97	0.03	0.04	0.44	0.43
Notch 2 (Cleaved-Ala1734)	0.98	Notch 2 (Cleaved-Ala1734)	218	170	0.04	0.07	0.77	0.76
CLCC1	0.98	CLCC1	238	186	0.00	0.11	0.84	0.83
ALDOB	0.98	ALDOB	215	168	0.02	0.13	0.76	0.75
YES1	0.98	YES1	140	109	0.05	0.05	0.49	0.48
Septin-1	0.98	Septin-1	343	268	0.00	0.12	1.21	1.19
TOP3B	0.98	TOP3B	304	238	0.06	0.07	1.07	1.06
CDCA3	0.98	CDCA3	345	270	0.07	0.07	1.22	1.20
CBLN3	0.98	CBLN3	270	211	0.15	0.04	0.95	0.94
BLCAP	0.98	BLCAP	512	400	0.02	0.04	1.81	1.78
JAK3	0.98	JAK3	137	107	0.07	0.05	0.48	0.48
STYK1	0.98	STYK1	183	143	0.03	0.09	0.64	0.63
PARK7	0.98	PARK7	169	132	0.08	0.05	0.60	0.59
Septin-3	0.98	Septin-3	218	170	0.02	0.06	0.77	0.76
IgE	0.98	IgE	143	112	0.01	0.04	0.51	0.50
RPC4	0.98	RPC4	275	214	0.06	0.09	0.97	0.95
IKBKB (IKK beta)	0.98	IKBKB (IKK beta)	127	99	0.04	0.03	0.45	0.44
RPC1	0.98	RPC1	399	311	0.09	0.05	1.41	1.38
MIPT3	0.98	MIPT3	215	168	0.06	0.00	0.76	0.75
FADD	0.98	FADD	312	243	0.10	0.05	1.10	1.08
TNFR4	0.98	TNFR4	271	211	0.05	0.05	0.96	0.94
Collagen IV alpha5	0.98	Collagen IV alpha5	296	230	0.04	0.08	1.04	1.02
CSTF2T	0.98	CSTF2T	262	204	0.03	0.01	0.92	0.91
ABHD12B	0.98	ABHD12B	228	177	0.05	0.02	0.80	0.79
SLC5A6	0.98	SLC5A6	246	191	0.07	0.05	0.87	0.85
CLIC3	0.98	CLIC3	252	196	0.02	0.02	0.89	0.87
LEG7	0.98	LEG7	288	224	0.04	0.10	1.02	1.00
MYST1	0.98	MYST1	131	102	0.01	0.02	0.46	0.45
CKI-alpha1/L	0.98	CKI-alpha1/L	272	212	0.03	0.00	0.96	0.94
BMX (ETK)	0.98	BMX (ETK)	133	103	0.07	0.04	0.47	0.46
CD38	0.98	CD38	256	199	0.17	0.01	0.90	0.89
RTN3	0.98	RTN3	265	206	0.11	0.09	0.93	0.91
CDH4	0.98	CDH4	316	246	0.00	0.01	1.12	1.09
ZP1	0.98	ZP1	204	158	0.14	0.05	0.72	0.70
CLIC4	0.98	CLIC4	284	221	0.00	0.07	1.00	0.98
ALDH1A2	0.98	ALDH1A2	291	226	0.11	0.01	1.03	1.00
Neuropilin (Cleaved-Val33)	0.98	Neuropilin (Cleaved-Val33)	244	189	0.06	0.10	0.86	0.84
AGR3	0.98	AGR3	428	332	0.08	0.03	1.51	1.48
CDH11	0.98	CDH11	214	166	0.01	0.09	0.76	0.74
GPRIN3	0.98	GPRIN3	239	185	0.04	0.05	0.84	0.82
CIB2	0.98	CIB2	294	228	0.03	0.09	1.04	1.01
TUFM	0.98	TUFM	216	168	0.11	0.10	0.76	0.75
C1S	0.98	C1S	232	180	0.08	0.14	0.82	0.80
ADRB1	0.98	ADRB1	336	261	0.03	0.10	1.19	1.16
RDX	0.98	RDX	296	229	0.02	0.08	1.04	1.02
Fibulin 5	0.98	Fibulin 5	136	105	0.06	0.09	0.48	0.47
HLAH	0.98	HLAH	198	153	0.08	0.02	0.70	0.68
Connexin 43	0.98	Connexin 43	446	346	0.26	0.02	1.58	1.54
MEF2C	0.98	MEF2C	193	150	0.03	0.07	0.68	0.67
COX41	0.97	COX41	310	240	0.06	0.01	1.09	1.07
BAGE3	0.97	BAGE3	210	163	0.08	0.08	0.74	0.72
PRKY	0.97	PRKY	195	151	0.04	0.06	0.69	0.67
Ku70/80	0.97	Ku70/80	453	351	0.08	0.11	1.60	1.56
Collagen I alpha2 (Cleaved-Gly1102)	0.97	Collagen I alpha2 (Cleaved-Gly1102)	265	205	0.07	0.07	0.94	0.91

Assay Data

Median Signal	283	225
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Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
0.55	0.53
1.00	0.97
0.45	0.44
0.49	0.48
0.95	0.93
1.13	1.10
1.58	1.54
1.07	1.04
0.47	0.45
0.92	0.90
0.46	0.44
0.42	0.41
0.96	0.93
0.48	0.47
1.19	1.16
0.63	0.62
0.59	0.57
0.96	0.94
0.57	0.55
1.32	1.28
1.05	1.02
1.54	1.49
0.48	0.46
1.61	1.57
1.09	1.06
0.98	0.95
0.57	0.55
0.73	0.71
0.65	0.63
1.00	0.97
0.86	0.84
0.68	0.66
0.94	0.91
1.18	1.15
0.48	0.46
1.36	1.32
1.32	1.27
1.26	1.22
0.63	0.61
0.87	0.84
1.65	1.60
0.93	0.90
1.14	1.11
1.23	1.19
1.45	1.40
0.98	0.95
0.45	0.44
1.74	1.68
0.49	0.47
1.13	1.09
0.85	0.82
0.88	0.85
1.27	1.22
0.71	0.68
0.68	0.66
1.40	1.35

Antibody Array Assay Results

Assay Data

Signaling Explorer Antibody Array

		Median Signal								
		283					225			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Protein List	Coefficient of Variation for Replicates		Protein List	Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample
ADD3	0.96	ADD3	308	235		0.06	0.01		1.09	1.05
ARHGEF3	0.96	ARHGEF3	221	169		0.02	0.05		0.78	0.75
Septin-8	0.96	Septin-8	288	220		0.07	0.00		1.02	0.98
LAMA4	0.96	LAMA4	352	269		0.01	0.07		1.24	1.19
TLE4	0.96	TLE4	440	336		0.13	0.15		1.55	1.49
PIGY	0.96	PIGY	231	176		0.04	0.16		0.81	0.78
Stefin A	0.96	Stefin A	400	305		0.12	0.11		1.41	1.36
EGR1	0.96	EGR1	144	110		0.04	0.03		0.51	0.49
HMGB1	0.96	HMGB1	336	256		0.06	0.02		1.19	1.14
FGR	0.96	FGR	386	295		0.02	0.02		1.36	1.31
p15 INK	0.96	p15 INK	485	370		0.00	0.05		1.71	1.65
STK39	0.96	STK39	194	148		0.00	0.02		0.69	0.66
CA19-9	0.96	CA19-9	175	134		0.15	0.01		0.62	0.59
PRIM1	0.96	PRIM1	337	257		0.12	0.07		1.19	1.14
CD69	0.96	CD69	143	109		0.03	0.07		0.50	0.48
ADA2L	0.96	ADA2L	279	212		0.03	0.07		0.98	0.94
CDH20	0.96	CDH20	293	223		0.00	0.01		1.04	0.99
MCL-1	0.96	MCL-1	136	104		0.10	0.10		0.48	0.46
Claudin 10	0.96	Claudin 10	414	315		0.01	0.04		1.46	1.40
Glucose-6-phosphate isomerase	0.96	Glucose-6-phosphate isomerase	142	108		0.02	0.05		0.50	0.48
FGF-2	0.96	FGF-2	109	83		0.06	0.03		0.38	0.37
ATP2C1	0.96	ATP2C1	182	138		0.00	0.11		0.64	0.61
CPNE8	0.96	CPNE8	359	273		0.12	0.09		1.27	1.21
Calreticulin	0.96	Calreticulin	192	146		0.06	0.12		0.68	0.65
CATZ (Cleaved-Leu62)	0.96	CATZ (Cleaved-Leu62)	275	209		0.03	0.02		0.97	0.93
ARSA	0.96	ARSA	237	180		0.07	0.10		0.84	0.80
DGKK	0.95	DGKK	290	220		0.01	0.04		1.02	0.98
BRCA2	0.95	BRCA2	323	245		0.08	0.14		1.14	1.09
ARHGEF5	0.95	ARHGEF5	354	268		0.02	0.00		1.25	1.19
CRYAB	0.95	CRYAB	139	105		0.03	0.03		0.49	0.47
ELOVL5	0.95	ELOVL5	279	212		0.07	0.02		0.99	0.94
IFN-gamma	0.95	IFN-gamma	126	96		0.07	0.04		0.45	0.42
MAPK9	0.95	MAPK9	322	244		0.06	0.02		1.14	1.09
RORA	0.95	RORA	357	271		0.04	0.02		1.26	1.20
KCNT1	0.95	KCNT1	332	252		0.05	0.02		1.17	1.12
CDKA1	0.95	CDKA1	204	155		0.01	0.06		0.72	0.69
p55CDC	0.95	p55CDC	229	173		0.08	0.03		0.81	0.77
Caspase 3 (Cleaved-Asp175)	0.95	Caspase 3 (Cleaved-Asp175)	301	228		0.03	0.05		1.06	1.01
CDK8	0.95	CDK8	340	257		0.02	0.02		1.20	1.14
AKR1CL2	0.95	AKR1CL2	255	193		0.02	0.05		0.90	0.86
ST6GAL1	0.95	ST6GAL1	302	229		0.04	0.16		1.07	1.02
SERPINB7	0.95	SERPINB7	156	118		0.01	0.04		0.55	0.53
GPR175	0.95	GPR175	154	116		0.00	0.02		0.54	0.52
Retinoid X Receptor gamma	0.95	Retinoid X Receptor gamma	330	249		0.01	0.04		1.16	1.11
Notch 2 (Cleaved-Val1697)	0.95	Notch 2 (Cleaved-Val1697)	235	177		0.13	0.08		0.83	0.79
E2F6	0.95	E2F6	495	374		0.01	0.09		1.75	1.66
UBAC1	0.95	UBAC1	175	132		0.05	0.06		0.62	0.59
CDH8	0.95	CDH8	330	249		0.00	0.07		1.16	1.11
TAF15	0.95	TAF15	307	232		0.00	0.04		1.08	1.03
MDM4	0.95	MDM4	134	101		0.03	0.11		0.47	0.45
UBTD1	0.95	UBTD1	203	153		0.12	0.03		0.72	0.68
Cyclin E1	0.95	Cyclin E1	487	367		0.08	0.05		1.72	1.63
Histone H3 (Acetyl-Lys9)	0.95	Histone H3 (Acetyl-Lys9)	318	240		0.00	0.09		1.12	1.07
MEF2B	0.95	MEF2B	480	362		0.03	0.01		1.70	1.61

Antibody Array Assay Results		Assay Data		
Signaling Explorer Antibody Array				

Antibody Array Assay Results		Assay Data							
Signaling Explorer Antibody Array									
		Median Signal							
		283							
		225							
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots			Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
RHG9	0.93	RHG9	227	168		0.07	0.03	0.80	0.75
RG51	0.93	RG51	319	237		0.09	0.07	1.13	1.05
CKI-alpha	0.93	CKI-alpha	271	201		0.06	0.05	0.96	0.89
Smad1/5/9	0.93	Smad1/5/9	282	209		0.14	0.12	1.00	0.93
LAT3	0.93	LAT3	520	385		0.08	0.12	1.84	1.71
RFWD2	0.93	RFWD2	294	218		0.03	0.06	1.04	0.97
CD8	0.93	CD8	135	100		0.08	0.03	0.48	0.44
CXADR	0.93	CXADR	322	239		0.06	0.13	1.14	1.06
ORCTL-2	0.93	ORCTL-2	330	244		0.07	0.03	1.16	1.09
Caspase 9 (Cleaved-Asp315)	0.93	Caspase 9 (Cleaved-Asp315)	389	288		0.07	0.04	1.37	1.28
SLC6A15	0.93	SLC6A15	362	268		0.08	0.09	1.28	1.19
SDCG1	0.93	SDCG1	380	281		0.19	0.03	1.34	1.25
CD3E	0.93	CD3E	131	97		0.05	0.04	0.46	0.43
MAP4K3	0.93	MAP4K3	202	149		0.07	0.01	0.71	0.66
MYBPC3	0.93	MYBPC3	173	128		0.23	0.13	0.61	0.57
RAB11FIP2	0.93	RAB11FIP2	312	231		0.00	0.04	1.10	1.03
GPR160	0.93	GPR160	266	197		0.16	0.03	0.94	0.87
IKK Alpha	0.93	IKK Alpha	130	96		0.02	0.07	0.46	0.43
ATF3	0.93	ATF3	325	240		0.03	0.00	1.15	1.07
CASP3 (p17,Cleaved-Asp175)	0.93	CASP3 (p17,Cleaved-Asp175)	994	734		0.06	0.00	3.51	3.26
MEKKK 1	0.93	MEKKK 1	307	227		0.02	0.01	1.08	1.01
Cytochrome P450 39A1	0.93	Cytochrome P450 39A1	307	226		0.00	0.03	1.08	1.01
CD45	0.93	CD45	128	94		0.03	0.05	0.45	0.42
CDKL3	0.93	CDKL3	217	160		0.10	0.10	0.77	0.71
RAB3GAP1	0.93	RAB3GAP1	365	269		0.02	0.09	1.29	1.19
MCL1	0.93	MCL1	528	389		0.03	0.02	1.86	1.73
SNCA (alpha-synuclein)	0.93	SNCA (alpha-synuclein)	209	154		0.05	0.12	0.74	0.68
MYH4	0.93	MYH4	197	145		0.24	0.02	0.70	0.65
EGFR	0.93	EGFR	140	103		0.11	0.14	0.49	0.46
E2F2	0.93	E2F2	227	167		0.11	0.08	0.80	0.74
UPF1	0.93	UPF1	375	276		0.11	0.04	1.32	1.23
ATP5G2	0.93	ATP5G2	435	320		0.06	0.10	1.54	1.42
SNAP25	0.93	SNAP25	310	228		0.03	0.03	1.10	1.01
ALDH1B1	0.93	ALDH1B1	282	207		0.04	0.05	0.99	0.92
PIP5K	0.93	PIP5K	312	229		0.09	0.02	1.10	1.02
ABL1	0.93	ABL1	402	296		0.03	0.07	1.42	1.31
Collagen IV alpha3 (Cleaved-Leu1425)	0.93	Collagen IV alpha3 (Cleaved-Leu1425)	279	205		0.09	0.01	0.99	0.91
RAB41	0.92	RAB41	382	281		0.00	0.12	1.35	1.25
Collagen IV alpha2	0.92	Collagen IV alpha2	282	207		0.02	0.01	1.00	0.92
MAPK15	0.92	MAPK15	600	440		0.09	0.19	2.12	1.96
Cytochrome P450 251	0.92	Cytochrome P450 251	387	284		0.01	0.01	1.37	1.26
S6K-alpha6	0.92	S6K-alpha6	237	174		0.06	0.03	0.84	0.77
RBM5	0.92	RBM5	265	194		0.05	0.09	0.93	0.86
ENAH	0.92	ENAH	383	281		0.05	0.09	1.35	1.25
EPHA7	0.92	EPHA7	293	215		0.02	0.05	1.03	0.95
ACTL6A	0.92	ACTL6A	249	183		0.07	0.01	0.88	0.81
CDC7	0.92	CDC7	275	202		0.04	0.04	0.97	0.90
JAK2	0.92	JAK2	137	100		0.08	0.04	0.48	0.44
TAF5L	0.92	TAF5L	350	256		0.03	0.06	1.23	1.14
CATG (Cleaved-Ile21)	0.92	CATG (Cleaved-Ile21)	342	251		0.02	0.07	1.21	1.11
MMP12 (Cleaved-Glu106)	0.92	MMP12 (Cleaved-Glu106)	234	171		0.03	0.09	0.83	0.76
Claudin 4	0.92	Claudin 4	458	335		0.09	0.05	1.62	1.49
3-Mar	0.92	3-Mar	310	227		0.08	0.03	1.09	1.01
ADCK3	0.92	ADCK3	205	150		0.01	0.05	0.72	0.67

Antibody Array Assay Results

Assay Data

Signaling Explorer Antibody Array

Median Signal

283

225

Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample
COT2	0.92	COT2	352	258
Fit-1 (VEGFR1)	0.92	Fit-1 (VEGFR1)	155	113
ARPP21	0.92	ARPP21	318	233
USP6NL	0.92	USP6NL	190	139
Cytochrome c-type Heme Lyase	0.92	Cytochrome c-type Heme Lyase	485	354
5-HT-4	0.92	5-HT-4	278	203
Cytochrome P450 4Z1	0.92	Cytochrome P450 4Z1	345	252
CST2	0.92	CST2	324	237
ITGAV (heavy chain,Cleaved-Lys889)	0.92	ITGAV (heavy chain,Cleaved-Lys889)	211	154
PEZR4	0.92	PEZR4	159	116
WASF4	0.92	WASF4	335	244
SLC28A2	0.92	SLC28A2	205	150
Histone H3 (Acetyl-Lys18)	0.92	Histone H3 (Acetyl-Lys18)	321	234
Cytochrome P450 2C19	0.92	Cytochrome P450 2C19	435	317
GRAH	0.92	GRAH	339	247
AARSD1	0.92	AARSD1	278	203
ACTN alpha-2/3	0.92	ACTN alpha-2/3	383	279
LEG4	0.92	LEG4	291	212
CSK	0.92	CSK	285	207
Rab25	0.92	Rab25	151	110
USP42	0.92	USP42	206	150
CD19	0.92	CD19	138	100
ARHGEF2	0.92	ARHGEF2	323	235
RAB11FIP3	0.92	RAB11FIP3	295	215
CDKL2	0.92	CDKL2	359	261
Dyskerin	0.91	Dyskerin	359	261
NF-kB p65 (Acetyl-Lys310)	0.91	NF-kB p65 (Acetyl-Lys310)	329	239
14-3-3 zeta	0.91	14-3-3 zeta	307	223
RON	0.91	RON	132	96
HOXA6	0.91	HOXA6	197	143
TP53INP2	0.91	TP53INP2	311	226
IL-1 beta	0.91	IL-1 beta	140	102
SLC30A1	0.91	SLC30A1	240	174
Cytochrome P450 3A4/5	0.91	Cytochrome P450 3A4/5	287	208
C1R (light chain,Cleaved-Ile464)	0.91	C1R (light chain,Cleaved-Ile464)	344	249
ATF7	0.91	ATF7	331	240
FGF18	0.91	FGF18	241	174
ADAR1	0.91	ADAR1	441	319
SLC30A4	0.91	SLC30A4	405	293
Adrenergic Receptor alpha-2B	0.91	Adrenergic Receptor alpha-2B	352	255
PC	0.91	PC	240	174
ERN1 (IRE1)	0.91	ERN1 (IRE1)	1930	1395
ACSL6	0.91	ACSL6	224	162
Cullin 3	0.91	Cullin 3	459	332
ADNP	0.91	ADNP	436	315
KSR2	0.91	KSR2	415	300
C140	0.91	C140	268	193
AVEN	0.91	AVEN	280	202
LRP10	0.91	LRP10	223	161
FOXA2	0.91	FOXA2	179	129
KCNJ9	0.91	KCNJ9	335	241
ME3	0.91	ME3	215	155
ATP5G3	0.91	ATP5G3	373	269
5-HT-1A	0.91	5-HT-1A	328	236

Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.02	0.01
0.00	0.04
0.08	0.09
0.11	0.08
0.04	0.06
0.01	0.02
0.02	0.00
0.02	0.07
0.02	0.11
0.00	0.07
0.07	0.03
0.07	0.00
0.17	0.05
0.04	0.06
0.00	0.03
0.02	0.04
0.12	0.14
0.06	0.05
0.02	0.08
0.11	0.12
0.06	0.07
0.03	0.01
0.08	0.03
0.00	0.08
0.05	0.09
0.03	0.02
0.03	0.02
0.06	0.11
0.02	0.11
0.21	0.01
0.04	0.05
0.03	0.01
0.01	0.10
0.07	0.05
0.13	0.01
0.01	0.01
0.04	0.02
0.04	0.01
0.05	0.12
0.10	0.01
0.02	0.05
0.03	0.34
0.09	0.14
0.04	0.02
0.00	0.05
0.06	0.04
0.03	0.16
0.02	0.03
0.09	0.02
0.01	0.12
0.04	0.07
0.06	0.03
0.11	0.07
0.05	0.04

Data Normalized to Median Signal	
Bigger Sample	Smaller Sample
1.24	1.15
0.55	0.50
1.12	1.03
0.67	0.62
1.71	1.58
0.98	0.90
1.22	1.12
1.14	1.05
0.75	0.69
0.56	0.52
1.18	1.09
0.72	0.67
1.13	1.04
1.54	1.41
1.20	1.10
0.98	0.90
1.35	1.24
1.03	0.94
1.01	0.92
0.53	0.49
0.73	0.67
0.49	0.44
1.14	1.04
1.04	0.95
1.27	1.16
1.27	1.16
1.16	1.06
1.08	0.99
0.46	0.42
0.69	0.63
1.10	1.00
0.49	0.45
0.85	0.77
1.01	0.93
1.22	1.11
1.17	1.07
0.85	0.77
1.56	1.42
1.43	1.30
1.24	1.13
0.85	0.77
6.82	6.21
0.79	0.72
1.62	1.47
1.54	1.40
1.47	1.33
0.95	0.86
0.99	0.90
0.79	0.71
0.63	0.57
1.18	1.07
0.76	0.69
1.32	1.19
1.16	1.05

Antibody Array Assay Results		Assay Data							
Signaling Explorer Antibody Array									
		Median Signal							
		283							
		225							
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots			Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
AATF	0.91	AATF	430	309		0.10	0.05	1.52	1.37
NF-kB p65	0.91	NF-kB p65	335	241		0.05	0.08	1.18	1.07
RBAK	0.91	RBAK	330	237		0.00	0.11	1.16	1.05
APLP2	0.90	APLP2	228	164		0.08	0.00	0.80	0.73
CYTL1	0.90	CYTL1	210	151		0.04	0.04	0.74	0.67
IRAK3	0.90	IRAK3	275	197		0.06	0.01	0.97	0.88
SLC30A8	0.90	SLC30A8	421	302		0.04	0.10	1.49	1.34
SNAI2 (SLUG)	0.90	SNAI2 (SLUG)	145	104		0.07	0.10	0.51	0.46
MYOM2	0.90	MYOM2	244	175		0.12	0.10	0.86	0.78
VANGL1	0.90	VANGL1	231	166		0.17	0.04	0.82	0.74
CD33	0.90	CD33	201	144		0.01	0.11	0.71	0.64
SOX2	0.90	SOX2	155	111		0.03	0.08	0.55	0.49
MARK4	0.90	MARK4	423	303		0.03	0.09	1.49	1.35
ATP5A1	0.90	ATP5A1	305	218		0.00	0.08	1.08	0.97
ADCY4	0.90	ADCY4	343	246		0.02	0.08	1.21	1.09
UBAP2L	0.90	UBAP2L	189	135		0.07	0.01	0.67	0.60
CDH3	0.90	CDH3	427	305		0.04	0.03	1.51	1.35
PDRG1	0.90	PDRG1	329	235		0.02	0.01	1.16	1.04
ICAM1	0.90	ICAM1	131	94		0.05	0.07	0.46	0.42
ATP6V1B1	0.90	ATP6V1B1	285	203		0.13	0.02	1.01	0.90
MAP3K9	0.90	MAP3K9	466	333		0.08	0.08	1.65	1.48
SAR1B	0.90	SAR1B	211	151		0.07	0.03	0.75	0.67
EFNB3	0.90	EFNB3	487	347		0.02	0.16	1.72	1.54
Cytochrome P450 4X1	0.90	Cytochrome P450 4X1	221	158		0.03	0.02	0.78	0.70
Histone H2B (Acetyl-Lys12)	0.90	Histone H2B (Acetyl-Lys12)	457	326		0.02	0.12	1.61	1.45
C56D2	0.90	C56D2	429	306		0.00	0.01	1.52	1.36
Fos	0.90	Fos	533	379		0.13	0.00	1.88	1.69
C9orf89	0.90	C9orf89	304	216		0.01	0.01	1.07	0.96
ATF1	0.90	ATF1	397	283		0.04	0.00	1.40	1.26
ADCK1	0.90	ADCK1	250	178		0.03	0.10	0.88	0.79
CLK1	0.90	CLK1	306	218		0.03	0.02	1.08	0.97
MLH1	0.89	MLH1	401	285		0.02	0.51	1.42	1.27
UBA5	0.89	UBA5	430	305		0.02	0.06	1.52	1.36
LRP3	0.89	LRP3	264	187		0.01	0.16	0.93	0.83
Collagen IV alpha6	0.89	Collagen IV alpha6	401	285		0.04	0.02	1.42	1.27
Keratin 10	0.89	Keratin 10	389	276		0.02	0.00	1.37	1.23
Collagen V alpha1	0.89	Collagen V alpha1	333	236		0.04	0.08	1.18	1.05
DDR1	0.89	DDR1	175	124		0.05	0.14	0.62	0.55
ATRX	0.89	ATRX	268	190		0.03	0.13	0.95	0.84
EPHA6	0.89	EPHA6	563	399		0.03	0.02	1.99	1.77
M3K13	0.89	M3K13	320	227		0.08	0.02	1.13	1.01
Cytochrome P450 2R1	0.89	Cytochrome P450 2R1	296	210		0.02	0.06	1.05	0.93
SLC24A6	0.89	SLC24A6	221	156		0.05	0.10	0.78	0.69
CDK2	0.89	CDK2	323	229		0.17	0.05	1.14	1.02
MAPK3	0.89	MAPK3	388	274		0.09	0.05	1.37	1.22
CMKLR1	0.89	CMKLR1	426	301		0.01	0.00	1.51	1.34
ARFGEF2	0.89	ARFGEF2	417	295		0.03	0.07	1.47	1.31
CaMK1-beta	0.89	CaMK1-beta	380	268		0.02	0.03	1.34	1.19
STAG3	0.89	STAG3	327	231		0.04	0.06	1.15	1.03
Cyclin G	0.89	Cyclin G	1053	742		0.17	0.01	3.72	3.30
RAB34	0.89	RAB34	279	197		0.13	0.08	0.99	0.87
DLEC1	0.89	DLEC1	277	195		0.13	0.07	0.98	0.87
Collagen XI alpha1	0.89	Collagen XI alpha1	350	246		0.03	0.07	1.23	1.09
NKX2.5	0.89	NKX2.5	150	106		0.08	0.09	0.53	0.47

Antibody Array Assay Results		Assay Data						
Signaling Explorer Antibody Array			Median Signal	283	225			
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots		Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
EMR1	0.89	EMR1	251	177	0.01	0.08	0.89	0.79
Aggrecan (Cleaved-Asp369)	0.89	Aggrecan (Cleaved-Asp369)	303	213	0.01	0.07	1.07	0.95
GRB2	0.89	GRB2	455	320	0.06	0.11	1.61	1.42
SESN1	0.88	SESN1	283	199	0.13	0.01	1.00	0.88
POLI	0.88	POLI	406	285	0.01	0.01	1.43	1.27
MAST4	0.88	MAST4	316	222	0.09	0.11	1.12	0.99
Foxp3	0.88	Foxp3	237	166	0.00	0.01	0.84	0.74
ARF4	0.88	ARF4	330	231	0.01	0.01	1.17	1.03
MMP17 (Cleaved-Gln129)	0.88	MMP17 (Cleaved-Gln129)	258	180	0.11	0.09	0.91	0.80
p53	0.88	p53	312	217	0.01	0.00	1.10	0.97
MET	0.88	MET	407	284	0.10	0.09	1.44	1.26
CA5B	0.88	CA5B	459	319	0.00	0.04	1.62	1.42
AMPD1	0.88	AMPD1	248	172	0.07	0.01	0.87	0.77
ACBD6	0.88	ACBD6	384	267	0.16	0.04	1.36	1.19
MCM5	0.87	MCM5	347	241	0.04	0.49	1.23	1.07
WDHD1	0.87	WDHD1	357	248	0.14	0.07	1.26	1.10
CaMK2beta/gamma	0.87	CaMK2beta/gamma	370	257	0.07	0.00	1.31	1.14
Collagen IV	0.87	Collagen IV	1246	864	0.32	0.02	4.40	3.84
SIAH2	0.87	SIAH2	362	251	0.05	0.01	1.28	1.12
SPTA2 (Cleaved-Asp1185)	0.87	SPTA2 (Cleaved-Asp1185)	331	230	0.05	0.00	1.17	1.02
MYL3	0.87	MYL3	178	123	0.00	0.15	0.63	0.55
CHML	0.87	CHML	345	239	0.05	0.05	1.22	1.06
S100A3	0.87	S100A3	369	255	0.01	0.03	1.30	1.13
UBE3B	0.87	UBE3B	310	215	0.08	0.01	1.10	0.95
Cytochrome P450 2A13	0.87	Cytochrome P450 2A13	338	234	0.02	0.19	1.19	1.04
KCNG3	0.87	KCNG3	456	313	0.02	0.07	1.61	1.39
FA12 (heavy chain,Cleaved-Arg372)	0.87	FA12 (heavy chain,Cleaved-Arg372)	524	360	0.02	0.06	1.85	1.60
EFNA4	0.86	EFNA4	666	457	0.01	0.02	2.35	2.03
ATP5D	0.86	ATP5D	461	317	0.07	0.02	1.63	1.41
Cofilin	0.86	Cofilin	395	271	0.06	0.07	1.40	1.21
DFF45 (Cleaved-Asp224)	0.86	DFF45 (Cleaved-Asp224)	299	205	0.04	0.10	1.06	0.91
PMS2/PMS2CL	0.86	PMS2/PMS2CL	563	385	0.08	0.01	1.99	1.71
TNNI3K	0.86	TNNI3K	512	350	0.03	0.10	1.81	1.56
POLG2	0.86	POLG2	340	233	0.04	0.03	1.20	1.03
ME1	0.86	ME1	293	200	0.10	0.00	1.03	0.89
LAMP3	0.86	LAMP3	319	218	0.00	0.01	1.13	0.97
AIG1	0.86	AIG1	228	155	0.07	0.01	0.80	0.69
ZADH2	0.86	ZADH2	292	199	0.02	0.03	1.03	0.88
SHC2	0.86	SHC2	458	312	0.10	0.05	1.62	1.39
WEE2	0.86	WEE2	439	299	0.09	0.03	1.55	1.33
APOF	0.86	APOF	316	215	0.09	0.03	1.12	0.96
MYL2	0.86	MYL2	283	192	0.06	0.12	1.00	0.85
FA10 (activated heavy chain,Cleaved-Ile235)	0.86	FA10 (activated heavy chain,Cleaved-Ile235)	382	260	0.11	0.12	1.35	1.15
Caspase 7 (Cleaved-Asp198)	0.86	Caspase 7 (Cleaved-Asp198)	904	614	0.19	0.02	3.19	2.73
Parkin	0.85	Parkin	488	331	0.11	0.04	1.72	1.47
Cytochrome P450 2C8/9/18/19	0.85	Cytochrome P450 2C8/9/18/19	416	282	0.03	0.02	1.47	1.25
Adrenergic Receptor alpha-2C	0.85	Adrenergic Receptor alpha-2C	298	202	0.09	0.02	1.05	0.90
CASP4 (p20,Cleaved-Gln81)	0.85	CASP4 (p20,Cleaved-Gln81)	239	162	0.12	0.02	0.84	0.72
CA181	0.85	CA181	353	239	0.03	0.03	1.25	1.06
Hexokinase-3	0.85	Hexokinase-3	307	207	0.06	0.22	1.08	0.92
STAT1	0.85	STAT1	337	228	0.18	0.01	1.19	1.01
Histone H4 (Acetyl-Lys12)	0.85	Histone H4 (Acetyl-Lys12)	583	394	0.03	0.09	2.06	1.75
Histone H2A (Acetyl-Lys5)	0.85	Histone H2A (Acetyl-Lys5)	370	250	0.27	0.12	1.31	1.11
p16 INK	0.85	p16 INK	427	288	0.07	0.15	1.51	1.28

Antibody Array Assay Results

Assay Data

Signaling Explorer Antibody Array

		Median Signal		283	225				
Protein List	Fold Change between Samples	Protein List	Average Signal of Replicate Spots			Coefficient of Variation for Replicates		Data Normalized to Median Signal	
	Smaller Sample/Bigger Sample		Bigger Sample	Smaller Sample		Bigger Sample	Smaller Sample	Bigger Sample	Smaller Sample
PAR4 (Cleaved-Gly48)	0.85	PAR4 (Cleaved-Gly48)	380	256		0.14	0.05	1.34	1.14
NSG1	0.85	NSG1	308	207		0.00	0.05	1.09	0.92
S6K-alpha2	0.85	S6K-alpha2	356	239		0.01	0.08	1.26	1.06
SHD	0.85	SHD	326	219		0.13	0.02	1.15	0.97
USP36	0.84	USP36	233	156		0.10	0.04	0.82	0.69
TAF1A	0.84	TAF1A	302	202		0.11	0.01	1.07	0.90
TNF12	0.84	TNF12	454	304		0.17	0.02	1.60	1.35
ADPGK	0.84	ADPGK	337	226		0.03	0.00	1.19	1.00
p97 MAPK	0.84	p97 MAPK	367	246		0.01	0.05	1.30	1.09
Collagen XIV alpha1	0.84	Collagen XIV alpha1	412	275		0.05	0.13	1.46	1.22
SOD1	0.84	SOD1	551	368		0.08	0.12	1.95	1.64
TACD1	0.84	TACD1	518	345		0.01	0.05	1.83	1.54
AASDHPPT	0.84	AASDHPPT	282	188		0.10	0.09	1.00	0.83
PARP (Cleaved-Gly215)	0.84	PARP (Cleaved-Gly215)	678	451		0.14	0.09	2.40	2.00
GPR150	0.84	GPR150	331	220		0.10	0.12	1.17	0.98
COPZ1	0.83	COPZ1	488	324		0.07	0.09	1.72	1.44
CATL2 (Cleaved-Leu114)	0.83	CATL2 (Cleaved-Leu114)	271	180		0.16	0.04	0.96	0.80
CASP2 (p18,Cleaved-Gly170)	0.83	CASP2 (p18,Cleaved-Gly170)	247	164		0.07	0.10	0.87	0.73
CASP8 (Cleaved-Asp384)	0.83	CASP8 (Cleaved-Asp384)	262	173		0.22	0.07	0.93	0.77
NCR3	0.83	NCR3	498	329		0.00	0.04	1.76	1.46
NOX5	0.83	NOX5	447	295		0.07	0.06	1.58	1.31
ABCA8	0.83	ABCA8	292	193		0.01	0.06	1.03	0.86
URB1	0.83	URB1	278	183		0.20	0.02	0.98	0.81
MYO1D	0.83	MYO1D	332	219		0.09	0.01	1.17	0.97
MMP3 (Cleaved-Phe100)	0.83	MMP3 (Cleaved-Phe100)	291	191		0.06	0.02	1.03	0.85
GRK3	0.82	GRK3	351	229		0.05	0.05	1.24	1.02
Histone H2AX	0.82	Histone H2AX	470	306		0.03	0.06	1.66	1.36
Cytochrome P450 2D6	0.82	Cytochrome P450 2D6	366	238		0.05	0.08	1.29	1.06
ARSD	0.82	ARSD	222	145		0.24	0.11	0.78	0.64
HMGGB2	0.82	HMGGB2	333	216		0.18	0.01	1.17	0.96
CD3	0.82	CD3	181	117		0.04	0.07	0.64	0.52
NOX3	0.82	NOX3	349	226		0.08	0.06	1.23	1.01
p57KIP2	0.81	p57KIP2	365	235		0.00	0.12	1.29	1.05
KCNV2	0.81	KCNV2	434	279		0.04	0.02	1.53	1.24
MRP9	0.81	MRP9	392	252		0.03	0.04	1.38	1.12
SGOL1	0.81	SGOL1	317	204		0.07	0.11	1.12	0.91
Histone H4 (Acetyl-Lys8)	0.81	Histone H4 (Acetyl-Lys8)	343	220		0.20	0.05	1.21	0.98
Androgen receptor	0.81	Androgen receptor	341	219		0.07	0.15	1.20	0.97
RAB18	0.81	RAB18	341	219		0.10	0.20	1.20	0.97
CKLF2	0.80	CKLF2	465	297		0.01	0.05	1.64	1.32
UNG	0.80	UNG	397	252		0.08	0.11	1.40	1.12
IgM	0.78	IgM	7177	4465		0.07	0.18	25.36	19.86
COX2	0.78	COX2	359	222		0.03	0.30	1.27	0.99
Collagen I	0.78	Collagen I	427	264		0.04	0.02	1.51	1.17
CASP5 (p20,Cleaved-Asp121)	0.78	CASP5 (p20,Cleaved-Asp121)	488	301		0.10	0.03	1.72	1.34
NCR1	0.77	NCR1	402	247		0.02	0.09	1.42	1.10
TTF2	0.77	TTF2	219	134		0.32	0.05	0.77	0.60
ADAM 17 (Cleaved-Arg215)	0.77	ADAM 17 (Cleaved-Arg215)	511	312		0.23	0.07	1.80	1.39
SLC39A1	0.77	SLC39A1	426	259		0.02	0.09	1.51	1.15
Cadherin-pan	0.77	Cadherin-pan	559	340		0.04	0.19	1.97	1.51
PE2R3	0.74	PE2R3	321	189		0.20	0.10	1.13	0.84
Cytochrome P450 1A1/2	0.73	Cytochrome P450 1A1/2	603	352		0.13	0.04	2.13	1.56
Caspase 9 (Cleaved-Asp330)	0.73	Caspase 9 (Cleaved-Asp330)	468	271		0.07	0.10	1.65	1.20
EFNA2 (Cleaved-Asn188)	0.73	EFNA2 (Cleaved-Asn188)	325	188		0.02	0.01	1.15	0.84

Assay Data

Median Signal	283	225
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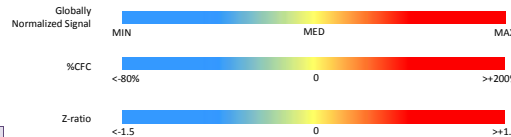
Coefficient of Variation for Replicates	
Bigger Sample	Smaller Sample
0.01	0.15
0.01	0.15
0.02	0.05
0.05	0.08
0.10	0.05
0.08	0.06
0.07	0.07
0.03	0.02
0.09	0.07
0.10	0.06
0.06	0.20
0.02	0.01
0.43	0.11
0.07	0.08
0.53	0.14
0.05	0.04

Bigger Sample	Smaller Sample
5.21	3.79
1.33	0.95
0.75	0.53
1.40	0.97
2.08	1.43
1.39	0.96
0.96	0.66
1.79	1.21
1.74	1.17
2.73	1.82
1.39	0.92
2.77	1.69
1.23	0.75
2.01	1.20
1.18	0.65
2.86	1.54

Appendix F

Pooled-Microarray

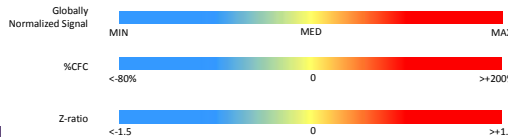
Sample IDs:		SAMPLE DETAILS		Globally Normalized Median																				Row		Column		Refseq		Uniprot Link	
				Control ID: Pooled Samples Larger																											
				Treated ID: Pooled Samples Smaller																											
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range Control	Log2 (Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range Treated	Log2 (Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	12	13												
1	NP186	4E-BP1	Pan-specific	Eukaryotic translation	0.0	1279	2	7	0.0	999	29	7	-22	-0.63	-0.83	-0.20	-0.874	4	6	1	NP_004086	Q13541									
2	PN001	4E-BP1	S65	Eukaryotic translation	0.0	1678	5	7	0.0	1185	2	7	-9	-0.67	-0.78	-0.11	-0.471	12	6	1	NP_004086	Q13541									
3	PN114	4E-BP1	T45	Eukaryotic translation	0.0	1638	5	7	0.0	1624	3	8	11	-0.45	-0.47	0.01	0.04	8	6	1	NP_004086	Q13541									
4	CN005	4G10	pTyr	Phosphotyrosine (Ctor	0.0	2906	70	70	0.0	4526	249	9	56	-0.16	0.06	0.22	0.80	N/A	6	1	N/A	N/A									
5	PK502	Y309	A6r	Twirlin-2	0.0	8478	21	10	0.0	9463	21	10	12	0.45	0.50	0.05	0.16	4	6	2	NP_009215.1	Q6B8S0									
6	PK503	AAK1	S637	AP2-associated protei	0.0	13538	63	10	0.0	12646	38	10	7	0.72	0.67	-0.05	-0.18	8	6	2	NP_058726.3	Q2N298									
7	PK501	Abi	Pan-Specific	Abelson proto-oncoge	0.0	43801	7	6	0.0	43838	4	7	63	-0.47	-0.66	0.21	0.87	4	6	3	NP_005148	P00519									
8	NK001-2	Abi	Pan-Specific	Abelson proto-oncoge	0.0	43951	4	12	0.0	69055	12	13	67	1.39	1.67	0.28	1.02	16	6	2	NP_005148	P00519									
9	PK001	Abi	S79	Abelson proto-oncoge	0.0	1981	11	8	0.0	1933	1	8	-2	-0.38	-0.24	-0.06	-0.23	12	6	2	NP_005148	P00519									
10	PN002	Abi	S79	Acetyl coenzyme A ca	0.0	19324	6	11	0.0	20525	2	11	6	0.92	0.96	0.03	0.12	8	6	3	NP_005148	Q13085									
11	NK002	ACK1	Pan-specific	Activated CD242 kina	0.0	2677	20	8	0.0	5211	3	9	95	-0.20	0.15	0.35	1.27	12	6	3	NP_005772	Q07912									
12	NK129-5	AKt1	Pan-Specific	Actin, alpha skeletin	0.0	41660	15	12	0.0	39455	12	12	-26	-1.36	1.19	-0.17	-0.80	4	6	3	NP_005154	P34128									
13	PN003-PN004	Adducin alg	S662	Adducin alpha (ADD1	0.0	5623	5	9	0.0	6256	19	9	11	0.22	0.25	0.04	0.13	4	6	4	NP_058432	P35611									
14	NN002	AIF	Pan-specific	Apoptosis inducing fa	0.0	1727	16	11	0.0	3018	71	8	75	-0.45	-0.18	0.28	1.01	8	6	4	NP_004199	Q92831									
15	NN003	AK2	Pan-specific	Adenylate kinase 2	0.0	4508	34	9	0.0	5073	23	9	13	0.09	0.13	0.04	0.13	12	6	4	NP_001614	P54819									
16	NK129-3	AKt1	Pan-Specific	RAC-alpha serine/thre	0.0	9868	12	10	0.0	6806	14	9	-31	0.54	0.30	-0.24	-0.86	16	6	4	NP_005154	P31749									
17	NK129-5	AKt1	Pan-Specific	RAC-alpha serine/thre	0.0	9868	12	10	0.0	6806	14	9	-31	0.54	0.30	-0.24	-0.86	16	6	4	NP_005154	P31749									
18	PK517	AKt1	Y326	RAC-alpha serine/thre	0.0	7039	89	9	0.0	6096	51	9	-13	0.35	0.24	-0.11	-0.39	8	6	5	NP_005154	P31749									
19	NK129	AKT1 (PK8a)	Pan-specific	RAC-alpha serine/thre	0.0	18678	16	11	0.0	17466	24	11	-6	0.90	0.86	-0.04	-0.16	4	6	6	NP_005154	P31749									
20	PK072-1	AKt1 (PK8a)	S473	RAC-alpha serine/thre	0.0	642	6	6	0.0	683	27	6	6	-1.02	-1.05	-0.04	-0.13	12	6	6	NP_005154	P31749									
21	PK072-3	AKt1 (PK8a)	S473	RAC-alpha serine/thre	0.0	622	8	6	0.0	364	14	6	-30	-1.14	-1.43	-0.29	-1.05	8	6	6	NP_005154	P31749									
22	PK072-5	AKt1 (PK8a)	S473	RAC-alpha serine/thre	0.0	4326	27	9	0.0	3312	12	9	-312	-0.07	-0.12	-0.05	-0.89	12	6	3	NP_005154	P31749									
23	PK148	AKt1 (PK8a)	Y474	RAC-alpha serine/thre	0.0	1982	77	8	0.0	2042	5	8	3	-0.38	-0.41	-0.03	-0.11	16	6	5	NP_005154	P31749									
24	NK130-4	AKt2	Pan-Specific	RAC-beta serine/thre	0.0	19180	10	11	0.0	12930	28	10	-33	0.92	0.88	-0.04	-0.26	16	6	6	NP_001617	P31761									
25	NK130-6	AKt2	Pan-specific	RAC-beta serine/thre	0.0	5060	9	9	0.0	5830	9	9	15	0.16	0.21	0.05	0.19	11	6	1	NP_001617	P31761									
26	NK130-7	AKt2	Pan-specific	RAC-beta serine/thre	0.0	4247	9	9	0.0	4247	9	9	33	0.19	0.19	0.13	0.49	15	6	1	NP_001617	P31761									
27	NK130-8	AKt2	Pan-Specific	RAC-beta serine/thre	0.0	54039	12	10	0.0	44572	26	12	1	1.39	1.39	0.02	0.11	11	6	1	NP_001617	P31761									
28	NK130-9	AKt2	Pan-Specific	RAC-beta serine/thre	0.0	54724	1	12	0.0	71378	10	13	30	1.52	1.69	0.17	0.63	7	6	1	NP_001617	P31761									
29	NK131-3	AKt3	Pan-Specific	RAC-gamma serine/th	0.0	52426	10	12	0.0	58269	18	13	11	1.49	1.57	0.08	0.29	3	6	2	NP_005456	Q9Y243									
30	NK003	ALK	Pan-specific	Anaplastic lymphoma	0.0	33389	7	12	0.0	34479	20	12	3	1.24	1.26	0.03	0.03	11	6	2	AAB71619	Q9LM73									
31	PK520	ALK	Pan-specific	Anaplastic lymphoma	0.0	10333	22	10	0.0	12764	2	10	24	0.57	0.68	0.11	0.68	7	6	2	AAB71619	Q9LM73									
32	AMPK2	AMPK2	S377	S-AMP-activated protei	0.0	10462	10	8	0.0	9465	10	8	0.53	0.56	0.03	0.11	0.53	11	6	2	NP_005456	P34483									
33	PK523	ANKRD3	S438	Ankyrin repeat domai	0.0	2430	49	8	0.0	2630	23	8	8	-0.26	-0.26	0.00	0.01	3	6	3	NP_065690.2	P50728									
34	PN504	ANXA2	Y238	Annexin A2	0.0	3259	5	12	0.0	3680	12	9	13	-0.09	-0.06	0.03	0.12	7	6	3	NP_001002857.1	Q07355									
35	NN004	APG1	Pan-specific	Hsp 70-related heat s	0.0	2431	33	8	0.0	5993	18	9	147	-0.26	0.23	0.49	1.77	11	6	3	NP_085093	Q95757									
36	NN122	APG2	Pan-specific	Hsp 70-related heat s	0.0	3145	33	8	0.0	9355	17	10	189	-0.11	-0.11	0.60	2.16	15	6	3	NP_085093	Q95757									
37	PN189	APP	S743	Amyloid beta A4 prote	0.0	445	5	-10	0.0	1396	81	3	114	-0.23	-0.63	0.40	2.16	15	6	4	NP_00475.1	P05067									
38	NK205-2	A-Raf	Pan-Specific	A-Raf proto-oncogene	0.0	2947	20	8	0.0	6471	272	9	120	-0.15	-0.13	0.02	0.42	15	6	5	NP_001645.1	P10398									
39	NK205-4	A-Raf	Pan-Specific	A-Raf proto-oncogene	0.0	77291	4	13	0.0	74399	1	13	-4	1.72	1.72	0.00	0.01	7	6	4	NP_001645.1	P10398									
40	NK205-5	A-Raf	Pan-Specific	A-Raf proto-oncogene	0.0	54134	10	12	0.0	46181	47	12	-15	1.51	1.44	-0.08	-0.38	11	6	4	NP_001645.1	P10398									
41	Y302	A-Raf	Pan-Specific	A-Raf proto-oncogene	0.0	13275	23	24	0.0	12135	24	23	9	0.71	0.71	0.00	0.01	15	6	4	NP_001645.1	P10398									
42	NN121	Arrestin b	Pan-specific	Arrestin beta 1	0.0	368	12	5	0.0	422	-14	5	-16	-1.22	-1.44	-0.22	-0.64	11	6	5	NP_004032	P49407									
43	PN133	Arrestin b	S412	Arrestin beta 1	0.0	13385	21	10	0.0	11838	24	10	-12	0.71	0.63	-0.08	-0.30	7	6	5	NP_004032	P49407									
44	NK007	ASK1	Pan-specific	Apoptosis signal regul	0.0	4306	16	10	0.0	8963	10	10	101	0.07	0.44	0.38	1.37	7	6	6	NP_005914	Q99833									
45	NK007-2	ASK1	Pan-specific	Apoptosis signal regul	0.0	6135	41	9	0.0	3643	110	9	-41	0.27	-0.07	-0.33	-1.21	3	6	6	NP_005914	Q99833									
46	PK143	SRB6	Pan-specific	Apoptosis signal regul	0.0	5266	15	3	0.0	5099	15	3	17	-1.13	-1.23	-0.10	-0.56	10	6	1	NP_005914	Q99833									
47	PN115	ATF2	S94/S112	Activating transcrip	0.0	2347	97	8	0.0	2347	58	8	-31	-0.07	-0.33	-0.26	-0.94	2	6	1	NP_001871	P15336									
48	PN006-1	ATF2	T69+T71	Activating transcrip	0.0	7831	19	10	0.0	7480	14	10	-4	0.41	0.36	-0.05	-0.18	15	6	6	NP_001871	P15336									
49	NK008-3	AurKA	Pan-Specific	Aurora Kinase A (seri	0.0	9509	22	14	0.0	13925	149	10	46	0.52	0.73	0.21	0.75	6	6	1	NP_040835	P14965									
50	NK008-4	AurKA	Pan-Specific	Aurora Kinase A (seri	0.0	58583	14	13	0.0	75240	3	13	31	1.53	1.71	0.18	0.65	10	6	1	NP_040835	P14965									
51	NK008-5	AurKA	Pan-Specific	Aurora Kinase A (seri	0.0	32540	37	12	0.0	34088	5	12	12	1.22	1.14	0.08	0.14	14	6	1	NP_040835	P14965									
52	NK193-2	AurKB	Pan-Specific	Aurora Kinase B (seri	0.0	27283	10	33	0.0	19213	33	11	-30	1.12	1.02	-0.20	-0.74	2	6	2	NP_004208	Q9BGD4									
53	NK193-3	AurKB	Pan-Specific	Aurora Kinase B (seri	0.0	40853	8	12	0.0	42532	7	12	4	1.35	1.39	0.04	0.13	6	6	2	NP_004208	Q9BGD4									
54	NK193-4	AurKB	Pan-Specific	Aurora Kinase B (seri	0.0	22551	308	11	0.0	11125	21	10	-51	1.01	0.59	-0.42	-1.51	10	6	2	NP_004208	Q9BGD4									
55	PK530	AurKB	S227	Aurora Kinase B (seri	0.0	25015	294	11	0.0	21895	194	11	-12	1.07	0.99	-0.08	-0.28	14	6	2	NP_004208	Q9BGD4									
56	NK009-2	B23 (NPM)	T234/237	B23 (nucleophosmin,	0.0	23079	35	5	0.0	17352	1	25	1	0.29	0.15	-0.14	-0.47	11	6	3	NP_002511	P06748									
57	PN008	B23 (NPM)	T234/237	B23 (nucleophosmin,	0.0	252	27	5	0.0	198	1	4	-21	-1.55	-1.79	-0.23	-0.80	10	6	3	NP_002511	P06748									
58	NN000	Bak	Pan-specific	Bcl2 homologous anta	0.0	3160	45	0.0	1929	43	7	-52	-0.11	-0.11	-0.58	-1.74	14	6	3	NP_001179	P10611										
60	NN005	Bax	Pan-specific	Apoptosis regulator B	0.0	9855	76	10	0.0	16330	34	11	66	0.94	0.82	0.28	0.64	2	6	4	NP_020116	Q07812									
61	NK257-1	BCL2 (BCL2K)	Pan-Specific	B-2-methyl-2-oxobutyl	0.0	14600	12	10	0.0	19697	16	45	11	0.16	0.15	0.01	0.11	14	6	4	NP_00116429.1	P10415									
62	NN006-1	BCL	Pan-Specific	B-cell lymphoma prote	0.0	286																									



SAMPLE DETAILS

Sample IDs: Control ID: Pooled Samples Larger
Treated ID: Pooled Samples Smaller

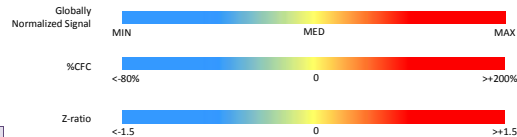
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Serial No.	Antibody Codes	Target Protein Names	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range Control	Log2(Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range Treated	Log2(Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link			
88	PK555	CaMK2a	T288	Calcium/calmodulin-d	0.0	10946	58	10	0.0	10994	76	10	-21	0.74	0.59	-0.15	-0.54	5	6	5	NP_057065.2	P0UJCM7			
89	NK019-2	CAMK2d	Pan-specific	Calcium/calmodulin-d	0.0	4695	57	9	0.0	5143	33	9	10	0.12	0.14	0.02	0.08	9	6	5	NP_742128	Q13557			
90	NK021-3	CaMK4	Pan-specific	Calcium/calmodulin-d	0.0	20776	22	11	0.0	19420	10	11	-7	0.97	0.92	-0.04	-0.15	1	6	6	NP_001735	Q16566			
91	PK556	CaMK4	T200	Calcium/calmodulin-d	0.0	4362	63	9	0.0	4651	51	9	7	0.07	0.08	0.00	0.02	13	6	5	NP_01735.1	Q16166			
92	NK211	CamKI		Calcium/calmodulin-d	0.0	1520	35	7	0.0	2661	8	8	75	-0.53	-0.25	0.28	1.00	5	6	6	NP_003647.1	Q14012			
93	NK022	CAMKK	Pan-Specific	Calcium/calmodulin-d	0.0	3908	6	9	0.0	4119	6	9	0	0.01	0.01	0.00	0.00	6	6	6	NP_006540	P04589			
94	PN505	Case1	Y168	Enhancer of filamentar	0.0	5199	36	11	0.0	5760	22	9	11	0.17	0.21	0.04	0.11	13	6	6	NP_00135965.1	Q14513			
95	NN011	Caspase 1	Pan-specific	Caspase 1 (Interleukin	0.0	4700	50	9	0.0	8615	51	10	88	0.12	0.46	0.34	1.23	4	6	7	NP_001214	P29466			
96	NN013	Caspase 3	Pan-specific	Caspase 3 (apoptin, c	0.0	408	44	5	0.0	397	25	5	-2	-1.28	-1.38	-0.09	-0.34	8	6	7	NP_004337	P42574			
97	NN016	Caspase 6	Pan-specific	Caspase 6 (apoptotic f	0.0	151	24	4	0.0	184	21	4	22	-1.84	-1.83	0.02	0.05	16	6	7	NP_001217	P56212			
98	NN017-2	Caspase 7	Pan-specific	Caspase 7 (ICE-like i	0.0	1159	29	7	0.0	1686	32	7	138	-0.68	-0.53	0.15	0.66	4	6	8	NP_001218	P56211			
99	PN142	Catenin a	S641	Catenin (cadherin-ass	0.0	1073	38	7	0.0	1136	29	8	6	-0.73	-0.75	-0.02	-0.10	7	6	8	NP_00127236.1	P33222			
100	NN021	Catenin b	Pan-specific	Catenin (cadherin-ass	0.0	2196	124	8	0.0	2086	7	8	-5	-0.32	-0.39	-0.08	-0.28	12	6	8	NP_001895	P35222			
101	PN166	Catenin b	S33	Catenin (cadherin-ass	0.0	1340	96	7	0.0	1673	42	7	25	-0.60	-0.53	0.07	0.27	16	6	8	NP_001895	P35222			
102	PN167	Catenin b	Y333	Catenin (cadherin-ass	0.0	501	1	6	0.0	653	20	6	30	-1.16	-1.08	0.08	0.29	4	6	9	NP_001895	P35222			
103	NK021-1	Catenin b1	Pan-Specific	Catenin (cadherin-ass	0.0	384	34	5	0.0	466	24	6	21	-1.31	-1.28	0.03	0.11	8	6	9	NP_001895	P35222			
104	PN167	Caveolin 1	YN167	Caveolin 1	0.0	119	20	4	0.0	155	43	4	15	-1.98	-1.93	0.05	0.16	9	6	9	NP_00116331.1	P03136			
105	PN167	Caveolin 1	Y14	Caveolin 1	0.0	351	11	5	0.0	336	26	5	-4	-1.36	-1.47	-0.11	-0.40	16	6	9	NP_00116356.1	Q03136			
106	NN022-1	Caveolin 2	Pan-specific	Caveolin 2	0.0	2291	10	8	0.0	1833	5	8	-20	-0.29	-0.47	-0.18	-0.64	8	6	10	NP_001224	P41636			
107	PN018	Caveolin 2	S36	Caveolin 2	0.0	3695	16	8	0.0	4001	29	9	8	-0.02	-0.01	0.01	0.04	4	6	10	NP_001224	P51636			
108	PN171	c-Cl	Y700	Signal transduction pr	0.0	285	1	5	0.0	258	66	5	9	-1.48	-1.63	-0.15	-0.53	12	6	10	NP_005179.2	P22481			
109	PN001	CD45	Pan-specific	Leukocyte common ar	0.0	853	36	6	0.0	714	23	6	17	-0.86	-0.77	0.09	0.17	16	6	10	NP_002829	P08372			
110	NN186	CD45	Pan-specific	CD45 Antigen	0.0	66642	23	13	0.0	6295	72	9	-91	1.63	0.26	-1.37	-4.97	4	6	11	NP_00124318.1	P08962			
111	NK025-6	Cdc2 p34	Pan-specific	Cyclin-dependent prot	0.0	705	81	6	0.0	1301	16	7	85	-0.97	-0.67	0.29	1.06	8	6	11	NP_001777	P06493			
112	NK025-6	Cdc2 p34	Pan-specific	Cyclin-dependent prot	0.0	5058	125	9	0.0	3644	8	9	-28	0.16	-0.07	-0.22	-0.81	12	6	11	NP_001777	P06493			
113	PN038-1	CD25A	Pan-Specific	Cell division cycle 25A	0.0	13432	17	10	0.0	8663	102	10	-36	0.72	0.45	-0.27	-0.98	16	6	11	NP_001780.2	P30304			
114	PN038-1	CD25B	Pan-Specific	Cell division cycle 25B	0.0	301887	32	12	0.0	31098	12	12	-32	4.20	-1.33	5.53	1.71	1	6	11	NP_001780.2	P30304			
115	PN038-3	CD25C	Pan-Specific	Cell division cycle 25C	0.0	8921	31	12	0.0	6221	43	9	8	0.93	0.25	-0.68	-0.84	8	7	1	NP_001780.2	P30304			
116	PN002	CD25B	Pan-Specific	Cell division cycle 25B	0.0	1769	25	7	0.0	1340	23	7	-24	-0.44	-0.66	-0.22	-0.78	3	6	7	NP_004349	P30305			
117	NP002-2	CD25B	Pan-Specific	Cell division cycle 25B	0.0	24698	37	11	0.0	21225	29	11	-14	1.06	0.98	-0.09	-0.32	12	7	1	NP_004349	P30305			
118	NP002-3	CD25B	Pan-Specific	Cell division cycle 25B	0.0	48033	11	12	0.0	47731	10	12	-1	1.44	1.45	0.01	0.04	16	7	1	NP_004349	P30305			
119	NP003	CD25C	Pan-Specific	Cell division cycle 25C	0.0	2485	46	8	0.0	2765	19	8	8	-0.25	-0.23	0.02	0.06	15	6	7	NP_001781	P30307			
120	NP003-2	CD25C	Pan-Specific	Cell division cycle 25C	0.0	52624	13	12	0.0	37410	7	13	9	0.74	1.56	0.82	1.82	10	6	7	NP_001781	P30307			
121	NP003-3	CD25C	Pan-Specific	Cell division cycle 25C	0.0	41174	18	12	0.0	41343	27	12	0	1.36	1.37	0.01	0.05	11	6	7	NP_001781	P30307			
122	NK024	CD2C15	Pan-specific	Cell division cycle 21C	0.0	3672	15	8	0.0	5759	42	9	57	-0.02	0.21	0.23	0.83	3	6	8	NP_003709	Q14004			
123	NN023	CD34	Pan-specific	Cell division cycle 34 (0.0	763	6	6	0.0	572	7	6	-25	-0.92	-1.16	-0.24	-0.86	7	6	8	NP_004350	P49427			
124	NN024	CD34	Pan-specific	Cell division cycle 34 (0.0	1059	9	7	0.0	759	6	7	-28	-0.73	-0.99	-0.26	-0.93	11	6	8	NP_001782	P06963			
125	PK558	CD37	Pan-specific	Cell division cycle 7-0	0.0	1784	9	7	0.0	1929	22	7	12	-0.44	-0.54	-0.10	-0.42	15	6	10	NP_00127891.1	Q03111			
126	NK025-1	CDK1	Pan-specific	Cyclin-dependent prot	0.0	13082	27	10	0.0	12138	18	10	7	0.70	0.65	-0.06	-0.20	3	6	9	NP_001777	P06493			
127	NK025-2	CDK1	Pan-specific	Cyclin-dependent prot	0.0	477	5	6	0.0	375	17	5	-21	-1.19	-1.41	-0.22	-0.80	7	6	9	NP_001777	P06493			
128	PK583	CDK1	Y19	Cyclin-dependent prot	0.0	8092	75	10	0.0	10129	84	10	25	0.43	0.54	0.11	0.41	11	6	9	NP_001777	P06493			
129	PK008	CDK1/2	Y14/Y15	Cyclin-dependent prot	0.0	1431	63	7	0.0	1191	15	7	-10	-0.56	-0.73	-0.16	-0.59	15	6	9	NP_001777	P06493			
130	PK007-1	CDK1/2	Y15	Cyclin-dependent prot	0.0	164	4	4	0.0	172	4	4	-12	-1.84	-1.87	-0.03	-0.12	7	6	10	NP_001777	P06493			
131	PK007-3	CDK1/2	Y15	Cyclin-dependent prot	0.0	224	4	4	0.0	272	41	5	22	-1.62	-1.60	0.02	-0.04	3	6	10	NP_001777	P06493			
132	PK008-1	CDK1/CD2C	T161	Cyclin-dependent prot	0.0	293	73	5	0.0	209	9	4	-29	-1.47	-1.75	-0.29	-1.08	11	6	10	NP_001777	P06493			
133	PK585	CDK1/1A	T583	Cell division cycle 2-lik	0.0	4899	4	9	0.0	4076	4	9	-17	0.14	0.00	-0.14	-0.55	15	6	10	NP_001781.2	Q0UQ88			
134	NK026-3	CDK2	Pan-specific	Cyclin-dependent prot	0.0	591	20	2	0.0	48	23	2	-5	-2.47	-2.62	-0.15	-0.55	15	6	11	NP_001789	P24941			
135	NK026-5	CDK2	Pan-specific	Cyclin-dependent prot	0.0	3432	8	9	0.0	4311	6	9	-36	0.36	0.33	0.03	0.03	13	6	11	NP_001789	P24941			
136	NK026-6	CDK2	Pan-specific	Cyclin-dependent prot	0.0	9381	435	10	0.0	7369	13	10	-21	0.35	0.35	0.00	-0.58	7	6	11	NP_001789	P24941			
137	NK026-7	CDK2	Pan-specific	Cyclin-dependent prot	0.0	2743	286	8	0.0	1645	36	7	-40	-0.19	-0.54	-0.34	-1.25	11	6	11	NP_001789	P24941			
138	NK027	CDK4	Pan-specific	Cyclin-dependent prot	0.0	28341	24	11	0.0	31368	16	12	11	1.14	1.21	0.06	0.23	12	6	7	NP_000066	P11802			
139	NK027-2	CDK4	Pan-specific	Cyclin-dependent prot	0.0	980	23	7	0.0	1196	12	7	22	-0.78	-0.72	0.06	0.20	7	7	1	NP_000066	P11802			
140	PK569	CDK4	T172	Cyclin-dependent prot	0.0	12242	10	10	0.0	10978	193	10	-10	0.66	0.59	-0.08	-0.28	3	7	1	NP_000066	P11802			
141	NK028-2	CDK5	Pan-specific	Cyclin-dependent prot	0.0	330622	11	14	0.0	330622	11	14	-1	-0.13	-0.12	0.01	-0.01	12	6	11	NP_004026	Q00538			
142	NK028-4	CDK5	Pan-specific	Cyclin-dependent prot	0.0	17087	972	11	9	4550	31	9	-73	0.85	0.07	-0.79	-2.85	11	7	1	NP_004026	Q00538			
143	NK028-5	CDK5	Pan-specific	Cyclin-dependent prot	0.0	3687	31	8	0.0	5521	30	9	50	-0.02	0.18	0.20	0.73	15	7	1	NP_004026	Q00538			
144	NK029	CDK6	Pan-specific	Cyclin-dependent prot	0.0	53698	12	12	0.0	56937	25	13	6	1.51	1.56	0.05	0.19	6	7	7	NP_001250	Q00534			
145	NK029-3	CDK6	Pan-specific	Cyclin-dependent prot	0.0	3031	277	8	0.0	969	64	7	68	-0.13	-0.65	-0.52	-2.59	14	6	7	NP_001250	Q00534			
146	PK165	CDK6	Y13	Cyclin-dependent prot	0.0	798	26	6	0.0	651	6	6	-19	-0.89	-1.08	-0.19	-0.78	10	6	7	NP_001250	Q00534			
147	NK030-2	CDK7	Pan-specific	Cyclin-dependent prot	0.0	934	14	7	0.0	7560	17	6	709	-0.81	-0.77	0.04	-0.24	2	6	8	NP_001790	P50813			
148	NK031-5	CDK8	Pan-specific	Cyclin-dependent prot	0.0	2257	16	8	0.0	2287	47	8	1	-0.30	-0.34	-0.04	-0.14	6	6	8	NP_001252	P49336			
149	NK032	CDK9	Pan-specific	Cyclin-dependent prot	0.0	4512	120	10	0.0	8403	185	10	86	0.09	0.43	0.33	1.21	2	6	9	NP_001252.1	P50750			
150	PK574	CDK9	S347	Cyclin-dependent prot	0.0																				



SAMPLE DETAILS

Sample IDs: Control ID: Pooled Samples Larger
Treated ID: Pooled Samples Smaller

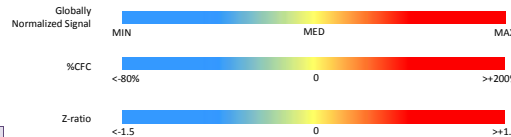
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										3433											4055										
Serial No.	Antibody codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range	Log2(Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range	Log2(Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link									
175	PN023	CREB1	S129/S133	cAMP response element-binding protein 1	0.0	3917	10	5	0.0	3917	13	5	-18	-1.32	-1.52	-0.20	-0.71	1	6	9	NP_004370	P16220									
176	PN024	CREB1	S133	cAMP response element-binding protein 1	0.0	18492	10	11	0.0	9990	13	10	-46	0.90	0.53	-0.37	-1.33	5	6	9	NP_004370	P16220									
177	NN182	CrkL (32H4)		Crk-like protein	0.0	11600	35	10	0.0	10671	17	10	-8	0.63	0.57	-0.06	-0.23	9	6	9	NP_005198.1	P46109									
178	NN149-1	Crystallin αB		Crystallin alpha B (heat shock domain-containing)	0.0	20231	7	11	0.0	19215	3	11	-5	0.95	0.92	-0.03	-0.12	5	6	10	NP_001876	P02811									
179	NN149-2	Crystallin αB		Crystallin alpha B (heat shock domain-containing)	0.0	2391	0	0	0.0	2674	18	0	-27	-0.27	-0.25	0.02	0.08	9	6	10	NP_001876	P02811									
180	PN025	Crystallin αB	S19	Crystallin alpha B (heat shock domain-containing)	0.0	23935	11	11	0.0	19310	38	11	-10	1.03	1.02	-0.11	0.02	9	6	10	NP_001876	P02811									
181	PN110	Crystallin αB	S45	Crystallin alpha B (heat shock domain-containing)	0.0	16114	25	11	0.0	10532	12	10	-35	0.82	1.56	-0.73	-0.93	1	6	9	NP_001876	P02811									
182	NK234-3	CSF1R	Pan-specific	Macrophage colony-stimulating factor receptor 1	0.0	52530	52	12	0.0	47202	41	12	-10	1.49	1.45	-0.05	-0.17	13	6	10	NP_01275634.1	P07333									
183	PK587	CSF1R	V699	Macrophage colony-stimulating factor receptor 1	0.0	3593	54	8	0.0	4522	39	9	26	-0.04	0.06	0.10	0.36	1	6	11	NP_01275634.1	P07333									
184	NK044	Osk	Pan-specific	C-terminus of Src tyrosine kinase	1.0	16491	14	11	1.0	3129	12	8	-81	0.83	-0.15	-0.99	-3.58	5	6	11	NP_004374	P14240									
185	NK044-2	Osk	Pan-specific	C-terminus of Src tyrosine kinase	0.0	1983	80	8	0.0	2012	36	8	2	-3.38	-0.42	-0.03	-0.13	9	6	11	NP_004374	P14240									
186	NN028	Cyclin A1	Pan-specific	Cyclin A1	0.0	32054	21	12	0.0	29325	21	12	0	1.17	1.17	-0.05	-0.16	3	7	11	NP_003905	P71338									
187	NN029	Cyclin B1	Pan-specific	Cyclin B1	0.0	1627	49	10	0.0	3071	10	8	-89	-0.49	-0.17	0.32	1.17	5	7	1	NP_114172	P14635									
188	PN190	Cyclin B1	S147	Cyclin B1	0.0	1529	28	7	0.0	1352	14	7	-12	-0.52	-0.65	-0.13	-0.46	1	7	1	NP_114172	P14635									
189	NN030-1	Cyclin D1	Pan-specific	Cyclin D1 (PRAD1)	0.0	20429	48	11	0.0	12767	24	10	-38	0.96	0.68	-0.28	-1.01	9	7	1	NP_444284	P24385									
190	NN031	Cytochrome E	Pan-specific	Cytochrome E	0.0	3347	74	8	0.0	12676	175	10	-279	-0.08	0.67	0.75	2.71	4	7	2	NP_001229	P24884									
191	PN191	Cytoskeleton	T098	Cytoskeleton	0.0	15912	16	7	0.0	15852	29	8	-29	-0.53	-0.43	-0.10	-0.13	7	1	NP_001229	P24884										
192	NN032	Cytoskeleton	Cytoskeleton	Cytoskeleton	0.0	4039	14	9	0.0	7605	215	10	88	0.03	0.37	0.34	1.23	8	7	2	NP_004051	P51959									
193	NN033	CytoC	Pan-specific	Cytochrome C	0.0	2605	6	8	0.0	18996	85	11	-629	-0.22	0.91	1.13	4.09	12	7	2	NP_061820	P99999									
194	PN026	Dab1	Y198	Disabled homolog 1	0.0	386	10	5	0.0	510	115	6	32	-1.31	-1.23	0.08	0.30	16	7	2	NP_00189450.1	P08345									
195	NK034	DAXX	Pan-specific	Death-associated protein 1	0.0	5658	96	9	0.0	3984	139	9	-30	0.22	-0.01	-0.24	-0.85	4	7	3	NP_001341	Q6UEJ7									
196	PK591	DRP1	Y789/cyt197	Epithelial dissection domain-containing protein 1	0.0	4449	102	7	0.0	4257	4	7	-4	0.09	0.43	-0.34	-0.21	4	7	3	NP_001189450.1	P08345									
197	NN219	DKK2	Pan-specific	Diacylglycerol kinase 2	0.0	3807	29	9	0.0	7605	20	10	100	0.00	0.37	0.37	1.36	12	7	3	NP_063290	Q13574									
198	NK048	DNAPK	Pan-specific	DNA-activated protein kinase	0.0	514	14	6	0.0	650	7	6	27	-1.15	-1.08	0.06	0.23	16	7	3	NP_008835	P78527									
199	PK595	DNAPK	T2609	DNA-activated protein kinase	0.0	2320	39	8	0.0	2853	28	8	23	-0.29	-0.21	0.08	0.28	4	7	4	NP_008835	P78527									
200	PN027	Dak2	Y142	Docking protein 2	0.0	5057	30	9	0.0	4141	22	9	-18	0.16	0.01	-0.15	-0.54	12	7	5	NP_034201	Q6D498									
201	PN027-2	Dak2	Y142	Docking protein 2	0.0	8258	38	10	0.0	5296	16	10	-38	0.44	0.16	-0.28	-0.49	16	7	5	NP_034201	Q6D498									
202	NK002	DRAK2	Pan-specific	DAP kinase-related ap	0.0	9602	32	10	0.0	11036	26	9	5	0.52	0.59	0.06	0.24	16	7	5	NP_004217	Q9A769									
203	PN006-2	DUSP1 (MKP1)	Pan-Specific	MAP kinase phosphatase 1	0.0	52371	4	12	0.0	57511	11	13	10	1.49	1.57	0.07	0.26	4	7	5	NP_004408.1	P28562									
204	PN006-3	DUSP1 (MKP1)	Pan-Specific	MAP kinase phosphatase 1	0.0	62341	13	13	0.0	67111	7	13	8	1.59	1.66	0.06	0.23	8	7	5	NP_004408.1	P28562									
205	PN047-2	DUSP10	Pan-Specific	Dual specificity protein	0.0	9001	83	10	0.0	5604	39	9	-38	0.49	0.19	-0.30	-1.08	12	7	5	NP_009138.1	Q9Y6W6									
206	PN045-2	DUSP11	Pan-Specific	Phosphatidylinositol-3-OH kinase-related protein 1	0.0	16396	1	11	0.0	13081	22	10	-9	0.90	0.69	-0.21	-0.74	16	7	5	NP_001558.3	O15367									
207	PN045-3	DUSP11	Pan-Specific	Phosphatidylinositol-3-OH kinase-related protein 1	0.0	12848	10	13	0.0	12344	3	13	-4	0.89	0.64	-0.24	-0.66	4	7	6	NP_001558.3	O15367									
208	PN046-2	DUSP12	Pan-Specific	Dual specificity protein	0.0	17597	21	11	0.0	6642	49	9	-62	0.87	0.29	-0.58	-2.10	12	7	6	NP_009171.1	Q9JUN6									
209	PN046-3	DUSP12	Pan-Specific	Dual specificity protein	0.0	20860	27	11	0.0	12860	22	10	-38	0.97	0.68	-0.29	-1.04	12	7	6	NP_009171.1	Q9JUN6									
210	PN008-2	DUSP2	Pan-Specific	Dual specificity protein	0.0	70537	2	13	0.0	82695	14	13	17	1.66	1.78	0.12	0.42	16	7	6	NP_004409.1	Q08923									
211	PN008-4	DUSP2	Pan-Specific	Dual specificity protein	0.0	89426	8	13	0.0	89796	3	13	-1	1.79	1.81	0.02	0.07	4	7	7	NP_004409.1	Q08923									
212	PN032-2	DUSP3	Pan-Specific	Dual specificity protein	0.0	10864	12	13	0.0	10864	1	13	-1	1.66	1.69	0.03	0.15	15	7	7	NP_004081.1	P51452									
213	PN030-3	DUSP3	Pan-Specific	Dual specificity protein	0.0	13683	15	10	0.0	7118	29	10	-48	0.73	0.33	-0.40	-1.43	12	7	7	NP_004081.1	P51452									
214	PN030-4	DUSP3	Pan-Specific	Dual specificity protein	0.0	29820	14	12	0.0	26743	8	12	1.17	1.11	1.11	-0.06	-0.21	16	7	7	NP_004081.1	P51452									
215	PN007-3	DUSP4	Pan-Specific	Dual specificity protein	0.0	51925	13	12	0.0	54063	0	12	4	1.49	1.53	0.04	0.15	3	7	2	NP_01385.1	Q13116									
216	PN007-4	DUSP4	Pan-Specific	Dual specificity protein	0.0	54019	13	12	0.0	63054	12	13	1.73	1.51	1.62	0.11	0.39	7	7	2	NP_01385.1	Q13116									
217	PN039-2	DUSP5	Pan-Specific	Dual specificity protein	0.0	10447	39	11	0.0	78764	73	10	-34	0.70	0.23	-0.47	-1.09	11	7	2	NP_004413.3	P28609									
218	PN040-1	DUSP6	Pan-Specific	Dual specificity protein	0.0	50481	29	12	0.0	51767	26	12	3	1.47	1.50	0.03	0.11	15	7	2	NP_001937.2	Q16828									
219	PN040-2	DUSP6	Pan-Specific	Dual specificity protein	0.0	20708	29	11	0.0	12832	10	10	-38	0.96	0.68	-0.28	-1.03	3	7	3	NP_001937.2	Q16828									
220	PN040-3	DUSP6	Pan-Specific	Dual specificity protein	0.0	15026	18	11	0.0	16153	15	11	8	0.78	0.81	0.03	0.12	7	7	3	NP_001937.2	Q16828									
221	PN041-1	DUSP7	Pan-Specific	Dual specificity protein	0.0	17620	30	11	0.0	14386	16	11	-18	0.87	0.75	-0.12	-0.45	11	7	3	NP_001938.2	Q16829									
222	PN041-2	DUSP7	Pan-Specific	Dual specificity protein	0.0	36261	23	12	0.0	35773	49	12	-7	1.28	1.25	-0.03	-0.12	15	7	3	NP_001938.2	Q16829									
223	PN041-3	DUSP7	Pan-Specific	Dual specificity protein	0.0	34024	2	12	0.0	29910	4	12	-3	1.26	1.18	-0.08	-0.28	3	7	4	NP_001938.2	Q16829									
224	PN042-3	DUSP8	Pan-Specific	Dual specificity protein	0.0	26583	3	11	0.0	22231	3	11	-16	1.11	1.10	-0.10	-0.37	7	7	4	NP_004411.2	Q13202									
225	PN043-2	DUSP9	Pan-Specific	Dual specificity protein	0.0	30618	29	12	0.0	26332	22	11	-14	1.19	1.10	-0.08	-0.30	11	7	4	NP_01386.1	Q99596									
226	PN509	eEF1A1	Y141	Elongation factor 1-α	0.0	2440	29	8	0.0	2663	33	8	9	-0.26	-0.25	0.01	0.02	15	7	4	NP_01393.1	P68104									
227	NN175	EphA5	Pan-Specific	Ephrin-A5	0.0	55	35	5	0.0	0	29	5	-29	-1.41	-1.70	-0.29	-1.05	3	7	5	NP_001953.1	P28203									
228	NK052-1	EGFR	Pan-specific	Epidermal growth factor receptor	0.0	21066	12	11	0.0	12781	12	11	19	0.90	0.80	-0.10	-0.39	3	7	5	NP_005219	P00533									
229	NK052-4	EGFR	Pan-Specific	Epidermal growth factor receptor	0.0	49060	9	12	0.0	51119	10	12	4	1.46	1.50	0.04	0.14	3	7	7	NP_005219	P00533									
230	NK052-6	EGFR	Pan-Specific	Epidermal growth factor receptor	0.0	54753	17	12	0.0	56445	17	12	0	1.52	1.53	0.02	0.06	11	7	6	NP_005219	P00533									
231	NK052-6	EGFR	Pan-Specific	Epidermal growth factor receptor	0.0	44239	16	12	0.0	45427	12	12	3	1.40	1.43	0.03	0.11	15	7	6	NP_005219	P00533									
232	PK121	EGFR	T693	Epidermal growth factor receptor	0.0	753	43	6	0.0	1209	160	7	61	-0.93	-0.72	0.21	0.77	11	7	5	NP_005219	P00533									
233	PK122-1	EGFR	Y1088	Epidermal growth factor receptor	0.0	1258	9	6	0.0	568	10	6	-1	1.07	1.07	0.00	0.00	11	7	5	NP_005219	P00533									
234	PK123	EGFR	Y1110	Epidermal growth factor receptor	0.0	729	10	7	0.0	1278	7	4	-4	-0.65	-0.68	-0.04	-0.13	15	7	5	NP_005219	P00533									
235	PK010	EGFR	Y1148	Epidermal growth factor receptor	0.0	1480	2	7	0.0	1316	28	7	-1	-0.54	-0.67	-0.12	-0.45	3	7	6	NP_005219	P00533									
236	PK010-2	EGFR	Y1148	Epidermal growth factor receptor	0.0	958	7	7	0.0	1305	66																				



SAMPLE DETAILS

Sample IDs: Control ID: Pooled Samples Larger
Treated ID: Pooled Samples Smaller

[illegible]

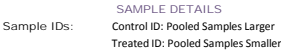


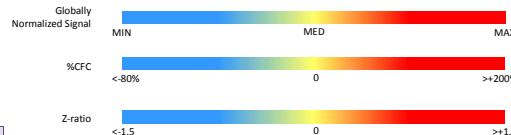
SAMPLE DETAILS

Sample IDs: Control ID: Pooled Samples Larger
Treated ID: Pooled Samples Smaller

						Globally Normalized Median							Globally Normalized Median												
						3433							4055												
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range Control	Log2 (Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range Treated	Log2 (Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link			
349	PN101	Histone H3	T3	Histone H3.3	0.0	20690	42	11	0.0	18338	25	11	-11	0.96	0.89	-0.07	-0.26	10	7	11	NP_033521	P84243			
350	PN101-2	Histone H3	T3	Histone H3.3	0.0	532	5	6	0.0	586	47	6	10	-1.13	-1.14	-0.02	-0.06	14	7	11	NP_033521	P84243			
351	NN052	HO1	Pan-specific	Heme oxygenase 1	0.0	19163	6	11	0.0	17993	11	11	-6	0.92	0.88	-0.04	-0.15	2	8	1	NP_002124	P09601			
352	NN053	HO2	Pan-specific	Heme oxygenase 2	0.0	20709	3	11	0.0	19407	5	11	-6	0.96	0.92	-0.04	-0.15	6	8	1	NP_002125	P30519			
353	NK072	HcK1	Pan-specific	Hematopoietic progenitor	0.0	5260	183	9	0.0	3561	11	9	-32	0.18	-0.08	-0.26	-0.11	10	8	1	NP_009112	O92918			
354	NN054	Hsp70	Pan-specific	Heat shock 70 kDa pr	0.0	14662	26	11	0.0	14662	60	7	11	-0.69	-0.52	-0.17	-0.64	14	8	1	NP_005886	P11142			
355	NN054-2	Hsp70	Pan-specific	Heat shock 70 kDa pr	0.0	20551	1	11	0.0	18527	13	11	-10	-0.96	0.90	-0.06	-0.23	2	8	2	NP_005886	P11142			
356	NN055	HSF4	Pan-specific	Heat shock transcript	0.0	611	68	6	0.0	466	52	6	-24	-1.05	-1.28	-0.23	-0.84	6	8	2	NP_001531	Q8ULV9			
357	NN062	Hsp105	Pan-specific	Heat shock 105 kDa p	0.0	2380	326	8	0.0	3608	247	9	52	-0.27	-0.07	0.20	0.73	10	8	2	NP_006635	O25268			
358	NN152-1	Hsp25	Pan-specific	Heat shock 27 kDa pr	0.0	19543	6	11	0.0	19701	16	11	1	0.93	0.93	0.00	0.01	1	7	8	NP_001531	P04792			
359	PN042-3	Hsp25	S82	Heat shock 27 kDa pr	0.0	1673	12	7	0.0	862	11	6	-48	-0.47	-0.92	-0.45	-1.61	14	8	2	NP_001531	P04792			
360	PN042-2	Hsp27	S15	Heat shock 27 kDa pr	0.0	6818	7	11	0.0	7325	7	6	7	0.33	0.35	0.02	0.03	13	7	8	NP_001531	P04792			
361	PN041	Hsp27	S78	Heat shock 27 kDa pr	0.0	29180	1	11	0.0	25255	2	11	-13	1.16	1.08	-0.08	-0.29	9	7	8	NP_001531	P04792			
362	PN042-1	Hsp27	S86	Heat shock 27 kDa pr	0.0	568	2	6	0.0	498	25	6	-12	-1.09	-1.24	-0.15	-0.54	5	7	8	NP_001531	P04792			
363	NN057-2	Hsp40	Pan-specific	DnaJ homolog, subfam	0.0	8026	5	10	0.0	9717	8	10	21	0.42	0.51	0.09	0.33	1	7	9	NP_006136	P25685			
364	NN057-3	Hsp40	Pan-specific	DnaJ homolog, subfam	0.0	15211	20	11	0.0	14353	11	11	6	-0.79	0.74	-0.04	-0.15	5	7	9	NP_006136	P25685			
365	NN058	Hsp40	Pan-specific	Heat shock 47 kDa pr	0.0	241	45	4	0.0	1665	247	6	8	-1.11	-1.65	-0.54	-1.11	7	9	NP_001226	P25683				
366	NN059-1	Hsp60	Pan-specific	Heat shock 60 kDa pr	0.0	2863	16	8	0.0	3822	8	9	33	0.47	-0.04	0.13	0.47	13	7	9	NP_002147	P10809			
367	NN059-2	Hsp60	Pan-specific	Heat shock 60 kDa pr	0.0	63447	26	13	0.0	65455	32	13	3	1.60	1.64	0.04	0.14	1	7	10	NP_002147	P10809			
368	NN059-3	Hsp60	Pan-specific	Heat shock 60 kDa pr	0.0	262	2	5	0.0	268	13	5	2	-1.53	-1.61	-0.08	-0.27	1	7	11	NP_002147	P10809			
369	NN060-2	Hsp70	Pan-specific	Heat shock 70 kDa pr	1.1	791	49	6	1.1	3813	40	9	892	-0.90	-0.04	0.86	3.12	5	7	10	NP_005336	P08107			
370	NN060-3	Hsp70	Pan-specific	Heat shock 70 kDa pr	0.0	29004	3	11	0.0	32166	8	11	29	1.07	1.22	0.15	0.15	9	7	10	NP_005336	P08107			
371	NN061	Hsp90	Pan-specific	Heat shock 90 kDa pr	0.0	7241	721	7	0.0	7281	62	10	168	-0.19	0.34	0.53	1.84	13	7	10	NP_005339	P07900			
372	NN061-16	Hsp90 alpha	Pan-specific	Heat shock 90 kDa pr	0.0	18853	3	11	0.0	18690	18	11	-1	0.91	0.90	-0.01	-0.03	5	7	11	NP_005339	P07900			
373	NN165-1	Hsp90 beta	Pan-specific	Heat shock 90 kDa pr	0.0	27928	12	11	0.0	30671	7	12	10	1.13	1.19	0.06	0.22	9	7	11	NP_031381	P08238			
374	NN166	Hsp90a	Pan-specific	Heat shock 90 kDa pr	0.0	9453	13	10	0.0	9669	17	10	14	0.45	0.51	0.06	0.22	13	7	11	NP_005339	P07900			
375	NN165	Hsp90b	Pan-specific	Heat shock 90 kDa pr	0.0	7354	13	9	0.0	5080	14	22	13	-0.19	0.23	-0.42	-0.52	6	8	2	NP_031381	P08238			
376	NN167	Hsp90b	Pan-specific	Heat shock 90 kDa pr	0.0	128	5	4	0.0	526	25	3	99	-1.94	-1.64	-0.30	-1.11	8	1	11	NP_031381	P08238			
377	NN063	HspBp1	Pan-specific	Hsp70 binding protein	0.0	628	28	6	0.0	579	12	8	21	-1.03	-0.43	0.61	2.18	9	8	1	NP_036399	O93351			
378	NK193	IKK-1	Pan-specific	Aurora Kinase B (seer	0.0	3555	44	4	0.0	1939	7	9	52	-0.04	0.17	0.21	0.76	13	8	1	NP_042008	Q96GD4			
379	PN103	Huntingtin	S421	Huntingtin's disease 1	0.0	12703	149	10	0.0	4850	103	9	-62	0.68	0.10	-0.58	-2.10	1	8	2	NP_002102	P42856			
380	NN064-2	Ikb-β	Pan-specific	Inhibitor of NF-κappa-B	0.0	2169	61	8	0.0	2370	5	8	9	-0.32	-0.32	0.01	0.02	3	8	4	NP_065390	P25963			
381	NN064-1	IKK-α	Pan-specific	Acidic leucine-rich	0.0	15192	1352	34	0.0	15552	24	10	-0.79	-0.08	0.71	-0.08	0.71	5	2	NP_008226	P25963				
382	NN131	SET	Pan-specific	Protein SET	0.0	21401	3	11	0.0	18313	19	11	-14	0.98	0.89	-0.09	-0.34	9	8	2	NP_030302	Q01105			
383	NN025	IAP1	Pan-specific	Cellular inhibitor of apc	0.0	1497	31	7	0.0	2128	19	8	42	-0.54	-0.38	0.15	0.55	13	8	2	NP_001156	Q13490			
384	PK655	IKK	Y156+Y157	Intestinal cell (MAK-ik	0.0	7925	66	10	0.0	11593	183	10	46	0.42	0.62	0.20	0.74	4	8	3	NP_05735.1	Q9UP29			
385	PK153	IGF1R	Y1165+Y1166	Insulin-like growth fact	0.0	288	15	5	0.0	292	29	5	2	-1.48	-1.56	-0.08	-0.29	16	8	3	NP_000866	P08269			
386	PK152	IGF1R	Y1280	Insulin-like growth fact	0.0	1117	12	7	0.0	1235	46	7	35	-0.36	-0.35	0.01	0.01	12	8	3	NP_000866	P08269			
387	PK658	IGF1R	Y1346	Insulin-like growth fact	0.0	2470	20	8	0.0	2678	31	8	8	-0.25	-0.25	0.00	0.01	8	8	3	NP_000866	P08269			
388	NN075-6	IKK-α	Pan-specific	Inhibitor of NF-κappa-B	0.0	5788	35	9	0.0	6343	22	9	10	0.24	0.30	0.03	0.10	4	8	4	NP_001289	O18111			
389	NN084	IKBα	Pan-specific	Inhibitor of NF-κappa-B	0.0	1752	14	7	0.0	2005	15	8	14	-0.45	-0.42	0.03	0.10	8	8	4	NP_065390	P25963			
390	PN164	IKBα	Y42	Inhibitor of NF-κappa-B	0.0	931	4	7	0.0	1194	8	7	28	-0.81	-0.72	0.08	0.30	12	8	4	NP_065390	P25963			
391	NN085	IKBβ	Pan-specific	Inhibitor of NF-κappa-B	0.0	1216	2	7	0.0	1593	6	11	10	-0.15	-0.15	0.00	0.00	16	8	4	NP_002494	P14563			
392	PN168	IKBε	S22	NF-κappa-B inhibitor ε	0.0	1816	19	7	0.0	2020	10	8	-43	-0.43	-0.41	0.01	0.04	4	8	5	NP_004547.2	Q03022			
393	NK075-2	IKKα	Pan-specific	Inhibitor of NF-κappa-B	0.0	968	15	7	0.0	2457	22	8	154	-0.79	-0.30	0.49	1.77	8	8	5	NP_001289	O18111			
394	NK075-3	IKKα	Pan-specific	Inhibitor of NF-κappa-B	0.0	8566	8	10	0.0	10877	20	10	27	0.46	0.58	0.12	0.44	16	8	5	NP_001289	O18111			
395	PK154	IKKα	T23	Inhibitor of NF-κappa-B	0.0	338	42	5	0.0	467	13	6	38	-1.39	-1.28	0.11	0.39	12	8	5	NP_001289	O18111			
396	NN161	IKKγ/NEMO	Pan-specific	I-κappa-B kinase gam	0.0	865	6	9	0.0	985	6	9	-81	-0.66	-0.66	-0.00	-0.00	6	8	6	NP_003630	O9P8Q9			
397	NK075-2	IKK1	Pan-specific	Integrin-linked protein	0.0	2096	30	10	0.0	2350	12	10	8	-0.32	-0.34	0.02	0.07	8	8	6	NP_001547	O14920			
398	PK662	ILK1	Y351	Integrin-linked protein	0.0	908	35	6	0.0	1144	32	7	26	-0.82	-0.75	0.07	0.26	12	8	6	NP_001547	O14920			
399	PK663	InsR	Y1189	INSR insulin receptor	0.0	2329	23	7	0.0	2887	8	8	24	-0.28	-0.20	0.08	0.29	16	8	6	NP_001099	P06213			
400	NK079	Integrin α4	Pan-specific	Integrin receptor beta c	0.0	931	157	8	0.0	498	30	6	-47	-0.81	-1.24	-0.43	-1.57	4	8	7	NP_001099	P06213			
401	PN043	Integrin α4	S988	Integrin alpha 4 (VL4A	0.0	23763	12	12	0.0	5206	2	12	-12	1.2	1.51	0.30	0.00	8	8	7	NP_000878	P13812			
402	PN044	Integrin β1	S785	Integrin beta 1 (fibron	0.0	2556	14	8	0.0	4159	6	8	-0.23	0.02	0.25	0.23	0.72	7	NP_002202	O05468					
403	PK032-1	IR	Y972	Integrin receptor	0.0	1220	24	7	0.0	1316	34	7	8	-0.65	-0.67	-0.01	-0.05	16	8	7	NP_001099	P06213			
404	PK033	IR/IGF1R	Y1162/Y1163	Insulin receptor / Insul	0.0	389	1	5	0.0	506	9	6	30	-1.31	-1.23	0.07	0.26	4	8	8	NP_000866	P06213			
405	NK080-2	IRAK1	Pan-specific	Interleukin 1 receptor	0.0	972	8	13	0.0	801	47	8	209	-0.78	-0.18	0.60	2.18	8	8	8	NP_001560	P51617			
406	NN081	IRAK2	Pan-specific	Interleukin 1 receptor	0.0	3967	7	9	0.0	3810	5	9	-4	0.02	-0.04	-0.06	-0.03	12	8	8	NP_00107654.1	Q41187			
407	PK665	IRAK4	T345+S346	Interleukin 1 receptor	0.0	1682	17	10	0.0	14286	87	11	8	-0.85	-0.74	0.10	0.38	15	8	8	NP_00107654.1	Q41187			
408	PN117	IRS1	S312	Insulin receptor subst	0.0	626	25	6	0.0	1742	7	7	178	-1.03	-0.50	0.53	1.93	7	8	3	NP_005533	P35568			
409	PN118	IRS1	S639	Insulin receptor subst	0.0	175	44	4	0.0	295	56	5	69	-1.76	-1.55	0.21	0.76	11	8	3	NP_005533	P35568			
410	PN046-2	IRS1	Y1179	Insulin receptor subst	0.0	5644	23	9	0.0	4947	4	9	-12	0.22	0.12	-0.11	-0.38	3	8	3	NP_005533	P35568			
411	PN045	IRS1	Y612	Insulin receptor subst	0.0	2456	95																		

SAMPLE DETAILS																						
Control ID: Pooled Samples Larger																						
Treated ID: Pooled Samples Smaller																						
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized Median 3433		Log2 (Intensity Corrected) - Control	Flag-Treated	Globally Normalized Median 4055		Log2 (Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link
						%Error Range Control	%Error Range Treated															
436	PN048-2	Jun	S73	Jun proto-oncogene-e	0.0	9708	4	10	0.0	10409	16	10	7	0.53	0.56	0.02	0.09	6	8	4	NP_002219	P05412
437	PN163	Jun	T91	Jun proto-oncogene-e	0.0	606	2	6	0.0	1795	73	8	166	-1.05	-0.48	0.57	2.06	2	8	4	NP_002219	P05412
438	PN155	Jun	Y170	Jun proto-oncogene-e	0.0	516	138	6	0.0	447	164	6	-13	-1.14	-1.30	-0.16	-0.58	14	8	3	NP_002219	P05412
439	NP004	KAP		Cyclin-dependent kin	0.0	1202	30	7	0.0	3610	51	9	200	-0.66	-0.07	0.59	2.14	2	8	5	NP_005163	Q16662
440	NN153	ER lum		ER lumen protein ret	0.0	1985	9	8	0.0	2444	22	8	23	-0.37	-0.30	0.07	0.27	6	8	5	NP_006792.1	P24390
441	NK241-2	Kit		Mast/stem cell growth	0.0	50161	1	12	0.0	53222	12	12	6	1.47	1.52	0.05	0.18	6	8	6	NP_006566	P10721
442	PK036	Kit	Y703	Mast/stem cell growth	0.0	8045	49	10	0.0	7174	29	10	-11	-0.42	0.34	-0.09	-0.32	10	8	5	NP_006566	P10721
443	PK150	Kit	Y721	Mast/stem cell growth	0.0	566	48	6	0.0	774	29	6	37	-1.09	-0.98	0.11	0.40	10	8	6	NP_006566	P10721
444	PK037	Kit	Y730	Mast/stem cell growth	0.0	7955	43	10	0.0	7226	37	10	-9	-0.42	0.34	-0.08	-0.28	14	8	5	NP_006566	P10721
445	PK038	Kit	Y936	Mast/stem cell growth	0.0	878	11	6	0.0	1768	157	7	101	-0.84	-0.49	0.35	1.26	2	8	6	NP_006566	P10721
446	NK090-2	Krs-1		Protein-serine kinase	0.0	1406	60	7	0.0	1921	58	8	37	-0.57	-0.44	0.13	0.47	14	8	6	AA050354.1	Q8V176
447	NK113-3	Krs-2		Mammalian STE20-lik	0.0	1113	94	7	0.0	3174	16	8	185	-0.71	-0.15	0.56	2.02	2	8	7	NP_006273	Q13043
448	NP005	LAR		LCA antigen-related	0.0	437	15	5	0.0	264	8	5	-39	-1.24	-1.62	-0.38	-1.36	6	8	7	NP_002831	P10586
449	NK092-2	Lck		Lymphocyte-specific p	0.0	1396	8	4	0.0	1233	4	7	-12	-0.13	-0.47	-0.34	-1.10	10	8	8	NP_005347	P06239
450	NK092-3	Lck		Lymphocyte-specific p	0.0	275	2	5	0.0	229	25	5	-17	-1.50	-1.70	-0.20	-0.71	14	8	8	NP_005347	P06239
451	PK039	Lck	S158	Lymphocyte-activated prot	0.0	4426	33	9	0.0	5575	24	9	26	0.08	0.19	0.10	0.37	14	8	7	NP_005347	P06239
452	PK040	Lck	Y192	Lymphocyte-specific p	0.0	7334	21	9	0.0	7012	4	9	-1	0.37	0.32	-0.05	-0.18	2	8	8	NP_005347	P06239
453	PK149	Lck	Y394	Lymphocyte-specific p	0.0	13640	19	10	0.0	13794	16	10	-4	0.73	0.72	0.00	-0.01	10	8	7	NP_005347	P06239
454	PK041	Lck	Y505	Lymphocyte-specific p	0.0	469	55	6	0.0	263	55	5	-44	-1.20	-1.52	-0.32	-1.52	6	8	8	NP_005347	P06239
455	NK093	LIMK1		LIM domain kinase 1	0.1	3197	515	8	0.1	1438	27	7	-55	-0.10	-0.61	-0.51	-1.85	1	8	3	NP_002305	P53667
456	PK042-PK144	LIMK1/2	Y507/Y508	LIM domain kinase 1	0.0	5363	34	9	0.0	4053	7	9	-24	0.19	0.00	-0.19	-0.70	5	8	3	NP_002305	P53667
457	NK227-2	LKB1		Serine/threonine-prote	0.0	61763	5	13	0.0	69262	10	13	12	1.59	1.67	0.09	0.32	9	8	3	NP_000446.1	Q15831
458	NK227-3	LKB1		Serine/threonine-prote	0.0	20178	51	11	0.0	20566	108	11	2	0.95	0.96	0.01	0.03	13	8	3	NP_000446.1	Q15831
459	NK227-4	LKB1		Serine/threonine-prote	0.0	14788	28	12	0.0	14788	28	12	-1	1.44	1.44	0.00	0.00	1	8	4	NP_000446.1	Q15831
460	NK095	Lyn		Yes-related protein-tyr	0.0	1348	3	7	0.0	4547	30	9	237	-0.60	0.07	0.66	2.40	5	8	4	NP_002341	P07348
461	NK097	MAPKAPK2		Mitogen-activated prot	0.0	1678	25	7	0.0	3115	17	8	86	-0.47	-0.16	0.31	1.13	13	8	4	NP_004750	P49137
462	PK044	MAPKAPK2	T222	Mitogen-activated prot	0.0	560	26	6	0.0	1120	56	7	100	-1.10	-0.76	0.34	1.21	1	8	5	NP_004750	P49137
463	PK045	MAPKAPK2	T334	Mitogen-activated prot	0.0	1445	16	7	0.0	1097	8	7	-24	-0.56	-0.77	-0.22	-0.79	9	8	4	NP_004750	P49137
464	PK093	MAPKAPK5	T186	MAP kinase-activated	0.0	16465	58	11	0.0	14079	106	11	-9	0.83	0.77	-0.06	-0.23	5	8	5	NP_003659.2	Q08441
465	PN050-1	MARCKS	S152/S156	Myristoylated alanine-r	0.0	135	51	4	0.0	290	9	5	115	-1.91	-1.56	0.35	1.26	9	8	5	NP_002347	P20966
466	PK694	MARK1	T215	MAP/microtubule affir	0.0	36305	34	12	0.0	28740	36	12	-21	1.28	1.16	-0.13	-0.47	13	8	5	NP_001273053.1	Q9P0L2
467	NN067	Mcl1		Myeloid cell leukemia 1	0.0	2271	11	8	0.0	2092	18	8	-8	-0.30	-0.39	-0.09	-0.34	1	8	6	NP_068779	P07820
468	PN169	MDM2	S166	Double minute 2	0.0	5473	18	9	0.0	5862	12	9	7	0.20	0.22	0.01	0.04	5	8	6	NP_001138699.1	Q00987
469	NN155	MEF-2		Myelin expression fact	0.0	2042	19	8	0.0	2342	19	8	77	-0.04	0.65	0.69	2.57	15	8	6	NP_057158.2	Q08265
470	NK099-1	MEK1		MAPK/ERK protein-se	0.0	639	52	6	0.0	618	23	6	-3	-1.02	-1.11	-0.09	-0.33	4	8	9	NP_002746	Q02750
471	NK099-3	MEK1		MAPK/ERK protein-se	0.0	20145	60	11	0.0	14186	65	11	-30	-0.95	-0.94	-0.21	-0.76	5	8	7	NP_002746	Q02750
472	NK099-7	MEK1		MAPK/ERK protein-se	0.0	38666	7	12	0.0	38143	19	12	3	1.29	1.32	0.03	0.11	1	8	8	NP_002746	Q02750
473	NK099-8	MEK1		MAPK/ERK protein-se	0.0	94544	22	12	0.0	83120	25	13	16	1.52	1.62	0.10	0.38	9	8	7	NP_002746	Q02750
474	NK099-9	MEK1		MAPK/ERK protein-se	0.0	21501	63	11	0.0	16995	46	11	-21	0.98	0.84	-0.14	-0.51	13	8	7	NP_002746	Q02750
475	PK046-2	MEK1	S292	MAPK/ERK protein-se	0.0	17494	17	11	0.0	13167	17	11	-25	0.87	0.69	-0.17	-0.63	5	8	8	NP_002746	Q02750
476	PK047-2	MEK1	S298	MAPK/ERK protein-se	0.0	15786	39	11	0.0	12678	10	-20	0.81	0.67	-0.14	-0.50	9	8	8	NP_002746	Q02750	
477	PK046-1	MEK1	T292	MAPK/ERK protein-se	0.0	18950	59	12	0.0	12969	49	10	-23	0.85	0.69	-0.16	-0.59	13	8	6	NP_002746	Q02750
478	PK048-1	MEK1	T386	MAPK/ERK protein-se	0.0	5174	49	9	0.0	3896	38	9	-25	0.17	-0.03	-0.20	-0.71	1	8	7	NP_002746	Q02750
479	PK048-2	MEK1	T386	MAPK/ERK protein-se	0.0	22688	28	11	0.0	18317	26	11	-19	1.02	0.89	-0.13	-0.46	13	8	8	NP_002746	Q02750
480	PK045-PN007	MEK1 + MEK2	S217-S221	B23 (nucleophosin, 1)	0.0	134	38	4	0.0	138	21	4	3	-1.91	-2.00	-0.08	-0.31	8	8	9	NP_002511	P06748
481	NK100-1	MEK2		MAPK/ERK protein-se	0.0	215	28	4	0.0	516	148	6	141	-1.64	-1.22	0.42	1.94	12	8	10	AAH00471.1	P36507
482	NK100-4	MEK2		MAPK/ERK protein-se	0.0	24011	27	11	0.0	27207	31	11	13	1.05	1.12	0.07	0.27	4	8	10	AAH00471.1	P36507
483	NK100-5	MEK2		MAPK/ERK protein-se	0.0	41022	8	12	0.0	45372	12	12	11	1.35	1.42	0.07	0.26	16	8	9	AAH00471.1	P36507
484	NK100-6	MEK2		MAPK/ERK protein-se	0.0	30589	6	12	0.0	30318	7	11	-34	1.19	0.95	-0.24	-0.85	8	8	10	AAH00471.1	P36507
485	PK049	MEK2	T394	MAPK/ERK protein-se	0.0	2252	10	8	0.0	3563	12	9	58	-0.30	-0.08	0.22	0.81	12	8	9	AAH00471.1	P36507
486	PK049-2	MEK2 human	T394	MAPK/ERK protein-se	0.0	4016	4	9	0.0	4041	15	9	1	0.03	0.00	-0.03	-0.11	16	8	10	AAH00471.1	P36507
487	PK050	MEK2 mouse	T394	MAPK/ERK protein-se	0.0	8516	18	10	0.0	6673	1	9	-22	0.46	0.29	-0.16	-0.59	4	8	11	NP_075627	P36507
488	NK101	MEK3	</																			

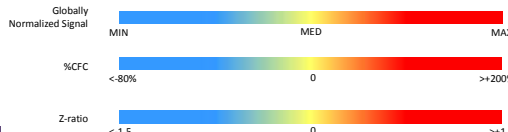




SAMPLE DETAILS

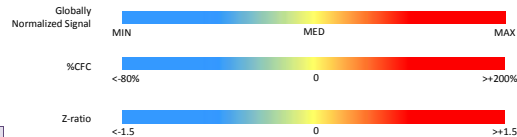
Sample IDs: Control ID: Pooled Samples Larger
Treated ID: Pooled Samples Smaller

										Globally Normalized Median		Globally Normalized Median		-1.5		0		>1.5											
										3433		4055																	
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range Control	Log2 (Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range Treated	Log2 (Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link							
610	NK123	PAK3		p21-activated kinase 3	0.0	2603	62	8	0.0	3002	63	9	92	-0.36	-0.02	0.34	1.22	15	9	6	NP_002569	Q75914							
611	PK752	PAK4	S474	p21-activated kinase 4	0.0	19767	28	11	0.0	24523	68	11	24	0.94	1.06	0.12	0.45	3	9	7	NP_001014831.1	Q98013							
612	NK200-2	PAKγ		p21-activated kinase 2	0.0	1573	30	0	0.0	3708	17	9	136	-0.51	-1.05	0.45	1.64	7	9	7	NP_002568.2	Q13177							
613	NN085-1	PARP1		Poly (ADP-ribose) poly	0.0	38105	7	12	0.0	51771	20	12	36	1.31	1.50	0.19	0.69	11	9	7	NP_001609	Q08874							
614	NN086	Paxillin		Paxillin 1	0.0	173	2	0	0.0	202	8	4	17	-1.77	-1.78	-0.01	-0.01	15	9	7	NP_002850	P49023							
615	PN069	Y118		Paxillin 1	0.0	465	4	4	0.0	1115	6	4	30	-0.46	-0.76	0.30	0.77	7	9	8	NP_002850	P49023							
616	PK59	Y31		Paxillin 1	0.0	1925	8	6	0.0	2367	8	6	7	-0.39	-0.40	0.01	-0.03	3	9	8	NP_002850	P49023							
617	NK125	PCTK1		PCTAIRE-1 protein-ase	0.0	3655	300	0	0.0	3370	95	8	7	-0.03	-0.11	-0.08	-0.31	11	9	8	NP_148978	Q00536							
618	PK756	PCKT2	S180	Cell division protein kin	0.0	4256	73	9	0.0	4423	67	9	4	0.06	0.05	-0.01	-0.04	15	9	8	NP_001163935.1	Q00537							
619	NK242-1	PDGFRα		Platelet-derived growth	0.0	46010	22	12	0.0	41257	4	12	-10	1.42	1.37	-0.05	-0.18	7	9	9	NP_006197.1	P16234							
620	NK242-2	PDGFRα		Platelet-derived growth	0.0	36176	12	12	0.0	43015	19	12	1.28	1.39	0.11	0.40	11	9	9	NP_006197.1	P16234								
621	PK757	PDGFRβ	S847-rp0848	Platelet-derived growth	0.0	8417	22	10	0.0	8417	22	10	0.45	0.63	0.18	0.63	14	9	9	NP_006197.1	P16234								
622	PK603	Y754		Platelet-derived growth	0.0	8031	32	10	0.0	6863	14	9	-15	0.42	0.31	-0.11	-0.41	3	9	9	NP_006197.1	P16234							
623	PK758	PDGFRα	Y762	Platelet-derived growth	0.0	7580	12	10	0.0	11262	4	10	49	0.39	0.60	0.21	0.77	2	9	4	NP_006197.1	P16234							
624	PK759	PDGFRα	Y768	Platelet-derived growth	0.0	2659	138	8	0.0	2225	42	8	-16	-0.21	-0.36	-0.15	-0.54	6	9	4	NP_006197.1	P16234							
625	NK243-1	PDGFRβ		Platelet-derived growth	0.0	5065	58	9	0.0	3817	78	9	27	0.16	-0.04	-0.20	-0.71	14	9	4	NP_002600.1	Q08619							
626	NK243-3	PDGFRβ		Platelet-derived growth	0.0	5409	2	10	0.0	19771	75	10	0.51	0.75	0.24	0.93	2	9	5	NP_002600.1	Q08619								
627	PK065	PDGFRβ	Y716	Platelet-derived growth	0.0	24812	10	8	0.0	3560	31	9	27	-0.18	-0.08	-0.10	0.35	10	9	4	NP_0032835	Q08619							
628	NN141-1	PDI		Protein disulfide-isom	0.0	21505	13	11	0.0	21298	12	11	-1	0.98	0.98	-0.01	-0.02	6	9	5	NP_00909.2	Q07237							
629	NK126-2	POK1		3-phosphoinositide-de	0.0	890	22	6	0.0	2874	144	8	223	-0.83	-0.21	0.63	2.27	2	9	6	NP_002604	Q15530							
630	NN179-1	POK1		Pyruvate dehydrogena	0.0	38600	10	12	0.0	46345	22	12	20	1.32	1.44	0.12	0.43	10	9	5	NP_001265478.1	Q15118							
631	NN179-2	POK1		Pyruvate dehydrogena	0.0	21817	22	11	0.0	19230	10	12	-12	0.99	0.92	-0.07	-0.14	9	5	5	NP_001265478.1	Q15118							
632	NN180-1	POK2		Pyruvate dehydrogena	0.0	34975	11	11	0.0	36205	12	12	1.26	1.26	0.00	0.28	6	9	6	NP_002602	Q15119								
633	NN180-2	POK2		Pyruvate dehydrogena	0.0	43078	56	12	0.0	35866	5	12	-17	1.38	1.29	-0.10	-0.35	10	9	6	NP_002602	Q15119							
634	NN181-1	POK3		Pyruvate dehydrogena	0.0	1040	19	7	0.0	1193	6	7	15	-0.74	-0.72	-0.02	0.07	14	9	6	NP_001135858.1	Q15120							
635	NN181-2	POK3		Pyruvate dehydrogena	0.0	39129	12	12	0.0	42523	35	12	16	1.33	1.42	0.10	0.35	2	9	7	NP_001135858.1	Q15120							
636	NN178-2	POK4		Pyruvate dehydrogen	0.0	38417	3	12	0.0	37331	32	12	-3	1.32	1.31	-0.01	-0.02	6	9	7	NP_002603.1	Q15054							
637	NN178-3	POK4		Pyruvate dehydrogen	0.0	37241	3	12	0.0	34441	6	12	-10	1.40	1.40	0.00	0.00	14	9	7	NP_002603.1	Q15054							
638	PN061	PEID5 (PEA15)	S116	Phosphoprotein-ench	0.0	2029	38	12	0.0	1772	5	7	-13	-0.36	-0.49	-0.13	-0.47	14	9	7	NP_003759	Q15121							
639	NN088	PERP		p53-induced protein 3	0.0	6504	26	9	0.0	4437	54	9	-32	0.30	0.05	-0.25	-0.91	2	9	8	NP_071404	Q9H230							
640	NN089	P13-Kinase		Phosphatidylinositol 3	0.0	1355	19	7	0.0	597	121	6	-56	-0.59	-1.13	-0.54	-1.96	6	9	8	NP_852664	P27896							
641	NK213	PITSLRE		PITSLRE serine/threo	0.0	2401	57	8	0.0	2315	15	8	-4	-0.27	-0.33	-0.07	-0.24	10	9	8	NP_001278274.1	P21127							
642	PKA	PKA		cAMP-dependent prot	0.0	364	24	5	0.0	364	24	5	-1	-1.42	-1.42	0.00	0.00	11	9	11	NP_002721	P17542							
643	PK067	PKA Cαb	T197	cAMP-dependent prot	0.0	7780	13	10	0.0	6167	15	9	-4	0.40	0.25	-0.16	-0.57	2	9	9	NP_002721	P17812							
644	PK068	PKA Cα	S338	cAMP-dependent prot	0.0	1893	2	8	0.0	3065	64	8	62	-0.40	-0.17	0.23	0.85	6	9	9	NP_002722	P22694							
645	PK069	S98		cAMP-dependent prot	0.0	156	20	4	0.0	193	28	4	24	-1.83	-1.80	0.03	0.09	10	9	9	NP_523671	P13861							
646	NK130-5	PKBζ-PCT		RAC-beta serine/threo	0.0	11474	66	10	0.0	7541	17	10	-34	0.63	0.36	-0.26	-0.95	14	9	9	NP_001817	P31751							
647	NK130-6	PKCβ1		Protein kinase C β1a	0.0	10216	29	7	0.0	10714	29	7	-73	-0.79	-0.20	0.63	2.99	4	9	4	NP_005046.2	P24742							
648	NK132	PKCα		Protein-serine kinase	0.0	753	39	6	0.0	813	14	6	8	-0.93	-0.95	-0.02	-0.09	5	9	8	NP_002728	P17252							
649	PK073	PKCα	S657	Protein-serine kinase	0.0	5228	10	9	0.0	6129	29	9	17	0.18	0.24	0.06	0.23	9	9	4	NP_002728	P17252							
650	NK133-2	PKCβ		Protein-serine kinase	0.0	10630	10	10	0.0	11104	25	10	4	0.58	0.59	0.01	0.04	13	9	4	NP_002729	P06771							
651	PK076-2	PKCβ2	T641	Protein-serine kinase	0.0	2893	113	8	0.0	2962	47	8	2	-0.16	-0.19	-0.03	-0.10	1	9	5	NP_002729	P06771							
652	NK133	PKCβ1		Protein-serine kinase	0.0	1918	19	7	0.0	2104	48	73	-65	-0.65	-0.59	-0.06	-0.10	13	9	5	NP_002729	P06771							
653	PK075-2	PKCβ12	T500	Protein-serine kinase	0.0	3765	301	1	0.0	3016	28	1	8	-0.01	0.18	0.19	0.57	9	9	5	NP_002729	P06771							
654	NK135	PKCβ		Protein-serine kinase	0.0	6180	1	9	0.0	8896	28	10	0.27	0.46	0.19	0.68	9	9	6	NP_002729	Q05655								
655	PK079-1	PKCα	S645	Protein-serine kinase	0.0	483	32	6	0.0	522	13	6	-18	-1.18	-1.21	-0.03	-0.11	5	9	6	NP_006245	Q05655							
656	PK080	PKCα	S664	Protein-serine kinase	0.0	2583	28	8	0.0	1625	1	7	-37	-0.22	-0.54	-0.32	-1.15	1	9	6	NP_006245	Q05655							
657	PK077-1	PKCα	Y311	Protein-serine kinase	0.0	10811	40	10	0.0	9700	29	10	0.59	0.59	0.00	-0.08	-0.29	13	9	5	NP_006245	Q05655							
658	PK078-1	PKCα	Y311	Protein-serine kinase	0.0	20526	28	11	0.0	20526	28	11	0.96	0.96	0.00	0.83	0.83	0.83	10	9	5	NP_006245	Q05655						
659	NK136	PKCε		Protein-serine kinase	0.0	1798	17	7	0.0	4000	28	9	122	-0.43	-0.01	0.42	1.53	5	9	7	NP_005391	Q02156							
660	NK136-2	PKCε		Protein-serine kinase	0.0	1526	23	7	0.0	2074	27	8	36	-0.53	-0.40	-0.13	0.46	9	9	7	NP_005391	Q02156							
661	PK081-1	PKCε	S729	Protein-serine kinase	0.0	1114	43	7	0.0	1078	28	7	-3	-0.70	-0.78	-0.08	-0.29	13	9	7	NP_005391	Q02156							
662	PK081-2	PKCε	S729	Protein-serine kinase	0.0	671	18	6	0.0	567	15	6	-16	-0.99	-1.18	-0.17	-0.62	1	9	7	NP_005391	Q02156							
663	PK082-1	PKCγ	TS14	Protein-serine kinase	0.0	2155	21	9	0.0	2254	10	9	0.26	0.26	0.00	0.26	0.26	9	9	8	NP_002730	P05129							
664	PK082-1	PKCγ	TS14	Protein-serine kinase	0.0	655	17	9	0.0	5732	10	9	-13	0.31	0.24	-0.07	-0.38	1	9	8	NP_002730	P05129							
665	PK082-2	PKCγ	TS14	Protein-serine kinase	0.0	17795	19	11	0.0	15132	14	11	-15	0.88	0.78	-0.10	-0.36	13	9	8	NP_002730	P05129							
666	PK083	PKCγ	T655	Protein-serine kinase	0.0	8305	5	10	0.0	7342	5	10	-12	0.44	0.35	-0.09	-0.34	5	9	8	NP_002730	P05129							
667	PK084	PKCγ	T674	Protein-serine kinase	0.0	10573	10	10	0.0	8342	10	10	-21	0.58	0.42	-0.16	-0.56	1	9	9	NP_002730	P05129							
668	PK085	PKCγ	T655	Protein-serine kinase	0.0	11523	9	10	0.0	10967	5	10	-5	0.63	0.59	-0.04	-0.16	5	9	9	NP_006246	P24722							
669	NK138-1	PKCζ		Protein-serine kinase	0.0	4027	23	9	0.0	5532	20	9	0.03	0.40	0.37	0.93	13	9	9	NP_002731	P41743								
670	PK082	PKCζ	T555/T563	Protein-serine kinase	0.0	1513	10	7	0.0	1379	37	7	-9	-0.53	-0.64	-													



Sample IDs: Control ID: Pooled Samples Larger Treated ID: Pooled Samples Smaller

					Globally Normalized Median 3433						Globally Normalized Median 4055															
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range Control	Log2 (Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range Treated	Log2 (Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link				
697	NP019	PP4/A2		Protein-serine phosph	0.0	45533	3	12	0.0	41310	4	12	-9	1.41	1.37	-0.04	-0.16	11	9	10	NP_005125	Q8T105				
698	NP020	PP4C (X/C)		Protein-serine phosph	0.0	39829	1	12	0.0	35203	1	12	-12	1.34	1.28	-0.06	-0.22	15	9	10	NP_002711	P60510				
699	NP020-2	PP4C (X/C)		Protein-serine phosph	0.0	53155	18	12	0.0	49504	6	12	-7	1.50	1.48	-0.02	-0.09	3	9	11	NP_002711	P60510				
700	NP021	PP5R/PP1		Protein-serine phosph	0.0	532	17	6	0.0	461	9	6	-13	0.13	0.29	0.16	0.16	7	9	11	NP_000238	P53441				
701	PN532	PPP1R11	Y64	Protein phosphatase 1	0.0	3083	118	8	0.0	1545	26	7	-50	-0.12	-0.57	-0.45	-1.62	11	9	11	NP_068778.1	O80927				
702	PN062	PRAS40	T246	Proline-rich Akt substr	0.0	1628	35	7	0.0	1396	30	7	-14	-0.49	-0.63	-0.14	-0.52	15	9	11	NP_115751	O96B36				
703	NK149	PRK2		Protein kinase C-relat	0.0	17130	3	11	0.0	11951	8	10	-30	0.86	0.64	-0.22	-0.79	3	10	1	NP_006247	Q16513				
704	NK149-2	PRK2		Protein kinase C-relat	0.0	1256	2	7	0.0	2329	0	8	85	-0.64	-0.33	0.31	0.11	7	10	1	NP_006247	Q16513				
705	NK048-4	PRKDC (DNAPK)		DNA-activated protein	0.0	47335	2	12	0.0	40545	6	12	-2	1.44	1.44	0.00	0.02	11	10	1	NP_001075109.1	P78527				
706	NK048-5	PRKDC (DNAPK)		DNA-activated protein	0.0	35148	3	12	0.0	43390	7	12	23	1.27	1.40	0.13	0.48	15	10	1	NP_001075109.1	P78527				
707	NK048-6	PRKDC (DNAPK)		DNA-activated protein	0.0	46880	14	12	0.0	43481	2	12	-7	1.43	1.40	-0.03	-0.11	3	10	2	NP_001075109.1	P78527				
708	NK048-7	PRKDC (DNAPK)		DNA-activated protein	0.0	39928	3	12	0.0	44350	10	12	11	1.34	1.41	0.07	0.27	7	10	2	NP_001075109.1	P78527				
709	NK151	PRKWNK4		Putative protein-serine	0.0	2062	5	8	0.0	2850	10	8	38	-0.35	-0.21	0.14	0.52	11	10	2	NP_115763	Q86392				
710	PN104	PRKWNK4		Putative protein-serine	0.0	463	6	8	0.0	550	46	8	19	-0.02	0.08	0.06	0.08	15	10	2	NP_000917	P26401				
711	PK786	PRF4K	T649	Protein-serine kinase f	0.0	3358	35	8	0.0	3306	12	8	-2	-0.07	-0.12	-0.05	-0.17	3	10	3	NP_003904.3	Q13523				
712	NN142	PSD-95		Disks large homolog 4	0.0	310	14	5	0.0	1937	34	8	526	-1.44	-0.44	1.00	3.91	7	10	3	NP_001356.1	P78352				
713	NP023	PTEN		Phosphatidylinositol-3	0.0	3599	12	8	0.0	25090	58	11	59	-0.04	1.07	1.11	4.02	15	10	4	NP_000305	P60484				
714	NP023-3	PTEN		Phosphatidylinositol-3	0.0	9447	63	10	0.0	14249	70	11	51	0.52	0.74	0.23	0.82	3	10	4	NP_000305.3	P60484				
715	NP023-5	PTEN		Phosphatidylinositol-3	0.0	35773	5	12	0.0	33261	5	12	-7	1.28	1.24	-0.03	-0.12	7	10	4	NP_000305	P60484				
716	PP003	PTEN	S380/S382/S385	Phosphatidylinositol-3	0.0	2750	5	8	0.0	2356	6	8	-14	-0.19	-0.32	-0.13	-0.48	15	10	3	NP_000305	P60484				
717	PP006	PTEN	S380/S382/S385	Phosphatidylinositol-3	0.0	267	57	5	0.0	347	36	5	35	-1.54	-1.45	0.09	0.32	11	10	3	NP_000305	P60484				
718	PP006-1	PTEN	S380/S382/S385	Phosphatidylinositol-3	0.0	713	15	6	0.0	755	7	6	6	-0.96	-0.99	-0.04	-0.13	11	10	4	NP_000305	P60484				
719	NP024	PTPFB		Protein-tyrosine phosph	0.0	1112	33	7	0.0	1215	50	7	6	-0.71	-0.71	-0.01	-0.03	2	9	10	NP_002818	P18031				
720	NP025	PTP1C		Protein-tyrosine phosph	0.0	1225	3	7	0.0	1529	25	6	-57	-0.65	-0.55	-0.10	-0.55	6	9	10	NP_002822	P29350				
721	NP026	PTP1D/SHP2		Protein-tyrosine phosph	0.0	2148	0	8	0.0	1270	36	7	-41	-0.33	-0.69	-0.36	-1.29	10	9	10	NP_002825	O06124				
722	NP036	PTP1D		Protein-tyrosine phosph	0.0	16379	27	11	0.0	13269	31	10	-19	0.83	0.70	-0.13	-0.47	14	9	10	NP_088970.2	Q16825				
723	NP027	PTP-PEST		Protein tyrosine phosph	0.0	4726	42	9	0.0	7382	18	10	56	0.12	0.35	0.23	0.84	2	9	11	NP_001124480.1	Q05209				
724	PG001	PYK	pTyr	Generic phosphotyros	0.0	8650	148	10	0.0	6809	76	9	-21	0.47	0.30	-0.16	-0.58	6	9	11	N/A	N/A				
725	NK154	PyK2		Protein-tyrosine kinase	0.0	1855	83	8	0.0	2338	25	8	26	-0.41	-0.33	0.09	0.31	14	9	11	NP_004094	Q14289				
726	PK097-3	PKYK2	Y579	Protein-tyrosine kinase	0.0	344	17	5	0.0	347	9	5	1	-1.37	-1.45	-0.08	-0.29	10	9	11	NP_004094	Q14289				
727	PG005	PKXSD8	pTyr	Phosphotyrosine resid	0.0	28208	15	11	0.0	21601	37	11	-23	1.14	0.99	-0.15	-0.55	2	10	1	N/A	N/A				
728	NN092-1	Rac1		Ras-related G3 botulin	0.0	784	39	6	0.0	565	12	6	-28	-0.91	-1.17	-0.26	-0.95	6	10	1	NP_001782	P63300				
729	PN063	Rac1tcd42	S71	Ras-related G3 botulin	0.0	1041	25	7	0.0	890	24	7	-14	-0.74	-0.90	-0.15	-0.56	10	10	1	NP_008839	P76300				
730	PN064	Rad17	S645	Rad17 homolog	0.0	148	37	4	0.0	150	31	4	2	-1.86	-1.95	-0.09	-0.33	14	10	1	NP_579921	Q75843				
731	PK098	Raf1	S259	Raf1 proto-oncogene+	0.0	182	48	4	0.0	186	37	4	2	-1.74	-1.82	-0.08	-0.30	2	10	2	NP_002871	P04049				
732	NK155-4	Raf-1		Raf1 homolog	0.0	3382	24	8	0.0	1418	20	7	-58	-0.07	-0.62	-0.55	-2.00	14	10	2	NP_002871	P04049				
733	NK155-5	Raf-1		Raf1 proto-oncogene+	0.0	26125	1	11	0.0	34069	13	12	30	1.10	1.26	0.16	0.58	6	10	2	NP_002871	P04049				
734	NK155-6	Raf-1		Raf1 proto-oncogene+	0.0	14130	7	10	0.0	6493	17	9	-54	0.75	0.28	-0.47	-1.70	10	10	2	NP_002871	P04049				
735	NN093	Rb	S612	Retinoblastoma-associ	0.0	1039	35	7	0.0	971	20	7	-7	-0.74	-0.85	-0.10	-0.37	5	9	10	NP_000312	P06400				
736	PN113	Rb	S608	Retinoblastoma-associ	0.0	2094	24	8	0.0	2184	16	8	4	-0.34	-0.37	-0.02	-0.08	1	9	10	NP_000312	P06400				
737	PN066	Rb	S612	Retinoblastoma-associ	0.0	20004	21	11	0.0	15533	29	11	-22	0.94	0.79	-0.15	-0.55	6	10	3	NP_000312	P06400				
738	PN067	Rb	S780	Retinoblastoma-associ	0.0	2895	18	8	0.0	3365	16	8	16	-0.16	-0.11	0.05	0.17	6	10	4	NP_000312	P06400				
739	PN131-1	Rb	S795	Retinoblastoma-associ	0.0	657	114	6	0.0	613	66	6	-101	-1.01	-1.12	-0.11	-0.41	14	10	4	NP_000312	P06400				
740	PN068	Rb	S807	Retinoblastoma-associ	0.0	6471	6	9	0.0	6569	11	9	2	0.30	0.28	-0.02	-0.06	10	10	3	NP_000312	P06400				
741	PN069	Rb	S807+S811	Retinoblastoma-associ	0.0	1518	24	7	0.0	1685	38	7	11	-0.53	-0.52	0.01	0.03	10	10	4	NP_000312	P06400				
742	PN065	Rb	T356	Retinoblastoma-associ	0.0	9358	37	10	0.0	7428	31	10	0.1	0.51	0.38	-0.15	-0.56	2	10	3	NP_000312	P06400				
743	PN070	Rb	T821	Retinoblastoma-associ	0.0	914	45	6	0.0	659	8	6	-28	-0.82	-1.08	-0.26	-0.93	14	10	3	NP_000312	P06400				
744	PN071	Rb	T826	Retinoblastoma-associ	0.0	9549	10	10	0.0	9387	12	10	0	0.52	0.49	-0.03	-0.10	2	10	4	NP_000312	P06400				
745	NN170	ReB		Transcription factor Re	0.0	106	40	3	0.0	125	4	4	14	-2.05	-2.08	-0.03	-0.11	9	9	10	NP_006500.2	Q01201				
746	PN151	ReB	S552	Transcription factor Re	0.0	1299	164	7	0.0	485	13	6	-63	-0.62	-1.26	-0.64	-2.32	13	9	10	NP_006500.2	Q01201				
747	NK244-1	Ret		Proto-oncogene tyrosin	0.0	31360	15	12	0.0	37508	21	12	20	1.20	1.31	0.11	0.41	1	9	11	NP_065681	P07849				
748	NK244-2	Ret		Proto-oncogene tyrosin	0.0	31968	11	12	0.0	40109	32	12	25	1.21	1.35	0.14	0.51	5	9	11</						



SAMPLE DETAILS

Sample IDs: Control ID: Pooled Samples Larger
Treated ID: Pooled Samples Smaller

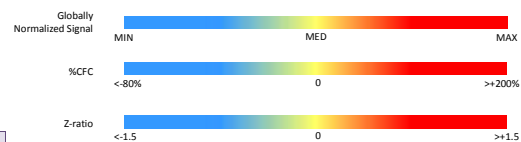
						Globally Normalized Median							Globally Normalized Median										
						3433							4055										
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range	Log2(Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range	Log2(Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z-score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link	
774	PNI195	Smad2	T220	Mothers against decar.	0.0	4174	15	8	0.0	4174	47	101	-0.35	0.02	0.36	1.32	12	10	9	NP_001003852	Q15798		
785	NN096	Smad2/3		SMAD- and mothers ag.	0.0	1586	20	7	0.0	543	62	6	-0.50	-1.09	-0.59	-2.12	16	10	9	NP_005892	Q15798		
786	PNI25	SMC1	S957	Structural maintenanc	0.0	18598	83	11	0.0	14092	9	10	0.90	0.73	-0.17	-0.61	4	10	10	NP_006297.2	Q14883		
787	NK233-1	SMG1		Lambda/Iota protein ki	0.0	68702	2	13	0.0	58870	1	13	-1.15	1.65	1.58	-0.07	-0.26	8		10	NP_055907.3	Q9BQ15	
788	NK233-3	SMG1		Lambda/Iota protein ki	0.0	43423	2	12	0.0	43552	4	12	0	1.39	1.40	0.01	0.05	12	10	10	NP_055907.3	Q9BQ15	
789	PK197	NCA (a-Synuclein	S129	Alpha-synuclein	0.0	561	89	6	0.0	755	6	12	-1.16	-1.00	-0.17	0.60	6	11	6	NP_000336.1	Q37460		
790	NK251-1	SNF-1k		Serin/threonine-prote	0.0	44022	3	12	0.0	49477	12	12	1.39	1.48	0.10	0.13	10	10	10	NP_775490.2	Q31359		
791	NK146	Snk		Polo-like protein kinase	0.0	1972	4	0	0.0	3886	50	9	0.97	-0.38	-0.03	0.35	1.27	3	10	5	NP_006613	Q9NYY3	
792	NN145	SOC52		Suppressor of cytokini	0.0	3565	107	8	0.0	6744	606	9	89	-0.04	0.30	0.34	1.23	7	10	5	NP_003868.1	Q14508	
793	NN097	SOC54		Suppressor of cytokini	0.0	8428	20	10	0.0	2971	7	8	65	0.45	-0.19	-0.64	-2.30	11	10	5	NP_543143	Q8WXX45	
794	NN098	SOD (Cu/Zn)		Superoxide dismutase	0.0	740	39	6	0.0	921	4	6	-30	-0.94	-1.21	-0.28	-1.00	15	10	5	NP_000445	Q9JSD4	
795	NN099	SOD3		Silencer of death dom	0.0	7386	0	7	0.0	7386	58	7	-0.54	0.62	1.16	1.66	11	10	7	NP_004885	Q9H432		
796	NN077	SOX9	S18Y (sex determining		0.0	3396	1	8	0.0	4101	39	9	-0.07	0.00	0.07	0.27	7	10	6	NP_000437	P48436		
797	NN100	SPHK1		Sphingosine kinase 1	0.0	2382	28	8	0.0	3136	17	8	32	-0.27	-0.15	0.12	0.42	11	10	6	NP_892010	Q9NYA1	
798	NN101	SPHK2		Sphingosine kinase 2	0.0	3001	19	8	0.0	4466	11	9	49	-0.14	0.06	0.19	0.70	15	10	6	NP_064511	Q9NR40	
799	NK172-2	Src		Src proto-oncogene-e	0.0	59224	18	13	0.0	68613	12	13	16	1.56	1.67	0.11	0.38	3	10	8	NP_005408	P12931	
800	NK172-3	Src		Src proto-oncogene-e	0.0	1459	20	7	0.0	11653	64	20	1	0.62	1.16	0.54	1.16	11	10	7	NP_005408	P12931	
801	NK172-4	Src		Src proto-oncogene-e	0.0	736	17	6	0.0	2552	26	6	94	-0.94	-0.28	0.67	2.41	15	10	7	NP_005408	P12931	
802	PK107	Src	Y418	Src proto-oncogene-e	0.0	1658	42	7	0.0	1495	40	7	-10	-0.48	-0.59	-0.11	-0.41	3	10	7	NP_005408	P12931	
803	PK108	Src	Y529	Src proto-oncogene-e	0.0	1192	60	7	0.0	1246	3	7	5	-0.67	-0.70	-0.03	-0.12	7	10	7	NP_005408	P12931	
804	NN102-NN124	STAT1		Signal transducer and	0.0	2586	122	8	0.0	2510	49	8	-3	-0.22	-0.29	-0.06	-0.22	11	10	9	NP_009330	P42224	
805	PN078-PNI35	STAT1		Signal transducer and	0.0	757	19	1	0.0	760	6	1	75	-0.33	-0.99	-0.66	-0.24	15	10	8	NP_009330	P42224	
806	PN079-PNI36	STAT1	Y701	Signal transducer and	0.0	1557	8	3	0.0	3044	3	3	95	-0.51	-0.17	0.34	0.22	15	10	3	NP_009330	P42224	
807	NN103	STAT2		Signal transducer and	0.0	4211	1	9	0.0	3775	13	9	-10	0.05	-0.04	-0.10	-0.36	3	10	9	NP_005410	P52630	
808	PN080	STAT2	Y689	Signal transducer and	0.0	229	119	4	0.0	133	45	4	-42	-1.61	-2.02	-0.42	-1.50	7	10	9	NP_005410	P52630	
809	NN104	STAT3		Signal transducer and	0.0	2818	85	8	0.0	4707	88	9	67	-0.18	0.09	0.26	0.95	15	10	9	NP_003141	P40763	
810	PN082-1	STAT3	Y704	Signal transducer and	0.0	6701	20	9	0.0	5576	10	9	-17	0.32	0.19	-0.13	-0.48	11	10	9	NP_003141	P40763	
811	PN107	STAT4		Signal transducer and	0.0	1817	1838	46	7	0.0	1838	5	7	-0.42	-0.59	-0.17	-0.42	3	10	9	NP_003142	Q14761	
812	PN083-1	STAT5	Y694	Signal transducer and	0.0	1332	243	7	0.0	811	19	6	-39	-0.60	-0.95	-0.35	-1.27	7	10	10	NP_003143	P42229	
813	NN105	STAT5A		Signal transducer and	0.0	3822	57	9	0.0	2716	8	8	-29	0.00	-0.24	-0.24	-0.86	11	10	10	NP_003143	P42229	
814	PN119	STAT5A	S780	Signal transducer and	0.0	743	26	6	0.0	1003	48	7	35	-0.94	-0.83	0.11	0.39	15	10	10	NP_003143	P42229	
815	NN106	STAT5B		Signal transducer and	0.0	741	5	6	0.0	1992	57	8	169	-0.94	-0.42	0.52	0.87	2	10	5	NP_065890	P51692	
816	NN107	STAT6		Signal transducer and	0.0	1176	50	7	0.0	1774	60	7	67	-0.54	0.51	1.05	0.61	6	10	5	NP_003144	P42229	
817	NN108	ST11		Stress induced phosph	0.0	572	25	6	0.0	353	32	5	-38	-1.09	-1.44	-0.36	-1.30	10	10	5	NP_006810	P31948	
818	NN134	Striatin		Striatin	1.0	12578	4	10	1.0	12598	33	10	0	0.68	0.67	-0.01	-0.04	14	10	5	NP_003153.2	Q43818	
819	NK174	Syk		Spleen protein-tyrosin	0.0	9998	12	10	0.0	8751	6	10	-12	0.55	0.45	-0.10	-0.23	6	10	6	NP_003168	P43405	
820	PK159	Syk	Y323	Spleen protein-tyrosin	0.0	890	9	6	0.0	217	10	4	-69	-0.98	-1.73	-0.75	-1.00	10	10	6	NP_003168	P43405	
821	PK1821	Syk	Y323	Spleen protein-tyrosin	0.0	3844	9	0	0.0	3844	0	9	0.37	0.46	0.10	0.27	6	10	6	NP_003168	P43405		
822	NN171	Synapsin 1		Synapsin 1 isoform la	0.0	394	934	5	0.0	275	308	5	-30	-1.30	-1.49	-0.19	-1.06	14	10	6	NP_008881	P17600	
823	PN111	Synapsin 1	S603	Synapsin 1 isoform la	0.0	180	5	4	0.0	307	64	5	71	-1.75	-1.53	0.22	0.79	2	10	7	NP_008881	P17600	
824	NK175-5	TAK1		TGF-beta-activated pr	0.0	2031	212	8	0.0	1961	64	8	-3	-0.36	-0.43	-0.07	-0.25	6	10	7	NP_063306	Q43318	
825	PN085	Tau	S199	Microtubule-associat	0.0	2602	18	8	0.0	2229	10	8	-14	-0.22	-0.36	-0.13	-0.49	10	10	7	NP_059901	P10636	
826	PN086	Tau	S199/202	Microtubule-associat	0.0	2162	23	7	0.0	1387	19	7	-68	-0.64	-0.84	0.04	0.16	14	10	7	NP_059901	P10636	
827	PK091	Tau	S400	Microtubule-associat	0.0	706	64	7	0.0	657	33	6	-97	-0.97	-1.11	-0.13	-0.47	10	10	8	NP_059901	P10636	
828	PN092	Tau	S404	Microtubule-associat	0.0	1273	28	7	0.0	989	5	7	-22	-0.63	-0.84	-0.21	-0.75	10	10	8	NP_059901	P10636	
829	PN107	Tau	S422	Microtubule-associat	0.0	2092	14	8	0.0	2188	5	8	5	-0.35	-0.37	-0.02	-0.08	14	10	8	NP_059901	P10636	
830	PN090	Tau	S713	Microtubule-associat	0.0	982	30	7	0.0	948	15	7	-3	-0.78	-0.86	-0.08	-0.30	2	10	8	NP_059901	P10636	
831	PN090-2	Tau	S713	Microtubule-associat	0.0	627	0	6	0.0	645	15	6	0	-1.03	-1.09	-0.06	-0.20	2	10	9	NP_059901	P10636	
832	PN122	Tau	T205	Microtubule-associat	0.0	540	49	5	0.0	540	49	5	-1	-1.12	-1.25	-0.13	-0.25	9	10	8	NP_059901	P10636	
833	PN122	Tau	T231	Microtubule-associat	0.0	328	30	5	0.0	324	8	5	-1	-1.40	-1.50	-0.09	-0.34	10	10	8	NP_059901	P10636	
834	NK220-2	TBK1		Serin/threonine-prote	0.0	2246	35	8	0.0	2612	13	8	16	-0.30	-0.26	0.04	0.15	14	10	9	NP_037386	Q9UHD2	
835	PK828	TBK1	S172	Serin/threonine-prote	0.0	32295	21	12	0.0	31054	20	12	-4	1.22	1.20	-0.02	-0.06	2	10	10	NP_037386	Q9UHD2	
836	PK829	TEC	Y519	Tyrosine-protein kinas	0.0	20981	88	11	0.0	27145	305	11	29	0.97	1.12	0.15	0.55	6	10	10	NP_003206.2	P42880	
837	PK18AD0	TNK1		Tumor necrosis facto	0.0	2110	59	8	0.0	1440	24	8	-24	-0.61	-0.74	-0.13	-0.46	10	10	9	NP_003789	Q14662	
838	NN111	Trail		Tumor necrosis facto	0.0	1370	14	7	0.0	1131	5	7	-17	-0.59	-0.76	-0.17	-0.61	14	10	10	NP_003801	P50591	
839	NK178	TrkA		Nerve growth facto (N	0.0	309	41	5	0.0	491	50	6	59	-1.44	-1.25	0.19	0.68	1	10	5	NP_002520	P40429	
840	NK179	TrkB		BDNF/NT3/4/5 recept	0.0	1766	20	7	0.0	2271	10	8	29	-0.44	-0.34	0.10	0.35	5	10	5	NP_006171	Q16820	
841	PK160	TrkB	Y705	BDNF/NT3/4/5 recept	0.0	2910	19	8	0.0	3314	36	8	38	-0.28	-0.19	0.09	0.52	9	10	5	NP_006171	Q16820	
842	NK180	TrkK		Dual specificity prote	0.0	2436	20	8	0.0	4760	10	9	62	-0.15	0.02	0.24	0.66	13	10	5	AA061239.1	Q34981	
843	PK092	Tubulin		Tubulin	0.0	3950	10	9	0.0	7143	19	10	24	-0.51	1.33	1.84	1.33	1	10	6	NP_001061.2	Q24258	
844	NK181	Tyk2		Protein-tyrosine kinas	0.0	641	38	6	0.0	1413	0	7	28	-0.87	-0.62	0.24	0.87	1	10	7	NP_003322	P29597	
845	NK181-2	Tyk2		Protein-tyrosine kinas	0.0	601	15	6	0.0	2342	29	8	290	-1.06	-0.33	0.73	2.64	5	10	7	NP_003322	P29597	
846	NK181-3	Tyk2		Protein-tyrosine kinas																			

Sample IDs:

SAMPLE DETAILS

Control ID: Pooled Samples Larger

Treated ID: Pooled Samples Smaller



						Globally Normalized Median 3433			Globally Normalized Median 4055	Z-ratio <div><div><-1.5</div><div>0</div><div>>+1.5</div></div>												
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag-Control	Globally Normalized - Control	%Error Range Control	Log2 (Intensity Corrected) - Control	Flag-Treated	Globally Normalized - Treated	%Error Range Treated	Log2 (Intensity Corrected) - Treated	%CFC (Treated from Control)	Z score (Control)	Z score (Treated)	Z score Difference (Treated-Control)	Z-ratio (Treated, Control)	Block	Row	Column	Refseq	Uniprot Link
871	NK186-2	Yes	Pan-specific	Yamaguchi sarcoma p	0.0	251	21	5	0.0	319	58	5	27	-1.55	-1.50	0.05	0.18	6	10	11	NP_005424	P07947
872	NK214	YSK1	Pan-specific	Serine/threonine-prote	0.0	6380	9	11	0.0	11299	2	10	77	0.29	0.60	0.31	1.13	10	10	11	NP_006365.2	Q00506
873	NK250-2	YSK4	Pan-specific	ZIPK1/STK20-related f	0.0	10243	25	11	0.0	17363	20	11	5	0.89	0.86	-0.03	-0.02	14	10	11	NP_001018054.1	Q26496
874	NK187	ZAP70	Pan-specific	Zeta-chain (TCR) assoc	0.0	1058	44	7	0.0	17363	21	8	120	-0.73	0.33	0.40	1.47	5	10	11	NP_003168	P43403
875	NK187-2	ZAP70	Pan-specific	Zeta-chain (TCR) assoc	0.0	1595	1	7	0.0	2581	35	8	62	-0.50	-0.27	0.23	0.84	1	10	11	NP_003168	P43403
876	NK188-1	ZIPK	Pan-specific	ZIP kinase (death ass	0.0	3626	35	8	0.0	6255	13	9	73	-0.03	0.25	0.29	1.03	13	10	11	NP_001339	Q43293
877	NK188-2	ZIPK	Pan-specific	ZIP kinase (death ass	0.0	3799	15	9	0.0	4003	20	9	5	0.00	-0.01	-0.01	-0.02	9	10	11	NP_001339	Q43293

Appendix G

Individual Microarray

[illegible]

Full Analysis: 10 Individual Wounds

[illegible]

Full Analysis: 10 Individual Words

Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag- Patient 1-Smaller	Flag- Patient 2-Smaller	Flag- Patient 3-Smaller	Flag- Patient 4-Smaller	Flag- Patient 5-Smaller	Globally Normalized - Patient 1-Smaller	Globally Normalized - Patient 2-Smaller	Globally Normalized - Patient 3-Smaller	Globally Normalized - Patient 4-Smaller	Globally Normalized - Patient 5-Smaller	Average - Smaller	S.Dev. - Smaller	%S.Dev. Smaller	Flag- Patient 1-Bigger	Flag- Patient 2-Bigger	Flag- Patient 3-Bigger	Flag- Patient 4-Bigger	Flag- Patient 5-Bigger	Globally Normalized - Patient 1-Bigger	Globally Normalized - Patient 2-Bigger	Globally Normalized - Patient 3-Bigger	Globally Normalized - Patient 4-Bigger	Globally Normalized - Patient 5-Bigger	Average - Larger	S.Dev. - Larger	%S.Dev. - Larger	NCPC - Average Larger from Average Smaller	Student T test p value	Block	Row	Column	Refseq	Uniprot Link				
681	NA132	PRC9	pan-specific	Protein-serine kinase C, gamma	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1078	1494	1330	1150	943	1101	168	17	13	472	9	9	8	NP_007270	P04126				
682	NA153-4	AurKB	pan-specific	Aurora Kinase B1 (serine/threonine protein kinase) (2)	0	0	0	0	0	1592	1273	2078	2963	2447	2002	660	33	0	0	0	0	0	0	1315	1262	2751	3402	2443	1107	267	853	38	13	161	10	6	2	NP_004208	P04204		
683	NA153-5	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
684	NA154	AP31	pan-specific	Map 70-related heat shock protein 1 (serine/threonine protein kinase) (DSPA4)	0	0	0	0	0	105	1036	839	943	1447	1023	220	21	0	0	0	0	0	0	74	968	961	969	2321	1167	607	82	13	538	11	6	3	NP_005053	P05053			
685	NA155	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
686	NA156	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
687	NA157	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
688	NA158	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
689	NA159	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
690	NA160	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
691	NA161	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
692	NA162	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
693	NA163	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
694	NA164	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
695	NA165	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
696	NA166	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
697	NA167	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
698	NA168	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
699	NA169	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
700	NA170	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
701	NA171	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
702	NA172	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
703	NA173	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
704	NA174	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
705	NA175	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
706	NA176	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
707	NA177	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
708	NA178	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
709	NA179	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237
710	NA180	PRK22	pan-specific	Protein-serine kinase PRK22 homolog B	0	0	0	0	0	242	207	242	242	242	202	20	0	0	0	0	0	0	0	237	237	237	237	237	237	237	237	237	237	237	237	237	237	237	23		

Full Analysis: 10 Individual Wounds

[illegible]

Full Analysis: 10 Individual Wounds

Serial No.			Antibody Codes			Target Protein Name			Phospho Site (Residue)			Full Target Protein Name			Globally Normalized Median					Average - Smaller			S. Dev. - Smaller			%S.Dev. Smaller			Globally Normalized Median					Average - Larger			S. Dev. - Larger			%S.Dev. Larger			N/CRC Average Larger from Average Smaller			Student t test p value			Block			Row			Column			Refseq			Uniprot Link		
															1545	1490	1854	1726	2278										1507	1688	1753	1745	1646																														
712	NP030-2	DURP3	Pro-pan-specific	Onco-specific protein phosphatase 3	0.0	0.0	0.0	1.0	0.0	14950	21099	15068	11459	10050	14878	3655	25	0.0	0.0	0.0	1.0	0.0	17010	18115	10102	10050	8726	13342	4603	35	8	7	7	NP 004048.1	P14146																												
713	NP030-8	BRG1	Pro-pan-specific	MRN-ICCA protein-enzyme kinase 1 (BRG1)	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
714	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
717	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
718	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784	19548	22971	1150	14	8	361	0	0	NP 005168.1	P14146																											
719	NP030-9	CDK28	Pro-pan-specific	Cell division cycle 28B phosphatase	0.0	0.0	0.0	0.0	0.0	18228	15726	22782	24313	23536	20016	4843	23	0.0	0.0	0.0	0.0	0.0	22220	23097	25826	27784																																					

[illegible]

Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name	Flag- Patient-1 Smaller	Flag- Patient-2 Smaller	Flag- Patient-3 Smaller	Flag- Patient-4 Smaller	Flag- Patient-5 Smaller	Flag- Patient-6 Smaller	Flag- Patient-7 Smaller	Flag- Patient-8 Smaller	Flag- Patient-9 Smaller	Flag- Patient-10 Smaller	Flag- Patient-11 Smaller	Flag- Patient-12 Smaller	Flag- Patient-13 Smaller	Flag- Patient-14 Smaller	Flag- Patient-15 Smaller	Flag- Patient-16 Smaller	Flag- Patient-17 Smaller	Flag- Patient-18 Smaller	Flag- Patient-19 Smaller	Flag- Patient-20 Smaller	Flag- Patient-21 Smaller	Flag- Patient-22 Smaller	Flag- Patient-23 Smaller	Flag- Patient-24 Smaller	Flag- Patient-25 Smaller	Flag- Patient-26 Smaller	Flag- Patient-27 Smaller	Flag- Patient-28 Smaller	Flag- Patient-29 Smaller	Flag- Patient-30 Smaller	Flag- Patient-31 Smaller	Flag- Patient-32 Smaller	Flag- Patient-33 Smaller	Flag- Patient-34 Smaller	Flag- Patient-35 Smaller	Flag- Patient-36 Smaller	Flag- Patient-37 Smaller	Flag- Patient-38 Smaller	Flag- Patient-39 Smaller	Flag- Patient-40 Smaller	Flag- Patient-41 Smaller	Flag- Patient-42 Smaller	Flag- Patient-43 Smaller	Flag- Patient-44 Smaller	Flag- Patient-45 Smaller	Flag- Patient-46 Smaller	Flag- Patient-47 Smaller	Flag- Patient-48 Smaller	Flag- Patient-49 Smaller	Flag- Patient-50 Smaller	Flag- Patient-51 Smaller	Flag- Patient-52 Smaller	Flag- Patient-53 Smaller	Flag- Patient-54 Smaller	Flag- Patient-55 Smaller	Flag- Patient-56 Smaller	Flag- Patient-57 Smaller	Flag- Patient-58 Smaller	Flag- Patient-59 Smaller	Flag- Patient-60 Smaller	Flag- Patient-61 Smaller	Flag- Patient-62 Smaller	Flag- Patient-63 Smaller	Flag- Patient-64 Smaller	Flag- Patient-65 Smaller	Flag- Patient-66 Smaller	Flag- Patient-67 Smaller	Flag- Patient-68 Smaller	Flag- Patient-69 Smaller	Flag- Patient-70 Smaller	Flag- Patient-71 Smaller	Flag- Patient-72 Smaller	Flag- Patient-73 Smaller	Flag- Patient-74 Smaller	Flag- Patient-75 Smaller	Flag- Patient-76 Smaller	Flag- Patient-77 Smaller	Flag- Patient-78 Smaller	Flag- Patient-79 Smaller	Flag- Patient-80 Smaller	Flag- Patient-81 Smaller	Flag- Patient-82 Smaller	Flag- Patient-83 Smaller	Flag- Patient-84 Smaller	Flag- Patient-85 Smaller	Flag- Patient-86 Smaller	Flag- Patient-87 Smaller	Flag- Patient-88 Smaller	Flag- Patient-89 Smaller	Flag- Patient-90 Smaller	Flag- Patient-91 Smaller	Flag- Patient-92 Smaller	Flag- Patient-93 Smaller	Flag- Patient-94 Smaller	Flag- Patient-95 Smaller	Flag- Patient-96 Smaller	Flag- Patient-97 Smaller	Flag- Patient-98 Smaller	Flag- Patient-99 Smaller	Flag- Patient-100 Smaller	Flag- Patient-101 Smaller	Flag- Patient-102 Smaller	Flag- Patient-103 Smaller	Flag- Patient-104 Smaller	Flag- Patient-105 Smaller	Flag- Patient-106 Smaller	Flag- Patient-107 Smaller	Flag- Patient-108 Smaller	Flag- Patient-109 Smaller	Flag- Patient-110 Smaller	Flag- Patient-111 Smaller	Flag- Patient-112 Smaller	Flag- Patient-113 Smaller	Flag- Patient-114 Smaller	Flag- Patient-115 Smaller	Flag- Patient-116 Smaller	Flag- Patient-117 Smaller	Flag- Patient-118 Smaller	Flag- Patient-119 Smaller	Flag- Patient-120 Smaller	Flag- Patient-121 Smaller	Flag- Patient-122 Smaller	Flag- Patient-123 Smaller	Flag- Patient-124 Smaller	Flag- Patient-125 Smaller	Flag- Patient-126 Smaller	Flag- Patient-127 Smaller	Flag- Patient-128 Smaller	Flag- Patient-129 Smaller	Flag- Patient-130 Smaller	Flag- Patient-131 Smaller	Flag- Patient-132 Smaller	Flag- Patient-133 Smaller	Flag- Patient-134 Smaller	Flag- Patient-135 Smaller	Flag- Patient-136 Smaller	Flag- Patient-137 Smaller	Flag- Patient-138 Smaller	Flag- Patient-139 Smaller	Flag- Patient-140 Smaller	Flag-
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Average	3991	3991	3991	3991	3991		3991		
Median	1545	1430	1884	1728	2278		1754	402	25
Maximum	40061	58080	47720	60269	74340		57260		

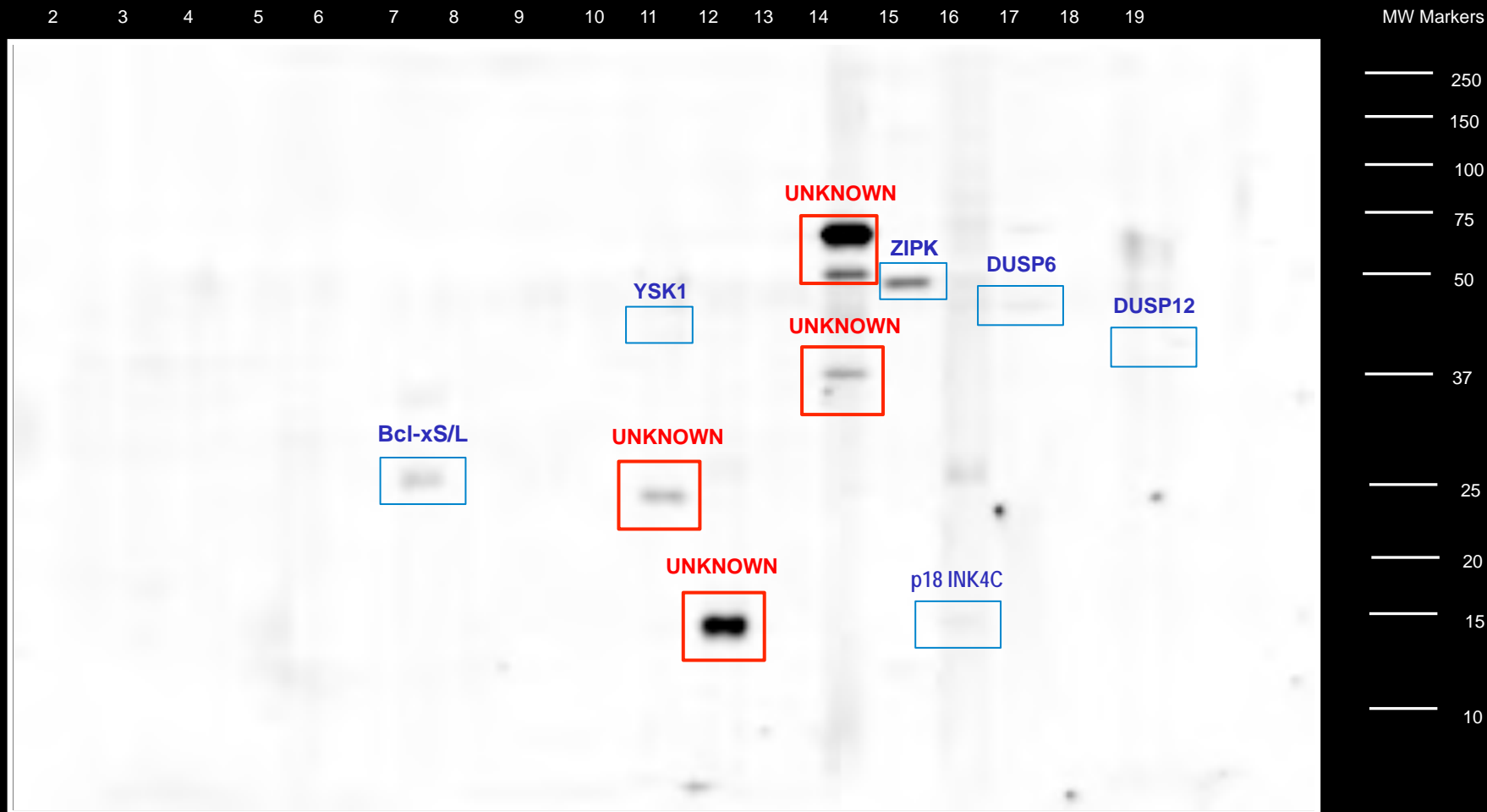
Full Analysis: 10 Individual Wounds

										Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median											Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median	Globally Normalized Median											Average - Smaller	S. Dev. - Smaller	%S.Dev. Smaller																																						
										1545	1490	1864	1726	2278											1597	1698	1753	1745	1646											Average - Larger	S. Dev. - Larger	%S.Dev. - Larger																																						
Serial No.	Antibody Codes	Target Protein Name	Phospho Site (Human)	Full Target Protein Name						Flag Patient 1- Smaller	Flag Patient 2- Smaller	Flag Patient 3- Smaller	Flag Patient 4- Smaller	Flag Patient 5- Smaller	Globally Normalized - Patient 1- Smaller	Globally Normalized - Patient 2- Smaller	Globally Normalized - Patient 3- Smaller	Globally Normalized - Patient 4- Smaller	Globally Normalized - Patient 5- Smaller											Globally Normalized - Patient 1- Bigger	Globally Normalized - Patient 2- Bigger	Globally Normalized - Patient 3- Bigger	Globally Normalized - Patient 4- Bigger	Globally Normalized - Patient 5- Bigger											NCFC - Average Larger from Average Smaller	Student T test p value	Block	Row	Column	Refseq	Uniprot Link																													
Minimum										13	5	16	11	23	Minimum										5	8	14	Minimum										5	8	14	Minimum										5	8	14											13																
Total										3500000	3500000	3500000	3500000	3500000	Total										3500000	3500000	3500000	3500000	3500000	Total										3500000	3500000	3500000	3500000	3500000	Total										3500000	3500000	3500000	3500000	3500000											3500000										

Appendix H

Pre-screen Results

Pre-Screen #1



Target Proteins from Pre-Screen #1

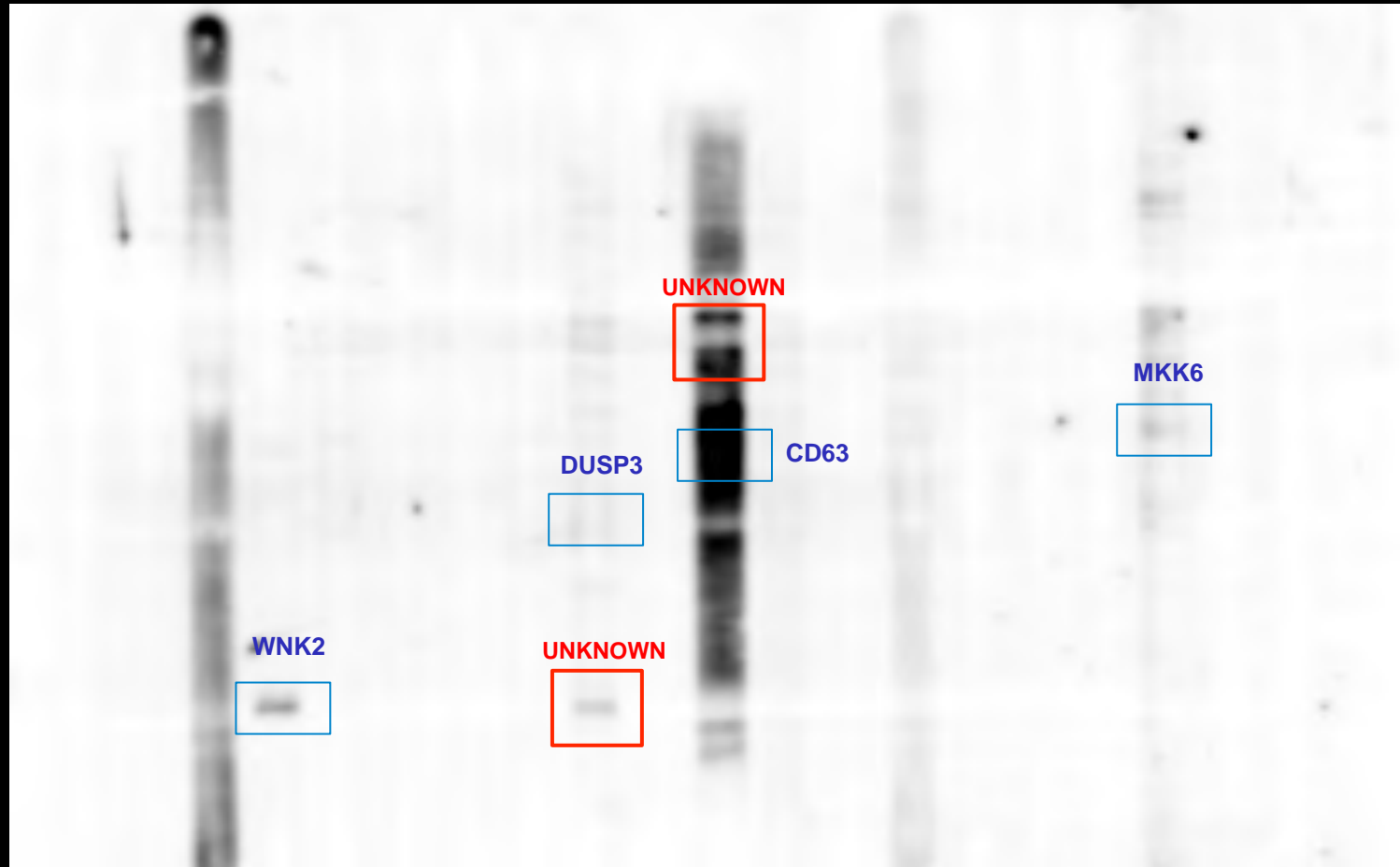
No. Lane Ab Code Target Protein Site Strength

1	7	NN008	Bcl-xS/L	Bcl-xS/L	Pan-specific	Strong target
2	11	NK214	YSK1	YSK1	Pan-specific	Weak target
3	11	NK214	YSK1	Unknown	Pan-specific	Moderate x-reactive
4	12	NK002	ACK1	Unknown	Pan-specific	Strong x-reactive
5	14	NK001-2	Abl1	Unknown	Pan-Specific	Moderate x-reactive
6	14	NK001-2	Abl1	Unknown	Pan-Specific	Weak x-reactive
7	15	NK188-1	ZIPK	ZIPK	Pan-specific	Strong Target
8	16	NN077	p18 INK4c	p18 INK4c	Pan-specific	Weak target
9	17	NP040-2	DUSP6	DUSP6	Pan-specific	Weak target
10	19	NP046-3	DUSP12	DUSP12	Pan-specific	Weak target

Pre-Screen #2

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

MW Markers



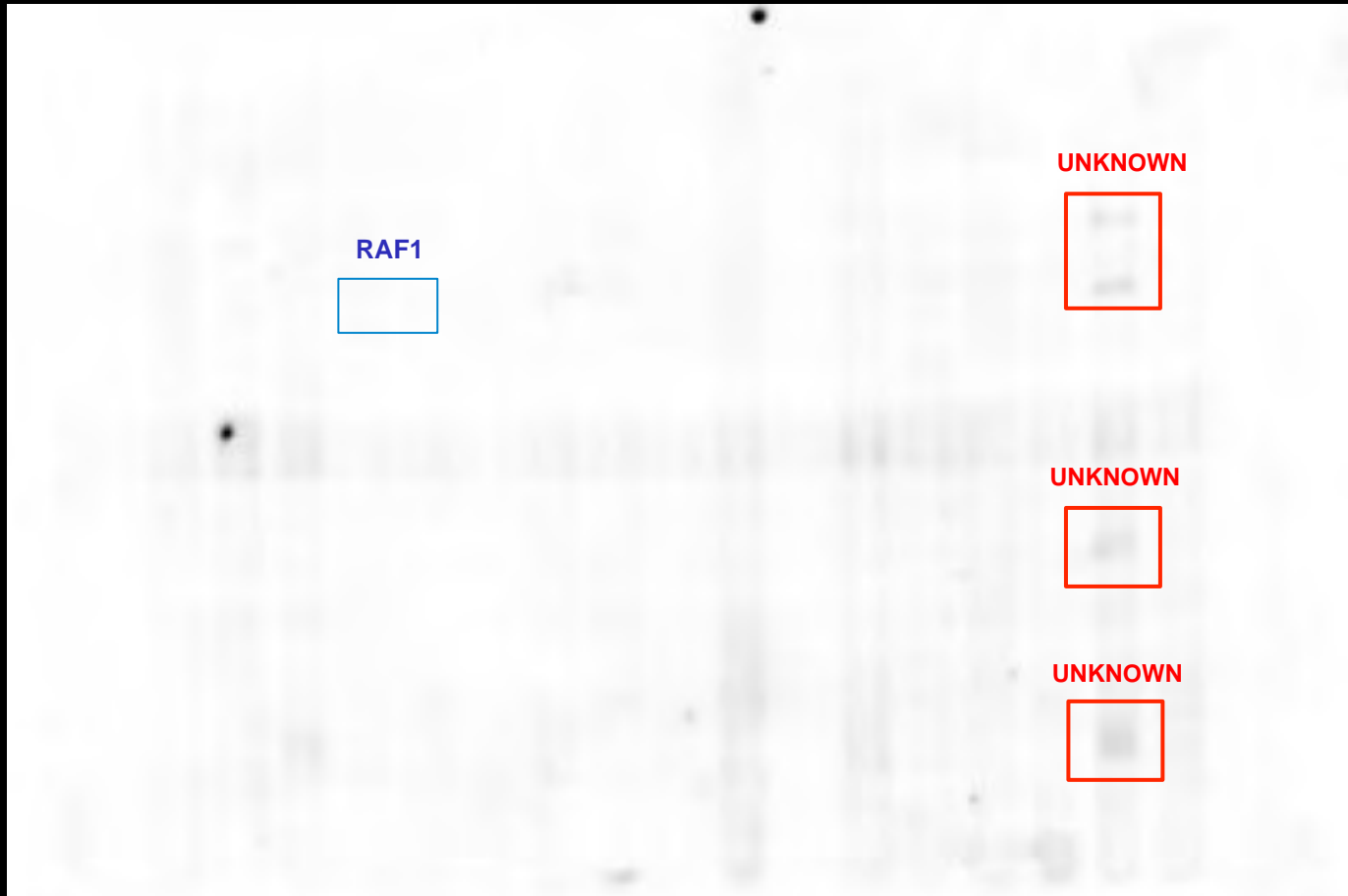
Target Proteins from Pre-Screen #2

No.	Lane	Ab Code	Target	Protein	Site	Strength
1	4	NK253-3	WNK2	Unknown	Pan-specific	Strong x-reactive
2	9	NP030-3	DUSP3	DUSP3	Pan-specific	Weak target
3	9	NP030-3	DUSP3	Unknown	Pan-specific	Weak x-reactive
4	11	NN186	CD63	Unknown	Pan-specific	Moderate cross x-reactive
5	11	NN186	CD63	CD63	Pan-specific	Strong target (dirty)
6	18	NK105-5	MKK6	MKK6	Pan-specific	Weak target

Pre-Screen #3

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

MW Markers



250

150

100

75

50

37

25

20

15

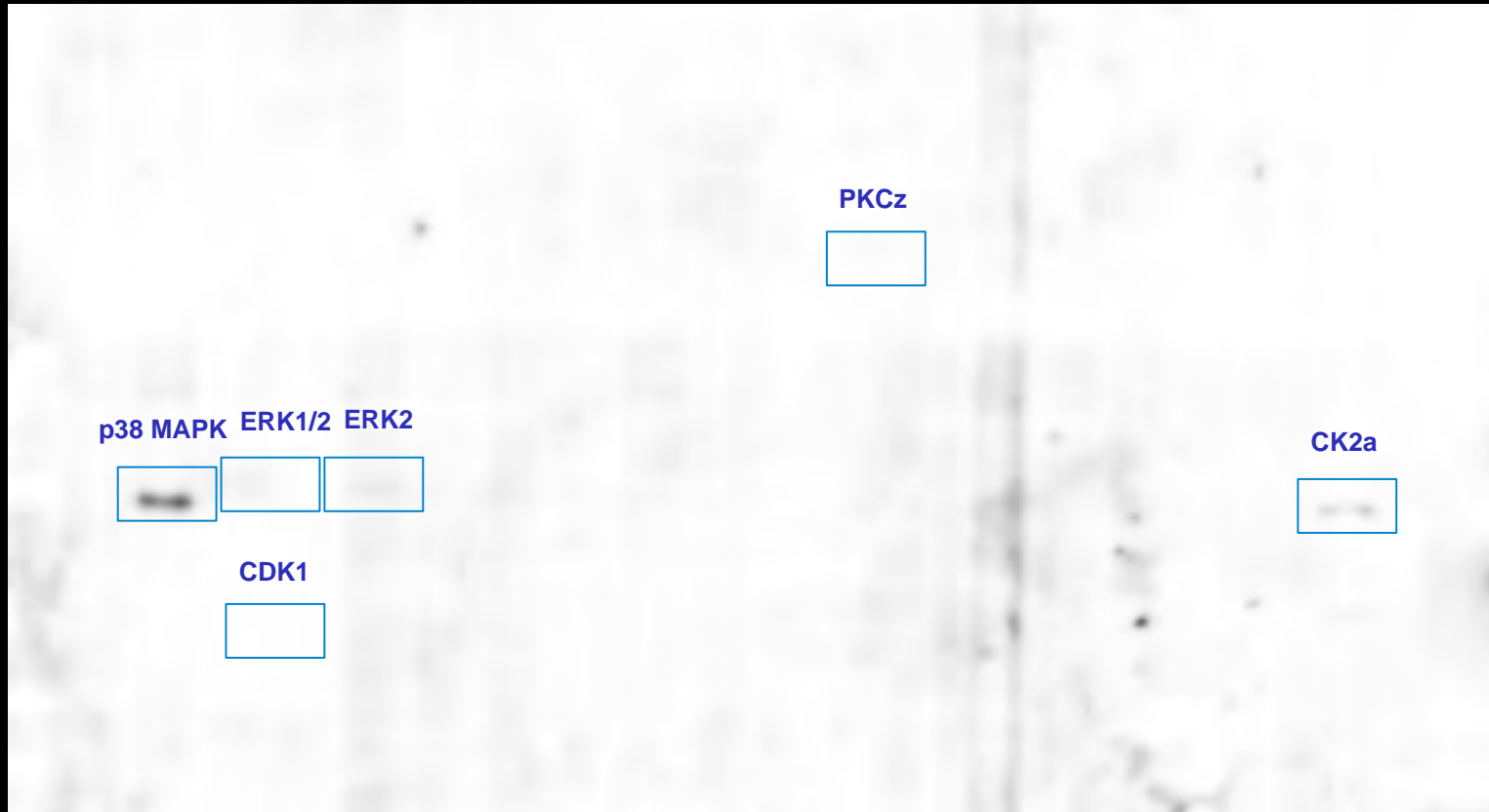
Target Proteins from Pre-Screen #3

No.	Lane	Ab Code	Target	Protein	Site	Strength
1	6	NK155-6	RAF1	RAF1	Pan-specific	Weak target
2	18	PK800	Ron	Unknown	Y1238	Weak x-reactive
3	18	PK800	Ron	Unknown	Y1238	Weak x-reactive
4	18	PK800	Ron	Unknown	Y1238	Weak x-reactive

Pre-Screen #4

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

MW Markers



250
150
100
75
50
37
25
20
15

Target Proteins from Pre-Screen #4

No. Lane Ab Code Target Protein Site Strength

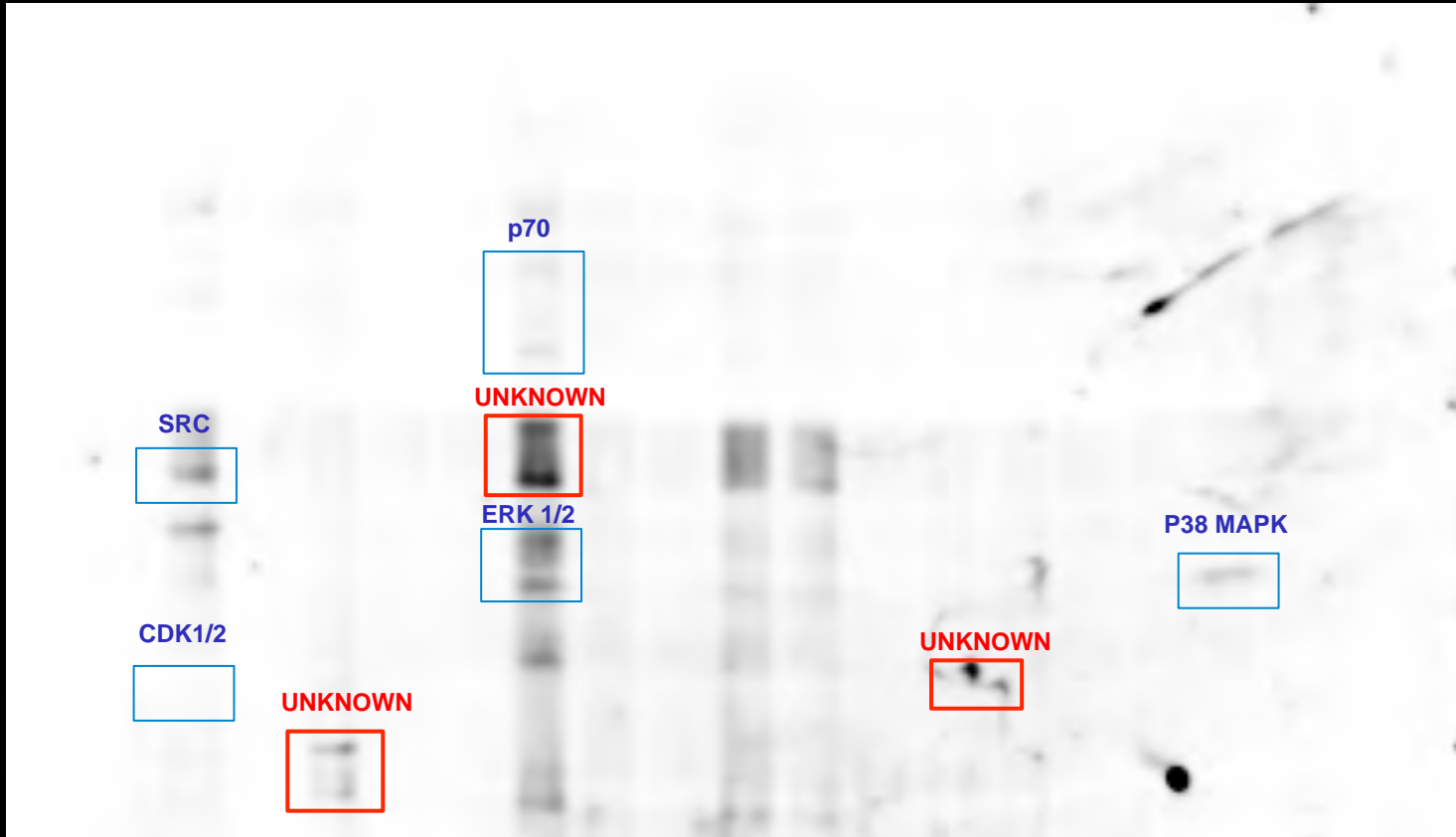
1	3	NK120-3	p38a MAPK	p38a MAPK	Pan-specific	Strong Target
2	4	NK025-2	CDK1	CDK1 (CDC2)	Pan-specific	Weak target
3	4	NK055-NK056	Erk1/2	Erk1/2	Pan-specific	Weak target
4	6	NK0456	Erk2	Erk2	Pan-specific	Weak target
5	13	NK141	PKCz	PKCz	Pan-specific	Weak target
6	20	NK041	CK2a	CK2a	Pan-specific	Moderate target

Pre-Screen #5

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

MW Markers

— 250
— 150
— 100
— 75
— 50
— 37
— 25
— 20
— 15



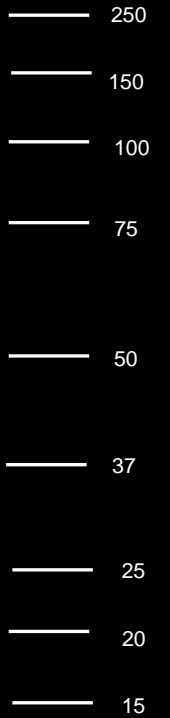
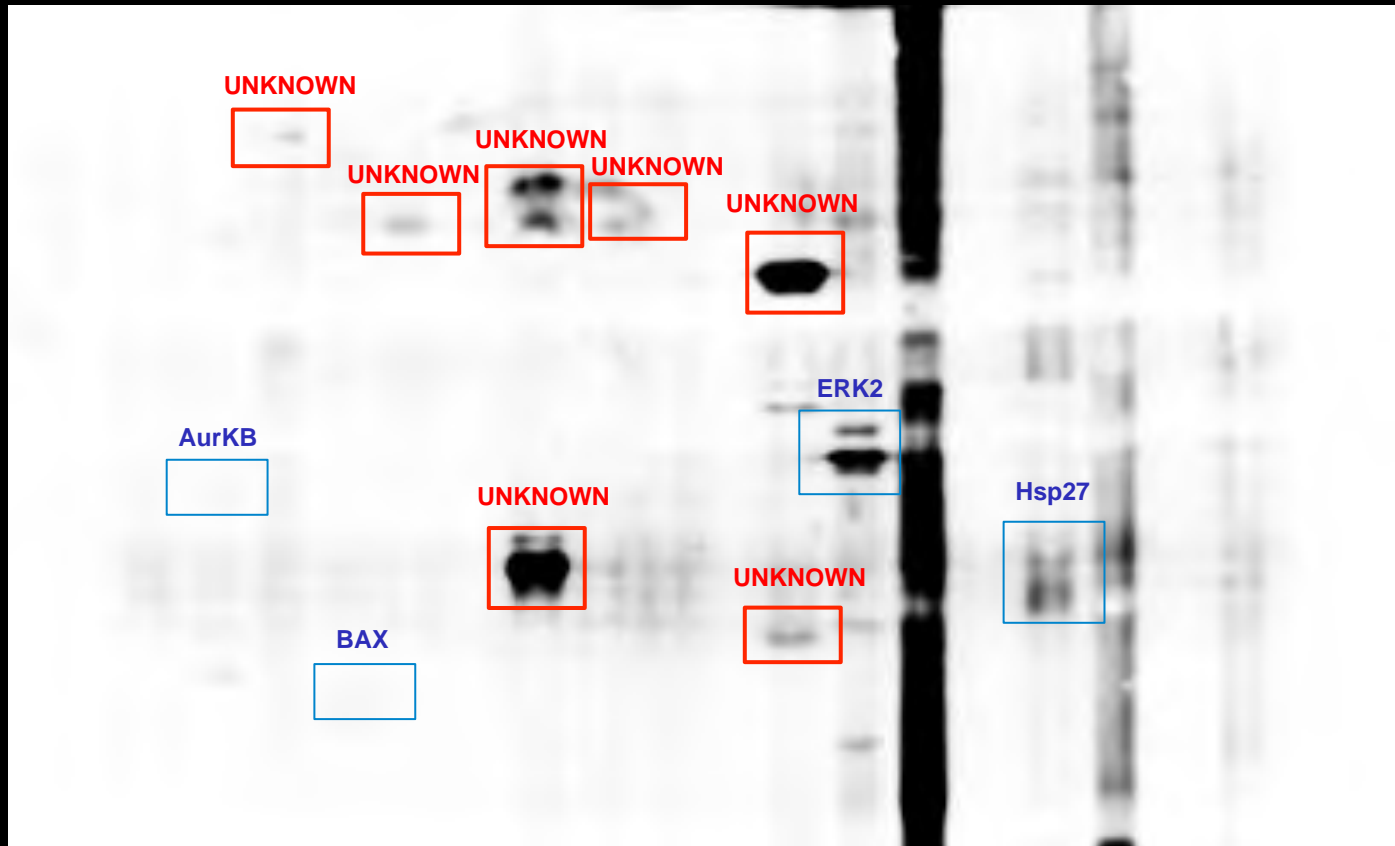
Target Proteins from Pre-Screen #5

No.	Lane	Ab Code	Target	Protein	Site	Strength
1	3	PK108	Src	Src	Y530	Strong target
2	3	PK007-2	CDK1/2	CDK1/2	Y15	Weak target
3	5	PK073/PK107	PKCa or Src	Unknown	S657 / Y419	Moderate x-reactive
4	8	PK147	p70 S6 Kinase	p70 S6K	T412	Weak target
5	8	PK147/PK168/PK170	p70 or Erk1/2	Unknown	Phospho-site	Strong x-reactive
6	8	PK168-PK169	p44/42 MAPK	Erk1/2	Y204/Y187	Strong target
6	8	PK170-PK171	p44/42 MAPK	Erk1/2	T202/T185	Strong target
7	14	PK072	PKBa (Akt1)	Unknown	S473	Moderate x-reactive
8	18	PK060-3	p38a MAPK	p38a MAPK	T180/Y182	Moderate target

Pre-Screen #6

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

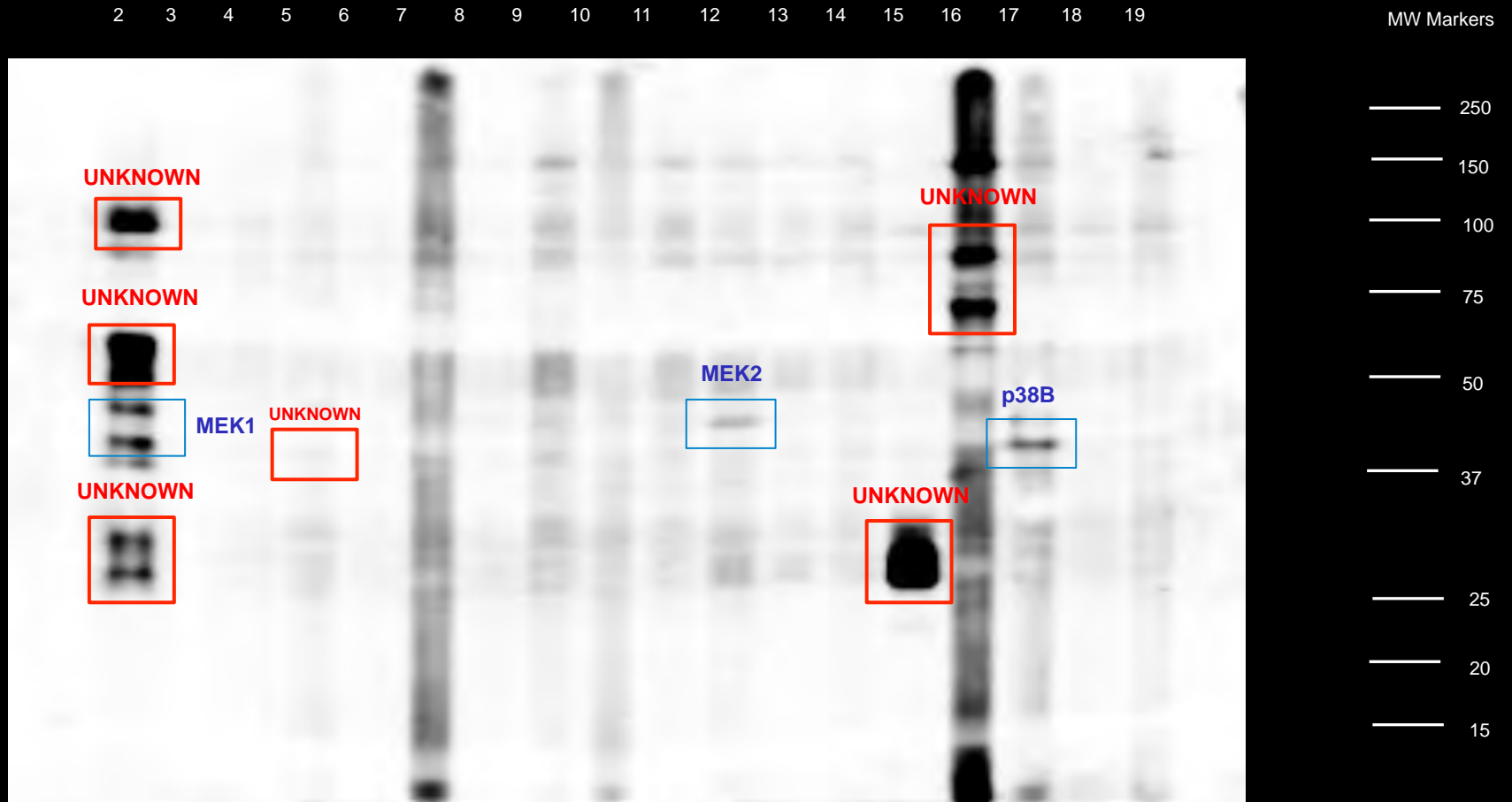
MW Markers



Target Proteins from Pre-Screen #6

No.	Lane	Ab Code	Target	Protein	Site	Strength
1	3	NK193-4	AurKB	AurKB	Pan-specific	Weak target
2	4	NK130-9	Akt2	Unknown	Pan-specific	Weak x-reactive
3	5	NN005	Bax	Bax	Pan-specific	Weak target
4	6	NN011	Caspase 1	Unknown	Pan-specific	Weak x-reactive
5	8	NK055-1	ERK1	Unknown	Pan-Specific	Strong x-reactive
6	8	NK055-1	ERK1	Unknown	Pan-Specific	Strong x-reactive
7	9	NK028-4	Cdk5	Unknown	Pan-specific	Moderate x-reactive
8	12	NK236-3	FGFR3	Unknown	Pan-specific	Strong x-reactive
9	12	NK236-3	FGFR3	Unknown	Pan-specific	Moderate x-reactive
10	13	NK056-4	ERK2	ERK2	Pan-Specific	Strong target
11	16	NN165-1	Hsp90 beta	Hsp90 beta	Pan-specific	Strong target

Pre-Screen #7



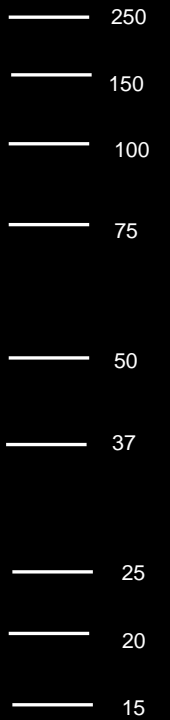
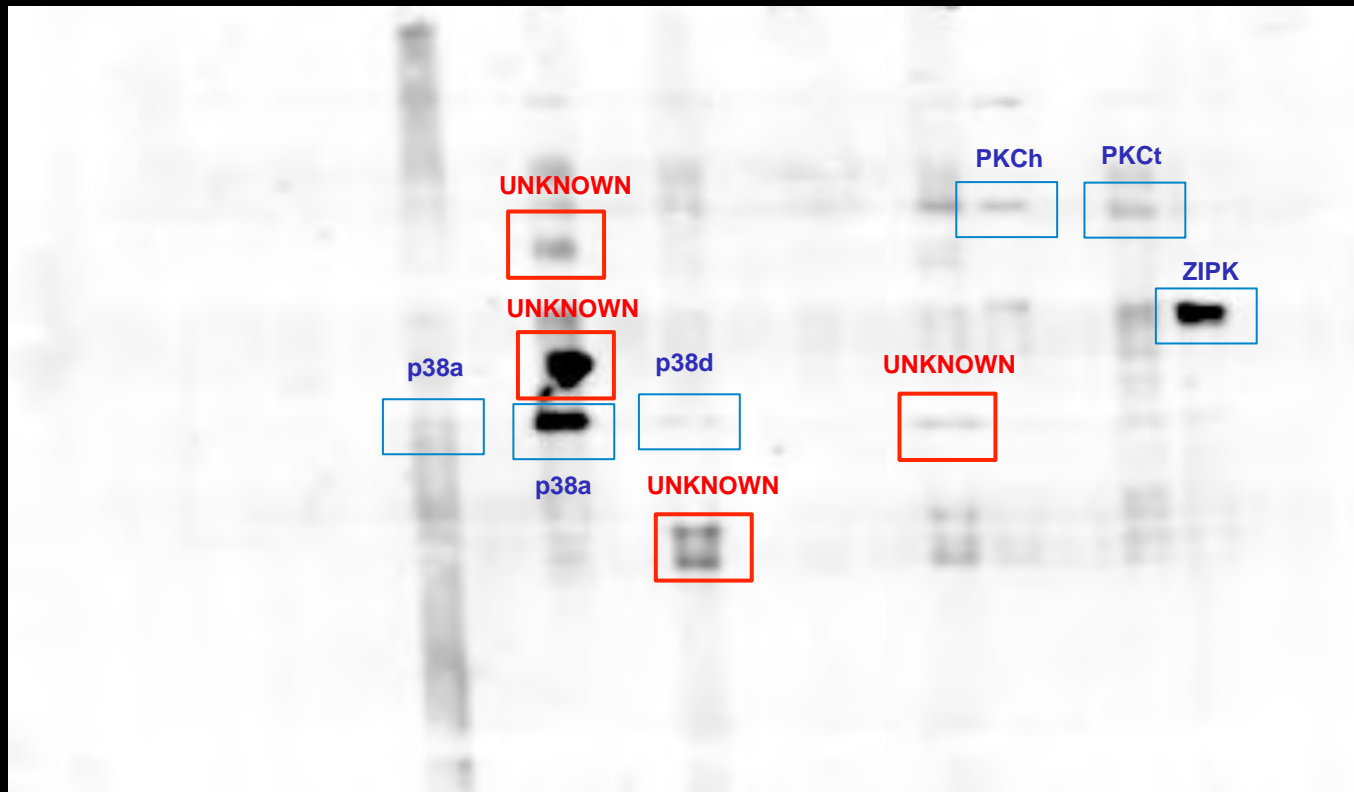
Target Proteins from Pre-Screen #7

No.	Lane	Ab Code	Target	Protein	Site	Strength
1	2	NK099-8	MEK1	Unknown	Pan-Specific	Strong x-reactive
2	2	NK099-8	MEK1	Unknown	Pan-Specific	Strong x-reactive
3	2	NK099-8	MEK1	MEK1 (MAP2K1)	Pan-Specific	Strong target
4	2	NK099-8	MEK1	Unknown	Pan-Specific	Strong x-reactive
5	5	NK155-5	Raf1	Unknown	Pan-specific	Weak x-reactive
6	12	NK100-6	MEK2	MEK2 (MAP2K2)	Pan-Specific	Strong Target
7	15	NK172-2	Src	Unknown	Pan-specific	Strong x-reactive
8	16	NK106-5	MKK7	Unknown	Pan-specific	Strong x-reactive (dirty)
9	17	NK248-1	p38b MAPK	p38b MAPK	Pan-specific	Strong target

Pre-Screen #8

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

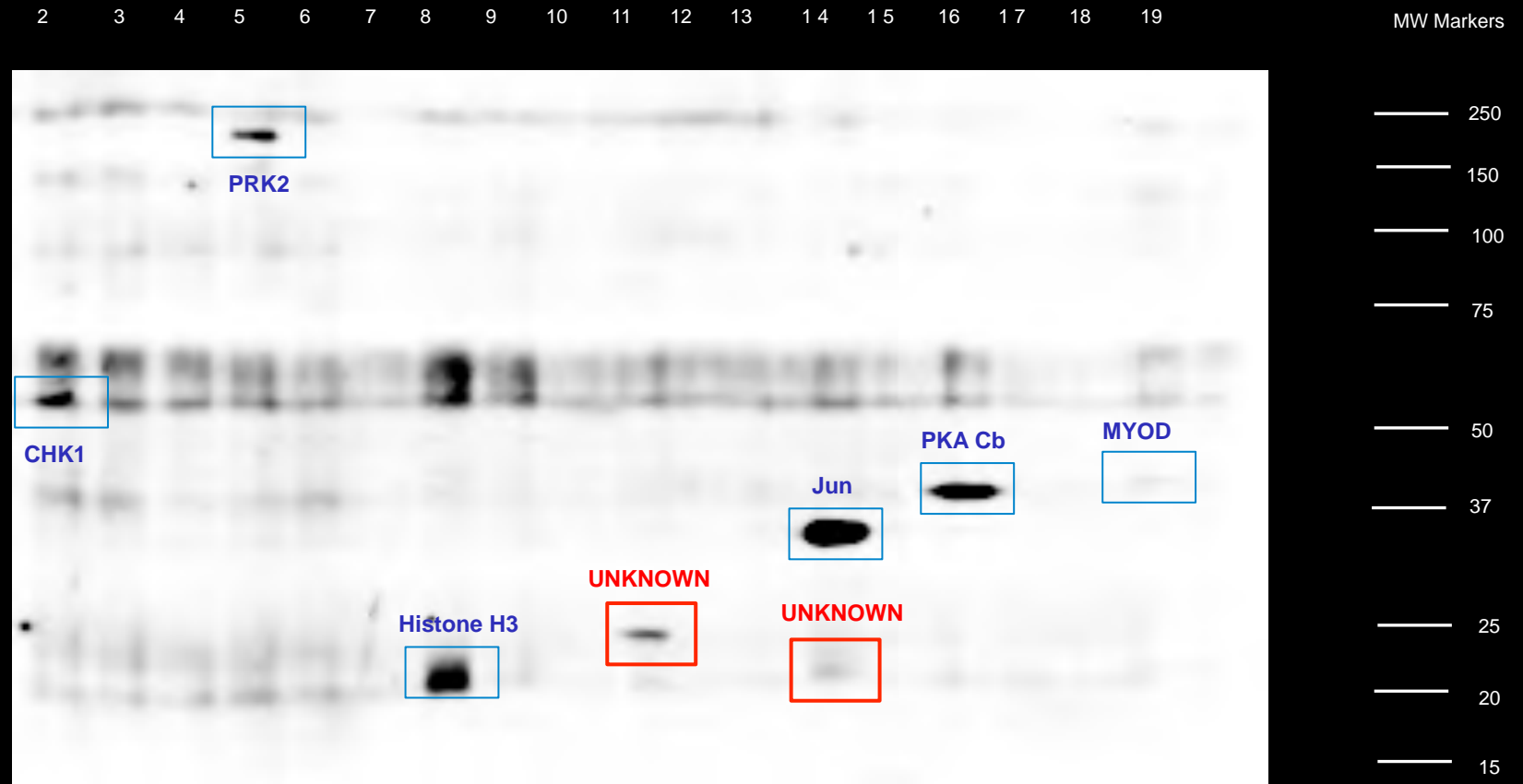
MW Markers



Target Proteins from Pre-Screen #8

No.	Lane	Ab Code	Target	Protein	Site	Strength
1	6	PK739	p38a MAPK	p38a MAPK	T180+Y182	Weak target (dirty)
2	8	NK120-3	p38a MAPK	Unknown	Pan-specific	Moderate x-reactive
3	8	NK120-3	p38a MAPK	Unknown	Pan-specific	Strong x-reactive
4	8	NK120-3	p38a MAPK	p38a MAPK	Pan-specific	Strong target
5	10	NK121-4	p38d MAPK	p38d MAPK	Pan-specific	Weak target
6	10	NK121-4	p38d MAPK	Unknown	Pan-specific	Moderate x-reactive
7	14	NN156	PLC R(PLCg2)	Unknown	Pan-specific	Moderate x-reactive
8	15	NK218	nPKC h	PKC h	Pan-specific	Moderate Target
9	17	PK089-1	PKCt	PKCq	S676	Moderate Target
10	18	NK188-1	ZIPK	ZIPK	Pan-specific	Strong target

Pre-Screen #9



Target Proteins from Pre-Screen #9

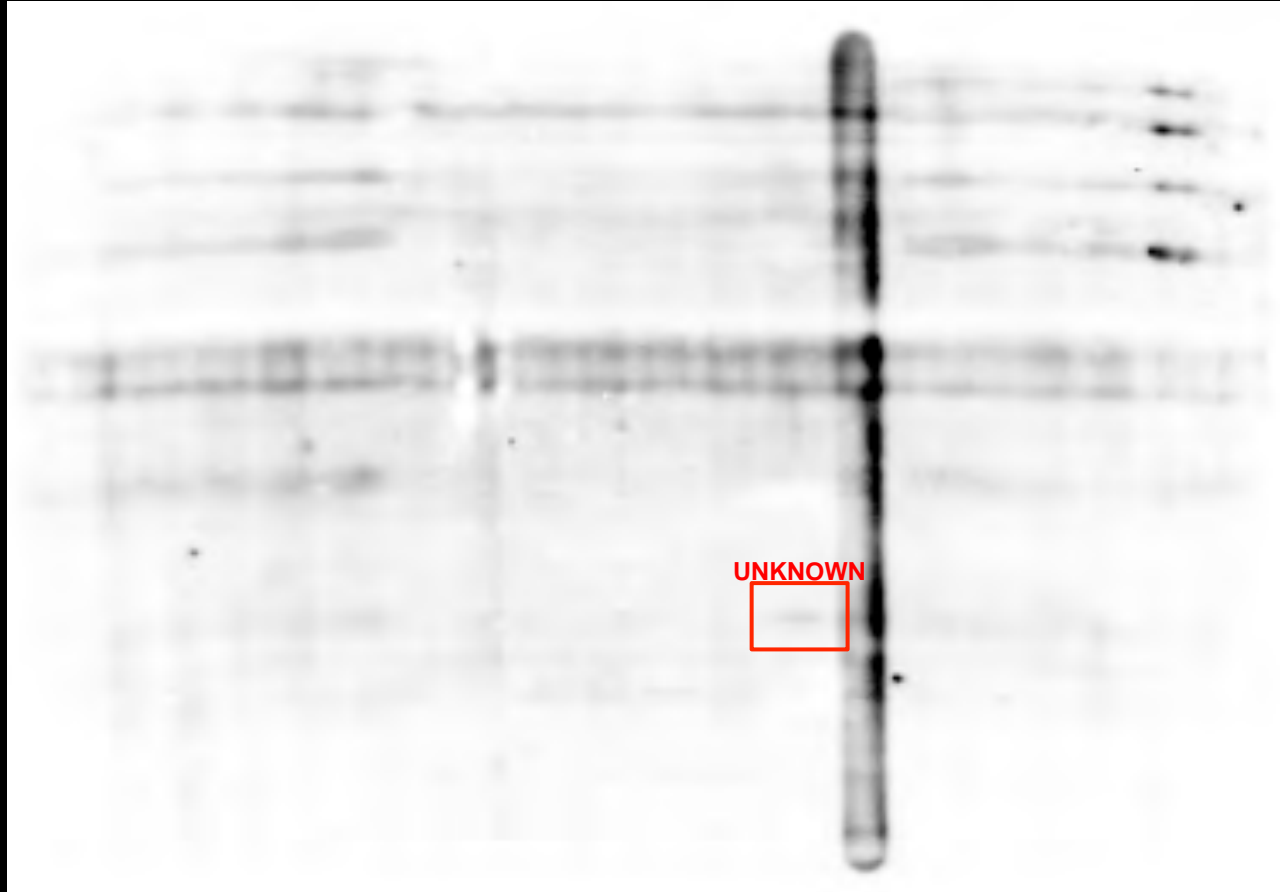
No. Lane Ab Code Target Protein Site Strength

1	2	PK577	Chk1	Chk1	S280	Moderate target
2	5	NK149	PRK2	PRK2 (PKN2)	Pan-specific	Strong target
3	8	PN100	Histone H3	Unknown	T11	Strong target
4	11	NN093	Rb	Unknown	Pan-specific	Moderate x-reactive
5	14	PN163	Jun	Jun	T91	Strong target
6	15	NK187	ZAP70	Unknown	Pan-specific	Weak x-reactive
7	16	PK068	PKA Cb	PKA Cb	S338	Strong target
8	19	PN182	MyoD	MyoD	S200	Weak target

Pre-Screen #10

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

MW Markers



— 250

— 150

— 100

— 75

— 50

— 37

— 25

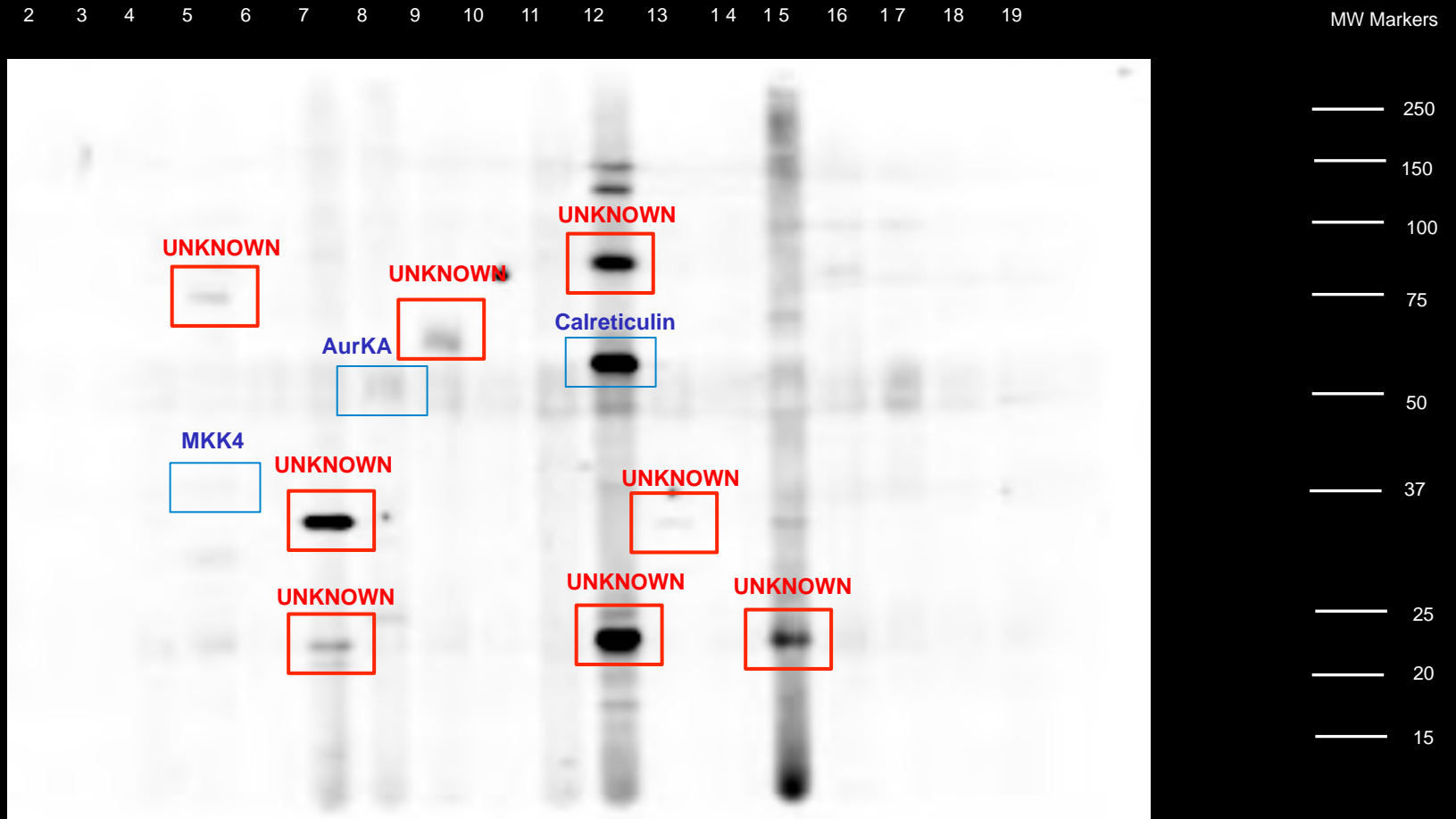
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Target Proteins from Pre-Screen #10

No.	Lane	Ab Code	Target	Protein	Site	Strength
1	13	NK157	RIP2/RICK	Unknown	Pan-specific	Weak x-reactive

Pre-Screen #11



Target Proteins from Pre-Screen #11

No. Lane Ab Code Target Protein Site Strength

1	5	NK103-6	MKK4	MKK4	Pan-specific	Weak target
2	5	NK103-6	MKK4	Unknown	Pan-specific	Weak x-reactive
3	7	NK054-4	ErbB2	Unknown	Pan-Specific	Strong x-reactive
4	7	NK054-4	ErbB2	Unknown	Pan-Specific	Weak x-reactive
5	8	NK008-3	AurKA	AurKa	Pan-Specific	Weak target
6	9	NK244-2	Ret	Unknown	Pan-specific	Strong x-reactive
7	12	NN137-1	Calreticulin	Target	Pan-specific	Strong target (dirty)
8	12	NN137-1	Calreticulin	Unknown	Pan-specific	Strong x-reactive (dirty)
9	12	NN137-1	Calreticulin	Unknown	Pan-specific	Strong x-reactive (dirty)
10	13	PN071	Rb	Unknown	T826	Weak x-reactive
11	15	NK250-1	SIK3	Unknown	Pan-specific	Strong x-reactive (dirty)

Appendix I

Quantitative

Microarray

Average Concentration	AG ID	Code	Study Time	protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
	1	ECPU-A	56	10.70	515.2	1546.4	1118.2	2169.0	77.6	3459.2
	2	ECPU-B	7	1.88	932.7	326.7	276.3	1579.1	351.7	816.1
	3	ECPU-B	56	4.29	1191.1	840.1	757.7	848.8	67.8	770.7
	4	ECPU-C	35	2.73	227.9	1528.3	362.7	4431.5	962.0	828.0
	5	ECPU-C	48	1.16	211.5	2472.1	257.1	4795.8	1067.1	679.1
	6	ECPU-D	21	0.26	133.5	506.4	85.9	1993.2	1069.5	802.3
	7	ECPU-D	35	0.14	52.1	143.7	1.5	2460.7	1125.6	530.3
	8	ECPU-E	28	0.30	48.0	324.1	31.6	3570.9	1147.2	391.7
	9	ECPU-F	21	4.52	140.7	1100.5	147.3	1050.8	1026.2	1592.2
	10	ECPU-G	21	3.93	113.4	1043.4	233.2	1314.6	1081.5	1938.1
	11	ECPU-H	34	0.45	132.1	947.2	306.5	1076.9	1121.6	446.5
	12	ECPU-H	48	1.70	155.3	1016.5	483.1	1188.8	1136.0	879.7
	13	ECPU-J	14	1.66	204.0	3548.9	319.6	1390.0	1121.6	382.7
	14	ECPU-J	21	1.46	78.1	507.1	381.6	1608.5	1010.2	1073.8
	15	ECPU-J	28	1.97	68.4	752.6	167.9	1428.0	1043.8	1028.9
	16	ECPU-J	49	3.91	78.1	2228.1	349.4	1161.1	931.6	929.8
	17	ECPU-L	20	8.77	456.5	3963.6	2203.7	4655.6	269.7	3133.4
	18	ECPU-M	21	0.82	133.5	260.1	411.8	1052.0	1133.6	222.8
	19	ECPU-M	42	0.59	130.6	721.4	260.6	1315.5	1119.2	97.5
	20	ECPU-N	14	0.63	1595.0	554316.3	5462.6	1342.7	74.5	2548.1
	21	ECPU-N	21	18.83	1638.3	2341.9	8814.1	1092.9	41.7	10037.7
	22	ECPU-N	42	7.07	1481.2	394980.0	1640.3	1678.4	78.5	571.8
	23	ECPU-N	56	5.23	1313.4	327487.5	1113.2	2873.0	1033.4	492.8
	24	ECPU-O	7	1.63	178.8	1652.1	2699.1	1520.1	1124.8	1139.5
	25	ECPU-O	21	1.20	87.9	719.9	819.8	1543.2	1167.3	341.3
	26	ECPU-O	28	1.92	117.7	2710.1	1049.6	1519.5	1079.9	625.2
	27	ECPU-O	36	0.33	58.9	470.3	274.1	1265.4	1132.8	314.7
	28	ECPU-O	43	2.32	153.8	4351.8	1543.7	1617.8	1107.2	684.9
	29	ECPU-P	20	1.04	80.9	383.8	258.0	1220.2	1101.5	362.8
	30	ECPU-P	27	4.21	218.9	222.6	2354.4	959.3	961.2	4242.9
	31	ECPU-P	34	0.39	67.1	210.3	293.3	1630.0	1158.5	606.0
	32	ECPU-P	41	1.08	102.0	395.6	309.4	2341.4	1134.4	472.4
	33	ECPU-P	57	4.07	211.5	140.3	2422.5	1224.6	427.4	3876.0
	34	ECPU-Q	6	0.77	177.3	500.4	125.0	1179.3	1097.5	241.6
	35	ECPU-Q	20	0.27	19.3	77.2	119.6	945.3	1019.0	265.7
	36	ECPU-Q	34	0.25	9.5	78.2	59.5	979.3	1094.3	100.6
	37	ECPU-Q	41	0.21	9.5	11.7	70.0	76.3	109.6	124.1
	38	ECPU-R	15	0.98	152.4	333.7	549.7	1164.8	1111.2	712.1
	39	ECPU-R	20	0.73	139.3	324.1	351.3	1277.5	1116.0	222.8
	40	ECPU-R	34	3.77	277.9	935.3	1735.7	1609.8	1006.1	3638.1
	41	ECPU-R	57	1.64	78.1	983.9	382.7	1173.3	1122.4	446.5
	42	ECPU-S	15	1.06	201.0	336.4	630.5	1082.7	1136.8	1172.5
	43	ECPU-S	27	0.97	201.0	377.9	333.0	1017.9	1129.6	690.7
	44	ECPU-S	57	1.02	150.9	333.5	342.4	1649.3	1135.2	571.8
	45	ECPU-T	9	1.82	181.7	308.7	1005.4	879.5	1104.8	1760.8
	46	ECPU-T	21	0.37	32.2	87.9	232.1	726.0	1080.7	274.4
	47	ECPU-T	42	0.49	63.0	228.3	231.8	1407.4	1095.1	182.5
	48	ECPU-U	55	5.38	2440.2	843.3	1688.8	2666.9	303.7	4206.2
	49	ECPU-A	7	6.88	2274.9	3537.4	1553.3	1542.6	1048.6	650.1
	50	ECPU-A	14	12.63	3325.8	166280.1	2514.1	1104.9	144.0	1447.0
	51	ECPU-A	21	33.54	803.7	3152.1	2430.1	1103.2	85.5	4446.4
	52	ECPU-A	49	5.55	524.8	9186.8	943.9	1071.5	68.1	1301.5
	53	ECPU-B	14	2.22	1445.1	421.0	499.2	1566.3	193.5	498.4
	54	ECPU-B	35	2.76	398.3	356.8	526.2	884.1	1039.8	1330.9
	55	ECPU-B	42	26.49	2490.2	534.9	7246.5	143.8	7.8	7947.9
	56	ECPU-B	49	26.32	1971.4	157.6	6406.8	44.0	2.8	7273.2
	57	ECPU-C	28	5.41	293.1	1499.4	296.2	519.4	351.2	790.4
	58	ECPU-C	42	3.95	244.5	4003.9	760.7	997.9	119.2	943.9
	59	ECPU-C	55	2.04	210.0	2128.4	429.5	904.8	1033.4	562.3

Average Concentration	AG ID	Code	Study Time	protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
	60	ECPU-D	8	4.62	648.6	11896.6	256.4	981.0	152.5	71.7
	61	ECPU-D	28	0.32	183.2	174.3	20.7	1374.4	1117.6	154.6
	62	ECPU-D	41	0.49	49.4	290.2	1.9	1188.1	985.3	321.8
	63	ECPU-D	50	0.12	44.0	54.6	34.6	1231.5	1079.9	496.6
	64	ECPU-E	21	11.78	270.3	743.8	488.1	1079.8	62.5	3583.1
	65	ECPU-E	35	0.31	53.4	207.9	15.7	1393.5	1051.0	162.8
	66	ECPU-E	56	4.93	96.3	161.9	318.8	337.6	73.6	2316.8
	67	ECPU-F	14	4.14	82.3	428.7	324.1	1112.6	1051.8	1949.1
	68	ECPU-F	28	3.47	78.1	595.4	197.4	984.2	1059.1	1607.2
	69	ECPU-G	14	2.50	74.0	1547.1	262.8	1343.2	1025.4	1502.3
	70	ECPU-G	34	3.05	36.1	390.7	217.4	893.8	1052.6	1802.2
	71	ECPU-H	13	2.67	462.8	5558.8	589.1	1171.4	1055.8	774.7
	72	ECPU-I	34	1.13	72.6	433.5	259.0	951.7	1083.9	426.3
	73	ECPU-I	48	9.07	392.1	447843.2	2618.3	1306.4	101.0	657.8
	74	ECPU-J	7	2.36	109.1	10315.1	379.8	1452.4	990.9	195.9
	75	ECPU-J	35	0.30	129.2	425.8	73.2	943.7	1107.2	130.4
	76	ECPU-J	42	0.89	24.4	1154.3	83.0	988.1	1133.6	149.7
	77	ECPU-J	56	8.53	68.4	1444.3	707.2	941.9	98.4	1568.6
	78	ECPU-K	13	0.90	381.2	1039.7	232.1	1281.4	988.5	444.7
	79	ECPU-L	7	3.15	532.7	1636.6	254.2	1751.8	1011.0	828.0
	80	ECPU-L	28	5.47	407.7	4507.4	703.8	1594.0	431.5	1902.9
	81	ECPU-N	7	12.14	8225.1	343037.1	3509.1	1165.9	95.9	4705.9
	82	ECPU-N	29	5.32	790.5	12075.9	1500.6	1386.4	219.1	1440.6
	83	ECPU-N	49	5.95	1083.2	345957.6	1433.1	1078.9	165.3	85.2
	84	ECPU-O	15	0.30	50.7	412.0	431.9	1125.7	1026.2	337.8
	85	ECPU-O	51	2.34	241.5	7535.7	1744.6	1140.1	1051.8	1145.6
	86	ECPU-O	58	2.07	205.2	2023.5	2087.4	302.4	8472.2	476.3
	87	ECPU-Q	15	0.82	77.7	138.7	406.1	296.1	2555.9	167.2
	88	ECPU-Q	27	3.38	115.9	443.7	772.1	295.6	8051.5	2292.4
	89	ECPU-R	6	0.24	31.7	102.7	1.9	274.3	8635.8	50.3
	90	ECPU-R	27	2.34	117.1	422.2	534.9	304.0	3329.8	1661.9
	91	ECPU-S	6	0.20	205.2	336.9	82.2	309.7	8472.2	57.0
	92	ECPU-S	20	0.45	254.0	262.0	233.9	312.5	8834.4	160.1
	93	ECPU-S	34	1.35	1339.6	945.6	284.6	297.3	8986.3	494.4
	94	ECPU-T	28	2.07	550.2	175.0	1019.0	280.5	1671.5	1694.1
	95	ECPU-U	7	4.46	750.6	887.6	877.5	285.2	672.5	1092.3
	96	ECPU-U	14	21.07	2487.7	1451.0	8940.3	239.0	12.8	15495.3
Replicate 1	AG ID	Code	Study Time	protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
	1	ECPU-A	56	10.70	562.1	1541.8	1250.1	2012.8	75.3	3531.9
	2	ECPU-B	7	1.88	996.2	365.4	302.4	1434.6	334.3	815.7
	3	ECPU-B	56	4.29	1259.2	930.0	820.8	763.2	63.8	762.5
	4	ECPU-C	35	2.73	240.5	1657.7	366.7	3977.0	903.4	817.5
	5	ECPU-C	48	1.16	222.7	2627.2	259.4	5116.4	1191.2	669.2
	6	ECPU-D	21	0.26	136.1	527.3	83.9	2058.3	1155.6	765.2
	7	ECPU-D	35	0.14	49.8	146.6	1.4	2536.1	1213.8	504.8
	8	ECPU-E	28	0.30	51.0	324.0	29.4	3673.0	1234.7	384.8
	9	ECPU-F	21	4.52	148.0	1069.5	135.7	1069.8	1093.2	1548.2
	10	ECPU-G	21	3.93	113.2	993.5	214.4	1335.7	1149.8	1880.7
	11	ECPU-H	34	0.45	131.6	821.8	335.0	1045.0	1138.7	432.5
	12	ECPU-H	48	1.70	150.1	864.1	512.2	1118.7	1118.6	826.2
	13	ECPU-J	14	1.66	203.7	2955.9	350.2	1351.6	1141.1	371.4
	14	ECPU-J	21	1.46	77.9	474.5	417.3	1560.9	1025.7	1040.0
	15	ECPU-J	28	1.97	68.1	690.0	173.5	1383.0	1057.8	934.8
	16	ECPU-J	49	3.91	91.6	2067.9	360.3	1099.8	876.1	843.0
	17	ECPU-L	20	8.77	518.8	4454.7	2195.1	4400.9	253.1	2721.8
	18	ECPU-M	21	0.82	151.4	286.4	409.3	922.9	1044.8	193.2
	19	ECPU-M	42	0.59	147.8	741.4	250.5	1151.7	1029.4	82.6
	20	ECPU-N	14	0.63	1729.6	558190.9	5240.5	1173.1	64.3	2156.0

Average Concentration

AG ID	Code	Study Time	protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
21	ECPU-N	21	18.83	1772.9	2310.6	8438.8	1048.4	35.9	8476.1
22	ECPU-N	42	7.07	1599.8	358140.3	1441.7	1606.9	75.1	525.7
23	ECPU-N	56	5.23	1415.7	290944.6	976.5	2745.2	922.7	452.2
24	ECPU-O	7	1.63	202.8	1438.1	2814.5	1355.2	1002.3	1168.9
25	ECPU-O	21	1.20	91.5	745.0	853.1	1373.0	1010.0	349.5
26	ECPU-O	28	1.92	132.7	2747.8	1020.2	1276.2	932.5	597.2
27	ECPU-O	36	0.33	62.4	423.8	265.9	1060.7	976.3	287.1
28	ECPU-O	43	2.32	165.1	4313.4	1431.6	1536.9	1081.3	638.6
29	ECPU-P	20	1.04	79.2	372.7	238.8	1119.7	1073.7	337.7
30	ECPU-P	27	4.21	213.7	215.7	2372.5	1040.5	935.1	3861.6
31	ECPU-P	34	0.39	60.8	189.5	277.7	1820.8	1081.6	529.4
32	ECPU-P	41	1.08	85.3	355.8	292.4	2610.1	1057.1	411.8
33	ECPU-P	57	4.07	197.7	140.3	2569.4	1362.4	430.9	3658.9
34	ECPU-Q	6	0.77	158.3	499.3	123.7	1309.4	1056.8	227.6
35	ECPU-Q	20	0.27	19.1	87.0	118.1	981.3	1061.6	249.8
36	ECPU-Q	34	0.25	8.7	87.9	68.7	981.1	1137.8	87.2
37	ECPU-Q	41	0.21	9.9	13.2	80.6	76.3	113.7	107.3
38	ECPU-R	15	0.98	154.6	366.8	619.7	1303.1	1128.7	603.1
39	ECPU-R	20	0.73	159.7	352.7	392.0	1414.6	1122.1	186.8
40	ECPU-R	34	3.77	304.5	997.2	1933.0	1779.1	1009.6	3043.8
41	ECPU-R	57	1.64	85.5	1027.8	425.3	1294.1	1124.0	372.8
42	ECPU-S	15	1.06	212.8	344.3	678.4	1155.9	1102.0	1099.8
43	ECPU-S	27	0.97	212.4	379.0	357.6	1084.5	1092.8	646.6
44	ECPU-S	57	1.02	149.6	327.7	366.8	1753.8	1096.1	534.2
45	ECPU-T	9	1.82	178.3	297.2	1066.3	925.7	1055.8	1628.3
46	ECPU-T	21	0.37	31.5	83.0	245.7	762.6	1030.7	253.2
47	ECPU-T	42	0.49	61.5	242.1	244.8	1475.4	1042.4	168.1
48	ECPU-U	55	5.38	2312.3	876.5	1730.1	2566.5	280.3	3757.1
49	ECPU-A	7	6.88	2227.5	3602.5	1644.3	1534.0	1000.2	600.1
50	ECPU-A	14	12.63	3250.0	165916.8	2656.1	1096.5	137.1	1332.9
51	ECPU-A	21	33.54	783.8	3081.6	2562.3	1092.6	81.2	4087.6
52	ECPU-A	49	5.55	485.2	9092.1	993.2	1018.6	64.6	1194.1
53	ECPU-B	14	2.22	1333.4	370.4	524.2	1486.0	183.1	456.4
54	ECPU-B	35	2.76	355.8	307.5	551.5	837.1	981.9	1216.1
55	ECPU-B	42	26.49	2219.7	451.7	7579.5	135.9	7.4	7248.2
56	ECPU-B	49	26.32	1982.1	136.8	6687.8	41.5	2.6	6619.6
57	ECPU-C	28	5.41	294.1	1275.3	308.6	488.8	329.6	718.0
58	ECPU-C	42	3.95	232.6	3336.8	790.9	937.3	111.6	855.6
59	ECPU-C	55	2.04	199.3	1947.9	445.7	848.2	966.2	508.7
60	ECPU-D	8	4.62	614.5	10667.8	265.5	917.7	142.3	64.7
61	ECPU-D	28	0.32	173.3	153.2	21.4	1283.2	1040.7	139.3
62	ECPU-D	41	0.49	51.3	249.8	1.9	1040.4	915.7	289.4
63	ECPU-D	50	0.12	43.8	46.0	35.7	1076.4	1001.6	445.7
64	ECPU-E	21	11.78	268.3	690.0	501.4	941.9	57.9	3312.1
65	ECPU-E	35	0.31	52.9	189.0	16.1	1213.1	970.9	150.2
66	ECPU-E	56	4.93	95.3	146.8	326.2	293.3	67.9	2133.0
67	ECPU-F	14	4.14	78.8	377.1	308.4	1061.4	967.8	1790.9
68	ECPU-F	28	3.47	74.6	522.7	187.4	937.0	972.5	1473.8
69	ECPU-G	14	2.50	70.5	1355.7	249.1	1276.1	939.7	1374.9
70	ECPU-G	34	3.05	37.9	341.7	205.6	847.5	962.7	1813.2
71	ECPU-H	13	2.67	485.5	5459.1	556.0	1108.5	963.7	777.9
72	ECPU-I	34	1.13	76.0	424.9	244.0	898.8	987.4	427.2
73	ECPU-I	48	9.07	393.3	438052.1	2461.2	1231.3	91.8	657.9
74	ECPU-J	7	2.36	109.2	10069.4	356.3	1366.1	899.0	184.1
75	ECPU-J	35	0.30	129.0	414.8	68.6	885.9	1002.5	118.9
76	ECPU-J	42	0.89	23.6	1122.3	77.6	925.7	1024.4	144.7
77	ECPU-J	56	8.53	66.2	1401.5	659.4	880.7	88.8	1512.5
78	ECPU-K	13	0.90	356.8	1006.8	216.0	1195.7	889.7	427.9
79	ECPU-L	7	3.15	468.6	1581.7	236.1	1631.4	908.1	795.2

Average Concentration	AG ID	Code	Study Time	α protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
	80	ECPU-L	28	5.47	391.9	4648.0	758.2	1736.2	451.0	2133.1
	81	ECPU-N	7	12.14	8403.2	377192.8	3864.2	1225.4	98.1	5164.4
	82	ECPU-N	29	5.32	831.9	13676.6	1702.1	1500.9	221.9	1564.9
	83	ECPU-N	49	5.95	1174.0	374576.3	1645.2	1203.0	167.1	92.4
	84	ECPU-O	15	0.30	56.6	459.5	490.9	1211.3	1129.3	365.4
	85	ECPU-O	51	2.34	277.7	8034.1	1962.9	1183.9	1120.5	1199.8
	86	ECPU-O	58	2.07	233.6	2135.8	2325.1	303.0	9007.2	497.8
	87	ECPU-Q	15	0.82	87.6	144.9	447.8	286.3	2711.8	180.4
	88	ECPU-Q	27	3.38	129.3	458.9	842.9	275.8	8455.7	2447.4
	89	ECPU-R	6	0.24	35.0	105.2	2.1	247.0	9051.2	53.6
	90	ECPU-R	27	2.34	128.1	428.0	572.4	272.8	3332.9	1767.1
	91	ECPU-S	6	0.20	222.2	338.2	87.1	268.2	8224.0	58.7
	92	ECPU-S	20	0.45	272.2	260.4	245.3	282.3	8861.4	170.6
	93	ECPU-S	34	1.35	1374.0	930.2	295.5	259.1	8995.8	525.7
	94	ECPU-T	28	2.07	558.7	170.4	1047.4	242.1	1669.9	1689.9
	95	ECPU-U	7	4.46	754.5	855.8	892.9	271.2	623.5	1087.4
	96	ECPU-U	14	21.07	2475.7	1385.0	9006.3	225.0	11.9	14777.9
Replicate 2	AG ID	Code	Study Time	α protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
	1	ECPU-A	56	10.70	468.3	1551.1	986.2	2325.2	79.8	3386.6
	2	ECPU-B	7	1.88	869.2	288.0	250.2	1723.6	369.1	816.5
	3	ECPU-B	56	4.29	1123.0	750.2	694.5	934.3	71.9	779.0
	4	ECPU-C	35	2.73	215.4	1398.9	358.7	4886.1	1020.7	838.4
	5	ECPU-C	48	1.16	200.3	2317.0	254.8	4475.1	943.0	689.0
	6	ECPU-D	21	0.26	130.9	485.5	87.9	1928.0	983.3	839.3
	7	ECPU-D	35	0.14	54.4	140.8	1.6	2385.3	1037.4	555.7
	8	ECPU-E	28	0.30	45.1	324.2	33.8	3468.9	1059.8	398.6
	9	ECPU-F	21	4.52	133.5	1131.4	158.9	1031.8	959.2	1636.2
	10	ECPU-G	21	3.93	113.5	1093.2	251.9	1293.5	1013.2	1995.4
	11	ECPU-H	34	0.45	132.5	1072.6	277.9	1108.9	1104.4	460.6
	12	ECPU-H	48	1.70	160.5	1168.9	454.0	1258.9	1153.5	933.2
	13	ECPU-J	14	1.66	204.3	4142.0	289.1	1428.3	1102.0	393.9
	14	ECPU-J	21	1.46	78.4	539.7	346.0	1656.0	994.6	1107.5
	15	ECPU-J	28	1.97	68.8	815.2	162.3	1473.0	1029.9	1123.0
	16	ECPU-J	49	3.91	64.7	2388.4	338.5	1222.4	987.1	1016.5
	17	ECPU-L	20	8.77	394.2	3472.5	2212.4	4910.4	286.3	3545.1
	18	ECPU-M	21	0.82	115.6	233.7	414.2	1181.2	1222.5	252.5
	19	ECPU-M	42	0.59	113.4	701.4	270.7	1479.3	1209.0	112.3
	20	ECPU-N	14	0.63	1460.5	550441.7	5684.6	1512.2	84.7	2940.2
	21	ECPU-N	21	18.83	1503.6	2373.1	9189.3	1137.3	47.5	11599.2
	22	ECPU-N	42	7.07	1362.7	431819.8	1838.9	1749.8	81.9	617.9
	23	ECPU-N	56	5.23	1211.2	364030.4	1250.0	3000.8	1144.1	533.5
	24	ECPU-O	7	1.63	154.8	1866.1	2583.7	1685.1	1247.3	1110.0
	25	ECPU-O	21	1.20	84.3	694.8	786.4	1713.4	1324.6	333.2
	26	ECPU-O	28	1.92	102.7	2672.4	1078.9	1762.8	1227.3	653.2
	27	ECPU-O	36	0.33	55.4	516.8	282.4	1470.1	1289.4	342.3
	28	ECPU-O	43	2.32	142.5	4390.1	1655.8	1698.8	1133.0	731.1
	29	ECPU-P	20	1.04	82.7	394.9	277.3	1320.7	1129.4	388.0
	30	ECPU-P	27	4.21	224.1	229.4	2336.2	878.0	987.4	4624.1
	31	ECPU-P	34	0.39	73.4	231.1	308.8	1439.3	1235.3	682.7
	32	ECPU-P	41	1.08	118.7	435.4	326.3	2072.7	1211.8	533.0
	33	ECPU-P	57	4.07	225.2	140.3	2275.5	1086.8	423.9	4093.1
	34	ECPU-Q	6	0.77	196.3	501.4	126.2	1049.2	1138.3	255.6
	35	ECPU-Q	20	0.27	19.5	67.3	121.0	909.2	976.4	281.6
	36	ECPU-Q	34	0.25	10.3	68.4	50.3	977.5	1050.9	114.0
	37	ECPU-Q	41	0.21	9.2	10.3	59.4	76.3	105.5	140.8
	38	ECPU-R	15	0.98	150.1	300.5	479.6	1026.4	1093.6	821.1
	39	ECPU-R	20	0.73	118.9	295.5	310.6	1140.3	1109.9	258.8
	40	ECPU-R	34	3.77	251.2	873.4	1538.5	1440.6	1002.7	4232.4

Average Concentration

AG ID	Code	Study Time	protein ug/ul	MIG, pg/ml	MMP-9, ng/ml	RBP-4, ng/ml	S100A8, ng/ml	S100A9, ng/ml	TGFBR3, pg/ml
41	ECPU-R	57	1.64	70.8	940.0	340.0	1052.5	1120.8	520.2
42	ECPU-S	15	1.06	189.2	328.4	582.7	1009.5	1171.6	1245.2
43	ECPU-S	27	0.97	189.6	376.9	308.5	951.2	1166.4	734.8
44	ECPU-S	57	1.02	152.3	339.3	317.9	1544.8	1174.4	609.4
45	ECPU-T	9	1.82	185.2	320.2	944.5	833.4	1153.7	1893.3
46	ECPU-T	21	0.37	32.8	92.9	218.6	689.4	1130.7	295.5
47	ECPU-T	42	0.49	64.4	214.4	218.7	1339.5	1147.9	197.0
48	ECPU-U	55	5.38	2568.1	810.1	1647.5	2767.4	327.0	4655.4
49	ECPU-A	7	6.88	2322.3	3472.4	1462.3	1551.2	1097.0	700.2
50	ECPU-A	14	12.63	3401.6	166643.3	2372.1	1113.2	151.0	1561.1
51	ECPU-A	21	33.54	823.6	3222.5	2298.0	1113.7	89.7	4805.3
52	ECPU-A	49	5.55	564.4	9281.6	894.6	1124.4	71.6	1409.0
53	ECPU-B	14	2.22	1556.9	471.7	474.1	1646.6	203.9	540.5
54	ECPU-B	35	2.76	440.9	406.1	500.9	931.1	1097.7	1445.6
55	ECPU-B	42	26.49	2760.6	618.1	6913.4	151.7	8.3	8647.7
56	ECPU-B	49	26.32	1960.6	178.4	6125.7	46.5	3.0	7926.9
57	ECPU-C	28	5.41	292.1	1723.5	283.8	549.9	372.7	862.9
58	ECPU-C	42	3.95	256.4	4671.1	730.5	1058.5	126.7	1032.1
59	ECPU-C	55	2.04	220.6	2308.9	413.4	961.5	1100.6	615.9
60	ECPU-D	8	4.62	682.6	13125.5	247.3	1044.2	162.7	78.7
61	ECPU-D	28	0.32	193.2	195.5	20.0	1465.6	1194.5	169.9
62	ECPU-D	41	0.49	47.5	330.6	1.8	1335.7	1054.9	354.2
63	ECPU-D	50	0.12	44.3	63.1	33.6	1386.7	1158.2	547.5
64	ECPU-E	21	11.78	272.2	797.5	474.8	1217.8	67.2	3854.1
65	ECPU-E	35	0.31	53.9	226.8	15.3	1574.0	1131.2	175.4
66	ECPU-E	56	4.93	97.4	176.9	311.4	381.9	79.3	2500.6
67	ECPU-F	14	4.14	85.8	480.2	339.9	1163.9	1135.9	2107.3
68	ECPU-F	28	3.47	81.6	668.0	207.3	1031.5	1145.6	1740.6
69	ECPU-G	14	2.50	77.4	1738.6	276.6	1410.2	1111.1	1629.8
70	ECPU-G	34	3.05	34.2	439.7	229.2	940.1	1142.6	1791.1
71	ECPU-H	13	2.67	440.1	5658.5	622.2	1234.4	1148.0	771.5
72	ECPU-I	34	1.13	69.2	442.1	274.1	1004.6	1180.5	425.4
73	ECPU-I	48	9.07	390.9	457634.3	2775.4	1381.5	110.2	657.8
74	ECPU-J	7	2.36	109.0	10560.8	403.4	1538.6	1082.8	207.6
75	ECPU-J	35	0.30	129.3	436.8	77.9	1001.5	1211.8	142.0
76	ECPU-J	42	0.89	25.2	1186.3	88.5	1050.5	1242.8	154.8
77	ECPU-J	56	8.53	70.7	1487.2	754.9	1003.2	108.1	1624.6
78	ECPU-K	13	0.90	405.6	1072.6	248.2	1367.1	1087.3	461.4
79	ECPU-L	7	3.15	596.9	1691.5	272.3	1872.2	1113.8	860.8
80	ECPU-L	28	5.47	423.6	4366.7	649.5	1451.8	412.0	1672.6
81	ECPU-N	7	12.14	8047.1	308881.4	3153.9	1106.3	93.6	4247.4
82	ECPU-N	29	5.32	749.2	10475.1	1299.1	1271.9	216.3	1316.4
83	ECPU-N	49	5.95	992.3	317338.9	1221.0	954.7	163.5	78.1
84	ECPU-O	15	0.30	44.8	364.5	373.0	1040.1	923.0	310.1
85	ECPU-O	51	2.34	205.3	7037.3	1526.3	1096.3	983.2	1091.5
86	ECPU-O	58	2.07	176.8	1911.3	1849.7	301.7	7937.1	454.8
87	ECPU-Q	15	0.82	67.8	132.5	364.4	305.8	2399.9	154.1
88	ECPU-Q	27	3.38	102.5	428.4	701.3	315.4	7647.3	2137.5
89	ECPU-R	6	0.24	28.4	100.2	1.8	301.6	8220.4	47.0
90	ECPU-R	27	2.34	106.2	416.3	497.5	335.2	3326.7	1556.6
91	ECPU-S	6	0.20	188.3	335.7	77.3	351.3	8720.3	55.2
92	ECPU-S	20	0.45	235.8	263.7	222.5	342.8	8807.4	149.6
93	ECPU-S	34	1.35	1305.2	960.9	273.8	335.4	8976.9	463.0
94	ECPU-T	28	2.07	541.7	179.5	990.6	318.9	1673.1	1698.3
95	ECPU-U	7	4.46	746.6	919.4	862.1	299.2	721.5	1097.2
96	ECPU-U	14	21.07	2499.6	1516.9	8874.4	252.9	13.8	16212.6

Appendix J

SRM Transition Parameters

Protein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ion	MS2 Re Dwell Fragmentor	Collision Energy	Cell Accelerator V	Ion Name
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	321.700306 Unit	5	380	24.1	6 y6
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	345.22448 Unit	5	380	24.1	4 y3
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	356.697429 Unit	5	380	24.1	4 b7
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	371.192511 Unit	5	380	24.1	4 b4
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	390.229762 Unit	5	380	24.1	4 y7
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	413.239461 Unit	5	380	24.1	4 b8
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	442.277243 Unit	5	380	24.1	4 y4
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	446.771794 Unit	5	380	24.1	4 y8
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	481.768917 Unit	5	380	24.1	4 b9
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	484.276575 Unit	5	380	24.1	4 b5
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	496.306001 Unit	5	380	24.1	4 y9
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	525.284931 Unit	5	380	24.1	4 b10
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	555.361307 Unit	5	380	24.1	4 y5
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	560.827297 Unit	5	380	24.1	4 y10
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	581.826963 Unit	5	380	24.1	4 b11
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	613.319168 Unit	5	380	24.1	4 b6
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	617.369329 Unit	5	380	24.1	4 y11
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	630.353345 Unit	5	380	24.1	4 b12
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	642.393336 Unit	5	380	24.1	4 y6
26S proteasome non-ATPase regulatory subunit 6 isoform X1	GAEILEVLHSLPAVR	802.461947 Unit	665.871902 Unit	5	380	24.1	4 b13
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	204.134267 Unit	5	380	15	4 y2
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	227.175404 Unit	5	380	15	4 b2
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	231.121357 Unit	5	380	15	4 y5
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	236.153614 Unit	5	380	15	4 b4
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	264.664346 Unit	5	380	15	4 b5
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	275.171381 Unit	5	380	15	4 y3
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	287.663389 Unit	5	380	15	4 y6
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	316.174121 Unit	5	380	15	4 y7
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	321.206378 Unit	5	380	15	4 b6
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	346.208495 Unit	5	380	15	4 y4
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	358.215889 Unit	5	380	15	4 b3
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	372.716153 Unit	5	380	15	4 y8
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	378.71985 Unit	5	380	15	4 b7
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	414.238407 Unit	5	380	15	4 b8
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	438.236395 Unit	5	380	15	4 y9
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	449.756964 Unit	5	380	15	4 b9
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	461.235438 Unit	5	380	15	4 y5
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	471.299953 Unit	5	380	15	4 b4
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	478.267695 Unit	5	380	15	4 b10
ADP-ribosylation Factor (ARF-6)	ILMLGLDAAGK	551.320459 Unit	494.778427 Unit	5	380	15	4 y10
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	490.748378 Unit	5	380	41.1	4 y10
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	491.738771 Unit	5	380	41.1	4 b8
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	526.266935 Unit	5	380	41.1	4 y11
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	536.253731 Unit	5	380	41.1	4 b4
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	556.260068 Unit	5	380	41.1	4 b9
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	563.303518 Unit	5	380	41.1	4 y5
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	591.787178 Unit	5	380	41.1	4 y12
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	607.290845 Unit	5	380	41.1	4 b5
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	620.289356 Unit	5	380	41.1	4 b10
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	650.335546 Unit	5	380	41.1	4 y6
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	656.308474 Unit	5	380	41.1	4 y13
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	684.810653 Unit	5	380	41.1	4 b11
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	720.337763 Unit	5	380	41.1	4 y14
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	720.374909 Unit	5	380	41.1	4 b6
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	737.367575 Unit	5	380	41.1	4 y7

Protein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ion	MS2 Re Dwell Fragmentor	Collision Energy	Cell Accelerator V	Ion Name
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	750.330895 Unit	5	380	41.1	4 b12
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	784.85906 Unit	5	380	41.1	4 y15
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	785.849452 Unit	5	380	41.1	4 b13
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	808.404688 Unit	5	380	41.1	4 y8
Beta Actin	LC[IAA alkylation]YVALDFEQEMATAASSSSLEK	1275.590554 Unit	835.401852 Unit	5	380	41.1	4 b7
CDC34	GLQEEPVEGFR	630.814584 Unit	279.131922 Unit	5	380	17.9	4 b5
CDC34	GLQEEPVEGFR	630.814584 Unit	299.171381 Unit	5	380	17.9	4 b3
CDC34	GLQEEPVEGFR	630.814584 Unit	304.163556 Unit	5	380	17.9	4 y5
CDC34	GLQEEPVEGFR	630.814584 Unit	322.187366 Unit	5	380	17.9	4 y2
CDC34	GLQEEPVEGFR	630.814584 Unit	327.658304 Unit	5	380	17.9	4 b6
CDC34	GLQEEPVEGFR	630.814584 Unit	352.689938 Unit	5	380	17.9	4 y6
CDC34	GLQEEPVEGFR	630.814584 Unit	377.192511 Unit	5	380	17.9	4 b7
CDC34	GLQEEPVEGFR	630.814584 Unit	379.208829 Unit	5	380	17.9	4 y3
CDC34	GLQEEPVEGFR	630.814584 Unit	417.211235 Unit	5	380	17.9	4 y7
CDC34	GLQEEPVEGFR	630.814584 Unit	428.213974 Unit	5	380	17.9	4 b4
CDC34	GLQEEPVEGFR	630.814584 Unit	441.713807 Unit	5	380	17.9	4 b8
CDC34	GLQEEPVEGFR	630.814584 Unit	470.224539 Unit	5	380	17.9	4 b9
CDC34	GLQEEPVEGFR	630.814584 Unit	481.732531 Unit	5	380	17.9	4 y8
CDC34	GLQEEPVEGFR	630.814584 Unit	508.251423 Unit	5	380	17.9	4 y4
CDC34	GLQEEPVEGFR	630.814584 Unit	543.758746 Unit	5	380	17.9	4 b10
CDC34	GLQEEPVEGFR	630.814584 Unit	545.76182 Unit	5	380	17.9	4 y9
CDC34	GLQEEPVEGFR	630.814584 Unit	557.256568 Unit	5	380	17.9	4 b5
CDC34	GLQEEPVEGFR	630.814584 Unit	602.303852 Unit	5	380	17.9	4 y10
CDC34	GLQEEPVEGFR	630.814584 Unit	607.319837 Unit	5	380	17.9	4 y5
CDC34	GLQEEPVEGFR	630.814584 Unit	654.309331 Unit	5	380	17.9	4 b6
Cdk3	IGEGTYGVVYK	593.311146 Unit	229.615908 Unit	5	380	16.6	4 b5
Cdk3	IGEGTYGVVYK	593.311146 Unit	254.660118 Unit	5	380	16.6	4 y4
Cdk3	IGEGTYGVVYK	593.311146 Unit	283.17085 Unit	5	380	16.6	4 y5
Cdk3	IGEGTYGVVYK	593.311146 Unit	300.155397 Unit	5	380	16.6	4 b3
Cdk3	IGEGTYGVVYK	593.311146 Unit	310.176132 Unit	5	380	16.6	4 y2
Cdk3	IGEGTYGVVYK	593.311146 Unit	311.147572 Unit	5	380	16.6	4 b6
Cdk3	IGEGTYGVVYK	593.311146 Unit	339.658304 Unit	5	380	16.6	4 b7
Cdk3	IGEGTYGVVYK	593.311146 Unit	357.176861 Unit	5	380	16.6	4 b4
Cdk3	IGEGTYGVVYK	593.311146 Unit	364.702514 Unit	5	380	16.6	4 y6
Cdk3	IGEGTYGVVYK	593.311146 Unit	389.192511 Unit	5	380	16.6	4 b8
Cdk3	IGEGTYGVVYK	593.311146 Unit	409.244546 Unit	5	380	16.6	4 y3
Cdk3	IGEGTYGVVYK	593.311146 Unit	415.226354 Unit	5	380	16.6	4 y7
Cdk3	IGEGTYGVVYK	593.311146 Unit	438.726718 Unit	5	380	16.6	4 b9
Cdk3	IGEGTYGVVYK	593.311146 Unit	443.737085 Unit	5	380	16.6	4 y8
Cdk3	IGEGTYGVVYK	593.311146 Unit	458.224539 Unit	5	380	16.6	4 b5
Cdk3	IGEGTYGVVYK	593.311146 Unit	508.258382 Unit	5	380	16.6	4 y9
Cdk3	IGEGTYGVVYK	593.311146 Unit	508.31296 Unit	5	380	16.6	4 y4
Cdk3	IGEGTYGVVYK	593.311146 Unit	520.258382 Unit	5	380	16.6	4 b10
Cdk3	IGEGTYGVVYK	593.311146 Unit	536.769114 Unit	5	380	16.6	4 y10
Cdk3	IGEGTYGVVYK	593.311146 Unit	565.334424 Unit	5	380	16.6	4 y5
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	363.187425 Unit	5	380	24.9	4 y3
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	372.684133 Unit	5	380	24.9	4 b6
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	387.703243 Unit	5	380	24.9	4 y7
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	406.165584 Unit	5	380	24.9	4 b3
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	438.204375 Unit	5	380	24.9	4 b7
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	453.223485 Unit	5	380	24.9	4 y8
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	478.214368 Unit	5	380	24.9	4 y4
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	502.251857 Unit	5	380	24.9	4 b8
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	503.218348 Unit	5	380	24.9	4 b4
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	517.252774 Unit	5	380	24.9	4 y9

Protein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ion	MS2 Re Dwell Fragmentor	Collision Energy	Cell Accelerator V	Ion Name
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	549.251482 Unit	5	380	24.9	4 y5
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	550.778239 Unit	5	380	24.9	4 b9
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	573.794806 Unit	5	380	24.9	4 y10
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	586.296796 Unit	5	380	24.9	4 b10
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	616.302412 Unit	5	380	24.9	4 b5
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	622.321188 Unit	5	380	24.9	4 y11
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	643.810267 Unit	5	380	24.9	4 b11
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	646.304246 Unit	5	380	24.9	4 y6
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	687.326281 Unit	5	380	24.9	4 b12
CUGBP Elav-like family member 2 isoform X22	MHHPIQMKPADSEK	824.900342 Unit	690.850644 Unit	5	380	24.9	4 y12
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	147.594247 Unit	5	380	14.2	4 y2
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	151.589161 Unit	5	380	14.2	4 b3
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	197.128454 Unit	5	380	14.2	4 y3
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	215.139019 Unit	5	380	14.2	4 b2
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	225.123368 Unit	5	380	14.2	4 b4
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	247.652293 Unit	5	380	14.2	4 y4
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	281.6654 Unit	5	380	14.2	4 b5
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	294.181218 Unit	5	380	14.2	4 y2
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	302.171047 Unit	5	380	14.2	4 b3
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	304.194325 Unit	5	380	14.2	4 y5
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	332.18924 Unit	5	380	14.2	4 b6
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	377.728532 Unit	5	380	14.2	4 y6
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	381.723447 Unit	5	380	14.2	4 b7
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	393.249632 Unit	5	380	14.2	4 y3
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	421.244546 Unit	5	380	14.2	4 y7
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	449.239461 Unit	5	380	14.2	4 b4
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	455.257654 Unit	5	380	14.2	4 b8
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	471.768386 Unit	5	380	14.2	4 y8
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	494.29731 Unit	5	380	14.2	4 y4
Cullin-2 (CUL-2)	LTSFITVFK	528.310418 Unit	562.323525 Unit	5	380	14.2	4 b5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	175.071333 Unit	5	380	12.5	4 b2
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	182.097351 Unit	5	380	12.5	4 y3
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	201.123368 Unit	5	380	12.5	4 b4
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	217.615908 Unit	5	380	12.5	4 y4
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	234.144832 Unit	5	380	12.5	4 y2
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	265.152657 Unit	5	380	12.5	4 b5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	281.645196 Unit	5	380	12.5	4 y5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	288.155397 Unit	5	380	12.5	4 b3
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	300.671214 Unit	5	380	12.5	4 b6
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	338.187228 Unit	5	380	12.5	4 y6
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	363.187425 Unit	5	380	12.5	4 y3
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	365.192511 Unit	5	380	12.5	4 b7
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	394.72926 Unit	5	380	12.5	4 y7
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	401.239461 Unit	5	380	12.5	4 b4
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	408.708525 Unit	5	380	12.5	4 b8
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	434.224539 Unit	5	380	12.5	4 y4
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	438.245275 Unit	5	380	12.5	4 y8
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	529.298038 Unit	5	380	12.5	4 b5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	562.283117 Unit	5	380	12.5	4 y5
DCC-interacting protein 13-alpha	SSILQAESK	481.761289 Unit	600.335152 Unit	5	380	12.5	4 b6
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	347.167359 Unit	5	380	23.3	4 y3
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	356.217997 Unit	5	380	23.3	4 b3
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	357.687061 Unit	5	380	23.3	4 b6
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	359.671942 Unit	5	380	23.3	4 y6
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	421.71635 Unit	5	380	23.3	4 b7

Protein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ion	MS2 Re Dwell Fragmentor	Collision Energy	Cell Accelerator V	Ion Name
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	423.701231 Unit	5	380	23.3	4 y7
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	457.265676 Unit	5	380	23.3	4 b4
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	476.209952 Unit	5	380	23.3	4 y4
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	486.237647 Unit	5	380	23.3	4 b8
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	488.222528 Unit	5	380	23.3	4 y8
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	542.779679 Unit	5	380	23.3	4 b9
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	552.251817 Unit	5	380	23.3	4 y9
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	585.324253 Unit	5	380	23.3	4 b5
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	589.294016 Unit	5	380	23.3	4 y5
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	602.775656 Unit	5	380	23.3	4 y10
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	607.300975 Unit	5	380	23.3	4 b10
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	664.814447 Unit	5	380	23.3	4 b11
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	667.296952 Unit	5	380	23.3	4 y11
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	693.325178 Unit	5	380	23.3	4 b12
kinesin-like protein KIF15 isoform X2	LLETQEQEIEDGR	780.381016 Unit	714.366846 Unit	5	380	23.3	4 b6
L-selectin	AEIEYLEK	497.758215 Unit	138.581336 Unit	5	380	13.1	4 y2
L-selectin	AEIEYLEK	497.758215 Unit	147.112804 Unit	5	380	13.1	4 y1
L-selectin	AEIEYLEK	497.758215 Unit	157.589161 Unit	5	380	13.1	4 b3
L-selectin	AEIEYLEK	497.758215 Unit	195.123368 Unit	5	380	13.1	4 y3
L-selectin	AEIEYLEK	497.758215 Unit	201.086983 Unit	5	380	13.1	4 b2
L-selectin	AEIEYLEK	497.758215 Unit	222.110458 Unit	5	380	13.1	4 b4
L-selectin	AEIEYLEK	497.758215 Unit	276.155397 Unit	5	380	13.1	4 y2
L-selectin	AEIEYLEK	497.758215 Unit	276.655033 Unit	5	380	13.1	4 y4
L-selectin	AEIEYLEK	497.758215 Unit	303.642122 Unit	5	380	13.1	4 b5
L-selectin	AEIEYLEK	497.758215 Unit	314.171047 Unit	5	380	13.1	4 b3
L-selectin	AEIEYLEK	497.758215 Unit	341.176329 Unit	5	380	13.1	4 y5
L-selectin	AEIEYLEK	497.758215 Unit	360.184154 Unit	5	380	13.1	4 b6
L-selectin	AEIEYLEK	497.758215 Unit	389.239461 Unit	5	380	13.1	4 y3
L-selectin	AEIEYLEK	497.758215 Unit	397.718361 Unit	5	380	13.1	4 y6
L-selectin	AEIEYLEK	497.758215 Unit	424.705451 Unit	5	380	13.1	4 b7
L-selectin	AEIEYLEK	497.758215 Unit	443.21364 Unit	5	380	13.1	4 b4
L-selectin	AEIEYLEK	497.758215 Unit	462.239658 Unit	5	380	13.1	4 y7
L-selectin	AEIEYLEK	497.758215 Unit	552.302789 Unit	5	380	13.1	4 y4
L-selectin	AEIEYLEK	497.758215 Unit	606.276969 Unit	5	380	13.1	4 b5
L-selectin	AEIEYLEK	497.758215 Unit	681.345383 Unit	5	380	13.1	4 y5
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	449.680496 Unit	5	380	32.5	4 y7
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	452.186903 Unit	5	380	32.5	4 b8
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	470.224539 Unit	5	380	32.5	4 b5
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	485.199053 Unit	5	380	32.5	4 y8
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	502.710742 Unit	5	380	32.5	4 b9
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	506.220516 Unit	5	380	32.5	4 y4
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	535.722892 Unit	5	380	32.5	4 y9
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	553.234581 Unit	5	380	32.5	4 b10
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	586.246731 Unit	5	380	32.5	4 y10
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	588.753138 Unit	5	380	32.5	4 b11
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	621.247459 Unit	5	380	32.5	4 y5
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	629.762745 Unit	5	380	32.5	4 y11
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	645.774602 Unit	5	380	32.5	4 b12
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	656.303852 Unit	5	380	32.5	4 b6
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	709.77807 Unit	5	380	32.5	4 y12
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	727.306266 Unit	5	380	32.5	4 b13
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	784.310788 Unit	5	380	32.5	4 y6
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	784.819737 Unit	5	380	32.5	4 b14
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	802.817726 Unit	5	380	32.5	4 y13
matrix metalloproteinase-9	SDGLPWC[IAA alkylation]STTANYDTDDR	1037.426358 Unit	816.334501 Unit	5	380	32.5	4 b7

Protein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ion	MS2 Re Dwell	Fragmentor	Collision Energy	Cell Accelerator V	Ion Name
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	373.25578 Unit	5	380	24.3	4	y3
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	380.710348 Unit	5	380	24.3	4	y6
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	384.705588 Unit	5	380	24.3	4	b7
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	387.202681 Unit	5	380	24.3	4	b3
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	424.226362 Unit	5	380	24.3	4	y7
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	428.221602 Unit	5	380	24.3	4	b8
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	459.744919 Unit	5	380	24.3	4	y8
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	486.271095 Unit	5	380	24.3	4	b4
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	501.314357 Unit	5	380	24.3	4	y4
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	508.236927 Unit	5	380	24.3	4	b9
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	516.766383 Unit	5	380	24.3	4	y9
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	557.771134 Unit	5	380	24.3	4	b10
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	565.292765 Unit	5	380	24.3	4	y10
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	583.323859 Unit	5	380	24.3	4	b5
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	600.382771 Unit	5	380	24.3	4	y5
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	614.826972 Unit	5	380	24.3	4	y11
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	621.800422 Unit	5	380	24.3	4	b11
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	658.342986 Unit	5	380	24.3	4	y12
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	671.334629 Unit	5	380	24.3	4	b12
pre-mRNA-processing factor 19	IWSVPNASC[IAA alkylation]VQVVVR	807.924674 Unit	697.366787 Unit	5	380	24.3	4	b6
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	336.663586 Unit	5	380	24.5	4	b6
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	365.174318 Unit	5	380	24.5	4	b7
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	384.689081 Unit	5	380	24.5	4	y6
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	403.229959 Unit	5	380	24.5	4	y3
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	429.234376 Unit	5	380	24.5	4	b4
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	429.695615 Unit	5	380	24.5	4	b8
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	449.210377 Unit	5	380	24.5	4	y7
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	477.721109 Unit	5	380	24.5	4	y8
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	503.229821 Unit	5	380	24.5	4	b9
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	534.270443 Unit	5	380	24.5	4	y4
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	535.234581 Unit	5	380	24.5	4	y9
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	546.745836 Unit	5	380	24.5	4	b10
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	557.292953 Unit	5	380	24.5	4	b5
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	599.26387 Unit	5	380	24.5	4	y10
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	612.266078 Unit	5	380	24.5	4	b11
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	621.302472 Unit	5	380	24.5	4	y5
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	655.805902 Unit	5	380	24.5	4	y11
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	669.77955 Unit	5	380	24.5	4	b12
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	672.319896 Unit	5	380	24.5	4	b6
profilin-1	DSLLQDGEFSMDLR	813.377419 Unit	712.347934 Unit	5	380	24.5	4	y12
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	447.235044 Unit	5	380	34	4	y3
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	463.218725 Unit	5	380	34	4	b4
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	466.727249 Unit	5	380	34	4	y8
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	470.22655 Unit	5	380	34	4	b8
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	495.237981 Unit	5	380	34	4	y9
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	526.768583 Unit	5	380	34	4	b9
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	551.780013 Unit	5	380	34	4	y10
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	562.261987 Unit	5	380	34	4	y4
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	583.310615 Unit	5	380	34	4	b10
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	592.261319 Unit	5	380	34	4	b5
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	608.322045 Unit	5	380	34	4	y11
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	611.821346 Unit	5	380	34	4	b11
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	633.299101 Unit	5	380	34	4	y5
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	651.838059 Unit	5	380	34	4	y12
protein S100-A7	IDFSEFLSLLGDIADYHK	1077.541319 Unit	669.334818 Unit	5	380	34	4	b12

Protein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ion	MS2 Re Dwell Fragmentor	Collision Energy	Cell Accelerator V	Ion Name
protein S100-A7	IDFSEFLSLGDIAADYHK	1077.541319 Unit	704.336215 Unit	5	380	34	4 y6
protein S100-A7	IDFSEFLSLGDIAADYHK	1077.541319 Unit	708.380091 Unit	5	380	34	4 y13
protein S100-A7	IDFSEFLSLGDIAADYHK	1077.541319 Unit	725.87685 Unit	5	380	34	4 b13
protein S100-A7	IDFSEFLSLGDIAADYHK	1077.541319 Unit	739.329733 Unit	5	380	34	4 b6
protein S100-A7	IDFSEFLSLGDIAADYHK	1077.541319 Unit	761.395407 Unit	5	380	34	4 b14
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	311.153189 Unit	5	380	21.4	4 b6
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	361.677028 Unit	5	380	21.4	4 y6
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	367.695221 Unit	5	380	21.4	4 b7
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	405.22448 Unit	5	380	21.4	4 b4
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	418.21906 Unit	5	380	21.4	4 y7
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	423.223811 Unit	5	380	21.4	4 y3
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	424.716684 Unit	5	380	21.4	4 b8
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	468.742899 Unit	5	380	21.4	4 y8
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	480.245275 Unit	5	380	21.4	4 y4
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	488.745973 Unit	5	380	21.4	4 b9
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	517.256705 Unit	5	380	21.4	4 b10
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	520.251423 Unit	5	380	21.4	4 b5
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	526.256371 Unit	5	380	21.4	4 y9
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	574.782753 Unit	5	380	21.4	4 y10
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	581.778001 Unit	5	380	21.4	4 b11
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	608.303852 Unit	5	380	21.4	4 y5
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	621.299101 Unit	5	380	21.4	4 b6
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	643.312208 Unit	5	380	21.4	4 y11
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	655.312208 Unit	5	380	21.4	4 b12
protein S100-A9	LGH PDTLNQGEFK	728.364972 Unit	671.82294 Unit	5	380	21.4	4 y12
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	381.195053 Unit	5	380	26.5	4 b7
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	432.71021 Unit	5	380	26.5	4 y8
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	437.206446 Unit	5	380	26.5	4 y4
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	437.737085 Unit	5	380	26.5	4 b8
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	456.245275 Unit	5	380	26.5	4 b4
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	489.252242 Unit	5	380	26.5	4 y9
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	502.258382 Unit	5	380	26.5	4 b9
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	508.24356 Unit	5	380	26.5	4 y5
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	527.282388 Unit	5	380	26.5	4 b5
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	562.786449 Unit	5	380	26.5	4 y10
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	566.287671 Unit	5	380	26.5	4 b10
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	606.302464 Unit	5	380	26.5	4 y11
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	607.311974 Unit	5	380	26.5	4 y6
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	614.314417 Unit	5	380	26.5	4 b6
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	615.821878 Unit	5	380	26.5	4 b11
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	641.82102 Unit	5	380	26.5	4 y12
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	651.340435 Unit	5	380	26.5	4 b12
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	698.363052 Unit	5	380	26.5	4 y13
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	700.874642 Unit	5	380	26.5	4 b13
pterin-4-alpha-carbinolamine dehydratase isoform 1	DINLASFIEQVAVSMT	869.44002 Unit	735.370552 Unit	5	380	26.5	4 y7
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	508.236927 Unit	5	380	42.2	4 b8
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	512.235104 Unit	5	380	42.2	4 y9
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	543.755484 Unit	5	380	42.2	4 b9
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	559.272218 Unit	5	380	42.2	4 y5
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	562.758943 Unit	5	380	42.2	4 y10
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	591.269675 Unit	5	380	42.2	4 y11
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	601.268955 Unit	5	380	42.2	4 b10
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	640.803882 Unit	5	380	42.2	4 y12
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	641.340572 Unit	5	380	42.2	4 b5
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGFTFTDTEPAK	1306.585803 Unit	660.319896 Unit	5	380	42.2	4 y6

Protein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ion	MS2 Re Dwell Fragmentor	Collision Energy	Cell Accelerator V	Ion Name
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	666.789197 Unit	5	380	42.2	4 b11
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	706.324124 Unit	5	380	42.2	4 y13
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	716.323404 Unit	5	380	42.2	4 b12
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	744.834136 Unit	5	380	42.2	4 b13
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	756.367515 Unit	5	380	42.2	4 b6
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	763.837596 Unit	5	380	42.2	4 y14
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	775.346839 Unit	5	380	42.2	4 y7
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	795.357976 Unit	5	380	42.2	4 b14
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	799.356153 Unit	5	380	42.2	4 y15
retinol-binding protein 4	LLNNWDVC[IAA alkylation]ADMVGTFDTEDPAK	1306.585803 Unit	855.435929 Unit	5	380	42.2	4 b7
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	393.237056 Unit	5	380	25.9	4 y6
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	421.747787 Unit	5	380	25.9	4 y7
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	433.224342 Unit	5	380	25.9	4 b9
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	461.735074 Unit	5	380	25.9	4 b10
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	462.245943 Unit	5	380	25.9	4 y3
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	479.261259 Unit	5	380	25.9	4 y8
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	495.292559 Unit	5	380	25.9	4 b5
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	518.277106 Unit	5	380	25.9	4 b11
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	527.787641 Unit	5	380	25.9	4 y9
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	559.298707 Unit	5	380	25.9	4 y4
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	566.329673 Unit	5	380	25.9	4 b6
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	571.303655 Unit	5	380	25.9	4 y10
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	574.819138 Unit	5	380	25.9	4 b12
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	606.822212 Unit	5	380	25.9	4 y11
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	623.34552 Unit	5	380	25.9	4 b13
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	653.361701 Unit	5	380	25.9	4 b7
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	663.843676 Unit	5	380	25.9	4 y12
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	672.382771 Unit	5	380	25.9	4 y5
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	712.370058 Unit	5	380	25.9	4 y13
Stat-1	LLGPNASPDGLIPWTR	853.964854 Unit	716.385176 Unit	5	380	25.9	4 b14
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	340.702514 Unit	5	380	27.6	4 b7
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	362.708662 Unit	5	380	27.6	4 y6
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	385.25578 Unit	5	380	27.6	4 y3
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	397.244546 Unit	5	380	27.6	4 b8
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	419.250694 Unit	5	380	27.6	4 y7
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	445.770928 Unit	5	380	27.6	4 b9
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	454.769251 Unit	5	380	27.6	4 y8
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	455.286411 Unit	5	380	27.6	4 b4
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	481.289485 Unit	5	380	27.6	4 b10
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	482.308544 Unit	5	380	27.6	4 y4
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	503.295633 Unit	5	380	27.6	4 y9
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	537.831517 Unit	5	380	27.6	4 b11
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	552.339175 Unit	5	380	27.6	4 b5
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	559.837665 Unit	5	380	27.6	4 y10
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	595.356222 Unit	5	380	27.6	4 y11
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	596.351471 Unit	5	380	27.6	4 y5
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	601.860806 Unit	5	380	27.6	4 b12
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	609.360639 Unit	5	380	27.6	4 b6
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	623.866954 Unit	5	380	27.6	4 y12
TGFBR3	ILLDPGALPALQNPPIR	899.532903 Unit	658.88227 Unit	5	380	27.6	4 b13
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	370.689938 Unit	5	380	19.9	4 b6
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	374.668346 Unit	5	380	19.9	4 y6
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	398.218666 Unit	5	380	19.9	4 b3
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	408.191131 Unit	5	380	19.9	4 y3
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	419.21632 Unit	5	380	19.9	4 b7

Prortein Name	Peptide Sequence (one peptide for each protein)	Precursor Ion	MS1 Re: Product Ion	MS2 Re Dwell	Fragmentor	Collision Energy	Cell Accelerator V	Ion Name
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	438.697634 Unit	5	380	19.9	4	y7
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	483.245609 Unit	5	380	19.9	4	b8
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	488.231841 Unit	5	380	19.9	4	y8
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	497.28708 Unit	5	380	19.9	4	b4
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	533.769448 Unit	5	380	19.9	4	b9
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	536.249708 Unit	5	380	19.9	4	y4
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	561.766048 Unit	5	380	19.9	4	y9
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	613.784772 Unit	5	380	19.9	4	b10
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	618.30808 Unit	5	380	19.9	4	y10
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	625.345657 Unit	5	380	19.9	4	b5
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	633.302472 Unit	5	380	19.9	4	y5
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	740.3726 Unit	5	380	19.9	4	b6
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	748.329415 Unit	5	380	19.9	4	y6
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	837.425364 Unit	5	380	19.9	4	b7
VEGF-A	HLFVQDPQTC[IAA alkylation]K	686.837536 Unit	876.387993 Unit	5	380	19.9	4	y7