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Proteomics Identifies Thymidine Phosphorylase As a Key Regulator of the Angiogenic Potential of Colony-Forming Units and Endothelial Progenitor Cell Cultures

Giordano Pula,* Ursula Mayr,* Colin Evans, Marianna Prokopi, Dina S. Vara, Xiaoke Yin, Zoe Astroulakis, Qingzhong Xiao, Jonathan Hill, Qingbo Xu, Manuel Mayr

Abstract—Endothelial progenitor cell (EPC) cultures and colony-forming units (CFUs) have been extensively studied for their therapeutic and diagnostic potential. Recent data suggest a role for EPCs in the release of proangiogenic factors. To identify factors secreted by EPCs, conditioned medium from EPC cultures and CFUs was analyzed using a matrix-assisted laser desorption/ionization tandem time-of-flight mass spectrometer combined with offline peptide separation by nanoflow liquid chromatography. Results were verified by RT-PCR and multiplex cytokine assays and complemented by a cellular proteomic analysis of cultured EPCs and CFUs using difference in-gel electrophoresis. This extensive proteomic analysis revealed the presence of the proangiogenic factor thymidine phosphorylase (TP). Functional experiments demonstrated that inhibition of TP by 5-bromo-6-amino-uracil or gene silencing resulted in a significant increase in basal and oxidative stress-induced apoptosis, whereas supplementation with 2-deoxy-D-ribose-1-phosphate (dRP), the enzymatic product of TP, abrogated this effect. Moreover, dRP produced in EPC cultures stimulated endothelial cell migration in a paracrine manner, as demonstrated by gene-silencing experiments in transmigration and wound repair assays. RGD peptides and inhibitory antibodies to integrin $\alpha v \beta 3$ attenuated the effect of conditioned medium from EPC cultures on endothelial migration. Finally, the effect of TP on angiogenesis was investigated by implantation of Matrigel plugs in mice. In these in vivo experiments, dRP strongly promoted neovascularization. Our data support the concept that EPCs exert their proangiogenic activity in a paracrine manner and demonstrate a key role of TP activity in their survival and proangiogenic potential. (*Circ Res.* 2009;104:32-40.)

Key Words: angiogenesis ■ endothelium ■ progenitor cells ■ proteomics ■ vascular biology

Human endothelial progenitor cells (EPCs) are attracting considerable attention in cardiovascular research,^{1,2} but multiple culture methods from peripheral blood mononuclear cells (PB-MNCs) have been described³⁻⁷ and studied for their clinical relevance.^{6,8-12} EPCs are commonly identified by cell surface antigen expression of CD133, CD34, and the vascular endothelial growth factor receptor-2 (VEGFR-2) (KDR).¹³ CD34 and VEGFR-2, however, are also expressed in hematopoietic stem cells¹⁴; thus, EPCs cannot yet be unambiguously defined. One alternative approach to flow cytometry has used the colony-forming unit (CFU) assay as a surrogate marker for EPCs.¹⁵ This method has been fundamental to many of the clinical studies published on EPCs to date, which predominantly reported low numbers of CFUs to be correlated to cardiovascular disease risk. Nonetheless, recent publications have cast doubts about the origin of CFUs by demonstrating that they may be clonally derived from the hematopoietic system, possess myeloid progenitor cell activity, and differentiate into phagocytic macrophages.¹⁶ Thus, there is an urgent need to provide a

mechanistic underpinning for the correlation between CFUs and cardiovascular disease^{6,15} and for the beneficial effects of endothelial progenitor transplantation in vivo.^{11,16}

Although it is commonly accepted that circulating progenitors may play an important role in revascularization and angiogenesis, the mechanisms by which they act remain unclear. Currently, there is little evidence of permanent engraftment of EPCs into blood vessels.^{8,17,18} It has therefore been suggested that EPCs stimulate endothelial repair by exerting a local paracrine effect.^{3,4,7,19} EPC-secreted factors, however, have not yet been fully characterized at the protein level. Although transcriptome analysis can generate a cell-specific signature,¹⁹ it cannot detail true cell phenotypes because of translational regulation and protein degradation. The addition of a proteome analysis offers an opportunity to characterize progenitor cells more comprehensively, leading to a better understanding of their role in vascular biology.²⁰⁻²²

In the present study, we use state-of-the-art proteomic techniques to analyze the secretome of EPC cultures and

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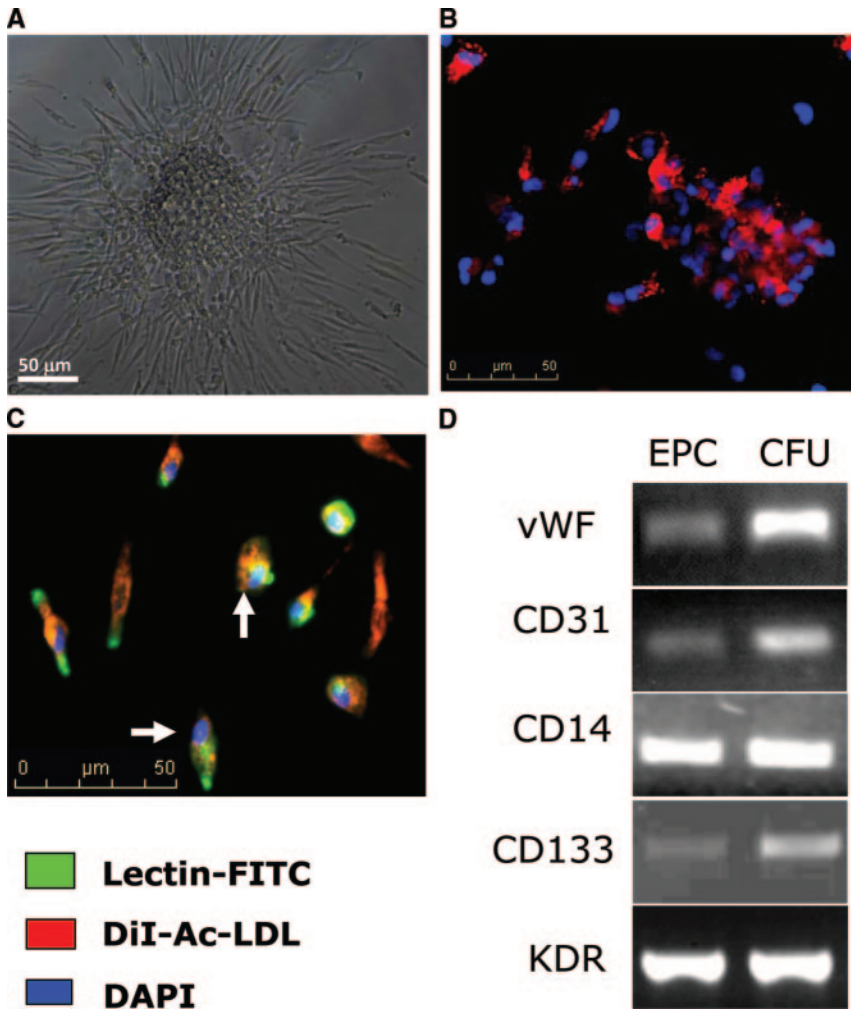


Figure 1. EPC cultures and CFUs. A and B, Morphology of CFUs (A) and endocytosis of acLDL (red fluorescence) (B). C, EPC cultures endocytose acLDL (red fluorescence) and bind to the lectin *Ulex europaeus* agglutinin (green fluorescence). Arrows indicate double positive cells. Blue labeling represents nuclear staining by DAPI. D, Assessment of mRNA levels for EPC cultures and CFUs by RT-PCR, including von Willebrand factor (vWF), CD31, CD14, CD133, and KDR (from top to bottom). The results shown are representative of at least 3 independent experiments.

CFUs by performing a nanoflow liquid chromatography matrix-assisted laser desorption/ionization tandem time-of-flight mass spectrometry (MALDI-TOF/TOF) analysis on culture media conditioned by EPCs. This approach was complemented by difference in-gel electrophoresis (DIGE) and cytokine antibody multiplex array analysis. Among the angiogenic factors revealed by proteomics, was thymidine phosphorylase (TP), also known as platelet-derived endothelial cell growth factor (PD-ECGF). This growth factor and deoxyribose phosphate (dRP), the product of its enzymatic activity, were shown to be essential for EPC survival and paracrine effects on endothelial cell migration and angiogenesis.

Materials and Methods

An expanded Material and Methods section is available in the online data supplement at <http://circres.ahajournals.org>. Key techniques involved adaptations of previously published protocols, including those for difference in-gel electrophoresis (DIGE)²³ and tandem mass spectrometry,²⁴ which are also available on our web site at <http://www.vascular-proteomics.com>.

CFUs and EPC Culture

Human blood was drawn from healthy volunteers. Informed consent was obtained and the study was approved by the ethics review board of King's College London. The CFU assay was performed as described previously.¹⁵ In brief, PB-MNCs were resuspended in growth medium containing medium 199 with 20% FBS on human

fibronectin-coated 6-well plates. After 48 hours, nonadherent cells were replated on human fibronectin-coated plates. For isolation of EPCs, PB-MNCs were separated onto Lymphoprep solution. EPC cultures were obtained using endothelial basal medium (EBM, Clonetics cc-3121, Lonza) containing human VEGF (10 ng/mL), as previously described.⁶ For secretome analysis, cells were incubated with serum-free culture medium for 24 hours before collection of the conditioned medium on day 7.

Matrix-Assisted Laser Desorption/Ionization Tandem Time-of-Flight Mass Spectrometry

For CFUs and EPCs, conditioned medium was concentrated using a Microcon Ultracel YM-10. A total volume of 1.5 mL conditioned medium was concentrated approximately 50-fold. The samples were digested overnight with trypsin, and the tryptic peptides were separated by nano liquid chromatography on a C18 column (PepMap) with a mobile phase formed from (1) high-performance liquid chromatography (HPLC)-grade water containing 5% acetonitrile and 0.1% TFA and (2) HPLC-grade acetonitrile containing 20% H₂O and 0.1% TFA. The HPLC was interfaced to a spotting robot (Dionex Probot). Several hundred fractions per sample were collected on MALDI target plates and mixed with matrix.

Peptides were subsequently analyzed using a TOF/TOF analyzer (4800 ToF/ToF, Applied Biosystems). Results were filtered using ProteinPilot software (Applied Biosystems). Assignments were accepted when the total score was ≥ 2.0 (corresponding to a 99% confidence of the protein identification). Results were further filtered for a minimum of ≥ 2 peptides per protein identification.

Table. Secretome of EPC Cultures and CFUs

Protein Name	Swiss Protein Accession No.	CFU		EPC	
		Total Ion Score	No. of Peptides	Total Ion Score	No. of Peptides
Angiogenic factors					
MMP-9	P14780	1262	24	ND	ND
IL-8	P10145	242	5	ND	ND
Pre-B cell-enhancing factor (PBEF)	P43490	233	6	216	6
Macrophage migration inhibitory factor (MIF)	P14174	168	3	89	2
Cathepsins					
Cathepsin B	P07858	598	11	567	11
Cathepsin S	P25774	374	6	325	6
Cathepsin Z	Q9UBR2	358	6	114	4
Cathepsin C	P53634	286	6	166	4
Cathepsin D	P07339	214	6	276	5
Cathepsin L	P07711	83	2	55	2
Protease inhibitors					
Inter- α -trypsin inhibitor complex component II	P19823	308	5	221	4
Metalloproteinase inhibitor 1 precursor (TIMP-1)	P01033	154	2	ND	ND
Cystatin-C	P01034	112	2	321	6
Serpin B9	P50453	95	3	101	3
α -2-Macroglobulin	P01023	92	3	88	3
Cystatin-B	P04080	82	1	75	2
S100 proteins					
Protein S100-A11	P31949	167	3	151	3
Protein S100-A8	P05109	71	2	65	2
Protein S100-A4	P26447	60	1	ND	ND
Miscellaneous					
Plasminogen activator inhibitor 2	P05120	739	11	466	10
Secretory granule proteoglycan core protein	P10124	239	5	26	1
Apolipoprotein E	P02649	202	6	985	22

Identifications were obtained by proteomic analysis of the conditioned medium of CFUs and EPC cultures by MALDI-TOF/TOF mass spectrometry. The average number of tryptic peptides and total ion scores are reported. The table highlights proteins that were chosen for their potential importance in the physiological activity of EPCs. The complete list of identified proteins is available in supplemental Table I. All peptide identifications are provided in supplemental Table II. ND indicates not detected.

Results

The Secretome of CFUs and EPC Cultures

CFUs consisted of a central cluster of rounded cells surrounded by multiple thin cells (Figure 1A), which showed endocytosis of acetylated LDL (red fluorescence) (Figure 1B). EPC cultures were characterized by single spindle-shaped cells positive for lectin staining and acetylated LDL uptake (Figure 1C). Both cell types express markers consistent with existing definitions of an EPC phenotype, such as von Willebrand factor, CD31 (platelet endothelial cell adhesion molecule-1), CD133, and VEGFR-2 (KDR) (Figure 1D). Analyses of the secretome of CFUs from 3 independent preparations resulted in the identification of 272 nonredundant proteins present in at least 2 samples (Table I in the online data supplement), of which 124 were also found in cultured EPCs. All identified peptides are provided in supplemental Table II. Secreted factors considered of potential relevance for the function of EPCs in the vascular system are

highlighted in the Table. Although some of the factors, such as cathepsins, have previously been reported to contribute to the angiogenic potential of EPCs,²⁵ others, such as the protein S100 family have not been implicated so far. A semiquantitative comparison based on the peptide count indicated that different members of the cathepsin family were present at similar concentrations under both culture conditions, whereas matrix metalloproteinase (MMP)-9 and interleukin (IL)-8 were secreted at higher levels by CFUs than cultured EPCs.

To further characterize cultured EPCs and CFUs, cellular protein extracts were labeled with Cy-dyes and separated by DIGE (Figure 2A and 2B). Overall, the proteome of CFUs was similar to EPC cultures and showed surprisingly little interindividual variability (supplemental Figure I). The analysis of 53 differentially expressed protein spots ($P < 0.05$, 1-way ANOVA) by ion trap tandem mass spectrometry resulted in the identification of 37 nonredundant proteins (supplemental Table III). Notably, the proangiogenic factor

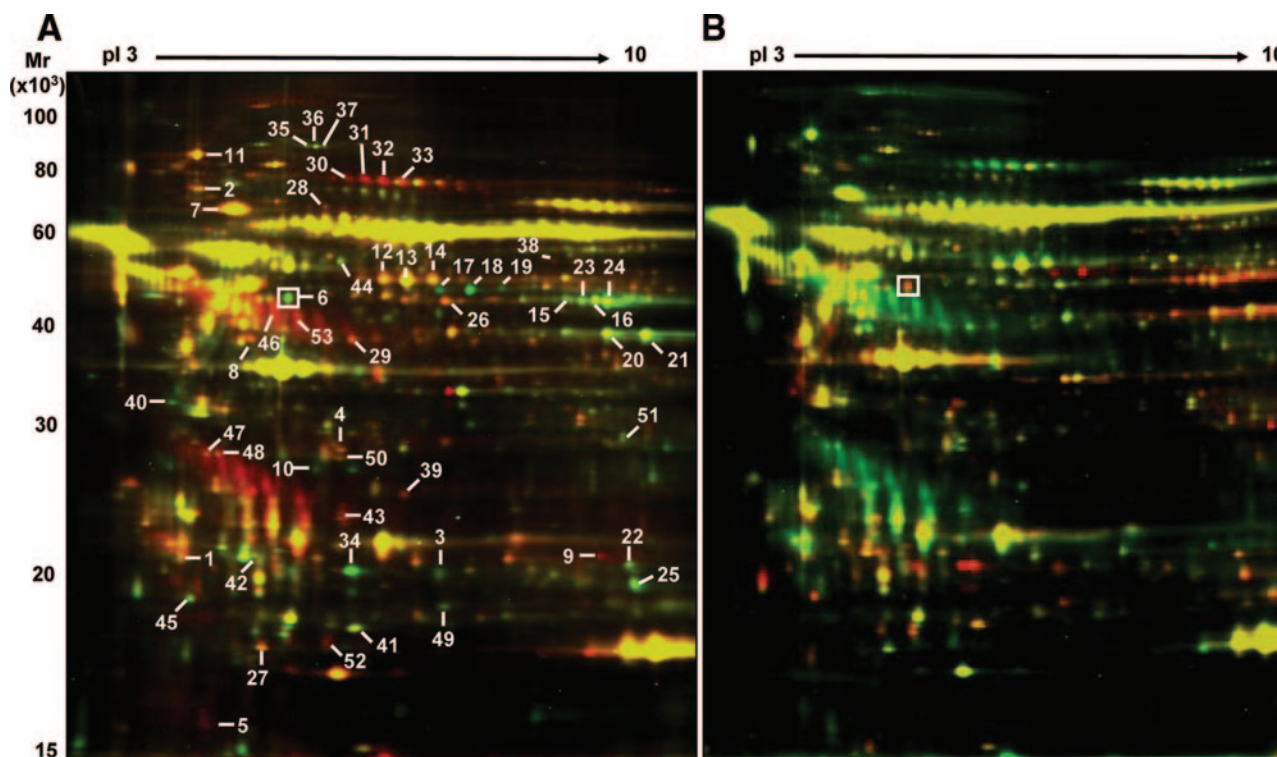


Figure 2. Difference in-gel electrophoresis. A, The proteins from CFUs are stained in green, whereas the proteins from EPC cultures are stained in red. B, Results are reproduced with different biological replicates using reverse-labeling (red for CFUs and green for EPCs). The protein corresponding to TP is highlighted with a box. Differentially expressed proteins ($P < 0.05$; 1-way ANOVA, SameSpot software, Nonlinear Dynamics) are numbered and listed in supplemental Table III.

TP,²⁶ although present in both EPC cultures and CFUs, was expressed at higher levels in cellular extracts of CFUs.

Validation of the Proteomic Findings

Cytokine concentrations in the conditioned media of CFUs ($n=15$) and EPC cultures ($n=13$) were quantified using a multiplex assay (supplemental Table IV). IL-8, as indicated by the proteomic analysis (Table), was confirmed to be the most abundant cytokine in the secretome of CFUs (76.1 ± 6.4 ng/mL) and cultured EPCs (1.4 ± 0.4 ng/mL). Its expression, along with other angiogenic factors, was verified by RT-PCR (Figure 3A). TP was further investigated by immunoblotting. This proangiogenic factor was predominantly present in CFUs, but also in EPC cultures and PB-MNCs, but not in human umbilical vein endothelial cells (HUVECs) (Figure 3B and 3C). Immunofluorescence experiments revealed the presence of TP in the cytosol and nucleus (Figure 3D), possibly because of its role in nucleotide metabolism.²⁶

TP Is a Survival Factor

To evaluate the functional role of TP in EPCs, cells were treated with 5-bromo-6-amino-uracil (5Br-6Am-U), an inhibitor of TP. Inhibition of TP resulted in a significant increase in baseline apoptosis as quantified by histone protein release (Figure 4A) and flow cytometric analysis of annexin V/propidium iodide staining (supplemental Figure II, A). Supplementation with deoxyribose phosphate (dRP), the product of TP, abrogated this effect. dRP also protected EPCs against apoptosis in response to diethyl maleate, a sulfhydryl-reactive agent, which induces oxidative stress by depleting intracel-

lular glutathione levels. In contrast, inhibition of TP by 5Br-6Am-U aggravated the proapoptotic effect of diethyl maleate. These findings were replicated by ablation of TP expression using small interfering (si)RNA-mediated gene silencing (Figure 4B and supplemental Figure II, B). Again, dRP reversed the effect of gene silencing of TP by siRNA on constitutive and stress-induced apoptosis. Knockdown efficiency was assessed by immunoblotting (supplemental Figure III, A). The proapoptotic effect of TP gene silencing was independent of VEGF (supplemental Figure III, B). On the other hand, inhibition of TP by 5Br-6Am-U or treatment with dRP did not alter apoptosis in HUVECs (supplemental Figure III, C), whereas prolonged inhibition (7 days, supplemental Figure III, D) or genetic ablation of TP (supplemental Figure III, E) significantly reduced EPC numbers in culture. Interestingly, dRP increased the expression of Bcl-2 in response to oxidative stress, which mitigates the proapoptotic effects of Bax but had no effect on redox-sensitive p38 mitogen-activated protein kinase (MAPK) signaling (Figure 5 and supplemental Figure IV).

Deoxyribose Phosphate Stimulates Focal Adhesion Formation and Enhances Integrin $\beta 3$ Expression

Besides its antiapoptotic effect, TP has been shown to stimulate endothelial cell motility,^{27,28} providing a likely explanation for its angiogenic activity. Therefore, we analyzed the formation of focal adhesions in HUVECs in response to the conditioned medium from EPCs. The conditioned medium of EPCs significantly increased the

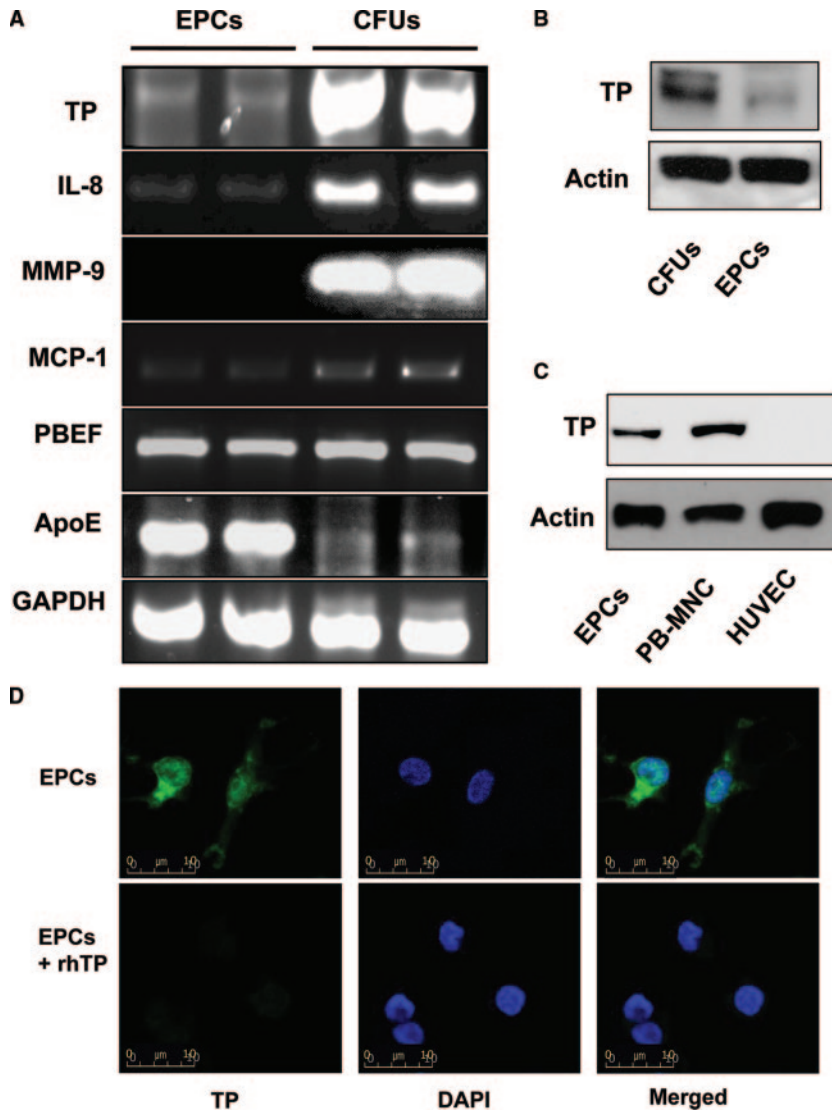


Figure 3. Expression of TP among other angiogenic factors. A, mRNA expression of TP, IL-8, MMP-9, MCP-1, pre-B cell-enhancing factor 4 (PBEF), and apolipoprotein E (ApoE) in EPC cultures and CFUs as assessed by RT-PCR. GAPDH was used as loading control. B, Protein expression of TP in EPC cultures and CFUs as assessed by immunoblotting. C, Levels of TP in EPCs, PB-MNCs, and HUVECs. Actin was used as loading control. The RT-PCR and immunoblot results are representative of 3 independent experiments. D, The cellular distribution of TP was visualized by immunofluorescence. Nuclei were counterstained with DAPI. To confirm the specificity of the antibody, immunostaining was repeated in the presence of 10 ng/mL recombinant human TP (rhTP).

number and dimension of focal adhesions (Figure 6A and supplemental Figure V, A). Untreated HUVECs and HUVECs treated with the conditioned medium from TP knockdown EPCs (TP KD) served as controls. Supplementing the conditioned medium from TP knockdown EPCs with dRP restored its ability to enhance focal adhesion formation in HUVECs, confirming that TP-derived dRP is the active compound in the conditioned medium. Notably, treatment with dRP increased endothelial expression of integrin $\beta 3$, but not integrin $\beta 1$ or αv , whereas other focal adhesion-associated proteins, such as vinculin and vasodilator stimulated phosphoprotein, were not affected (Figure 6B and supplemental Figure V, B).

TP Stimulates Endothelial Cell Migration

Next, we assessed the effect of TP on endothelial cell motility in a modified Boyden chamber. The presence of EPCs in the bottom compartment stimulated the migration of HUVECs migrating from the top insert (Figure 7A), confirming the importance of paracrine factors in EPC-endothelial cell interactions. The genetic ablation of TP in

EPCs by siRNA transfection significantly reduced the number of transmigrating HUVECs. The addition of 50 $\mu\text{mol/L}$ dRP in the bottom chamber, but not in the insert, reversed this effect, suggesting that the product of TP in the conditioned medium of EPCs acts as a chemotactic stimulus on HUVECs. Moreover, the presence of RGD peptides or an anti-integrin $\alpha v\beta 3$ inhibitory antibody attenuated the chemotactic activity, suggesting that dRP acts via integrins, in particular $\alpha v\beta 3$ (Figure 7B).

TP Enhances Wound Healing In Vitro and Angiogenesis In Vivo

The contribution of TP to the stimulatory activity of conditioned medium on endothelial motility was further investigated in a wound-healing assay. The process of endothelial wound-healing was attenuated in the presence of conditioned medium from TP-ablated EPC cultures compared to cultures treated with scrambled siRNA, suggesting that the activity of TP in EPCs promotes HUVEC motility in a paracrine manner (Figure 7C and supplemental Figure VI, A). The presence of an anti-integrin $\alpha v\beta 3$

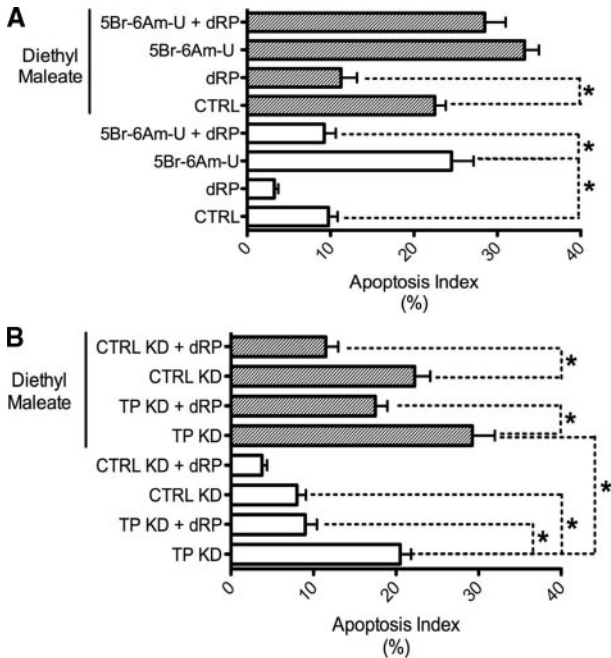


Figure 4. TP protects against apoptosis. A, Apoptosis in EPC cultures following treatment with 5Br-6Am-U (100 μ mol/L) was assessed by ELISA. Where indicated, apoptosis was induced by diethyl maleate (5 mmol/L, 12 hours). B, Apoptosis following knockdown of TP in EPC cultures by siRNA (TP KD) in the presence or absence of dRP (50 μ mol/L) as quantified by ELISA. Controls were transfected with scrambled siRNA (CTRL KD). Flow cytometric analyses of annexin V and propidium iodide staining are shown in supplemental Figure II.

inhibitory antibody (supplemental Figure VI, B) or RGD peptides (supplemental Figure VI, C) abolished the difference between conditioned medium from TP-ablated and control EPCs. Finally, the angiogenic effect of TP and its product dRP was investigated by implanting Matrigel plugs into healthy mice and assessing the vascularization of the plugs over the implantation period. Whereas both control plugs and plugs treated with 5Br-6Am-U showed cell invasion, dRP facilitated vessel formation (Figure 7D and supplemental Figure VII).

Discussion

This study is the first to use state-of-the art proteomic techniques to better characterize CFUs and EPC cultures. Although it has become apparent that the markers currently used for defining EPCs are insufficient,¹⁴ EPCs have never been studied comprehensively at the protein level. By analyzing their secretome, we provide additional support to the concept that exogenously administered EPCs may augment neovascularization and endothelial repair via paracrine mechanisms.^{4,19}

Paracrine Effects of EPCs

Despite the controversy regarding the origin of EPCs, a contribution of circulating progenitors to blood vessel growth has been shown in different animal models^{3,11,16,29–31} and administration of bone marrow cells appears to be beneficial in some,^{32–34} but not all clinical trials conducted so far.³⁵

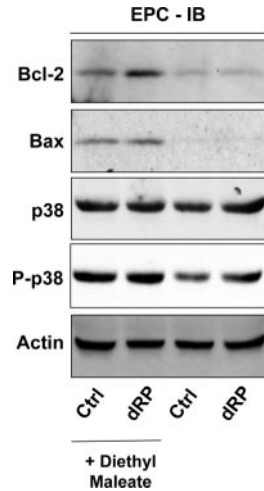


Figure 5. dRP enhances Bcl-2 expression under oxidative stress. EPC cultures with and without supplementation of dRP (50 μ mol/L) were subjected to treatment with diethyl maleate (5 mmol/L) and probed for Bcl-2, Bax, p38 MAPK, and phospho-p38 MAPK by immunoblotting. Actin served as loading control. Protein expression was quantified by densitometry (means \pm SEM, n=3; supplemental Figure IV).

Although it is commonly accepted that EPCs have potential for use in angiogenic therapies, the mechanisms by which they improve revascularization remain unsettled.³⁶ Their baseline incorporation rate is low and there is currently limited evidence of long-term engraftment of EPCs into newly formed blood vessels.^{37,38} Additionally, it has been shown that EPCs can cause neovascularization without physically building endothelial structures,³⁹ supporting the concept of a paracrine effect on the vasculature. Therefore, further investigations are required to characterize paracrine factors that could mediate their proangiogenic effects. Our proteomic analysis revealed that CFUs secrete high levels of MMP-9, IL-8, and cathepsins, previously described as characteristics of EPCs.^{7,25} In addition, we found novel factors, in particular TP, which was further characterized for its functional relevance in the biology of EPCs.

TP Improves EPC Survival

TP is an angiogenic enzyme catalyzing the reversible phosphorolysis of 2'-deoxythymidine to dRP and thymine. The antiapoptotic role of TP has been investigated in cancer cells.^{40,41} The proposed mechanism of action is not clear, but it has been suggested that the protective effect of TP is mediated by 2-deoxy-D-ribose, a product of dephosphorylation of the primary TP product dRP.⁴⁰ In this study, we report the presence of TP in CFUs and EPC cultures. Whereas apoptosis of mature endothelial cells was not influenced by dRP, the activity of TP correlated with levels of basal and oxidative stress-induced apoptosis in EPC cultures. Notably, dRP enhances the expression of the antiapoptotic protein Bcl-2, which heterodimerizes with Bax and thereby antagonizes its proapoptotic effect.^{42,43} Thus, it is likely that dRP conveys resistance to oxidative stress and apoptosis by increasing the Bcl-2/Bax ratio.

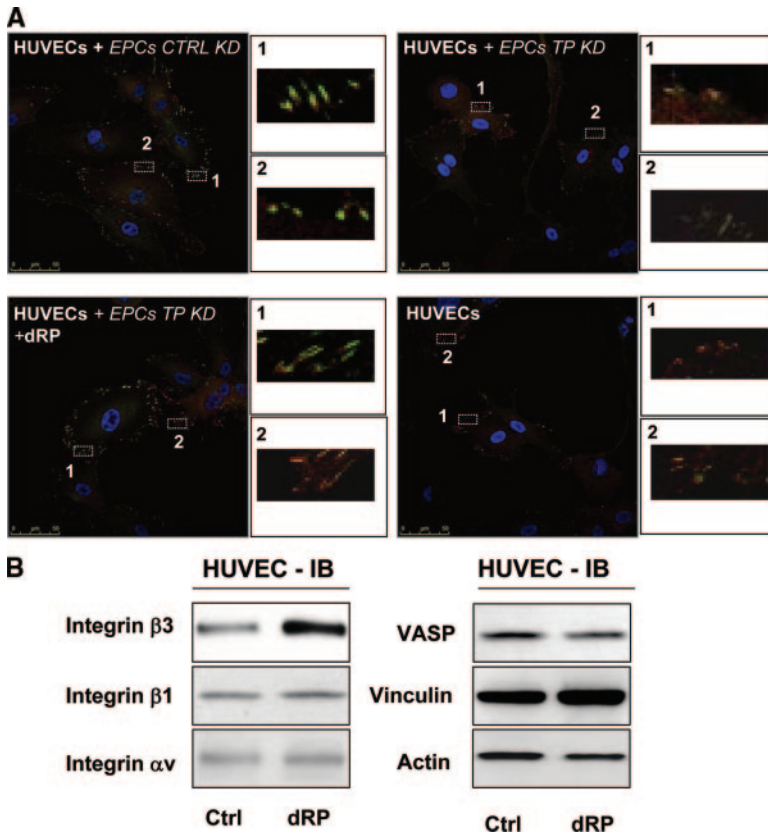


Figure 6. TP expression and release of dRP by EPCs stimulates focal adhesion formation and integrin $\beta 3$ expression in HUVECs. A, HUVECs were cultured for 24 hours in the presence of conditioned medium from EPC cultures (ratio 1:2) treated with either siRNA directed toward TP (TP KD) (top right) or scrambled controls (CTRL KD) (top left). dRP (50 $\mu\text{mol/L}$) was added where indicated (bottom left). HUVECs cultured in growth medium supplemented with nonconditioned EPC medium served as a reference (bottom right). Focal adhesions were visualized by the colocalization (yellow) of anti-integrin $\beta 3$ (FITC, green) and anti-vinculin (TRITC, red) staining. Two areas are magnified in the adjacent boxes (area 1 and 2), and the intensity of staining was quantified by densitometry (supplemental Figure V, A). The images are representative of 3 independent experiments. B, HUVECs were treated with 50 $\mu\text{mol/L}$ dRP for 24 hours and protein extracts were probed for expression of integrin $\beta 3$, integrin $\beta 1$, integrin αv , vasodilator stimulated phosphoprotein (VASP), and vinculin. Untreated HUVECs served as controls. The densitometric data were normalized to actin (means \pm SEM, $n=3$; supplemental Figure V, B).

TP Mediates Paracrine Effects on Endothelial Cells

It has long been suspected that EPCs may release paracrine factors to enhance endothelial repair. Our proteomic experiments revealed TP to be involved: First, the presence of EPC cultures in the bottom of a Boyden chamber markedly stimulated migration of HUVECs across the membrane, demonstrating the former cell type is able to induce endothelial migration in a paracrine manner. Second, downregulation of TP by siRNA attenuated this paracrine effect, suggesting that TP expression in EPC cultures plays a key role in the stimulation of endothelial migration. This is in agreement with previous observations that supplementation of dRP or TP-expressing tumor cells induce HUVEC chemotaxis.²⁷ Third, the addition of dRP to the bottom of a Boyden chamber with EPCs, but not to the top insert with HUVECs, restored the effect on HUVEC migration. Thus, the product of TP, not the enzyme itself, is the chemotactic agent that stimulates HUVEC migration in the conditioned medium of EPCs. Fourth, the expression of TP was also responsible for the enhanced regeneration of a wounded endothelial monolayer in the presence of conditioned medium from EPCs. The upregulation of integrin $\beta 3$ and enhanced focal adhesion formation provide a potential mechanism of how dRP regulates endothelial cell motility.²⁸ In summary, although the proangiogenic potential of TP and dRP has previously been established,^{28,44} our observations demonstrate for the first time that dRP is among the major proangiogenic factors in the conditioned medium of CFUs and EPC cultures. Therefore, the release of dRP at sites of vascular

injury is likely to promote endothelial cell migration from intact neighboring regions, which could represent an important mechanism by which EPCs enhance vascular repair. In agreement with this model, the effect of dRP on angiogenesis and neovascularization was further confirmed by our *in vivo* experiments.

Clinical Implications

The number of CFUs is widely used as a measure of EPC function⁴⁵ and has been shown to correlate negatively with cardiovascular disease risk factors and positively with vascular function. However, recent evidence casts doubts over the identity of the cells that form the colonies, suggesting they may be derived from hematopoietic rather than endothelial cell precursors.⁴⁵ This raises an important question: if CFUs do not directly reflect numbers of circulating EPCs, why do they correlate with cardiovascular disease risk? Our data demonstrate that CFUs express and secrete proangiogenic factors. Thus, although CFUs may not represent endothelial precursors per se, the cellular aggregates forming the colonies could still be involved in vascular homeostasis, ie, CFUs may represent a surrogate marker for the proangiogenic potential among PB-MNCs. This alternative explanation would help to reconcile literature documenting the beneficial effects of circulating EPCs on cardiovascular function with the recent finding that CFUs may be hematopoietic rather than endothelial precursors.

Limitations of the Study

There is currently no consensus on which culture conditions are most successful in isolating the effective EPC popula-

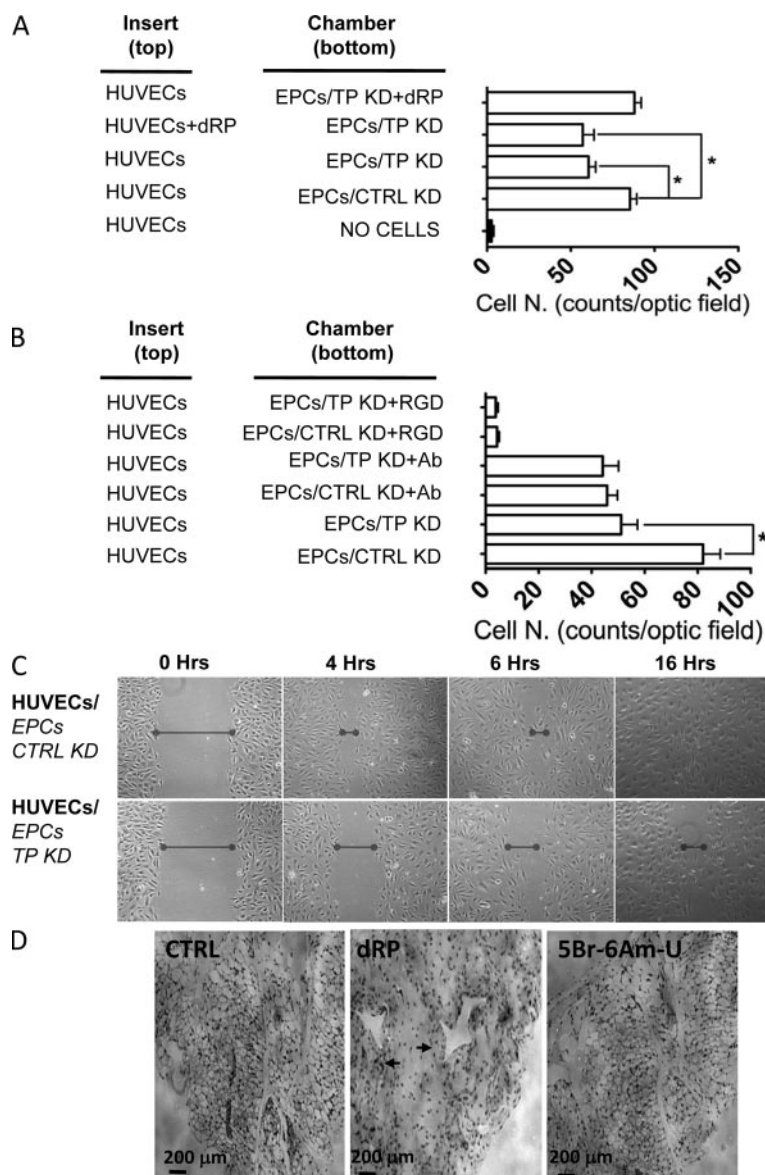


Figure 7. TP stimulates endothelial cell migration. The motility of HUVECs in response to paracrine factors released by EPCs was investigated in a modified Boyden chamber. The bottom chamber was either empty or seeded with EPCs treated with TP siRNA (TP KD) or scrambled control siRNA (CTRL KD). A and B, dRP (50 $\mu\text{mol/L}$), anti- $\alpha\text{v}\beta\text{3}$ inhibitory antibody (Ab) (10 $\mu\text{g/mL}$), or RGD peptide (10 $\mu\text{mol/L}$) was added where indicated. The number of transmigrated cells was counted in 3 independent experiments and presented as means \pm SEM. Statistical significance was tested by 1-way ANOVA with Bonferroni post test ($*P < 0.05$). C, Wound-healing of endothelial monolayers. HUVEC monolayers were scratched and conditioned medium from EPC cultures either pre-treated with TP siRNA (TP KD) (bottom images) or scrambled siRNA (CTRL KD) (top images) was added at a ratio of 1:2. The results presented are representative of 3 independent experiments. The width of the wound was measured (black bars) and plotted over time (supplemental Figure VI, A). Note that the effect was attenuated when experiments were repeated in the presence of 10 $\mu\text{g/mL}$ anti- $\alpha\text{v}\beta\text{3}$ inhibitory antibody or 10 $\mu\text{mol/L}$ RGD peptide (supplemental Figure VI, B and C). D, Angiogenesis in vivo. The neovascularization of Matrigel plugs containing PBS (Ctrl) ($n=4$), 250 $\mu\text{mol/L}$ dRP ($n=4$), or 500 $\mu\text{mol/L}$ 5Br-6Am-U ($n=3$) was measured (supplemental Figure VII). Arrows indicate vessels.

tions. In the present study, we used 2 of the most commonly used methods, but we cannot rule out that culture conditions used by other investigators may alter protein expression and secretion. In this respect, the present proteomic dataset could serve as a reference and contribute to standardizing EPC cultures. Although mass spectrometry has proven a valuable tool to array secreted proteins, it is important to note that minor components can remain undetected, especially in the presence of intracellular proteins released during cell death in culture.

Conclusion

In summary, the proteomic analysis reported in this study identified TP to be among the main proangiogenic factors in EPC cultures and CFUs, which might facilitate the development of new therapeutic strategies.

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Disclosures

None.

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SUPPLEMENT MATERIAL

Proteomics Identifies Thymidine Phosphorylase as a Key Regulator of the Angiogenic Potential of Colony-forming Units and Endothelial Progenitor Cell Cultures

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Material and Methods

EPC culture and colony-forming units (CFUs). Human blood was drawn from healthy volunteers. Informed consent was obtained and the study was approved by the ethics review board of King's College London. For isolation of EPCs, peripheral blood mononuclear cells (PBMCs) were collected by separation onto Lymphoprep™ solution (LYS3772, Axis-Shield) at a ratio of 1 ml blood: 1 ml separation solution. Cells were centrifuged for 20 minutes at 2 krpm, 20°C. Buffy coat PBMCs were collected and washed 3 times with PBS containing 2% fetal bovine serum. EPCs were obtained according to two commonly used methods: First, PBMCs were suspended using endothelial basal medium (EBM, Clonetics cc-3121, Lonza) containing 20% fetal bovine serum, epidermal growth factor (10 µg/ml), bovine brain extract (3 µg/ml), gentamicine (50 µg/ml), amphotericin-B (50 µg/ml), hydrocortisone (1 µg/ml), and human VEGF (10 ng/ml), as described previously¹. Cells were seeded at 5×10^6 cells.well⁻¹ on human fibronectin-coated 6-well plates. Growth medium was changed every 3 days. EPC numbers were assessed by double positive staining for DiI-Ac-LDL and Lectin on day 5 of culture. Second, the colony forming unit (CFU) assay was performed as described previously². In brief, PBMCs were suspended in growth medium containing Medium 199 (22340, Gibco) with 20% fetal bovine serum and seeded at 5×10^6 cells.well⁻¹ on human fibronectin-coated (F0895, Sigma) 6-well plates. Wells were washed with growth medium after 48 hours and non-adherent cells were re-plated at 4×10^6 cells.well⁻¹ on human fibronectin-coated plates kept in the same growth medium, which was changed every 3 days. For both culture methods, cells were harvested for experimentation after 7 days of culture at 37°C with 5% CO₂-enriched atmosphere. For secretome analyses, cells were incubated with serum-free

culture medium for 24 hours at 37°C. The conditioned medium was cleared by centrifugation (30 min, 3,000g) to eliminate floating cells or cell debris and stored at -80°C.

Culture of Human Umbilical Vein Endothelial Cells (HUVECs). HUVECs were isolated from human umbilical cords as described previously^{3, 4} and were cultured in M199 medium supplemented with 1ng/ml Endothelial Cell Growth Factor (ECGF), 3µg/ml Endothelial Cell Growth Supplement (ECGS), 10U/ml Heparin, 2.5 µg/ml Thymidine and 5% FBS. The cells were cultured in collagen I-coated T75 flasks at 37°C with 5% CO₂-enriched atmosphere for up to 10 passages.

MALDI-ToF-ToF. Conditioned medium was thawed at 4°C. For CFUs and early EPCs, 500 µl of conditioned medium was placed in a Microcon Ultracel YM-10 (Millipore, 42406) and centrifuged for 45 minutes at 13.2 krpm. This procedure was repeated three times. A total volume of 1.5 ml conditioned medium was concentrated approximately 50-fold. Protein concentration was determined using the Bradford method as described above. Subsequently, proteins were reduced with DTT then alkylated and subject to an overnight tryptic digest. Tryptic peptides were separated by nano liquid chromatography (Ultimate 3000™, Dionex) on a C18 column (PepMap 100, 75 µm I.D., 15 cm length, Dionex) with a mobile phase (A) formed from HPLC grade water containing 5% acetonitril and 0.1% TFA and (B) HPLC grade acetonitrile containing 20% H₂O and 0.1% TFA according to the gradient 5% solvent B (0-5 min); 5-30% Solvent B (5-120 min); 60-95% Solvent B (120-150 min); and 95% Solvent B (151-160 min) at a flow rate of 200 nl/min. The HPLC was interfaced to a spotting robot (Dionex Probot). Several hundred fractions were collected per sample

(fraction size: 10 sec) on matrix-assisted laser desorption/ionisation (MALDI) target plates and mixed with matrix (CHCA, 2 mg/ml in 70% acetonitril in 0.1% TFA). Peptides were subsequently analyzed using a TOF/TOF analyser (4800 ToF/ToF, Applied Biosystems). Results were searched against a human / bovine database (Uniprot) in Mascot and filtered with ProteinPilot™ software (Applied Biosystems). All peptide sequence assignments were required to result from fully tryptic cleavages of the corresponding proteins. Assignments were accepted when the total score was > 2.0. The total score is a measure of the confidence of the protein identification (e.g. total score of 2.0 corresponds to a confidence of 99%) and was calculated by ProteinPilot software as $-\log(1-\text{percent confidence}/100)$. Results were further filtered for a minimum of ≥ 2 peptides per protein identification.

Cytokine measurements and confirmation of protein expression. Cytokine concentrations in the EPC secretomes were measured using a commercial assay (Bio-Plex, Biorad). The conditioned medium from several independent EPC cultures and CFU preparations was analyzed according to the manufacturers' instructions.

Difference in-gel electrophoresis (DIGE). For cellular proteomics, cell monolayers were rinsed thoroughly with cold PBS to remove any serum components. Protein extracts were prepared from CFUs and cultured EPCs using a lysis buffer (8M urea, 4% w/v CHAPS, 30mM Tris-Cl, pH 8.5) compatible with DIGE labelling (GE healthcare). After centrifugation at 13,000 g for 10 min, the supernatant containing soluble proteins was harvested and the protein concentration was determined using a modification of the method described by Bradford⁵. The fluorescence dye labelling reaction was carried out at a dye/protein ratio of 400pmol/100µg. After incubation on

ice for 30 min, the labelling reaction was stopped by scavenging non-bound dyes with 10mM lysine (L8662, Sigma) for 15 min. For two-dimensional gel electrophoresis, samples were mixed with 2x buffer (8M urea, 4% w/v CHAPS, 2% w/v DTT, 2% v/v Pharmalytes 3-10 for IEF), 50µg per sample were diluted in rehydration solution (8M urea, 0.5% w/v CHAPS, 0.2% w/v DTT, and 0.2% v/v Pharmalyte pH 3-10) and loaded on IPG strips (18cm, pH 3-10, nonlinear, GE healthcare). After rehydration overnight, strips were focused at 0.05 mA/IPG strip for 60 kWh at 20°C (Multiphor II, GE healthcare). Once IEF was complete the strips were equilibrated in 6M urea containing 30% v/v glycerol, 2% w/v SDS and 0.01% w/v Bromphenol blue, with addition of 1% w/v DTT for 15 min, followed by the same buffer without DTT, but with the addition of 4.8% w/v iodoacetamide for 15 min. SDS-PAGE was performed using 12% T (total acrylamide concentration), 2.6% C (degree of cross-linking) polyacrylamide gels without a stacking gel, using the Ettan DALT system (GE healthcare). The second dimension was terminated when the Bromophenol blue dye front had migrated off the lower end to the gels. After electrophoresis, fluorescence images were acquired using the Typhoon variable mode imager 9400 (GE healthcare). Finally, gels were fixed overnight in methanol: acetic acid: water solution (4:1:5 v/v/v). Protein profiles were visualised by silver staining using the Plus one silver staining kit (GE healthcare). For documentation, silver-stained gels were scanned in transmission scan mode using a calibrated scanner (GS-800, Bio-Rad). DIGE gels were analysed using SameSpot version 3.2 software (Nonlinear Dynamics). Spots exhibiting differential expression ($p < 0.05$, one-way ANOVA) were excised for identification. A detailed methodology is available on our website <http://www.vascular-proteomics.com>.

Nano-LC MS/MS. Gel pieces containing selected protein spots were treated overnight with modified trypsin (Promega) according to a published protocol modified for use with an Investigator ProGest (Genomic Solutions, Huntington, UK) robotic digestion system. Following enzymatic degradation, peptides were separated by a nanoflow HPLC system (Ultimate 3000, Dionex) on a reverse-phase column and applied online to a LTQ XL ion-trap mass spectrometer. Spectra were collected from the ion-trap mass analyzer using full ion scan mode over the mass-to-charge (m/z) range 300-2000. MS-MS scans were performed on each ion using dynamic exclusion. Database search was performed using the TurboSEQUENT software (Thermo Finnigan). One missed cleavage per peptide was allowed and carbamidomethylation of cysteine as well as partial oxidation of methionine were assumed. The following filters were applied: Xcorr values of >2.0 (+1 charge), >2.5 (+2 charge) and >3.5 (+3 charge), deltaCN >0.1, a minimum of 2 peptides and a probability score < than $e^{-0.03}$.

mRNA isolation and assessment of gene regulation by rtPCR. Total mRNA was extracted from CFUs or cultured EPCs with RNeasy mini kit (Qiagen), following manufacturer's instructions. Briefly, 2.5 μ g of mRNA was converted to cDNA using Promega Reverse Transcription System (Promega). The cDNA products were amplified by PCR using gene-specific primers. The primers used were IL-8 forward: CTGCGCCAACACAGAAATTA; IL-8 reverse: GCTTGAAGTTTCACT GGCATC; MMP-9 forward: GAGACCGGTGAGCTGGATAG; MMP-9 reverse: CACCAA ACTGGATGACGATG; ApoE forward: CCAATCACAGGCAGGA AGAT; ApoE reverse: CTCCTGCACCTGCTCAGAC; TP forward: CATGGATCTGGAGGA GACCT; TP reverse: TCTGGGCTCTGGATGACATT; CD133 forward: ACCCA TTGGCATTCTCTTTG; PBEF forward: TATCCACCCAACACAAGCAA, PBEF

reverse: GCTCCTATGCCAGCAGTCTC; MCP-1 forward:
TCTGTGCCTGCTGCTCATAG, MCP-1 reverse: GCAATTTCCCAAGTCTCTG;
CD133 reverse: GGTGCATTTCTCCACCACAT; vWF forward:
GACCCTTTGTGCAGAAGGAA; VWF reverse: TCCCAAGA TACACGGAGAG;
CD14 forward: CTGCAACTTCTCCGAACCTC; CD14 reverse:
TAGGTCCTCGAGCGTCAGTT; KDR forward: GCTTTGGCCCAATAATCAGA;
KDR reverse: ACACGACTCCATGTTGGTCA; CD31 forward: TATTTTCCAA
GCCCGAACTG; CD31 reverse: ATGACCTCAAACCTGGGCATC; GAPDH
forward: CGGAGTCAACGGATTTG GTCGTAT; and GAPDH reverse:
AGCCTTCTCCATGGTGGTGAAGAC. PCR conditions were as follows: 94°C for 5
min and then 30 cycles at 94°C for 30 s, 58°C for 1 min and 72°C for 1 min, followed
by 72°C for 10 min. PCR products were separated by 1.5% agarose gel electrophoresis
and visualized by ethidium bromide staining.

Immunoblot. Cells were lysed with an equal volume of radioimmuno-
precipitation assay buffer (RIPA) (1% Triton X-100, 1% sodium deoxycholate, 0.1%
SDS, 150 mM NaCl, 50 mM Tris, 5 mM EDTA) containing protease inhibitors
(Complete mini, Roche). Proteins were quantified using the Bradford assay⁵ and
resolved by sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE)
using 8% to 10% polyacrylamide Tris-Glycine pre-cast gels (Invitrogen). Samples
were then transferred to ProTran nitrocellulose transfer membrane (Whatman) and
blocked with 10% w/v dry milk in TBS-T (25mM Tris, 150mM NaCl, 0.1% v/v
Tween20, pH 7.2). Immunostaining for thymidine phosphorylase was performed with
650 ng/ml anti-human PD-ECGF antibody (R&D Systems, AF1143) and 650 ng/ml
anti–mouse IgG HRP-conjugated antibodies (Dako). Primary antibodies against actin

(Santa Cruz Biotechnology, sc-1616), Bcl-2 (Santa Cruz Biotechnology, sc-783), Bax (Santa Cruz Biotechnology, sc-6236), integrin β 1 (Santa Cruz Biotechnology, sc-8978), integrin α v (Santa Cruz Biotechnology, sc-6616), integrin β 3 (R&D Systems, AF2266), p38 MAPK (Cell Signaling Technology, #9212), phospho-p38 MAPK (Cell Signaling Technology, #9211), VASP (Alexis Biochemicals, ALX-210-898-R100), and vinculin (Chemicon International, CBL233), were used at different concentration depending on their efficiency and specificity in combination with species-specific HRP-conjugated anti-IgG secondary antibodies (Dako). Bound peroxidase activity was detected using enhanced chemiluminescence (ECL).

Immunofluorescence. EPCs normally were cultured as described until day 6, then transferred to 22mm coverslips coated with fibronectin ($20 \mu\text{g ml}^{-1}$) and cultured for a further 2 days. Alternatively, HUVECs were cultured for 24 hours on collagen I-coated coverslips ($20 \mu\text{g/ml}$). On the day of the experiment, cells were fixed with 3.7% formaldehyde in TBS (25mM Tris, 150 mM NaCl, pH 7.2) and permeabilised with TBS containing 0.05% Triton X-100. For EPCs, the immunostaining was performed with $1.5 \mu\text{g/ml}$ anti-human PD-ECGF antibody (R&D Systems, AF1143), $1 \mu\text{g/ml}$ DAPI (Sigma), and $0.8 \mu\text{g/ml}$ fluorescein isothiocyanate (FITC)-labeled anti-mouse IgG antibody (Molecular Probes). For HUVECs, the staining was performed with $2 \mu\text{g/ml}$ anti-integrin β 3 antibody (R&D Systems, AF2266), $20 \mu\text{g/ml}$ FITC-conjugated anti-vinculin antibody (Sigma, F7053), $1 \mu\text{g/ml}$ DAPI and $0.8 \mu\text{g/ml}$ (TRITC)-labeled anti-goat IgG antibody (Molecular Probes). Coverslips were then mounted using Slow-Fade mounting medium and examined by microscopy on an upright Leica DMI 6000 CS inverted microscope connected to a Leica TCS SP5 confocal laser scanning system (objective: Leica HCX PL Apo 63x/1.40-0.60 oil).

Cell Death ELISA. EPCs were cultured until day 6, then different treatments were administered by adding biological/pharmacological agents to the culture medium. On day 7, apoptosis was analysed with Cell Death Detection ELISA Plus (Roche), according to the manufacturer's instructions. Briefly, after cells lysis, cytoplasm and intact nuclei were fractionated by centrifugation. The cytoplasmic fraction was analysed for the presence of histone proteins released from the nucleus, by incubating 20µl of the medium with anti-histone biotin-conjugated antibody and anti-DNA peroxidase-conjugated antibody in a streptavidin-conjugated microplate for 2 hours at room temperature. Histone protein absorbed to the microplate was detected by a colorimetric reaction using a peroxidase substrate and absorbance measurement at 405nm using a Genios Pro microplate reader (Tecan).

Gene knock-down by siRNA. On day 6 of the normal culture procedure, EPCs were incubated with 80 pmols/well of TP siRNA (TP KD) in the presence of siRNA Transfection Reagent (Santa Cruz) in the absence of foetal bovine serum for 8 hours. Similarly, control cells were incubated with scrambled control siRNA (CTRL KD). Foetal bovine serum was subsequently added to the normal final concentration and cells were cultured overnight before experimentation.

Flow cytometry. EPCs used for apoptosis studies were cultured until day 6, when different compounds were added to the culture medium. On day 7, apoptosis was analysed by flow cytometry using the Annexin V-FITC Apoptosis Detection Kit I (BD Pharmingen), according to manufacturer's instructions and as previously described⁶. Briefly, cells were detached by short trypsin treatment and quick blockade of the protease activity with foetal bovine serum. Cells were then washed in phosphate buffer saline (PBS: 4mM NaH₂PO₄, 16mM Na₂HPO₄, 150mM NaCl, pH 7.4) and

incubated with Annexin V and Propidium Iodide for 15 minutes at room temperature. The flow cytometric analysis was performed with a FACSCalibur flow cytometer (Becton Dickinson).

Cell transmigration analysis. The method was adapted from previous studies⁷. For HUVEC migration assays, 10^5 cells were added to the top inserts of 24 well-transmigration microplates (pore size 8 μm , Corning), coated with collagen-I (20 $\mu\text{g/ml}$, Sigma). The bottom chamber of the transmigration microplate was seeded with 2×10^5 EPCs (either TP KD or CTRL KD), following coating with fibronectin (20 $\mu\text{g/ml}$, Sigma). The gene knock-down procedure was performed on day 6 of the EPC culture, as described above, and 48 hours prior seeding onto the transmigration microplate. Transmigration was quantified 8 hours after assembly of the chemotaxis chamber by hematoxylin staining and phase-contrast microscopy (objective 4X/0.10, microscope Nikon Eclipse TS100, connected to a Nikon Digital Sight imaging system).

Wound-healing assay. HUVECs were cultured in 6 well-plates to confluence. The day of the experiment, the monolayer was injured manually, and following a brief wash with PBS, the conditioned medium from EPCs was added. The healing of the injury was followed at time 0, 2, 4, 6 and 16 hours by phase contrast microscopy (objective 4X/0.10, microscope Nikon Eclipse TS100, connected to a Nikon Digital Sight imaging system).

Matrigel plugs. 50 μl Matrigel was mixed with 250 μM dRP or 500 μM 5Br-6Am-U, and then injected subcutaneously into the back or flank of C57BL/6 mice. Three to four injections were performed for each group. The mice were killed on day 14, and the plugs were harvested and frozen immediately in liquid nitrogen, followed

by embedding with OCT, sectioning and hematoxylin-staining. The sections were visualized by phase contrast microscopy (objective 4X/0.10, microscope Nikon Eclipse TS100, connected to a Nikon Digital Sight imaging system).

Online Figures

Online Figure I. Cellular proteome of CFUs. A DIGE gel demonstrates the consistency of the proteomic profiles from CFUs of two different individuals, whose protein extracts were differentially labeled with Cy-dyes in green and red, respectively. Yellow color indicates proteins present in both samples.

Online Figure II. Flow cytometry. Apoptosis in EPC cultures following treatment with 5Br-6Am-U (100 μ M) was assessed by flow cytometric analysis of annexin V and propidium iodide staining (A). Apoptosis following knock-down of TP in EPC cultures by siRNA (TP KD) compared to scrambled control siRNA (CTRL KD) (B).

Online Figure III. TP gene silencing by siRNA. TP gene was knocked-down in cultured EPCs as described in the Methods section and protein extracts were obtained. The level of expression of TP was assessed by immunoblotting using a specific antibody (top panel). As a control, protein extracts were obtained from EPCs treated with a scrambled siRNA (A). Apoptosis induced in EPCs by TP knock-down with or without VEGF (10 ng/ml) was assessed by ELISA (B). Treatment with 5Br-6Am-U or dRP did not alter survival of HUVECs (C). The effect of 5Br-6Am-U or dRP or both (D), and TP knock-down by siRNA in the presence or absence of dRP (E) on cell numbers in EPC cultures (cells per optic field) is also presented. The data in the bar graphs are presented as mean \pm SEM from at least 3 independent experiments. Statistical significance was tested by one-way ANOVA with Bonferroni post-test (* = $p < 0.05$).

Online Figure IV. Densitometry. dRP enhances Bcl-2 expression in EPCs under oxidative stress (Figure 5). Statistical significance was tested by one-way ANOVA with Bonferroni post-test (* = $p < 0.05$).

Online Figure V. Quantification of focal adhesions. (A) HUVECs were cultured in the presence of conditioned medium from EPCs and the focal adhesions were visualized by immunofluorescence as described in the legend of Figure 6. The number of focal adhesions (FA) per cell is quantified in the bar graph (mean \pm SEM, *white bars*). Where indicated dRP (50 μ M) was added. HUVECs without EPC conditioned medium served as a control (*black column*). The pictures utilized for quantification were from 3 independent experiments. Statistical significance was tested by one-way ANOVA with Bonferroni post-test (* = $p < 0.05$; ** = $p < 0.01$). (B) Densitometry. dRP stimulates integrin $\beta 3$ expression in HUVECs (Figure 6B). Statistical significance was tested by one-way ANOVA with Bonferroni post-test (* = $p < 0.05$).

Online Figure VI. Quantification of wound healing. The width of the wound was measured and plotted over time (A). Statistical significance was tested by two-way ANOVA, * denotes $p < 0.05$. Note that the effect was attenuated when experiments were repeated in the presence of 10 μ g/ml anti- $\alpha v \beta 3$ inhibitory antibody (B) or 10 μ M RGD peptide (C).

Online Figure VII. Neovascularization of matrigel plugs. Values are means \pm SEM for Ctrl (n=4), 250 μ M dRP (n=4) or 500 μ M 5Br-6Am-U (n=3). Statistical significance was tested by one-way ANOVA with Bonferroni post-test (* = $p < 0.05$).

Online Tables**Online Table I. Proteins identified in the conditioned medium.**

Proteins in the conditioned medium of CFUs from 3 different individuals were identified by MALDI-TOF/TOF mass spectrometry. Proteins appearing in at least 2 samples are reported in the table and the results for the 3 biological replicates are highlighted in different colors (blue, red and black). The rank N is the position in the ranking of proteins in decreasing order of abundance. The total score is a measure of the confidence of the protein identification (e.g. total score of 2.0 corresponds to a confidence of 99%) and was calculated by ProteinPilot™ software as $-\log(1-\text{percent confidence}/100)$. Proteins also identified in cultured EPCs are highlighted in light grey.

Online Table II. Peptides identified in the conditioned medium.

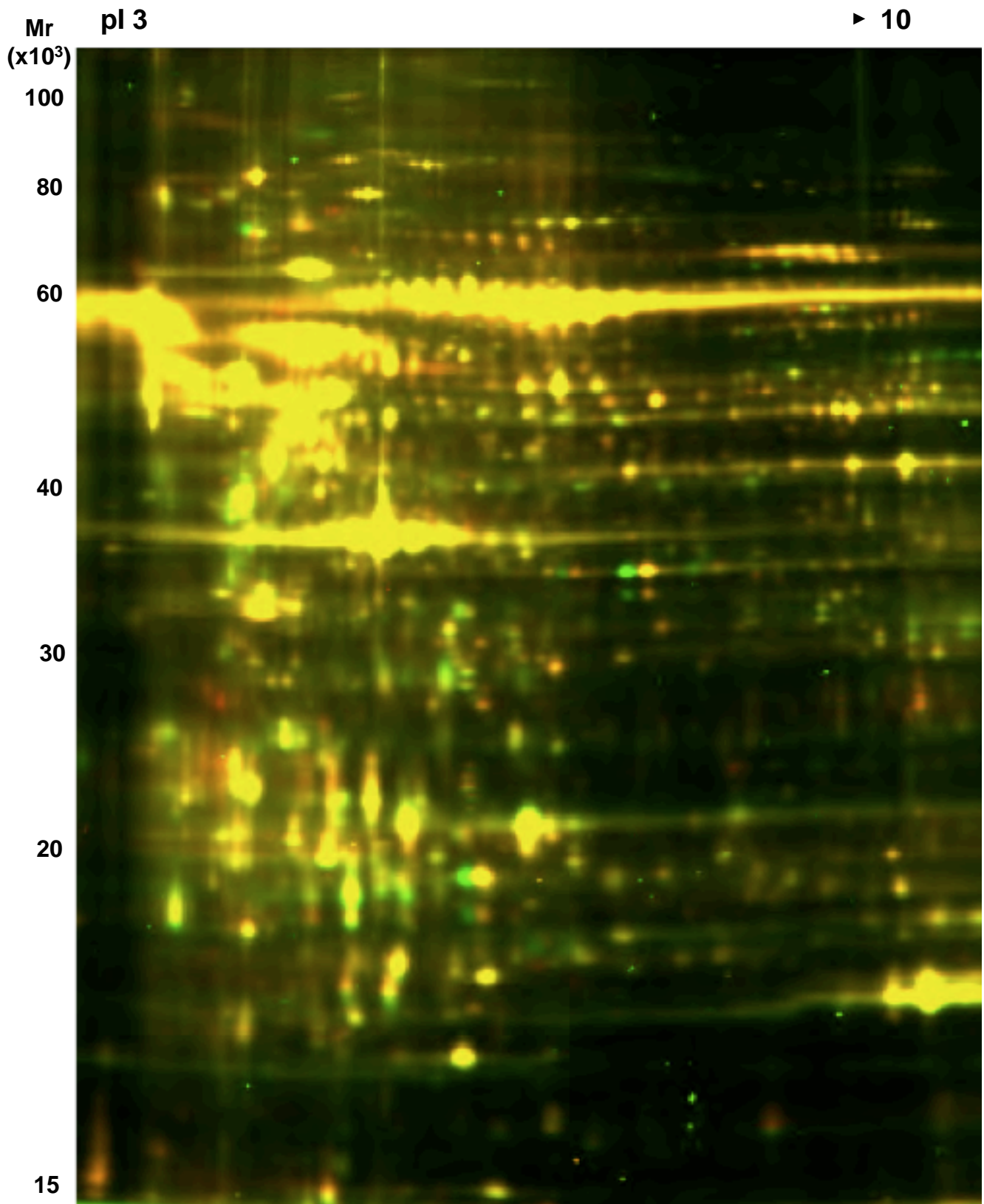
Peptides in the conditioned medium of CFUs as identified by MALDI-TOF/TOF mass spectrometry. The 3 biological replicates are highlighted in different colors (blue, red and black).

Online Table III. Differentially expressed proteins in CFUs compared to EPC cultures. CFUs and EPC cultures were compared by difference in-gel electrophoresis (DIGE). Results from 4 independent images were analyzed using SameSpot software (Nonlinear Dynamics). Spots exhibiting differential expression ($p < 0.05$, one-way ANOVA) were excised for identification and reported in the table.

Online Table IV. Cytokine secretion. Cytokine concentrations in the conditioned medium were measured using the 27-plex cytokine assay from Biorad. The conditioned media from the 13 independent EPC cultures and 15 independent CFU preparations were analyzed according to the manufacturers' instructions. Depending on the cytokine, the intraplate variability of the assay measured as %CV (percent coefficient of variation) is between 2 and 13%, while the interplate %CV is between 4.3 and 21.5%. The limit of detection (LOD) ranges from 0.2 to 19.3 pg/ml.

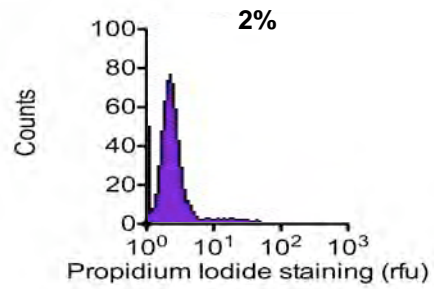
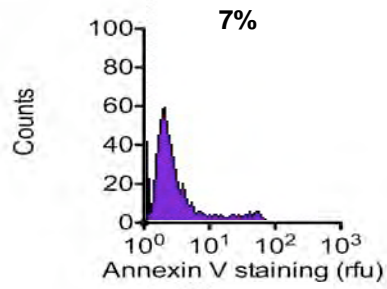
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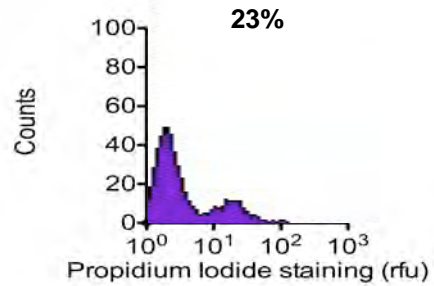
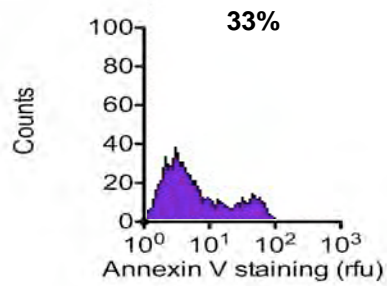


A

CTRL

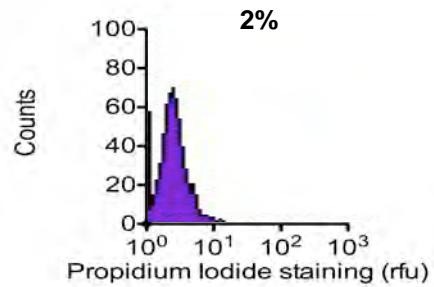
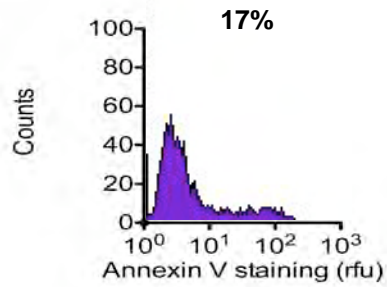


5Br-6Am-U

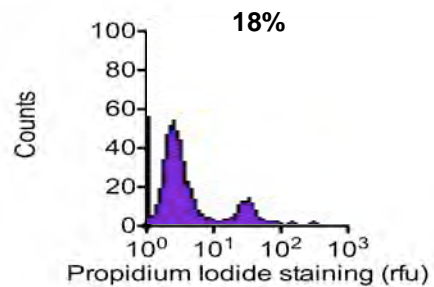
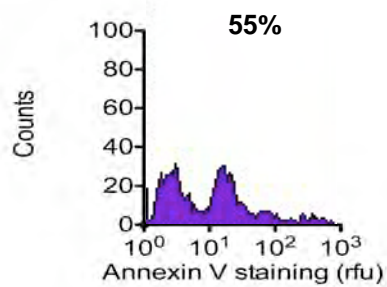


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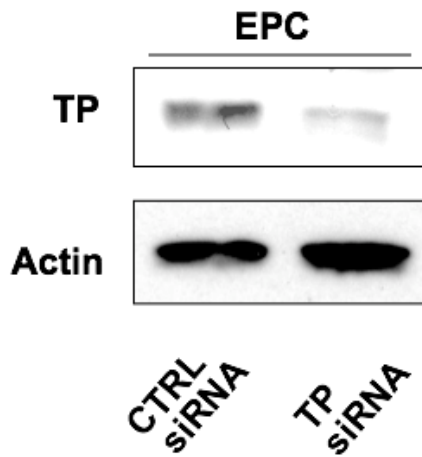
CTRL KD



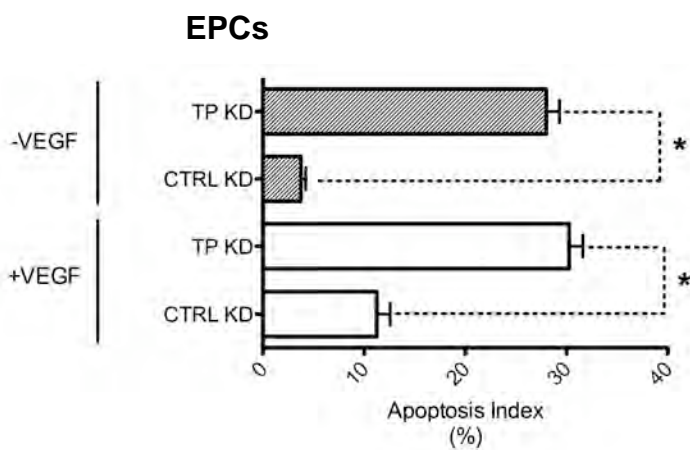
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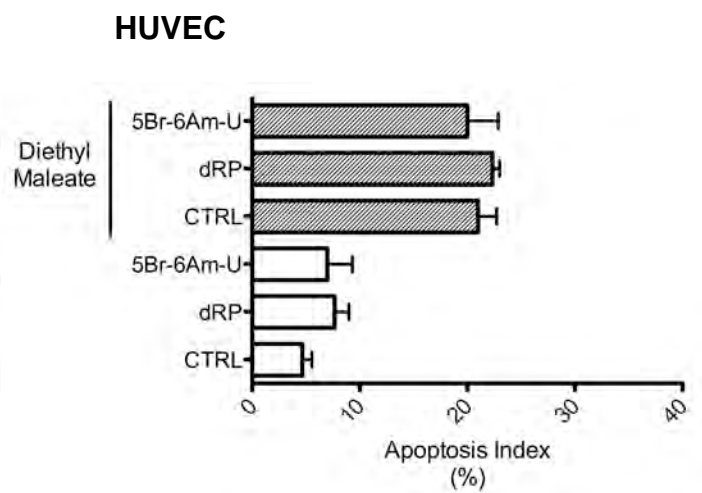
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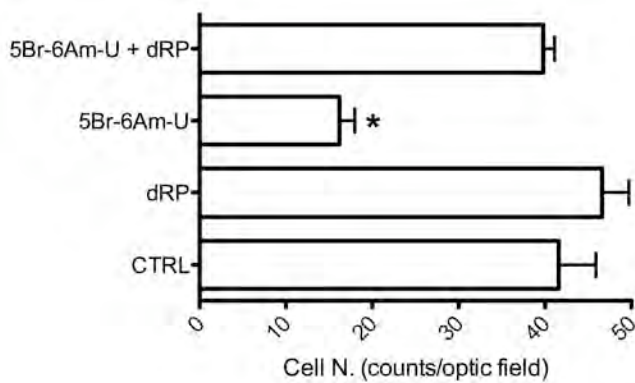
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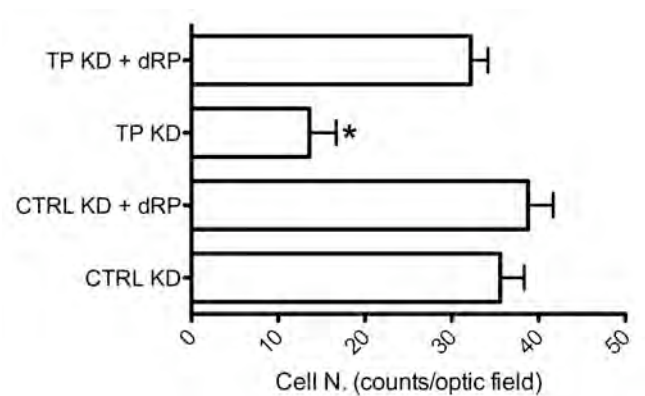
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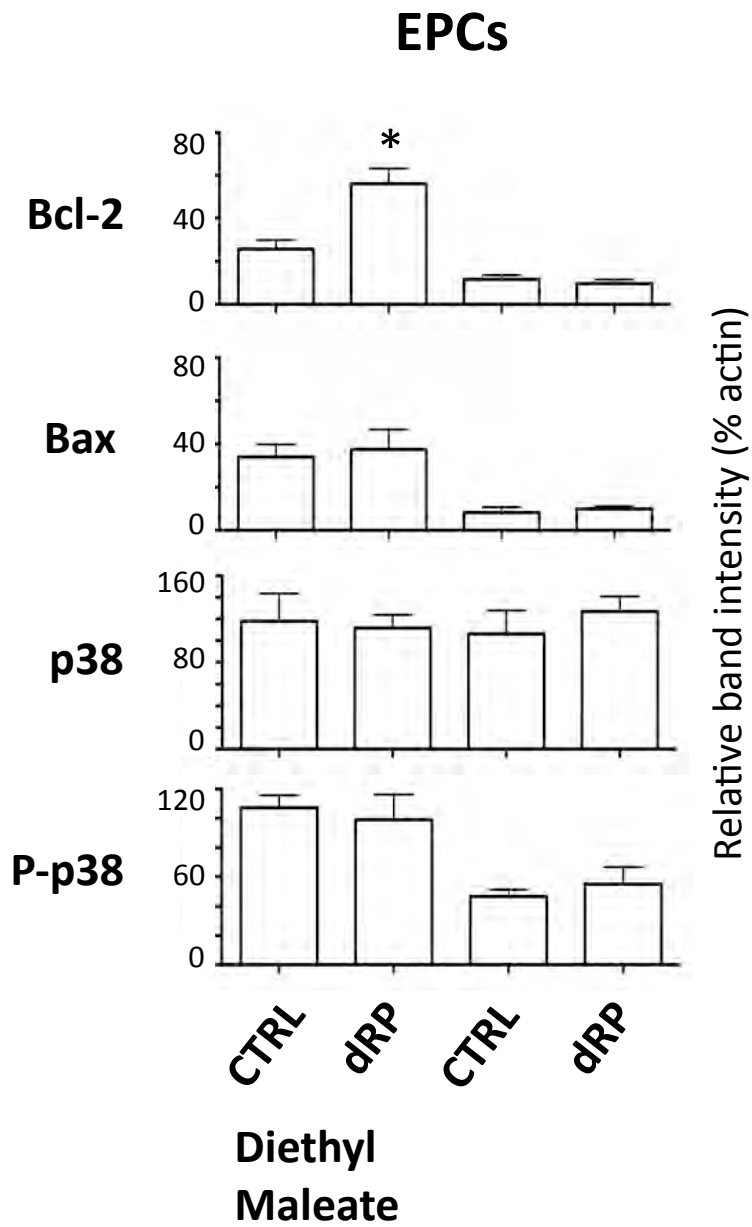


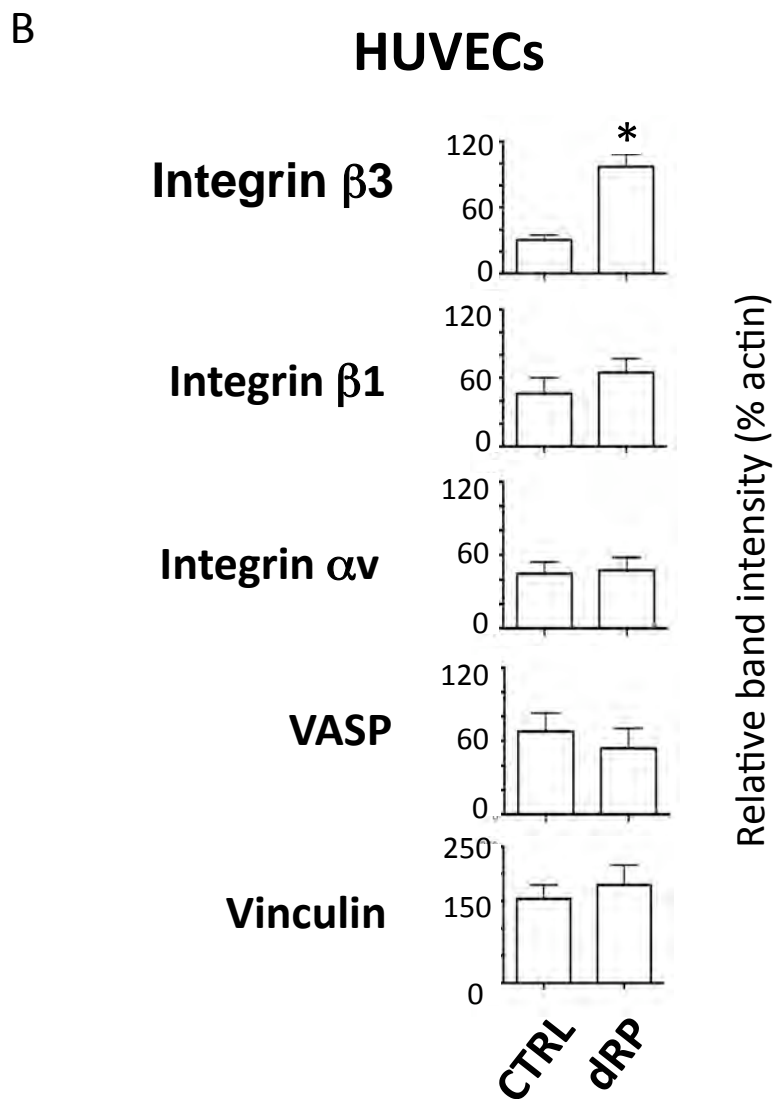
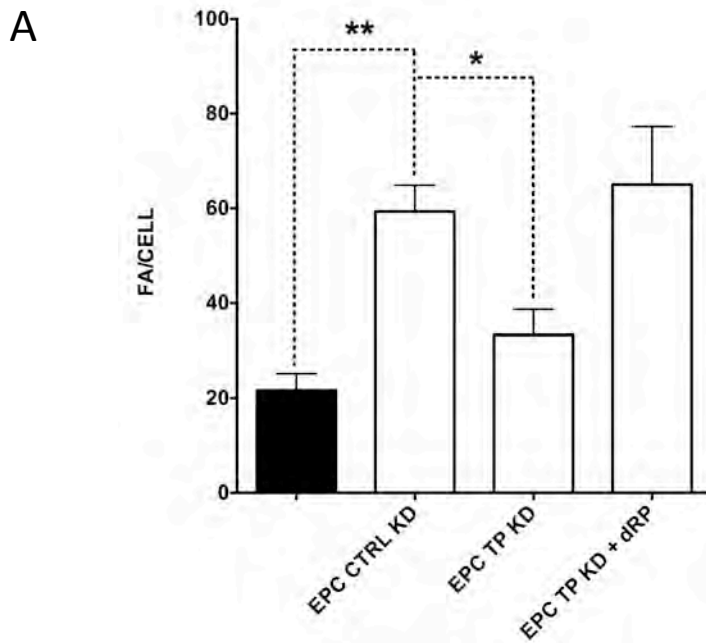
D

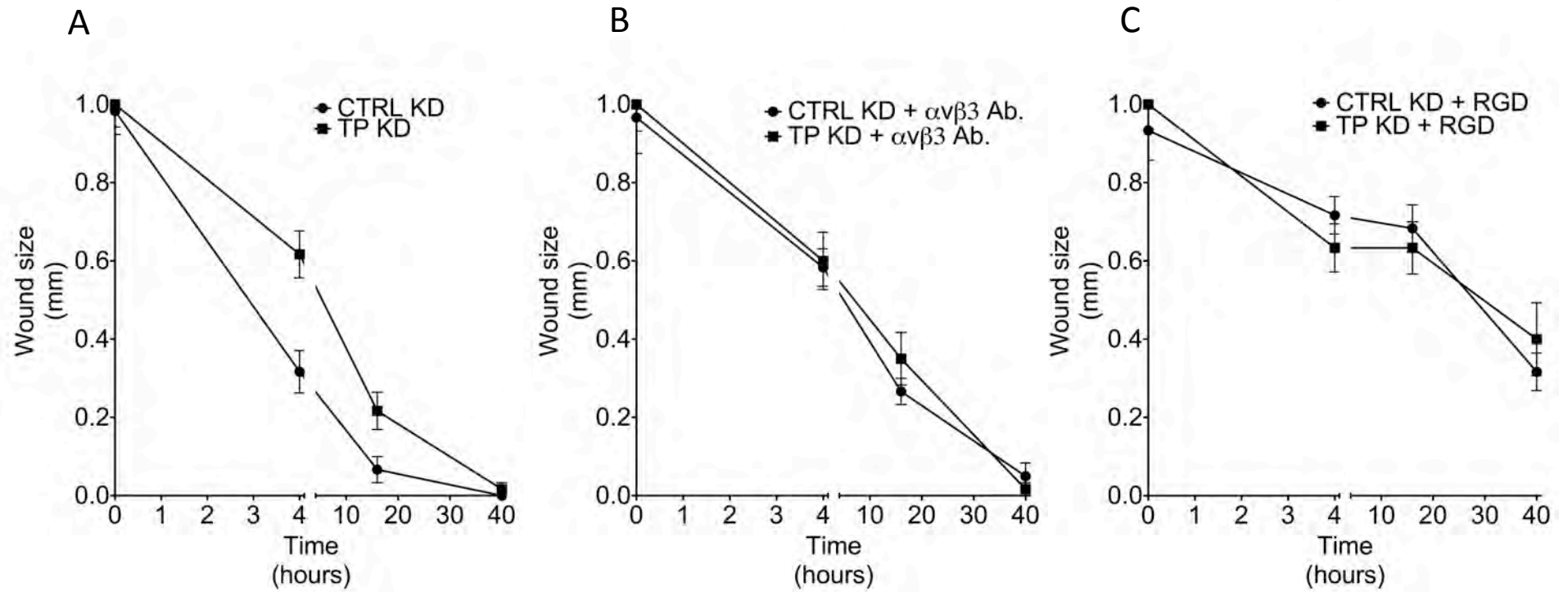


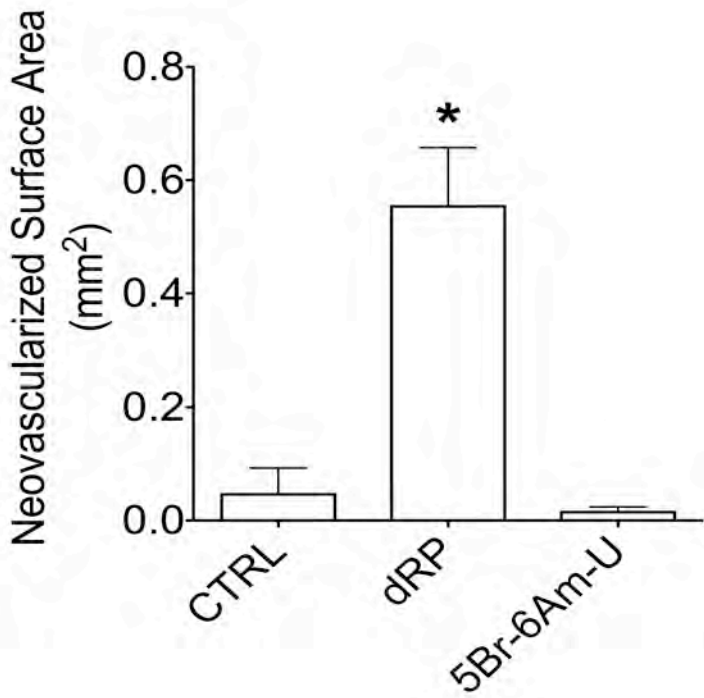
E











ONLINE TABLE I

HUMAN PROTEINS IDENTIFIED IN THE CONDITIONED MEDIUM OF CFUs (n=3)

Rank N.	Total Score	% Coverage	Accession	Protein name
108	8.2	20.7	O00299 CLIC1_HUMAN	Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (Chloride channel ABP) (Regulatory nuclear chloride ion channel protein) (hRNCC) - Homo sapiens (Human)
69	4.9	30.3	O00299 CLIC1_HUMAN	Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (Chloride channel ABP) (Regulatory nuclear chloride ion channel protein) (hRNCC) - Homo sapiens (Human)
123	9.5	31.1	O00299 CLIC1_HUMAN	Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (Chloride channel ABP) (Regulatory nuclear chloride ion channel protein) (hRNCC) - Homo sapiens (Human)
160	2.0	11.1	O00391 QSOX6_HUMAN	Sulfhydryl oxidase 1 precursor (EC 1.8.3.2) (Qulescin O6) (thSOX) - Homo sapiens (Human)
201	6.0	12.2	O00391 QSOX6_HUMAN	Sulfhydryl oxidase 1 precursor (EC 1.8.3.2) (Qulescin O6) (thSOX) - Homo sapiens (Human)
338	2.0	51.1	O00479 HMGN4_HUMAN	High-mobility group nucleosome-binding domain-containing protein 4 (Nonhistone chromosomal protein HMG-17-like 3) (Non-histone chromosomal protein) - Homo sapiens (Human)
285	4.0	44.4	O00479 HMGN4_HUMAN	High-mobility group nucleosome-binding domain-containing protein 4 (Nonhistone chromosomal protein HMG-17-like 3) (Non-histone chromosomal protein) - Homo sapiens (Human)
189	4.0	5.0	O14773 TPP1_HUMAN	Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase 1) (TPP-1) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC) (Cell growth-inhibiting gene 1 protein) - Homo sapiens (Human)
138	2.1	14.9	O14773 TPP1_HUMAN	Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase 1) (TPP-1) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC) (Cell growth-inhibiting gene 1 protein) - Homo sapiens (Human)
490	2.0	4.6	O14773 TPP1_HUMAN	Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase 1) (TPP-1) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC) (Cell growth-inhibiting gene 1 protein) - Homo sapiens (Human)
202	3.7	11.7	O14818 PSA7_HUMAN	Proteasome subunit alpha type 7 (EC 3.4.25.1) (Proteasome subunit RC6-1) (Proteasome subunit XAPC7) - Homo sapiens (Human)
177	6.5	17.3	O14818 PSA7_HUMAN	Proteasome subunit alpha type 7 (EC 3.4.25.1) (Proteasome subunit RC6-1) (Proteasome subunit XAPC7) - Homo sapiens (Human)
278	2.1	19.5	O14979 HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP-D-like protein) (hnHNP-DL) (JKT41-binding protein) (AU-rich element RNA-binding factor) (Protein laAUF1) - Homo sapiens (Human)
87	4.0	18.8	O14979 HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP-D-like protein) (hnHNP-DL) (JKT41-binding protein) (AU-rich element RNA-binding factor) (Protein laAUF1) - Homo sapiens (Human)
452	6.0	9.8	O14979 HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP-D-like protein) (hnHNP-DL) (JKT41-binding protein) (AU-rich element RNA-binding factor) (Protein laAUF1) - Homo sapiens (Human)
85	8.9	22.3	O15143 ARCB1_HUMAN	Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC) - Homo sapiens (Human)
128	2.3	24.7	O15143 ARCB1_HUMAN	Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC) - Homo sapiens (Human)
152	8.0	17.7	O15143 ARCB1_HUMAN	Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC) - Homo sapiens (Human)
151	4.7	11.7	O15144 ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (ARP2/3 complex 34 kDa subunit) (p34-ARC) - Homo sapiens (Human)
196	1.7	21.0	O15144 ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (ARP2/3 complex 34 kDa subunit) (p34-ARC) - Homo sapiens (Human)
172	6.7	20.7	O15144 ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (ARP2/3 complex 34 kDa subunit) (p34-ARC) - Homo sapiens (Human)
247	2.3	15.2	O15145 ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 (ARP2/3 complex 21 kDa subunit) (p21-ARC) - Homo sapiens (Human)
238	5.1	21.9	O15145 ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 (ARP2/3 complex 21 kDa subunit) (p21-ARC) - Homo sapiens (Human)
216	3.2	8.5	O15204 ADEC1_HUMAN	ADAM DEC1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain-like protein decysin 1) (ADAM-like protein decysin 1) - Homo sapiens (Human)
81	4.2	7.7	O15204 ADEC1_HUMAN	ADAM DEC1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain-like protein decysin 1) (ADAM-like protein decysin 1) - Homo sapiens (Human)
264	4.3	10.4	O15204 ADEC1_HUMAN	ADAM DEC1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain-like protein decysin 1) (ADAM-like protein decysin 1) - Homo sapiens (Human)
166	4.3	14.5	O43390 HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R) - Homo sapiens (Human)
267	4.2	20.7	O43390 HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R) - Homo sapiens (Human)
22	22.9	32.3	O43707 ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross-linking protein) - Homo sapiens (Human)
44	6.9	13.9	O43707 ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross-linking protein) - Homo sapiens (Human)
10	41.3	35.2	O43707 ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross-linking protein) - Homo sapiens (Human)
295	2.0	6.4	O43776 SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic (EC 6.1.1.22) (Asparagine--tRNA ligase) (AsnRS) - Homo sapiens (Human)
212	6.0	9.3	O43776 SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic (EC 6.1.1.22) (Asparagine--tRNA ligase) (AsnRS) - Homo sapiens (Human)
111	6.9	14.4	O75083 WDR1_HUMAN	WD repeat protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1) - Homo sapiens (Human)
125	2.3	14.9	O75083 WDR1_HUMAN	WD repeat protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1) - Homo sapiens (Human)
373	2.0	8.8	O75368 SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein - Homo sapiens (Human)
320	4.0	24.6	O75368 SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein - Homo sapiens (Human)
384	1.7	11.2	O75791 GRAP2_HUMAN	GRB2-related adapter protein 2 (GADS protein) (Growth factor receptor-binding protein) (GRBLG) (Grf40 adapter protein) (Grf-40) (GRB-2-like protein) (GRB2L) (GRBX) (P38) (Hematopoietic cell-associated adapter protein GrpL) (Adapter protein GRID) (SH3-SH2-SH3 adapter Mona) - Homo sapiens (Human)
553	2.0	3.3	O75791 GRAP2_HUMAN	GRB2-related adapter protein 2 (GADS protein) (Growth factor receptor-binding protein) (GRBLG) (Grf40 adapter protein) (Grf-40) (GRB-2-like protein) (GRB2L) (GRBX) (P38) (Hematopoietic cell-associated adapter protein GrpL) (Adapter protein GRID) (SH3-SH2-SH3 adapter Mona) - Homo sapiens (Human)
88	4.0	11.1	P00338 LDHA_HUMAN	L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH muscle subunit) (LDH-M) (Proliferation-inducing gene 19 protein) (Renal carcinoma antigen NY-REN-59) - Homo sapiens (Human)
129	11.3	30.4	P00338 LDHA_HUMAN	L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH muscle subunit) (LDH-M) (Proliferation-inducing gene 19 protein) (Renal carcinoma antigen NY-REN-59) - Homo sapiens (Human)
141	5.7	29.1	P00491 PNPH_HUMAN	Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine phosphorylase) (PNP) - Homo sapiens (Human)
166	7.0	32.9	P00491 PNPH_HUMAN	Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine phosphorylase) (PNP) - Homo sapiens (Human)
30	20.8	45.6	P00558 PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2) (Cell migration-inducing gene 10 protein) - Homo sapiens (Human)
76	4.6	30.5	P00558 PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2) (Cell migration-inducing gene 10 protein) - Homo sapiens (Human)
22	28.0	53.0	P00558 PGK1_HUMAN	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2) (Cell migration-inducing gene 10 protein) - Homo sapiens (Human)
18	26.1	17.1	P01023 AZMG_HUMAN	Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Human)
16	16.5	18.1	P01023 AZMG_HUMAN	Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Human)
65	15.3	11.9	P01023 AZMG_HUMAN	Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Human)
195	4.0	13.0	P01033 TIMP1_HUMAN	Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid-potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases) (Fibroblast collagenase inhibitor) (Collagenase inhibitor) - Homo sapiens (Human)
169	2.0	22.2	P01033 TIMP1_HUMAN	Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid-potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases) (Fibroblast collagenase inhibitor) (Collagenase inhibitor) - Homo sapiens (Human)
319	4.0	14.5	P01033 TIMP1_HUMAN	Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid-potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases) (Fibroblast collagenase inhibitor) (Collagenase inhibitor) - Homo sapiens (Human)
355	2.0	13.7	P01034 CYTC_HUMAN	Cystatin-C precursor (Cystatin-3) (Neuroendocrine basic polypeptide) (Gamma-trace) (Post-gamma-globulin) - Homo sapiens (Human)
104	3.4	26.0	P01034 CYTC_HUMAN	Cystatin-C precursor (Cystatin-3) (Neuroendocrine basic polypeptide) (Gamma-trace) (Post-gamma-globulin) - Homo sapiens (Human)
302	4.0	25.3	P01034 CYTC_HUMAN	Cystatin-C precursor (Cystatin-3) (Neuroendocrine basic polypeptide) (Gamma-trace) (Post-gamma-globulin) - Homo sapiens (Human)
188	4.0	31.1	P01834 KAC_HUMAN	Ig kappa chain C region - Homo sapiens (Human)
260	4.5	37.7	P01834 KAC_HUMAN	Ig kappa chain C region - Homo sapiens (Human)
203	3.7	28.6	P01842 LAC_HUMAN	Ig lambda chain C regions - Homo sapiens (Human)
64	5.3	19.0	P01842 LAC_HUMAN	Ig lambda chain C regions - Homo sapiens (Human)
332	3.67	39.0	P01842 LAC_HUMAN	Ig lambda chain C regions - Homo sapiens (Human)
106	7.6	17.2	P01871 MUC_HUMAN	Ig mu chain C region - Homo sapiens (Human)
195	1.7	7.0	P01871 MUC_HUMAN	Ig mu chain C region - Homo sapiens (Human)
570	1.7	1.8	P01871 MUC_HUMAN	Ig mu chain C region - Homo sapiens (Human)
337	2.0	14.3	P02746 C1QB_HUMAN	Complement C1q subcomponent subunit B precursor - Homo sapiens (Human)
95	4.0	13.5	P02746 C1QB_HUMAN	Complement C1q subcomponent subunit B precursor - Homo sapiens (Human)
354	2.0	10.2	P02747 C1QC_HUMAN	Complement C1q subcomponent subunit C precursor - Homo sapiens (Human)
190	2.0	3.7	P02747 C1QC_HUMAN	Complement C1q subcomponent subunit C precursor - Homo sapiens (Human)
386	2.4	14.7	P02747 C1QC_HUMAN	Complement C1q subcomponent subunit C precursor - Homo sapiens (Human)
27	21.3	16.4	P02751 FINC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (ClG) - Homo sapiens (Human)
22	13.3	13.7	P02751 FINC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (ClG) - Homo sapiens (Human)
584	1.4	1.1	P02751 FINC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (ClG) - Homo sapiens (Human)
370	2.0	8.6	P02792 FRIL_HUMAN	Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)
550	2.0	8.6	P02792 FRIL_HUMAN	Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)
114	6.7	62.3	P02795 MT2_HUMAN	Metallothionein-2 (MT-2) (Metallothionein-II) (MT-II) (Metallothionein-2A) - Homo sapiens (Human)
216	6.0	82.0	P02795 MT2_HUMAN	Metallothionein-2 (MT-2) (Metallothionein-II) (MT-II) (Metallothionein-2A) - Homo sapiens (Human)
159	4.5	13.6	P04004 VTNC_HUMAN	Vitronectin precursor (Serum-spreading factor) (S-protein) (V75) [Contains: Vitronectin V65 subunit: Vitronectin V10 subunit: Somatomedin B] - Homo sapiens (Human)
119	2.5	12.3	P04004 VTNC_HUMAN	Vitronectin precursor (Serum-spreading factor) (S-protein) (V75) [Contains: Vitronectin V65 subunit: Vitronectin V10 subunit: Somatomedin B] - Homo sapiens (Human)

482	2.0	6.1	P04004 VTNC_HUMAN	Vitronectin precursor (Serum-spreading factor) (S-protein) (V75) [Contains: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin B] - Homo sapiens (Human)
23	22.8	50.5	P04075 ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Lung cancer antigen NY-LU-1) - Homo sapiens (Human)
52	6.2	29.4	P04075 ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Lung cancer antigen NY-LU-1) - Homo sapiens (Human)
16	37.1	57.7	P04075 ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Lung cancer antigen NY-LU-1) - Homo sapiens (Human)
277	2.1	30.6	P04080 CYTB_HUMAN	Cystatin-B (Stefin-B) (Liver thiol proteinase inhibitor) (CPI-B) - Homo sapiens (Human)
318	4.0	36.7	P04080 CYTB_HUMAN	Cystatin-B (Stefin-B) (Liver thiol proteinase inhibitor) (CPI-B) - Homo sapiens (Human)
34	19.3	40.3	P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) - Homo sapiens (Human)
74	4.7	25.4	P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) - Homo sapiens (Human)
30	24.2	49.6	P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) - Homo sapiens (Human)
161	4.4	25.8	P05109 S10A8_HUMAN	Protein S100-A8 (S100 calcium-binding protein A8) (Calgranulin-A) (Migration inhibitory factor-related protein 8) (MRP-8) (Cystic fibrosis antigen) (CFAG) (P8) (Leukocyte L1 complex light chain) (Calprotectin L1L subunit) (Urinary stone protein band A) - Homo sapiens (Human)
317	4.0	25.8	P05109 S10A8_HUMAN	Protein S100-A8 (S100 calcium-binding protein A8) (Calgranulin-A) (Migration inhibitory factor-related protein 8) (MRP-8) (Cystic fibrosis antigen) (CFAG) (P8) (Leukocyte L1 complex light chain) (Calprotectin L1L subunit) (Urinary stone protein band A) - Homo sapiens (Human)
17	26.4	37.3	P05120 PAI2_HUMAN	Plasminogen activator inhibitor 2 precursor (PAI-2) (Placental plasminogen activator inhibitor) (Monocyte Arg-serpin) (Urokinase inhibitor) - Homo sapiens (Human)
38	8.1	21.2	P05120 PAI2_HUMAN	Plasminogen activator inhibitor 2 precursor (PAI-2) (Placental plasminogen activator inhibitor) (Monocyte Arg-serpin) (Urokinase inhibitor) - Homo sapiens (Human)
114	10.0	13.5	P05120 PAI2_HUMAN	Plasminogen activator inhibitor 2 precursor (PAI-2) (Placental plasminogen activator inhibitor) (Monocyte Arg-serpin) (Urokinase inhibitor) - Homo sapiens (Human)
353	2.0	10.9	P05161 UCRP_HUMAN	Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein (hUCRP) (Interferon-induced 15 kDa protein)] - Homo sapiens (Human)
502	2.0	12.7	P05161 UCRP_HUMAN	Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein (hUCRP) (Interferon-induced 15 kDa protein)] - Homo sapiens (Human)
369	2.0	2.1	P05362 ICAM1_HUMAN	Intercellular adhesion molecule 1 precursor (ICAM-1) (Major group rhinovirus receptor) (CD54 antigen) - Homo sapiens (Human)
569	1.7	2.1	P05362 ICAM1_HUMAN	Intercellular adhesion molecule 1 precursor (ICAM-1) (Major group rhinovirus receptor) (CD54 antigen) - Homo sapiens (Human)
251	2.2	15.7	P06576 ATPB_HUMAN	ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (Human)
316	4.0	6.6	P06576 ATPB_HUMAN	ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (Human)
12	31.0	55.8	P06733 ENO4_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein) - Homo sapiens (Human)
19	14.1	35.3	P06733 ENO4_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein) - Homo sapiens (Human)
15	38.3	62.9	P06733 ENO4_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein) - Homo sapiens (Human)
103	7.7	15.2	P06744 G6P1_HUMAN	Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin) (NLK) (Sperm antigen 36) (SA-36) - Homo sapiens (Human)
92	11.9	18.6	P06744 G6P1_HUMAN	Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin) (NLK) (Sperm antigen 36) (SA-36) - Homo sapiens (Human)
391	9.7	21.5	P06753 TPM3_HUMAN	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTMS) - Homo sapiens (Human)
255	16.4	40.8	P06753 TPM3_HUMAN	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTMS) - Homo sapiens (Human)
196	3.8	17.4	P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46) - Homo sapiens (Human)
207	4.0	20.1	P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46) - Homo sapiens (Human)
56	16.9	32.6	P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46) - Homo sapiens (Human)
298	2.0	6.7	P07237 PDIA1_HUMAN	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-hydroxylase subunit beta) (Cellular thyroid hormone-binding protein) (p55) - Homo sapiens (Human)
481	2.0	6.5	P07237 PDIA1_HUMAN	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-hydroxylase subunit beta) (Cellular thyroid hormone-binding protein) (p55) - Homo sapiens (Human)
149	4.9	16.0	P07339 CATD_HUMAN	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain] - Homo sapiens (Human)
70	4.9	20.9	P07339 CATD_HUMAN	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain] - Homo sapiens (Human)
199	6.0	18.2	P07339 CATD_HUMAN	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain] - Homo sapiens (Human)
47	15.8	30.0	P07437 TBBS_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) - Homo sapiens (Human)
26	11.9	22.5	P07437 TBBS_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) - Homo sapiens (Human)
21	28.5	47.3	P07437 TBBS_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) - Homo sapiens (Human)
89	8.3	11.8	P07602 SAP_HUMAN	Proactivator polypeptide precursor [Contains: Saposin A (Protein A); Saposin B-Val; Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator); Saposin C (Co-beta-glucosidase) (A1 activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D (Protein C) (Component C)] - Homo sapiens (Human)
92	4.0	5.7	P07602 SAP_HUMAN	Proactivator polypeptide precursor [Contains: Saposin A (Protein A); Saposin B-Val; Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator); Saposin C (Co-beta-glucosidase) (A1 activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D (Protein C) (Component C)] - Homo sapiens (Human)
204	6.0	9.7	P07602 SAP_HUMAN	Proactivator polypeptide precursor [Contains: Saposin A (Protein A); Saposin B-Val; Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator); Saposin C (Co-beta-glucosidase) (A1 activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D (Protein C) (Component C)] - Homo sapiens (Human)
225	2.9	22.2	P07711 CATL_HUMAN	Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP) [Contains: Cathepsin L heavy chain; Cathepsin L light chain] - Homo sapiens (Human)
210	1.4	5.1	P07711 CATL_HUMAN	Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP) [Contains: Cathepsin L heavy chain; Cathepsin L light chain] - Homo sapiens (Human)
438	2.0	7.8	P07711 CATL_HUMAN	Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP) [Contains: Cathepsin L heavy chain; Cathepsin L light chain] - Homo sapiens (Human)
29	20.9	61.4	P07737 PROF1_HUMAN	Profilin-1 (Profilin I) - Homo sapiens (Human)
21	13.4	61.4	P07737 PROF1_HUMAN	Profilin-1 (Profilin I) - Homo sapiens (Human)
36	22.5	82.1	P07737 PROF1_HUMAN	Profilin-1 (Profilin I) - Homo sapiens (Human)
48	15.7	34.2	P07858 CATB_HUMAN	Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (APP secretase) (APPS) [Contains: Cathepsin B light chain; Cathepsin B heavy chain] - Homo sapiens (Human)
71	4.9	28.0	P07858 CATB_HUMAN	Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (APP secretase) (APPS) [Contains: Cathepsin B light chain; Cathepsin B heavy chain] - Homo sapiens (Human)
51	17.4	38.3	P07858 CATB_HUMAN	Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (APP secretase) (APPS) [Contains: Cathepsin B light chain; Cathepsin B heavy chain] - Homo sapiens (Human)
117	16.0	29.9	P07900 HSP90A_HUMAN	Heat shock protein HSP 90-alpha (HSP 86) (Renal carcinoma antigen NY-REN-38) - Homo sapiens (Human)
75	4.7	23.5	P07900 HSP90A_HUMAN	Heat shock protein HSP 90-alpha (HSP 86) (Renal carcinoma antigen NY-REN-38) - Homo sapiens (Human)
20	29.4	29.9	P07900 HSP90A_HUMAN	Heat shock protein HSP 90-alpha (HSP 86) (Renal carcinoma antigen NY-REN-38) - Homo sapiens (Human)
213	3.2	27.5	P07910 HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1 / hnRNP C2) - Homo sapiens (Human)
241	5.0	8.8	P07910 HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1 / hnRNP C2) - Homo sapiens (Human)
126	5.0	23.2	P08107 HSP71_HUMAN	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2) - Homo sapiens (Human)
127	14.3	29.2	P08107 HSP71_HUMAN	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2) - Homo sapiens (Human)
37	18.7	28.2	P08238 HSP90B_HUMAN	Heat shock protein HSP 90-beta (HSP 84) (HSP 90) - Homo sapiens (Human)
197	3.6	24.4	P08238 HSP90B_HUMAN	Heat shock protein HSP 90-beta (HSP 84) (HSP 90) - Homo sapiens (Human)
57	27.8	30.9	P08238 HSP90B_HUMAN	Heat shock protein HSP 90-beta (HSP 84) (HSP 90) - Homo sapiens (Human)
182	4.0	18.1	P08571 CD14_HUMAN	Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein) [Contains: Monocyte differentiation antigen CD14, urinary form; Monocyte differentiation antigen CD14, membrane-bound form] - Homo sapiens (Human)
145	2.1	16.3	P08571 CD14_HUMAN	Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein) [Contains: Monocyte differentiation antigen CD14, urinary form; Monocyte differentiation antigen CD14, membrane-bound form] - Homo sapiens (Human)
548	2.0	4.8	P08571 CD14_HUMAN	Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein) [Contains: Monocyte differentiation antigen CD14, urinary form; Monocyte differentiation antigen CD14, membrane-bound form] - Homo sapiens (Human)
323	2.0	6.7	P08575 CD45_HUMAN	Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (T200) (CD45 antigen) - Homo sapiens (Human)
250	4.7	3.7	P08575 CD45_HUMAN	Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (T200) (CD45 antigen) - Homo sapiens (Human)
8	44.3	62.2	P08670 VIME_HUMAN	Vimentin - Homo sapiens (Human)
8	22.8	70.6	P08670 VIME_HUMAN	Vimentin - Homo sapiens (Human)
3	63.4	70.0	P08670 VIME_HUMAN	Vimentin - Homo sapiens (Human)
99	8.0	18.6	P09211 GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1) - Homo sapiens (Human)
47	6.6	23.3	P09211 GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1) - Homo sapiens (Human)
96	11.7	37.6	P09211 GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1) - Homo sapiens (Human)
142	5.7	29.6	P09382 LEG1_HUMAN	Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-I) (Lactose-binding lectin 1) (S-Lac lectin 1) (Galaptin) (14 kDa lectin) (HPL) (HBL) (Putative MAPK-activating protein MP12) - Homo sapiens (Human)
68	4.9	61.5	P09382 LEG1_HUMAN	Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-I) (Lactose-binding lectin 1) (S-Lac lectin 1) (Galaptin) (14 kDa lectin) (HPL) (HBL) (Putative MAPK-activating protein MP12) - Homo sapiens (Human)
99	11.2	61.5	P09382 LEG1_HUMAN	Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-I) (Lactose-binding lectin 1) (S-Lac lectin 1) (Galaptin) (14 kDa lectin) (HPL) (HBL) (Putative MAPK-activating protein MP12) - Homo sapiens (Human)
73	10.0	53.5	P09429 HMG81_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1) - Homo sapiens (Human)
40	7.5	33.5	P09429 HMG81_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1) - Homo sapiens (Human)
42	20.0	45.6	P09429 HMG81_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1) - Homo sapiens (Human)
203	1.5	11.3	P09496 CLCA_HUMAN	Clathrin light chain A (Lca) - Homo sapiens (Human)
315	4.0	12.9	P09496 CLCA_HUMAN	Clathrin light chain A (Lca) - Homo sapiens (Human)

65	13.9	51.1	P09651 ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) - Homo sapiens (Human)
32	28.6	63.4	P09651 ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) - Homo sapiens (Human)
224	2.9	3.9	P09874 PARP1_HUMAN	Poly (ADP-ribose) polymerase 1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)-ADP-ribosyltransferase 1) (Poly[ADP-ribose] synthetase 1) - Homo sapiens (Human)
125	9.4	16.2	P09874 PARP1_HUMAN	Poly (ADP-ribose) polymerase 1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)-ADP-ribosyltransferase 1) (Poly[ADP-ribose] synthetase 1) - Homo sapiens (Human)
342	2.0	5.1	P09960 LKHA4_HUMAN	Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase) (Leukotriene A(4) hydrolase) - Homo sapiens (Human)
115	9.9	14.1	P09960 LKHA4_HUMAN	Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase) (Leukotriene A(4) hydrolase) - Homo sapiens (Human)
82	9.0	39.2	P10124 PGSG_HUMAN	Secretory granule proteoglycan core protein precursor (Platelet proteoglycan core protein) (P.PG) (Hematopoietic proteoglycan core protein) (Serglycin) - Homo sapiens (Human)
48	6.5	39.2	P10124 PGSG_HUMAN	Secretory granule proteoglycan core protein precursor (Platelet proteoglycan core protein) (P.PG) (Hematopoietic proteoglycan core protein) (Serglycin) - Homo sapiens (Human)
179	6.4	39.2	P10124 PGSG_HUMAN	Secretory granule proteoglycan core protein precursor (Platelet proteoglycan core protein) (P.PG) (Hematopoietic proteoglycan core protein) (Serglycin) - Homo sapiens (Human)
105	7.7	56.6	P10145 IL8_HUMAN	Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-activating protein 1) (NAP-1) (Protein 3-10C) (Granulocyte chemotactic protein 1) (GCP-1) (Monocyte-derived neutrophil-activating peptide) (MONAP) (Emotakin) [Contains: MDNCF-a (IL8/NAP1 form I) (GCP/IL-8 protein IV); Interleukin-8 (IL-8(1-77)) (MDNCF-b) (IL8/NAP1 form II) (GCP/IL-8 protein II) ((Ala-IL-8)77); IL-8(5-77); IL-8(6-77) (Lymphocyte-derived neutrophil-activating factor) (LYNAP) (Neutrophil-activating factor) (NAF) (MDNCF-c) (IL8/NAP1 form III) (GCP/IL-8 protein I) ((Ser-IL-8)72); IL-8(7-77) (IL8/NAP1 form IV) (GCP/IL-8 protein V); IL-8(8-77) (IL8/NAP1 form V) (GCP/IL-8 protein VI); IL-8(9-77) (IL8/NAP1 form VI) (GCP/IL-8 protein III)] - Homo sapiens (Human)
73	4.8	43.4	P10145 IL8_HUMAN	Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-activating protein 1) (NAP-1) (Protein 3-10C) (Granulocyte chemotactic protein 1) (GCP-1) (Monocyte-derived neutrophil-activating peptide) (MONAP) (Emotakin) [Contains: MDNCF-a (IL8/NAP1 form I) (GCP/IL-8 protein IV); Interleukin-8 (IL-8(1-77)) (MDNCF-b) (IL8/NAP1 form II) (GCP/IL-8 protein II) ((Ala-IL-8)77); IL-8(5-77); IL-8(6-77) (Lymphocyte-derived neutrophil-activating factor) (LYNAP) (Neutrophil-activating factor) (NAF) (MDNCF-c) (IL8/NAP1 form III) (GCP/IL-8 protein I) ((Ser-IL-8)72); IL-8(7-77) (IL8/NAP1 form IV) (GCP/IL-8 protein V); IL-8(8-77) (IL8/NAP1 form V) (GCP/IL-8 protein VI); IL-8(9-77) (IL8/NAP1 form VI) (GCP/IL-8 protein III)] - Homo sapiens (Human)
133	8.4	49.5	P10145 IL8_HUMAN	Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-activating protein 1) (NAP-1) (Protein 3-10C) (Granulocyte chemotactic protein 1) (GCP-1) (Monocyte-derived neutrophil-activating peptide) (MONAP) (Emotakin) [Contains: MDNCF-a (IL8/NAP1 form I) (GCP/IL-8 protein IV); Interleukin-8 (IL-8(1-77)) (MDNCF-b) (IL8/NAP1 form II) (GCP/IL-8 protein II) ((Ala-IL-8)77); IL-8(5-77); IL-8(6-77) (Lymphocyte-derived neutrophil-activating factor) (LYNAP) (Neutrophil-activating factor) (NAF) (MDNCF-c) (IL8/NAP1 form III) (GCP/IL-8 protein I) ((Ser-IL-8)72); IL-8(7-77) (IL8/NAP1 form IV) (GCP/IL-8 protein V); IL-8(8-77) (IL8/NAP1 form V) (GCP/IL-8 protein VI); IL-8(9-77) (IL8/NAP1 form VI) (GCP/IL-8 protein III)] - Homo sapiens (Human)
107	3.2	41.7	P10319 I1B58_HUMAN	HLA class I histocompatibility antigen, B-58 alpha chain precursor (MHC class I antigen B*58) (Bw-58) - Homo sapiens (Human)
160	12.5	47.8	P10319 I1B58_HUMAN	HLA class I histocompatibility antigen, B-58 alpha chain precursor (MHC class I antigen B*58) (Bw-58) - Homo sapiens (Human)
160	7.7	24.2	P10412 H14_HUMAN	Histone H1.4 (Histone H1b) - Homo sapiens (Human)
74	14.0	18.3	P10412 H14_HUMAN	Histone H1.4 (Histone H1b) - Homo sapiens (Human)
81	9.1	42.9	P10599 THIO_HUMAN	Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphhydryl protein) (SASP) - Homo sapiens (Human)
80	4.3	33.3	P10599 THIO_HUMAN	Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphhydryl protein) (SASP) - Homo sapiens (Human)
113	10.0	42.9	P10599 THIO_HUMAN	Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphhydryl protein) (SASP) - Homo sapiens (Human)
83	10.6	15.3	P11021 GRP78_HUMAN	78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP) (Endoplasmic reticulum luminal Ca(2+)-binding protein grp78) - Homo sapiens (Human)
105	3.5	20.6	P11021 GRP78_HUMAN	78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP) (Endoplasmic reticulum luminal Ca(2+)-binding protein grp78) - Homo sapiens (Human)
104	13.3	22.3	P11021 GRP78_HUMAN	78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP) (Endoplasmic reticulum luminal Ca(2+)-binding protein grp78) - Homo sapiens (Human)
26	21.5	28.9	P11142 HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) - Homo sapiens (Human)
15	16.6	32.5	P11142 HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) - Homo sapiens (Human)
9	43.1	46.0	P11142 HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) - Homo sapiens (Human)
101	14.7	22.9	P11413 G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD) - Homo sapiens (Human)
205	1.5	6.8	P11413 G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD) - Homo sapiens (Human)
100	11.1	20.8	P11413 G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD) - Homo sapiens (Human)
322	2.0	2.5	P11717 MPRI_HUMAN	Cation-independent mannose-6-phosphate receptor precursor (CI Man-6-P receptor) (CI-MPR) (M6PR) (Insulin-like growth factor 2 receptor) (Insulin-like growth factor II receptor) (IGF-II receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (300 kDa mannose 6-phosphate receptor) (MPR 300) (MPR300) (CD222 antigen) - Homo sapiens (Human)
201	1.5	6.2	P11717 MPRI_HUMAN	Cation-independent mannose-6-phosphate receptor precursor (CI Man-6-P receptor) (CI-MPR) (M6PR) (Insulin-like growth factor 2 receptor) (Insulin-like growth factor II receptor) (IGF-II receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (300 kDa mannose 6-phosphate receptor) (MPR 300) (MPR300) (CD222 antigen) - Homo sapiens (Human)
199	3.7	11.9	P11940 PABP1_HUMAN	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) - Homo sapiens (Human)
117	2.6	18.4	P11940 PABP1_HUMAN	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) - Homo sapiens (Human)
194	6.0	21.2	P11940 PABP1_HUMAN	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) - Homo sapiens (Human)
367	2.0	2.0	P12955 PEPD_HUMAN	Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptidase) (Proline dipeptidase) (Prolidase) (Imidodipeptidase) - Homo sapiens (Human)
572	1.5	3.4	P12955 PEPD_HUMAN	Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptidase) (Proline dipeptidase) (Prolidase) (Imidodipeptidase) - Homo sapiens (Human)
227	2.9	11.8	P12956 KU70_HUMAN	ATP-dependent DNA helicase 2 subunit 1 (ATP-dependent DNA helicase II 70 kDa subunit) (Lupus Ku autoantigen protein p70) (Ku70) (70 kDa subunit of Ku antigen) (Thyroid-lupus autoantigen) (TLAA) (CTC box-binding factor 75 kDa subunit) (CTCBF) (CTC75) (DNA-repair protein XRCC6) - Homo sapiens (Human)
49	18.0	20.2	P12956 KU70_HUMAN	ATP-dependent DNA helicase 2 subunit 1 (ATP-dependent DNA helicase II 70 kDa subunit) (Lupus Ku autoantigen protein p70) (Ku70) (70 kDa subunit of Ku antigen) (Thyroid-lupus autoantigen) (TLAA) (CTC box-binding factor 75 kDa subunit) (CTCBF) (CTC75) (DNA-repair protein XRCC6) - Homo sapiens (Human)
366	2.0	4.2	P13284 GILT_HUMAN	Gamma-interferon-inducible lysosomal thiol reductase precursor (Gamma-interferon-inducible protein IP-30) - Homo sapiens (Human)
183	2.0	8.8	P13284 GILT_HUMAN	Gamma-interferon-inducible lysosomal thiol reductase precursor (Gamma-interferon-inducible protein IP-30) - Homo sapiens (Human)
545	2.0	4.2	P13284 GILT_HUMAN	Gamma-interferon-inducible lysosomal thiol reductase precursor (Gamma-interferon-inducible protein IP-30) - Homo sapiens (Human)
300	2.0	6.9	P13489 RINI_HUMAN	Ribonuclease inhibitor (Ribonuclease/angiogenin inhibitor 1) (RAI) (Placental ribonuclease inhibitor) (RNase inhibitor) (RI) - Homo sapiens (Human)
232	5.3	15.0	P13489 RINI_HUMAN	Ribonuclease inhibitor (Ribonuclease/angiogenin inhibitor 1) (RAI) (Placental ribonuclease inhibitor) (RNase inhibitor) (RI) - Homo sapiens (Human)
51	15.4	27.2	P13639 EF2_HUMAN	Elongation factor 2 (EF-2) - Homo sapiens (Human)
33	9.8	18.4	P13639 EF2_HUMAN	Elongation factor 2 (EF-2) - Homo sapiens (Human)
35	22.8	20.3	P13639 EF2_HUMAN	Elongation factor 2 (EF-2) - Homo sapiens (Human)
305	6.0	54.8	P13640 MT1G_HUMAN	Metallothionein-1G (MT-1G) (Metallothionein-IG) (MT-IG) (Metallothionein-1K) (MT-1K) - Homo sapiens (Human)
182	2.0	53.2	P13640 MT1G_HUMAN	Metallothionein-1G (MT-1G) (Metallothionein-IG) (MT-IG) (Metallothionein-1K) (MT-1K) - Homo sapiens (Human)
460	4.0	53.2	P13640 MT1G_HUMAN	Metallothionein-1G (MT-1G) (Metallothionein-IG) (MT-IG) (Metallothionein-1K) (MT-1K) - Homo sapiens (Human)
299	2.0	6.5	P13686 PPA5_HUMAN	Tartrate-resistant acid phosphatase type 5 precursor (EC 3.1.3.2) (TR-AP) (Tartrate-resistant acid ATPase) (TrATPase) (Acid phosphatase 5, tartrate resistant) - Homo sapiens (Human)
144	2.1	15.7	P13686 PPA5_HUMAN	Tartrate-resistant acid phosphatase type 5 precursor (EC 3.1.3.2) (TR-AP) (Tartrate-resistant acid ATPase) (TrATPase) (Acid phosphatase 5, tartrate resistant) - Homo sapiens (Human)
247	4.9	12.3	P13686 PPA5_HUMAN	Tartrate-resistant acid phosphatase type 5 precursor (EC 3.1.3.2) (TR-AP) (Tartrate-resistant acid ATPase) (TrATPase) (Acid phosphatase 5, tartrate resistant) - Homo sapiens (Human)
24	22.6	37.5	P13796 PLSL_HUMAN	Plastin-2 (L-plastin) (Lymphocyte cytosolic protein 1) (LCP-1) (LC64P) - Homo sapiens (Human)
18	14.2	31.4	P13796 PLSL_HUMAN	Plastin-2 (L-plastin) (Lymphocyte cytosolic protein 1) (LCP-1) (LC64P) - Homo sapiens (Human)
25	26.0	32.2	P13796 PLSL_HUMAN	Plastin-2 (L-plastin) (Lymphocyte cytosolic protein 1) (LCP-1) (LC64P) - Homo sapiens (Human)
194	4.0	17.4	P14174 MIF_HUMAN	Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) - Homo sapiens (Human)
94	4.0	17.4	P14174 MIF_HUMAN	Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) - Homo sapiens (Human)
193	6.0	22.6	P14174 MIF_HUMAN	Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) - Homo sapiens (Human)
153	4.6	17.9	P14317 HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75) - Homo sapiens (Human)
137	2.1	30.0	P14317 HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75) - Homo sapiens (Human)
130	8.7	13.8	P14317 HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75) - Homo sapiens (Human)
16	27.4	51.2	P14618 KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase muscle isozyme) (Pyruvate kinase 2/3) (Cytosolic thyroid hormone-binding protein) (CTHBP) (THBP1) - Homo sapiens (Human)
49	6.4	37.1	P14618 KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase muscle isozyme) (Pyruvate kinase 2/3) (Cytosolic thyroid hormone-binding protein) (CTHBP) (THBP1) - Homo sapiens (Human)
14	38.4	54.6	P14618 KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase muscle isozyme) (Pyruvate kinase 2/3) (Cytosolic thyroid hormone-binding protein) (CTHBP) (THBP1) - Homo sapiens (Human)
316	2.0	8.8	P14625 ENPL_HUMAN	Endoplasmic precursor (Heat shock protein 90 kDa beta member 1) (94 kDa glucose-regulated protein) (GRP94) (gp96 homolog) (Tumor rejection antigen 1) - Homo sapiens (Human)
467	2.0	5.5	P14625 ENPL_HUMAN	Endoplasmic precursor (Heat shock protein 90 kDa beta member 1) (94 kDa glucose-regulated protein) (GRP94) (gp96 homolog) (Tumor rejection antigen 1) - Homo sapiens (Human)
6	46.9	48.9	P14780 MMP9_HUMAN	Matrix metalloproteinase-9 precursor (EC 3.4.24.35) (MMP-9) (92 kDa type IV collagenase) (92 kDa gelatinase) (Gelatinase B) (GELB) [Contains: 67 kDa matrix metalloproteinase-9; 82 kDa matrix metalloproteinase-9] - Homo sapiens (Human)
6	31.5	42.9	P14780 MMP9_HUMAN	Matrix metalloproteinase-9 precursor (EC 3.4.24.35) (MMP-9) (92 kDa type IV collagenase) (92 kDa gelatinase) (Gelatinase B) (GELB) [Contains: 67 kDa matrix metalloproteinase-9; 82 kDa matrix metalloproteinase-9] - Homo sapiens (Human)

8	44.0	50.2	P14780 MMP9_HUMAN	Matrix metalloproteinase-9 precursor (EC 3.4.24.35) (MMP-9) (92 kDa type IV collagenase) (92 kDa gelatinase) (Gelatinase B) (GELB) [Contains: 67 kDa matrix metalloproteinase-9; 82 kDa matrix metalloproteinase-9] - Homo sapiens (Human)
155	4.6	65.1	P14854 CX6B1_HUMAN	Cytochrome c oxidase subunit VIb isoform 1 (EC 1.9.3.1) (COX VIb-1) - Homo sapiens (Human)
344	3.4	31.4	P14854 CX6B1_HUMAN	Cytochrome c oxidase subunit VIb isoform 1 (EC 1.9.3.1) (COX VIb-1) - Homo sapiens (Human)
356	2.0	5.2	P15153 RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 precursor (p21-Rac2) (Small G protein) (GX) - Homo sapiens (Human)
304	4.0	9.4	P15153 RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 precursor (p21-Rac2) (Small G protein) (GX) - Homo sapiens (Human)
67	23.1	38.4	P15311 EZRI_HUMAN	Ezrin (p81) (Cytovillin) (Villin-2) - Homo sapiens (Human)
127	10.3	24.9	P15311 EZRI_HUMAN	Ezrin (p81) (Cytovillin) (Villin-2) - Homo sapiens (Human)
46	27.2	41.1	P15311 EZRI_HUMAN	Ezrin (p81) (Cytovillin) (Villin-2) - Homo sapiens (Human)
156	4.6	7.5	P16070 CD44_HUMAN	CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (Heparan sulfate proteoglycan) (Epicin) (CDw44) - Homo sapiens (Human)
109	3.2	6.9	P16070 CD44_HUMAN	CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (Heparan sulfate proteoglycan) (Epicin) (CDw44) - Homo sapiens (Human)
346	3.3	4.0	P16070 CD44_HUMAN	CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (Heparan sulfate proteoglycan) (Epicin) (CDw44) - Homo sapiens (Human)
193	4.0	13.4	P16152 CBR1_HUMAN	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) (Prostaglandin-E(2) 9-reductase) (EC 1.1.1.189) (Prostaglandin 9-ketoreductase) (15-hydroxyprostaglandin dehydrogenase [NADP+]) (EC 1.1.1.197) - Homo sapiens (Human)
329	3.7	13.4	P16152 CBR1_HUMAN	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) (Prostaglandin-E(2) 9-reductase) (EC 1.1.1.189) (Prostaglandin 9-ketoreductase) (15-hydroxyprostaglandin dehydrogenase [NADP+]) (EC 1.1.1.197) - Homo sapiens (Human)
246	2.3	22.6	P16401 H15_HUMAN	Histone H1.5 (Histone H1a) - Homo sapiens (Human)
235	6.0	23.5	P16401 H15_HUMAN	Histone H1.5 (Histone H1a) - Homo sapiens (Human)
309	3.7	30.3	P16402 H13_HUMAN	Histone H1.3 (Histone H1c) - Homo sapiens (Human)
451	6.0	23.5	P16402 H13_HUMAN	Histone H1.3 (Histone H1c) - Homo sapiens (Human)
102	7.7	23.5	P16403 H12_HUMAN	Histone H1.2 (Histone H1d) - Homo sapiens (Human)
227	11.4	22.1	P16403 H12_HUMAN	Histone H1.2 (Histone H1d) - Homo sapiens (Human)
297	2.0	21.5	P16949 STMN1_HUMAN	Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia-associated phosphoprotein p18) (pp17) (Proslin) (Metablastin) (Protein Pr22) - Homo sapiens (Human)
149	2.0	12.8	P16949 STMN1_HUMAN	Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia-associated phosphoprotein p18) (pp17) (Proslin) (Metablastin) (Protein Pr22) - Homo sapiens (Human)
243	4.9	27.5	P16949 STMN1_HUMAN	Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia-associated phosphoprotein p18) (pp17) (Proslin) (Metablastin) (Protein Pr22) - Homo sapiens (Human)
192	4.0	10.0	P17931 LEG3_HUMAN	Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding protein) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Laminin-binding protein) (Lectin L-29) (L-31) (Galactoside-binding protein) (GALBP) - Homo sapiens (Human)
124	2.3	14.4	P17931 LEG3_HUMAN	Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding protein) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Laminin-binding protein) (Lectin L-29) (L-31) (Galactoside-binding protein) (GALBP) - Homo sapiens (Human)
357	3.2	10.0	P17931 LEG3_HUMAN	Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding protein) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Laminin-binding protein) (Lectin L-29) (L-31) (Galactoside-binding protein) (GALBP) - Homo sapiens (Human)
107	3.2	36.7	P18465 I1857_HUMAN	HLA class I histocompatibility antigen, B-57 alpha chain precursor (MHC class I antigen B*57) (Bw-57) - Homo sapiens (Human)
160	12.3	40.6	P18465 I1857_HUMAN	HLA class I histocompatibility antigen, B-57 alpha chain precursor (MHC class I antigen B*57) (Bw-57) - Homo sapiens (Human)
53	14.0	42.9	P18669 PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1) - Homo sapiens (Human)
36	8.6	38.6	P18669 PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1) - Homo sapiens (Human)
40	20.6	61.0	P18669 PGAM1_HUMAN	Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1) - Homo sapiens (Human)
128	6.0	33.9	P19105 MLRM_HUMAN	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC) - Homo sapiens (Human)
146	2.1	17.5	P19105 MLRM_HUMAN	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC) - Homo sapiens (Human)
151	8.0	29.2	P19105 MLRM_HUMAN	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC) - Homo sapiens (Human)
20	23.9	20.3	P19823 ITH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin inhibitor complex component II) (Serum-derived hyaluronan-associated protein) (SHAP) - Homo sapiens (Human)
31	10.0	12.4	P19823 ITH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin inhibitor complex component II) (Serum-derived hyaluronan-associated protein) (SHAP) - Homo sapiens (Human)
55	16.9	13.4	P19823 ITH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin inhibitor complex component II) (Serum-derived hyaluronan-associated protein) (SHAP) - Homo sapiens (Human)
107	7.5	23.0	P19971 TYPH_HUMAN	Thymidine phosphorylase precursor (EC 2.4.2.4) (TdRPase) (TP) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (Gliostatin) - Homo sapiens (Human)
416	2.1	8.9	P19971 TYPH_HUMAN	Thymidine phosphorylase precursor (EC 2.4.2.4) (TdRPase) (TP) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (Gliostatin) - Homo sapiens (Human)
100	7.8	27.6	P20700 LMNB1_HUMAN	Lamin-B1 - Homo sapiens (Human)
97	11.5	26.1	P20700 LMNB1_HUMAN	Lamin-B1 - Homo sapiens (Human)
214	5.2	7.8	P20742 PZP_HUMAN	Pregnancy zone protein precursor - Homo sapiens (Human)
358	7.7	8.4	P20742 PZP_HUMAN	Pregnancy zone protein precursor - Homo sapiens (Human)
360	2.0	7.8	P21291 CSR1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP1) (CRP) - Homo sapiens (Human)
527	2.0	7.8	P21291 CSR1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP1) (CRP) - Homo sapiens (Human)
36	18.9	13.4	P21333 FLNA_HUMAN	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin) - Homo sapiens (Human)
29	10.2	7.9	P21333 FLNA_HUMAN	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin) - Homo sapiens (Human)
24	27.7	14.3	P21333 FLNA_HUMAN	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin) - Homo sapiens (Human)
261	2.2	9.4	P22314 UBE1_HUMAN	Ubiquitin-activating enzyme E1 (A1S9 protein) - Homo sapiens (Human)
226	5.4	5.3	P22314 UBE1_HUMAN	Ubiquitin-activating enzyme E1 (A1S9 protein) - Homo sapiens (Human)
131	6.0	44.7	P22392 NDKB_HUMAN	Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B) (nm23-H2) (C-myc purine-binding transcription factor PUF) - Homo sapiens (Human)
140	8.0	48.7	P22392 NDKB_HUMAN	Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B) (nm23-H2) (C-myc purine-binding transcription factor PUF) - Homo sapiens (Human)
134	6.0	25.2	P23246 SFPO_HUMAN	Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF) (DNA-binding p52/p100 complex, 100 kDa subunit) (100 kDa DNA-pairing protein) (hPOMp100) - Homo sapiens (Human)
212	1.3	16.4	P23246 SFPO_HUMAN	Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF) (DNA-binding p52/p100 complex, 100 kDa subunit) (100 kDa DNA-pairing protein) (hPOMp100) - Homo sapiens (Human)
52	17.2	23.6	P23246 SFPO_HUMAN	Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF) (DNA-binding p52/p100 complex, 100 kDa subunit) (100 kDa DNA-pairing protein) (hPOMp100) - Homo sapiens (Human)
248	2.3	10.1	P23284 PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1) - Homo sapiens (Human)
142	2.1	6.7	P23284 PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1) - Homo sapiens (Human)
38	18.5	32.7	P23381 SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TrpRS) (IFP53) (hWRS) - Homo sapiens (Human)
110	3.1	24.8	P23381 SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TrpRS) (IFP53) (hWRS) - Homo sapiens (Human)
43	19.9	32.9	P23381 SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TrpRS) (IFP53) (hWRS) - Homo sapiens (Human)
54	13.7	60.2	P23528 COF1_HUMAN	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) - Homo sapiens (Human)
42	7.2	29.5	P23528 COF1_HUMAN	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) - Homo sapiens (Human)
37	22.3	51.8	P23528 COF1_HUMAN	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) - Homo sapiens (Human)
58	13.0	23.3	P25774 CATS_HUMAN	Cathepsin S precursor (EC 3.4.22.27) - Homo sapiens (Human)
39	8.0	30.2	P25774 CATS_HUMAN	Cathepsin S precursor (EC 3.4.22.27) - Homo sapiens (Human)
139	8.1	20.5	P25774 CATS_HUMAN	Cathepsin S precursor (EC 3.4.22.27) - Homo sapiens (Human)
144	5.3	26.2	P25786 PSA1_HUMAN	Proteasome subunit alpha type 1 (EC 3.4.25.1) (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain) (30 kDa prosomal protein) (PROS-30) - Homo sapiens (Human)
135	2.2	13.7	P25786 PSA1_HUMAN	Proteasome subunit alpha type 1 (EC 3.4.25.1) (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain) (30 kDa prosomal protein) (PROS-30) - Homo sapiens (Human)
118	9.7	26.2	P25786 PSA1_HUMAN	Proteasome subunit alpha type 1 (EC 3.4.25.1) (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain) (30 kDa prosomal protein) (PROS-30) - Homo sapiens (Human)
273	2.1	17.9	P25787 PSA2_HUMAN	Proteasome subunit alpha type 2 (EC 3.4.25.1) (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) - Homo sapiens (Human)
187	2.0	6.0	P25787 PSA2_HUMAN	Proteasome subunit alpha type 2 (EC 3.4.25.1) (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) - Homo sapiens (Human)
435	2.0	18.4	P25787 PSA2_HUMAN	Proteasome subunit alpha type 2 (EC 3.4.25.1) (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) - Homo sapiens (Human)
359	2.0	3.8	P25789 PSA4_HUMAN	Proteasome subunit alpha type 4 (EC 3.4.25.1) (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex subunit C9) (Proteasome subunit L) - Homo sapiens (Human)
147	2.0	12.6	P25789 PSA4_HUMAN	Proteasome subunit alpha type 4 (EC 3.4.25.1) (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex subunit C9) (Proteasome subunit L) - Homo sapiens (Human)
524	2.0	3.8	P25789 PSA4_HUMAN	Proteasome subunit alpha type 4 (EC 3.4.25.1) (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex subunit C9) (Proteasome subunit L) - Homo sapiens (Human)
7	44.9	56.7	P26038 MOES_HUMAN	Moesin (Membrane-organizing extension spike protein) - Homo sapiens (Human)
11	20.7	37.1	P26038 MOES_HUMAN	Moesin (Membrane-organizing extension spike protein) - Homo sapiens (Human)
5	53.4	55.3	P26038 MOES_HUMAN	Moesin (Membrane-organizing extension spike protein) - Homo sapiens (Human)

268	2.1	20.8	P26447 S10A4_HUMAN	Protein S100-A4 (S100 calcium-binding protein A4) (Metastasin) (Protein Mts1) (Placental calcium-binding protein) (Calvasculin) - Homo sapiens (Human)
181	2.0	19.8	P26447 S10A4_HUMAN	Protein S100-A4 (S100 calcium-binding protein A4) (Metastasin) (Protein Mts1) (Placental calcium-binding protein) (Calvasculin) - Homo sapiens (Human)
499	2.0	19.8	P26447 S10A4_HUMAN	Protein S100-A4 (S100 calcium-binding protein A4) (Metastasin) (Protein Mts1) (Placental calcium-binding protein) (Calvasculin) - Homo sapiens (Human)
264	8.2	39.7	P26583 HMG2_HUMAN	High mobility group protein B2 (High mobility group protein 2) (HMG-2) - Homo sapiens (Human)
288	16.0	50.7	P26583 HMG2_HUMAN	High mobility group protein B2 (High mobility group protein 2) (HMG-2) - Homo sapiens (Human)
159	2.0	28.9	P27695 APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP endonuclease 1) (APEX nuclease) (APEN) (Protein REF-1) - Homo sapiens (Human)
158	7.6	24.8	P27695 APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP endonuclease 1) (APEX nuclease) (APEN) (Protein REF-1) - Homo sapiens (Human)
123	6.0	13.9	P27797 CALR_HUMAN	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60) (grp60) - Homo sapiens (Human)
86	12.2	25.4	P27797 CALR_HUMAN	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60) (grp60) - Homo sapiens (Human)
131	2.2	13.0	P28062 PSB8_HUMAN	Proteasome subunit beta type 8 precursor (EC 3.4.25.1) (Proteasome component C13) (Macropain subunit C13) (Multicatalytic endopeptidase complex subunit C13) - Homo sapiens (Human)
149	8.0	21.7	P28062 PSB8_HUMAN	Proteasome subunit beta type 8 precursor (EC 3.4.25.1) (Proteasome component C13) (Macropain subunit C13) (Multicatalytic endopeptidase complex subunit C13) - Homo sapiens (Human)
190	4.0	14.1	P28066 PSA5_HUMAN	Proteasome subunit alpha type 5 (EC 3.4.25.1) (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) - Homo sapiens (Human)
169	6.7	26.6	P28066 PSA5_HUMAN	Proteasome subunit alpha type 5 (EC 3.4.25.1) (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) - Homo sapiens (Human)
136	2.2	22.3	P28070 PSB4_HUMAN	Proteasome subunit beta type 4 precursor (EC 3.4.25.1) (Proteasome beta chain) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain) (Proteasome chain 3) (HSN3) (HsBPROS26) - Homo sapiens (Human)
281	4.0	24.2	P28070 PSB4_HUMAN	Proteasome subunit beta type 4 precursor (EC 3.4.25.1) (Proteasome beta chain) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain) (Proteasome chain 3) (HSN3) (HsBPROS26) - Homo sapiens (Human)
175	4.0	11.9	P28482 MK01_HUMAN	Mitogen-activated protein kinase 1 (EC 2.7.11.24) (Extracellular signal-regulated kinase 2) (ERK-2) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2) (p42-MAPK) (ERT1) - Homo sapiens (Human)
167	2.0	15.0	P28482 MK01_HUMAN	Mitogen-activated protein kinase 1 (EC 2.7.11.24) (Extracellular signal-regulated kinase 2) (ERK-2) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK 2) (p42-MAPK) (ERT1) - Homo sapiens (Human)
229	2.8	13.2	P28799 GRN_HUMAN	Granulin precursor (Proepithelin) (PEPI) [Contains: Acrogranin; Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3 (Granulin B); Granulin-4 (Granulin A); Granulin-5 (Granulin C); Granulin-6 (Granulin D); Granulin-7 (Granulin E)] - Homo sapiens (Human)
368	2.9	10.1	P28799 GRN_HUMAN	Granulin precursor (Proepithelin) (PEPI) [Contains: Acrogranin; Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3 (Granulin B); Granulin-4 (Granulin A); Granulin-5 (Granulin C); Granulin-6 (Granulin D); Granulin-7 (Granulin E)] - Homo sapiens (Human)
32	20.0	37.2	P28838 AMPL_HUMAN	Cytosolic aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Leucine aminopeptidase 3) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase) (Peptidase S) - Homo sapiens (Human)
84	4.1	22.2	P28838 AMPL_HUMAN	Cytosolic aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Leucine aminopeptidase 3) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase) (Peptidase S) - Homo sapiens (Human)
44	19.5	30.1	P28838 AMPL_HUMAN	Cytosolic aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Leucine aminopeptidase 3) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase) (Peptidase S) - Homo sapiens (Human)
287	2.0	7.4	P29350 PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 (EC 3.1.3.48) (Protein-tyrosine phosphatase 1C) (PTP-1C) (Hematopoietic cell protein-tyrosine phosphatase) (SH-PTP1) (Protein-tyrosine phosphatase SHP-1) - Homo sapiens (Human)
128	9.2	25.0	P29350 PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 (EC 3.1.3.48) (Protein-tyrosine phosphatase 1C) (PTP-1C) (Hematopoietic cell protein-tyrosine phosphatase) (SH-PTP1) (Protein-tyrosine phosphatase SHP-1) - Homo sapiens (Human)
66	11.8	22.8	P29401 TKT_HUMAN	Transketolase (EC 2.2.1.1) (TK) - Homo sapiens (Human)
62	5.6	23.4	P29401 TKT_HUMAN	Transketolase (EC 2.2.1.1) (TK) - Homo sapiens (Human)
53	17.1	30.0	P29401 TKT_HUMAN	Transketolase (EC 2.2.1.1) (TK) - Homo sapiens (Human)
215	3.2	18.3	P30041 PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (Antioxidant protein 2) (1-Cys peroxidase) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2) (Non-selenium glutathione peroxidase) (EC 1.11.1.7) (NSGPx) (24 kDa protein) (Liver 2D page spot 40) (Red blood cells page spot 12) - Homo sapiens (Human)
561	1.7	12.9	P30041 PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.11.1.15) (Antioxidant protein 2) (1-Cys peroxidase) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (EC 3.1.1.-) (aiPLA2) (Non-selenium glutathione peroxidase) (EC 1.11.1.7) (NSGPx) (24 kDa protein) (Liver 2D page spot 40) (Red blood cells page spot 12) - Homo sapiens (Human)
365	2.0	9.3	P30046 DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II) - Homo sapiens (Human)
341	2.0	9.3	P30046 DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II) - Homo sapiens (Human)
331	2.0	17.0	P30050 RL12_HUMAN	60S ribosomal protein L12 - Homo sapiens (Human)
411	2.2	19.4	P30050 RL12_HUMAN	60S ribosomal protein L12 - Homo sapiens (Human)
184	4.0	31.0	P30086 PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (HCNPP) (Neuropeptide h3) (Raf kinase inhibitor protein) (RKIP) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNP)] - Homo sapiens (Human)
102	10.6	55.1	P30086 PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (HCNPP) (Neuropeptide h3) (Raf kinase inhibitor protein) (RKIP) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNP)] - Homo sapiens (Human)
97	8.0	16.4	P30101 PDIA3_HUMAN	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (Erp60) (58 kDa microsomal protein) (p58) (Erp57) (58 kDa glucose-regulated protein) - Homo sapiens (Human)
61	5.8	17.8	P30101 PDIA3_HUMAN	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (Erp60) (58 kDa microsomal protein) (p58) (Erp57) (58 kDa glucose-regulated protein) - Homo sapiens (Human)
63	15.7	23.6	P30101 PDIA3_HUMAN	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (Erp60) (58 kDa microsomal protein) (p58) (Erp57) (58 kDa glucose-regulated protein) - Homo sapiens (Human)
270	7.4	30.9	P30508 1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain precursor (MHC class I antigen Cw*12) - Homo sapiens (Human)
542	16.6	48.9	P30508 1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain precursor (MHC class I antigen Cw*12) - Homo sapiens (Human)
272	2.1	11.3	P30740 LEU1_HUMAN	Leukocyte elastase inhibitor (LEI) (Serp1 B1) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI) - Homo sapiens (Human)
155	7.7	14.0	P30740 LEU1_HUMAN	Leukocyte elastase inhibitor (LEI) (Serp1 B1) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI) - Homo sapiens (Human)
25	21.5	32.8	P31146 COR1A_HUMAN	Coronin-1A (Coronin-like protein p57) (Coronin-like protein A) (Clpin-A) (Tryptophan aspartate-containing coat protein) (TACO) - Homo sapiens (Human)
20	13.9	28.2	P31146 COR1A_HUMAN	Coronin-1A (Coronin-like protein p57) (Coronin-like protein A) (Clpin-A) (Tryptophan aspartate-containing coat protein) (TACO) - Homo sapiens (Human)
26	25.9	41.2	P31146 COR1A_HUMAN	Coronin-1A (Coronin-like protein p57) (Coronin-like protein A) (Clpin-A) (Tryptophan aspartate-containing coat protein) (TACO) - Homo sapiens (Human)
177	4.0	12.2	P31153 METK2_HUMAN	S-adenosylmethionine synthetase isoform type-2 (EC 2.5.1.6) (Methionine adenosyltransferase 2) (AdoMet synthetase 2) (Methionine adenosyltransferase II) (MAT-II) - Homo sapiens (Human)
239	5.0	18.7	P31153 METK2_HUMAN	S-adenosylmethionine synthetase isoform type-2 (EC 2.5.1.6) (Methionine adenosyltransferase 2) (AdoMet synthetase 2) (Methionine adenosyltransferase II) (MAT-II) - Homo sapiens (Human)
310	2.4	37.1	P31949 S10AB_HUMAN	Protein S100-A11 (S100 calcium-binding protein A11) (Protein S100C) (Calgizzarin) (MLN 70) - Homo sapiens (Human)
189	2.0	10.5	P31949 S10AB_HUMAN	Protein S100-A11 (S100 calcium-binding protein A11) (Protein S100C) (Calgizzarin) (MLN 70) - Homo sapiens (Human)
210	6.0	46.7	P31949 S10AB_HUMAN	Protein S100-A11 (S100 calcium-binding protein A11) (Protein S100C) (Calgizzarin) (MLN 70) - Homo sapiens (Human)
42	17.7	37.7	P32455 GBP1_HUMAN	Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1) (Guanine nucleotide-binding protein 1) (GBP-1) (HuGBP-1) - Homo sapiens (Human)
54	17.0	27.2	P32455 GBP1_HUMAN	Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1) (Guanine nucleotide-binding protein 1) (GBP-1) (HuGBP-1) - Homo sapiens (Human)
222	5.0	14.9	P32456 GBP2_HUMAN	Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2) (Guanine nucleotide-binding protein 2) (GBP-2) (HuGBP-2) - Homo sapiens (Human)
234	7.3	9.6	P32456 GBP2_HUMAN	Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2) (Guanine nucleotide-binding protein 2) (GBP-2) (HuGBP-2) - Homo sapiens (Human)
168	4.2	21.5	P33241 LSP1_HUMAN	Lymphocyte-specific protein 1 (Protein pp52) (52 kDa phosphoprotein) (Lymphocyte-specific antigen WP34) (47 kDa actin-binding protein) - Homo sapiens (Human)
84	12.3	35.7	P33241 LSP1_HUMAN	Lymphocyte-specific protein 1 (Protein pp52) (52 kDa phosphoprotein) (Lymphocyte-specific antigen WP34) (47 kDa actin-binding protein) - Homo sapiens (Human)
35	18.9	31.7	P35579 MYH9_HUMAN	Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle IIa) (Nonmuscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA) (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain A) (NMMHC-A) - Homo sapiens (Human)
17	36.9	25.6	P35579 MYH9_HUMAN	Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle IIa) (Nonmuscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA) (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain A) (NMMHC-A) - Homo sapiens (Human)
104	7.7	18.3	P36222 CH3L1_HUMAN	Chitinase-3-like protein 1 precursor (Cartilage glycoprotein 39) (GP-39) (39 kDa synovial protein) (HCgp-39) (YKL-40) - Homo sapiens (Human)
168	2.0	15.7	P36222 CH3L1_HUMAN	Chitinase-3-like protein 1 precursor (Cartilage glycoprotein 39) (GP-39) (39 kDa synovial protein) (HCgp-39) (YKL-40) - Homo sapiens (Human)
38	22.0	43.9	P36222 CH3L1_HUMAN	Chitinase-3-like protein 1 precursor (Cartilage glycoprotein 39) (GP-39) (39 kDa synovial protein) (HCgp-39) (YKL-40) - Homo sapiens (Human)
143	5.4	51.8	P37802 TAGL2_HUMAN	Transgelin-2 (SM22-alpha homolog) - Homo sapiens (Human)
97	3.8	32.7	P37802 TAGL2_HUMAN	Transgelin-2 (SM22-alpha homolog) - Homo sapiens (Human)
66	14.8	61.3	P37802 TAGL2_HUMAN	Transgelin-2 (SM22-alpha homolog) - Homo sapiens (Human)
220	3.1	18.4	P37837 TALDO_HUMAN	Transaldolase (EC 2.2.1.2) - Homo sapiens (Human)
209	1.4	6.8	P37837 TALDO_HUMAN	Transaldolase (EC 2.2.1.2) - Homo sapiens (Human)
219	5.9	11.9	P37837 TALDO_HUMAN	Transaldolase (EC 2.2.1.2) - Homo sapiens (Human)
294	2.0	39.4	P38159 HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein, X chromosome) (Glycoprotein p43) - Homo sapiens (Human)
151	2.0	33.2	P38159 HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein, X chromosome) (Glycoprotein p43) - Homo sapiens (Human)
107	10.1	32.5	P38159 HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein, X chromosome) (Glycoprotein p43) - Homo sapiens (Human)

231	2.0	3.9	P38919 IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (EC 3.6.1.-) (Eukaryotic translation initiation factor 4A isoform 3) (ATP-dependent RNA helicase eIF4A-3) (ATP-dependent RNA helicase DDX48) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Nuclear matrix protein 265) (hNMP 265) - Homo sapiens (Human)
164	2.0	17.0	P38919 IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (EC 3.6.1.-) (Eukaryotic translation initiation factor 4A isoform 3) (ATP-dependent RNA helicase eIF4A-3) (ATP-dependent RNA helicase DDX48) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Nuclear matrix protein 265) (hNMP 265) - Homo sapiens (Human)
428	2.0	3.9	P38919 IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (EC 3.6.1.-) (Eukaryotic translation initiation factor 4A isoform 3) (ATP-dependent RNA helicase eIF4A-3) (ATP-dependent RNA helicase DDX48) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Nuclear matrix protein 265) (hNMP 265) - Homo sapiens (Human)
72	10.1	30.2	P40121 CAPG_HUMAN	Macrophage-capping protein (Actin-regulatory protein CAP-G) - Homo sapiens (Human)
30	10.0	23.0	P40121 CAPG_HUMAN	Macrophage-capping protein (Actin-regulatory protein CAP-G) - Homo sapiens (Human)
181	6.4	19.3	P40121 CAPG_HUMAN	Macrophage-capping protein (Actin-regulatory protein CAP-G) - Homo sapiens (Human)
63	12.0	26.3	P40925 MDHC_HUMAN	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) - Homo sapiens (Human)
58	6.0	12.9	P40925 MDHC_HUMAN	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) - Homo sapiens (Human)
90	12.0	31.4	P40925 MDHC_HUMAN	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) - Homo sapiens (Human)
280	2.1	17.2	P40926 MDHM_HUMAN	Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Homo sapiens (Human)
71	14.1	42.6	P40926 MDHM_HUMAN	Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Homo sapiens (Human)
60	12.8	19.9	P42224 STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84) - Homo sapiens (Human)
83	4.1	11.2	P42224 STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84) - Homo sapiens (Human)
58	16.7	19.1	P42224 STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84) - Homo sapiens (Human)
55	13.4	20.2	P43490 NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase (EC 2.4.2.12) (NAMPTase) (Nampt) (Pre-B cell-enhancing factor) (Pre-B-cell colony-enhancing factor 1) (Visfatin) - Homo sapiens (Human)
341	3.4	6.3	P43490 NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase (EC 2.4.2.12) (NAMPTase) (Nampt) (Pre-B cell-enhancing factor) (Pre-B-cell colony-enhancing factor 1) (Visfatin) - Homo sapiens (Human)
244	2.3	24.9	P46777 RL5_HUMAN	60S ribosomal protein L5 - Homo sapiens (Human)
79	13.3	35.0	P46777 RL5_HUMAN	60S ribosomal protein L5 - Homo sapiens (Human)
210	3.3	47.9	P46781 RS9_HUMAN	40S ribosomal protein S9 - Homo sapiens (Human)
220	5.8	28.4	P46781 RS9_HUMAN	40S ribosomal protein S9 - Homo sapiens (Human)
162	4.4	11.2	P46940 IGOA1_HUMAN	Ras GTPase-activating-like protein IGOA1 (p195) - Homo sapiens (Human)
180	6.4	6.8	P46940 IGOA1_HUMAN	Ras GTPase-activating-like protein IGOA1 (p195) - Homo sapiens (Human)
329	2.0	10.3	P48739 PIPNB_HUMAN	Phosphatidylinositol transfer protein beta isoform (PtdIns transfer protein beta) (PtdInsTP) (PI-TP-beta) - Homo sapiens (Human)
473	2.0	14.4	P48739 PIPNB_HUMAN	Phosphatidylinositol transfer protein beta isoform (PtdIns transfer protein beta) (PtdInsTP) (PI-TP-beta) - Homo sapiens (Human)
285	2.0	14.7	P49368 TCPG_HUMAN	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRIC5) - Homo sapiens (Human)
87	12.2	23.9	P49368 TCPG_HUMAN	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRIC5) - Homo sapiens (Human)
91	8.1	20.4	P50395 GDI_B_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2) - Homo sapiens (Human)
54	6.1	16.0	P50395 GDI_B_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2) - Homo sapiens (Human)
75	13.8	25.4	P50395 GDI_B_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2) - Homo sapiens (Human)
379	1.7	12.2	P50453 SPB9_HUMAN	Serpin B9 (Cytoplasmic antiprotease 3) (CAP-3) (CAP3) (Protease inhibitor 9) - Homo sapiens (Human)
209	6.0	14.9	P50453 SPB9_HUMAN	Serpin B9 (Cytoplasmic antiprotease 3) (CAP-3) (CAP3) (Protease inhibitor 9) - Homo sapiens (Human)
138	5.8	21.1	P50552 VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP) - Homo sapiens (Human)
83	12.7	31.8	P50552 VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP) - Homo sapiens (Human)
113	2.9	7.3	P50990 TCPO_HUMAN	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Renal carcinoma antigen NY-REN-15) - Homo sapiens (Human)
208	6.0	6.4	P50990 TCPO_HUMAN	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Renal carcinoma antigen NY-REN-15) - Homo sapiens (Human)
209	3.4	11.6	P51149 RAB7A_HUMAN	Ras-related protein Rab-7a - Homo sapiens (Human)
362	3.0	20.3	P51149 RAB7A_HUMAN	Ras-related protein Rab-7a - Homo sapiens (Human)
208	3.7	29.6	P51991 ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3) - Homo sapiens (Human)
162	7.4	39.7	P51991 ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3) - Homo sapiens (Human)
50	15.5	26.3	P52209 6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) - Homo sapiens (Human)
121	2.4	10.8	P52209 6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) - Homo sapiens (Human)
414	2.2	13.5	P52209 6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) - Homo sapiens (Human)
86	8.8	51.0	P52565 GDIR_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) - Homo sapiens (Human)
82	4.1	26.0	P52565 GDIR_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) - Homo sapiens (Human)
28	24.6	49.0	P52565 GDIR_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) - Homo sapiens (Human)
269	2.1	49.3	P52566 GDIS_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI) - Homo sapiens (Human)
101	12.0	49.8	P52566 GDIS_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI) - Homo sapiens (Human)
330	2.7	12.3	P52597 HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo sapiens (Human)
234	6.0	20.7	P52597 HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo sapiens (Human)
282	2.1	15.4	P52907 CAZA1_HUMAN	F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human)
166	2.0	19.2	P52907 CAZA1_HUMAN	F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human)
233	5.3	19.9	P52907 CAZA1_HUMAN	F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human)
311	2.0	3.7	P53634 CATC_HUMAN	Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase) [Contains: Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase 1 exclusion domain chain); Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 heavy chain); Dipeptidyl-peptidase 1 light chain (Dipeptidyl-peptidase 1 light chain)] - Homo sapiens (Human)
101	3.5	11.9	P53634 CATC_HUMAN	Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase) [Contains: Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase 1 exclusion domain chain); Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 heavy chain); Dipeptidyl-peptidase 1 light chain (Dipeptidyl-peptidase 1 light chain)] - Homo sapiens (Human)
126	6.0	28.9	P54819 KAD2_HUMAN	Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo sapiens (Human)
118	2.6	30.5	P54819 KAD2_HUMAN	Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo sapiens (Human)
189	6.1	34.7	P54819 KAD2_HUMAN	Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo sapiens (Human)
61	12.8	18.7	P55072 TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP) - Homo sapiens (Human)
45	19.1	25.3	P55072 TERA_HUMAN	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP) - Homo sapiens (Human)
187	4.0	10.0	P55209 NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP) - Homo sapiens (Human)
98	3.8	10.2	P55209 NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP) - Homo sapiens (Human)
198	6.0	10.5	P55209 NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP) - Homo sapiens (Human)
181	4.0	6.7	P55786 PSA_HUMAN	Puromycin-sensitive aminopeptidase (EC 3.4.11.-) (PSA) - Homo sapiens (Human)
152	2.0	7.5	P55786 PSA_HUMAN	Puromycin-sensitive aminopeptidase (EC 3.4.11.-) (PSA) - Homo sapiens (Human)
407	2.3	3.8	P55786 PSA_HUMAN	Puromycin-sensitive aminopeptidase (EC 3.4.11.-) (PSA) - Homo sapiens (Human)
327	2.0	19.0	P59998 ARPC4_HUMAN	Actin-related protein 2/3 complex subunit 4 (ARP2/3 complex 20 kDa subunit) (p20-ARC) - Homo sapiens (Human)
123	2.3	23.8	P59998 ARPC4_HUMAN	Actin-related protein 2/3 complex subunit 4 (ARP2/3 complex 20 kDa subunit) (p20-ARC) - Homo sapiens (Human)
197	6.0	29.8	P59998 ARPC4_HUMAN	Actin-related protein 2/3 complex subunit 4 (ARP2/3 complex 20 kDa subunit) (p20-ARC) - Homo sapiens (Human)
40	18.1	57.0	P60174 TPIS_HUMAN	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Homo sapiens (Human)
13	18.3	66.7	P60174 TPIS_HUMAN	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Homo sapiens (Human)
23	28.0	61.0	P60174 TPIS_HUMAN	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Homo sapiens (Human)
122	6.1	50.3	P60660 MYL6_HUMAN	Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosin light chain alkali 6) (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3) (LC17) - Homo sapiens (Human)
65	5.2	31.1	P60660 MYL6_HUMAN	Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosin light chain alkali 6) (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3) (LC17) - Homo sapiens (Human)
112	10.0	50.3	P60660 MYL6_HUMAN	Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosin light chain alkali 6) (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3) (LC17) - Homo sapiens (Human)
5	31.5	66.4	P60709 ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)
449	54.1	69.9	P60709 ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)
356	2.0	5.2	P15153 RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 precursor (p21-Rac2) (Small G protein) (GX) - Homo sapiens (Human)
304	2.0	9.4	P15153 RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 precursor (p21-Rac2) (Small G protein) (GX) - Homo sapiens (Human)
231	2.7	12.3	P60842 IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (EC 3.6.1.-) (ATP-dependent RNA helicase eIF4A-1) (eIF4A-I) (eIF-4A-I) - Homo sapiens (Human)
428	2.1	10.8	P60842 IF4A1_HUMAN	Eukaryotic initiation factor 4A-I (EC 3.6.1.-) (ATP-dependent RNA helicase eIF4A-1) (eIF4A-I) (eIF-4A-I) - Homo sapiens (Human)
165	4.4	21.8	P60866 RS20_HUMAN	40S ribosomal protein S20 - Homo sapiens (Human)
354	3.2	29.4	P60866 RS20_HUMAN	40S ribosomal protein S20 - Homo sapiens (Human)
94	8.1	24.8	P60900 PSA6_HUMAN	Proteasome subunit alpha type 6 (EC 3.4.25.1) (Proteasome Iota chain) (Macropain Iota chain) (Multicatalytic endopeptidase complex Iota chain) (27 kDa prosomeal protein) (PROS-27) (p27K) - Homo sapiens (Human)
180	2.0	8.5	P60900 PSA6_HUMAN	Proteasome subunit alpha type 6 (EC 3.4.25.1) (Proteasome Iota chain) (Macropain Iota chain) (Multicatalytic endopeptidase complex Iota chain) (27 kDa prosomeal protein) (PROS-27) (p27K) - Homo sapiens (Human)
69	14.4	40.2	P60900 PSA6_HUMAN	Proteasome subunit alpha type 6 (EC 3.4.25.1) (Proteasome Iota chain) (Macropain Iota chain) (Multicatalytic endopeptidase complex Iota chain) (27 kDa prosomeal protein) (PROS-27) (p27K) - Homo sapiens (Human)
79	9.5	18.2	P61158 ARP3_HUMAN	Actin-like protein 3 (Actin-related protein 3) - Homo sapiens (Human)
111	10.0	14.4	P61158 ARP3_HUMAN	Actin-like protein 3 (Actin-related protein 3) - Homo sapiens (Human)
112	2.9	15.5	P61160 ARP2_HUMAN	Actin-like protein 2 (Actin-related protein 2) - Homo sapiens (Human)
141	8.0	24.6	P61160 ARP2_HUMAN	Actin-like protein 2 (Actin-related protein 2) - Homo sapiens (Human)
136	5.8	18.2	P61247 RS3A_HUMAN	40S ribosomal protein S3a - Homo sapiens (Human)

63	5.5	16.3	P61247 RS3A_HUMAN	40S ribosomal protein S3a - Homo sapiens (Human)
73	14.0	30.7	P61247 RS3A_HUMAN	40S ribosomal protein S3a - Homo sapiens (Human)
271	2.1	29.7	P61254 RL26_HUMAN	60S ribosomal protein L26 - Homo sapiens (Human)
445	2.0	15.2	P61254 RL26_HUMAN	60S ribosomal protein L26 - Homo sapiens (Human)
374	1.9	26.5	P61604 CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (CPN10) (Early-pregnancy factor) (EPF) - Homo sapiens (Human)
	5.7	26.5	P61604 CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (CPN10) (Early-pregnancy factor) (EPF) - Homo sapiens (Human)
45	16.3	68.2	P61626 LYSC_HUMAN	Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) - Homo sapiens (Human)
23	12.6	81.1	P61626 LYSC_HUMAN	Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) - Homo sapiens (Human)
41	20.4	81.8	P61626 LYSC_HUMAN	Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) - Homo sapiens (Human)
69	10.4	37.8	P61769 B2MG_HUMAN	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pI 5.3] - Homo sapiens (Human)
53	6.1	26.1	P61769 B2MG_HUMAN	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pI 5.3] - Homo sapiens (Human)
94	11.7	49.6	P61769 B2MG_HUMAN	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pI 5.3] - Homo sapiens (Human)
386	1.7	10.6	P61916 NPC2_HUMAN	Epididymal secretory protein E1 precursor (Niemann-Pick disease type C2 protein) (hE1) - Homo sapiens (Human)
536	2.0	10.6	P61916 NPC2_HUMAN	Epididymal secretory protein E1 precursor (Niemann-Pick disease type C2 protein) (hE1) - Homo sapiens (Human)
254	2.2	19.5	P62158 CALM_HUMAN	Calmodulin (CaM) - Homo sapiens (Human)
237	5.2	36.9	P62158 CALM_HUMAN	Calmodulin (CaM) - Homo sapiens (Human)
169	4.1	52.9	P62241 RS8_HUMAN	40S ribosomal protein S8 - Homo sapiens (Human)
106	10.1	52.4	P62241 RS8_HUMAN	40S ribosomal protein S8 - Homo sapiens (Human)
387	1.7	16.9	P62244 RS15A_HUMAN	40S ribosomal protein S15a - Homo sapiens (Human)
296	4.0	21.5	P62244 RS15A_HUMAN	40S ribosomal protein S15a - Homo sapiens (Human)
68	10.9	52.1	P62249 RS16_HUMAN	40S ribosomal protein S16 - Homo sapiens (Human)
106	3.3	35.6	P62249 RS16_HUMAN	40S ribosomal protein S16 - Homo sapiens (Human)
159	7.4	47.3	P62249 RS16_HUMAN	40S ribosomal protein S16 - Homo sapiens (Human)
256	3.5	18.8	P62258 I1433E_HUMAN	14-3-3 protein epsilon (14-3-3E) - Homo sapiens (Human)
109	12.0	37.3	P62258 I1433E_HUMAN	14-3-3 protein epsilon (14-3-3E) - Homo sapiens (Human)
135	5.9	37.5	P62269 RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) - Homo sapiens (Human)
164	7.2	34.9	P62269 RS18_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) - Homo sapiens (Human)
240	2.4	33.9	P62273 RS29_HUMAN	40S ribosomal protein S29 - Homo sapiens (Human)
379	2.6	33.9	P62273 RS29_HUMAN	40S ribosomal protein S29 - Homo sapiens (Human)
116	6.6	34.2	P62280 RS11_HUMAN	40S ribosomal protein S11 - Homo sapiens (Human)
72	4.9	25.3	P62280 RS11_HUMAN	40S ribosomal protein S11 - Homo sapiens (Human)
82	12.8	39.2	P62280 RS11_HUMAN	40S ribosomal protein S11 - Homo sapiens (Human)
361	2.0	7.8	P62310 LSM3_HUMAN	U6 snRNA-associated Sm-like protein LSm3 - Homo sapiens (Human)
311	4.0	28.4	P62310 LSM3_HUMAN	U6 snRNA-associated Sm-like protein LSm3 - Homo sapiens (Human)
333	2.0	19.8	P62318 SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (snRNP core protein D3) (Sm-D3) - Homo sapiens (Human)
207	6.0	38.9	P62318 SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (snRNP core protein D3) (Sm-D3) - Homo sapiens (Human)
28	21.1	97.7	P62328 TYB4_HUMAN	Thymosin beta-4 (T beta 4) (Tx) [Contains: Hematopoietic system regulatory peptide (Seraspenside)] - Homo sapiens (Human)
29	24.5	97.7	P62328 TYB4_HUMAN	Thymosin beta-4 (T beta 4) (Tx) [Contains: Hematopoietic system regulatory peptide (Seraspenside)] - Homo sapiens (Human)
179	2.0	15.8	P62633 CNBP_HUMAN	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9) - Homo sapiens (Human)
353	3.2	41.8	P62633 CNBP_HUMAN	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9) - Homo sapiens (Human)
93	8.1	28.1	P62701 RS4X_HUMAN	40S ribosomal protein S4, X isoform (Single copy abundant mRNA protein) (SCR10) - Homo sapiens (Human)
195	6.0	21.7	P62701 RS4X_HUMAN	40S ribosomal protein S4, X isoform (Single copy abundant mRNA protein) (SCR10) - Homo sapiens (Human)
291	2.0	24.9	P62753 RS6_HUMAN	40S ribosomal protein S6 (Phosphoprotein NP33) - Homo sapiens (Human)
140	2.1	37.8	P62753 RS6_HUMAN	40S ribosomal protein S6 (Phosphoprotein NP33) - Homo sapiens (Human)
192	6.0	27.3	P62753 RS6_HUMAN	40S ribosomal protein S6 (Phosphoprotein NP33) - Homo sapiens (Human)
31	20.7	88.3	P62805 H4_HUMAN	Histone H4 - Homo sapiens (Human)
46	6.6	70.9	P62805 H4_HUMAN	Histone H4 - Homo sapiens (Human)
64	15.6	82.5	P62805 H4_HUMAN	Histone H4 - Homo sapiens (Human)
147	5.0	20.4	P62826 RAN_HUMAN	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) (Androgen receptor-associated protein 24) - Homo sapiens (Human)
90	4.0	22.2	P62826 RAN_HUMAN	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) (Androgen receptor-associated protein 24) - Homo sapiens (Human)
397	2.3	28.7	P62826 RAN_HUMAN	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) (Androgen receptor-associated protein 24) - Homo sapiens (Human)
292	2.0	30.4	P62854 RS26_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human)
178	2.0	29.6	P62854 RS26_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human)
222	5.7	51.3	P62854 RS26_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human)
363	2.0	3.8	P62873 GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human)
534	2.0	3.8	P62873 GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human)
87	8.7	45.5	P62937 PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human)
17	16.0	57.0	P62937 PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human)
27	24.9	81.8	P62937 PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human)
191	4.0	25.0	P62942 FKBP1A_HUMAN	FK506-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human)
174	2.0	40.7	P62942 FKBP1A_HUMAN	FK506-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human)
215	6.0	29.6	P62942 FKBP1A_HUMAN	FK506-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human)
157	4.6	55.0	P62979 RS27A_HUMAN	40S ribosomal protein S27a - Homo sapiens (Human)
372	2.8	55.0	P62979 RS27A_HUMAN	40S ribosomal protein S27a - Homo sapiens (Human)
56	13.3	51.4	P63104 I1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human)
67	5.1	35.1	P63104 I1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human)
34	22.8	65.7	P63104 I1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human)
382	1.7	8.5	P63244 GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta 2-like 1 (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Receptor of activated protein kinase C 1) (RACK1) (Receptor for activated C kinase) - Homo sapiens (Human)
533	2.0	4.1	P63244 GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta 2-like 1 (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Receptor of activated protein kinase C 1) (RACK1) (Receptor for activated C kinase) - Homo sapiens (Human)
5	50.7	69.1	P63261 ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) - Homo sapiens (Human)
154	31.4	66.4	P63261 ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) - Homo sapiens (Human)
4	54.2	69.9	P63261 ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin) - Homo sapiens (Human)
173	2.0	15.8	P63279 UBC9_HUMAN	SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (SUMO-protein ligase) (Ubiquitin-conjugating enzyme E2 1) (Ubiquitin-protein ligase 1) (Ubiquitin carrier protein 1) (Ubiquitin carrier protein 9) (p18) - Homo sapiens (Human)
497	2.0	7.0	P63279 UBC9_HUMAN	SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (SUMO-protein ligase) (Ubiquitin-conjugating enzyme E2 1) (Ubiquitin-protein ligase 1) (Ubiquitin carrier protein 1) (Ubiquitin carrier protein 9) (p18) - Homo sapiens (Human)
57	13.2	49.6	P67936 TPM4_HUMAN	Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p1) - Homo sapiens (Human)
78	4.5	44.4	P67936 TPM4_HUMAN	Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p1) - Homo sapiens (Human)
39	21.0	45.6	P67936 TPM4_HUMAN	Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p1) - Homo sapiens (Human)
90	8.2	22.1	P68104 EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1) (Elongation factor Tu) (EF-Tu) (Leukocyte receptor cluster member 7) - Homo sapiens (Human)
129	2.3	10.2	P68104 EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1) (Elongation factor Tu) (EF-Tu) (Leukocyte receptor cluster member 7) - Homo sapiens (Human)
91	12.0	21.4	P68104 EF1A1_HUMAN	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1) (Elongation factor Tu) (EF-Tu) (Leukocyte receptor cluster member 7) - Homo sapiens (Human)
49	15.5	29.9	P68363 TBAK_HUMAN	Tubulin alpha-ubiquitous chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) - Homo sapiens (Human)
33	23.4	38.6	P68363 TBAK_HUMAN	Tubulin alpha-ubiquitous chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) - Homo sapiens (Human)
112	6.9	37.5	P68431 H3_HUMAN	Histone H3.1 (H3/a) (H3/b) (H3/c) (H3/d) (H3/f) (H3/h) (H3/i) (H3/j) (H3/k) (H3/l) - Homo sapiens (Human)
139	2.1	19.1	P68431 H3_HUMAN	Histone H3.1 (H3/a) (H3/b) (H3/c) (H3/d) (H3/f) (H3/h) (H3/i) (H3/j) (H3/k) (H3/l) - Homo sapiens (Human)
154	7.9	41.2	P68431 H3_HUMAN	Histone H3.1 (H3/a) (H3/b) (H3/c) (H3/d) (H3/f) (H3/h) (H3/i) (H3/j) (H3/k) (H3/l) - Homo sapiens (Human)
146	5.1	28.6	P78417 GSTO1_HUMAN	Glutathione transferase omega-1 (EC 2.5.1.18) (GSTO 1-1) - Homo sapiens (Human)
188	2.0	3.3	P78417 GSTO1_HUMAN	Glutathione transferase omega-1 (EC 2.5.1.18) (GSTO 1-1) - Homo sapiens (Human)
369	2.9	14.5	P78417 GSTO1_HUMAN	Glutathione transferase omega-1 (EC 2.5.1.18) (GSTO 1-1) - Homo sapiens (Human)
304	6.0	54.1	P80295 MT11_HUMAN	Metallothionein-11 (MT-11) (Metallothionein-II) - Homo sapiens (Human)
182	2.0	19.7	P80295 MT11_HUMAN	Metallothionein-11 (MT-11) (Metallothionein-II) - Homo sapiens (Human)
459	4.0	52.5	P80295 MT11_HUMAN	Metallothionein-11 (MT-11) (Metallothionein-II) - Homo sapiens (Human)
313	2.0	46.3	P84103 SRFS3_HUMAN	Splicing factor, arginine/serine-rich 3 (Pre-mRNA-splicing factor SRP20) - Homo sapiens (Human)
279	4.0	37.8	P84103 SRFS3_HUMAN	Splicing factor, arginine/serine-rich 3 (Pre-mRNA-splicing factor SRP20) - Homo sapiens (Human)
234	2.5	3.5	O00610 CLH1_HUMAN	Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)
408	2.3	3.6	O00610 CLH1_HUMAN	Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)
140	5.7	20.6	O00839 HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (pp120) - Homo sapiens (Human)
93	11.9	23.1	O00839 HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (pp120) - Homo sapiens (Human)

255	2.2	7.9	Q01082 SPTB2_HUMAN	Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1) (Beta-II spectrin) (Fodrin beta chain) - Homo sapiens (Human)
119	9.6	8.6	Q01082 SPTB2_HUMAN	Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1) (Beta-II spectrin) (Fodrin beta chain) - Homo sapiens (Human)
127	6.0	22.8	Q01105 SET_HUMAN	Protein SET (Phosphatase 2A inhibitor 12PP2A) (I-2PP2A) (Template-activating factor 1) (TAF-1) (HLA-DR-associated protein II) (PHAPI) (Inhibitor of granzyme A-activated DNase) (GAAD) - Homo sapiens (Human)
61	16.1	15.2	Q01105 SET_HUMAN	Protein SET (Phosphatase 2A inhibitor 12PP2A) (I-2PP2A) (Template-activating factor 1) (TAF-1) (HLA-DR-associated protein II) (PHAPI) (Inhibitor of granzyme A-activated DNase) (GAAD) - Homo sapiens (Human)
226	2.9	31.9	Q01469 FABPE_HUMAN	Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) - Homo sapiens (Human)
176	6.5	57.8	Q01469 FABPE_HUMAN	Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) - Homo sapiens (Human)
110	7.1	21.1	Q01518 CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1) - Homo sapiens (Human)
56	6.0	14.5	Q01518 CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1) - Homo sapiens (Human)
121	9.6	16.2	Q01518 CAP1_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1) - Homo sapiens (Human)
312	2.0	16.8	Q01844 EWS_HUMAN	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) - Homo sapiens (Human)
115	2.8	23.6	Q01844 EWS_HUMAN	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) - Homo sapiens (Human)
268	4.1	25.8	Q01844 EWS_HUMAN	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) - Homo sapiens (Human)
150	4.7	23.4	Q02818 NUCB1_HUMAN	Nucleobindin-1 precursor (CALNUC) - Homo sapiens (Human)
271	4.1	18.2	Q02818 NUCB1_HUMAN	Nucleobindin-1 precursor (CALNUC) - Homo sapiens (Human)
332	2.0	12.8	Q02878 RL6_HUMAN	60S ribosomal protein L6 (TAX-responsive enhancer element-binding protein 107) (TAXREB107) (Neoplasm-related protein C140) - Homo sapiens (Human)
355	3.2	21.2	Q02878 RL6_HUMAN	60S ribosomal protein L6 (TAX-responsive enhancer element-binding protein 107) (TAXREB107) (Neoplasm-related protein C140) - Homo sapiens (Human)
92	8.1	13.8	Q06033 ITHI3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3) (Inter-alpha-inhibitor heavy chain 3) (Serum-derived hyaluronan-associated protein) (SHAP) - Homo sapiens (Human)
100	3.5	8.6	Q06033 ITHI3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3) (Inter-alpha-inhibitor heavy chain 3) (Serum-derived hyaluronan-associated protein) (SHAP) - Homo sapiens (Human)
116	9.7	7.3	Q06033 ITHI3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3) (Inter-alpha-inhibitor heavy chain 3) (Serum-derived hyaluronan-associated protein) (SHAP) - Homo sapiens (Human)
59	12.9	34.1	Q06323 PSME1_HUMAN	Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease subunit 1) (11S regulator complex subunit alpha) (REG-alpha) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) - Homo sapiens (Human)
50	6.3	26.9	Q06323 PSME1_HUMAN	Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease subunit 1) (11S regulator complex subunit alpha) (REG-alpha) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) - Homo sapiens (Human)
68	14.7	38.2	Q06323 PSME1_HUMAN	Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease subunit 1) (11S regulator complex subunit alpha) (REG-alpha) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) - Homo sapiens (Human)
41	18.0	49.7	Q06830 PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Proliferation-associated gene protein) (PAG) (Natural killer cell-enhancing factor A) (NKEF-A) - Homo sapiens (Human)
25	12.3	52.8	Q06830 PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Proliferation-associated gene protein) (PAG) (Natural killer cell-enhancing factor A) (NKEF-A) - Homo sapiens (Human)
48	18.3	55.3	Q06830 PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Proliferation-associated gene protein) (PAG) (Natural killer cell-enhancing factor A) (NKEF-A) - Homo sapiens (Human)
276	2.1	7.5	Q08380 LG3BP_HUMAN	Galectin-3-binding protein precursor (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (Mac-2 BP) (MAC2BP) (Tumor-associated antigen 90K) - Homo sapiens (Human)
161	2.0	6.3	Q08380 LG3BP_HUMAN	Galectin-3-binding protein precursor (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (Mac-2 BP) (MAC2BP) (Tumor-associated antigen 90K) - Homo sapiens (Human)
436	2.0	9.1	Q08380 LG3BP_HUMAN	Galectin-3-binding protein precursor (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (Mac-2 BP) (MAC2BP) (Tumor-associated antigen 90K) - Homo sapiens (Human)
249	2.2	8.2	Q12906 ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Double-stranded RNA-binding protein 76) (DRBP76) (Translational control protein 80) (TCP80) (Nuclear factor associated with dsRNA) (NFAR) (M-phase phosphoprotein 4) (MPP4) - Homo sapiens (Human)
60	16.5	21.9	Q12906 ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Double-stranded RNA-binding protein 76) (DRBP76) (Translational control protein 80) (TCP80) (Nuclear factor associated with dsRNA) (NFAR) (M-phase phosphoprotein 4) (MPP4) - Homo sapiens (Human)
172	2.0	10.0	Q13093 PAFA_HUMAN	Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47) (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase) - Homo sapiens (Human)
529	2.0	3.6	Q13093 PAFA_HUMAN	Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47) (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase) - Homo sapiens (Human)
346	2.0	8.2	Q13151 ROAO_HUMAN	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0) - Homo sapiens (Human)
591	1.4	24.3	Q13151 ROAO_HUMAN	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0) - Homo sapiens (Human)
212	3.2	37.3	Q14019 COTL1_HUMAN	Coactosin-like protein - Homo sapiens (Human)
126	9.3	50.7	Q14019 COTL1_HUMAN	Coactosin-like protein - Homo sapiens (Human)
157	4.0	11.0	Q14103 HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human)
85	12.2	35.2	Q14103 HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human)
404	1.3	16.4	Q14152 IF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (eIF3 p167) (eIF3 p180) (eIF3 p185) (eIF3a) - Homo sapiens (Human)
137	8.2	16.1	Q14152 IF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (eIF3 p167) (eIF3 p180) (eIF3 p185) (eIF3a) - Homo sapiens (Human)
145	5.1	15.8	Q14764 MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human)
122	9.5	13.9	Q14764 MVP_HUMAN	Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human)
124	6.0	33.7	Q14847 LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human)
72	14.1	37.9	Q14847 LASP1_HUMAN	LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human)
232	2.6	21.4	Q15233 NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrnb)) (p54nrnb) (55 kDa nuclear protein) (NMT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human)
78	15.9	33.3	Q15233 NONO_HUMAN	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrnb)) (p54nrnb) (55 kDa nuclear protein) (NMT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human)
206	3.5	10.3	Q16181 SEPT7_HUMAN	Septin-7 (CDC10 protein homolog) - Homo sapiens (Human)
406	2.3	9.8	Q16181 SEPT7_HUMAN	Septin-7 (CDC10 protein homolog) - Homo sapiens (Human)
286	2.0	9.8	Q16555 DYPY2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human)
336	3.5	5.9	Q16555 DYPY2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human)
344	2.0	4.7	Q16558 FSCN1_HUMAN	Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human)
383	2.5	11.2	Q16558 FSCN1_HUMAN	Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human)
343	2.0	4.6	Q16881 TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic precursor (EC 1.8.1.9) (TR) (TR1) - Homo sapiens (Human)
392	2.4	9.2	Q16881 TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic precursor (EC 1.8.1.9) (TR) (TR1) - Homo sapiens (Human)
129	4.0	39.2	Q6F113 H2A2A_HUMAN	Histone H2A type 2-A (H2A.2) - Homo sapiens (Human)
111	3.1	52.3	Q6F113 H2A2A_HUMAN	Histone H2A type 2-A (H2A.2) - Homo sapiens (Human)
112	6.9	37.5	Q71D13 H32_HUMAN	Histone H3.2 (H3/m) (H3/o) - Homo sapiens (Human)
139	2.1	19.1	Q71D13 H32_HUMAN	Histone H3.2 (H3/m) (H3/o) - Homo sapiens (Human)
154	7.9	41.2	Q71D13 H32_HUMAN	Histone H3.2 (H3/m) (H3/o) - Homo sapiens (Human)
319	2.0	9.9	Q86UX7 URP2_HUMAN	Unc-112-related protein 2 (Kindlin-3) (MIG2-like) - Homo sapiens (Human)
409	2.2	12.7	Q86UX7 URP2_HUMAN	Unc-112-related protein 2 (Kindlin-3) (MIG2-like) - Homo sapiens (Human)
260	2.2	16.7	Q8NHJ6 LIRB4_HUMAN	Leukocyte immunoglobulin-like receptor subfamily B member 4 precursor (Leukocyte immunoglobulin-like receptor 5) (LIR-5) (Immunoglobulin-like transcript 3) (ILT-3) (Monocyte inhibitory receptor HM18) (CD85k antigen) - Homo sapiens (Human)
191	1.9	5.1	Q8NHJ6 LIRB4_HUMAN	Leukocyte immunoglobulin-like receptor subfamily B member 4 precursor (Leukocyte immunoglobulin-like receptor 5) (LIR-5) (Immunoglobulin-like transcript 3) (ILT-3) (Monocyte inhibitory receptor HM18) (CD85k antigen) - Homo sapiens (Human)
327	3.7	7.1	Q8NHJ6 LIRB4_HUMAN	Leukocyte immunoglobulin-like receptor subfamily B member 4 precursor (Leukocyte immunoglobulin-like receptor 5) (LIR-5) (Immunoglobulin-like transcript 3) (ILT-3) (Monocyte inhibitory receptor HM18) (CD85k antigen) - Homo sapiens (Human)
315	2.0	9.6	Q92598 HIS105_HUMAN	Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY-CO-25) - Homo sapiens (Human)
194	1.7	10.7	Q92598 HIS105_HUMAN	Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY-CO-25) - Homo sapiens (Human)
290	4.0	6.9	Q92598 HIS105_HUMAN	Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY-CO-25) - Homo sapiens (Human)
274	2.1	14.0	Q96C23 GALM_HUMAN	Aldose 1-epimerase (EC 5.1.3.3) (Galactose mutarotase) - Homo sapiens (Human)
148	8.0	19.3	Q96C23 GALM_HUMAN	Aldose 1-epimerase (EC 5.1.3.3) (Galactose mutarotase) - Homo sapiens (Human)
139	5.7	25.5	Q96CX2 KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftelin) (Predominantly fetal expressed T1 domain) - Homo sapiens (Human)
474	2.0	7.4	Q96CX2 KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pftelin) (Predominantly fetal expressed T1 domain) - Homo sapiens (Human)
395	1.5	7.6	Q96EP5 DAZP1_HUMAN	DAZ-associated protein 1 (Deleted in azoospermia-associated protein 1) - Homo sapiens (Human)
283	4.0	11.3	Q96EP5 DAZP1_HUMAN	DAZ-associated protein 1 (Deleted in azoospermia-associated protein 1) - Homo sapiens (Human)
236	2.5	11.4	Q96IU4 ABHEB_HUMAN	Abhydrolase domain-containing protein 14B (EC 3.-.-.-) (CCG1-interacting factor B) - Homo sapiens (Human)
308	4.0	11.4	Q96IU4 ABHEB_HUMAN	Abhydrolase domain-containing protein 14B (EC 3.-.-.-) (CCG1-interacting factor B) - Homo sapiens (Human)
253	2.2	7.4	Q96KP4 CNDP2_HUMAN	Cytosolic nonspecific dipeptidase (CNDP dipeptidase 2) (Glutamate carboxypeptidase-like protein 1) - Homo sapiens (Human)
347	3.3	8.4	Q96KP4 CNDP2_HUMAN	Cytosolic nonspecific dipeptidase (CNDP dipeptidase 2) (Glutamate carboxypeptidase-like protein 1) - Homo sapiens (Human)
266	2.1	20.1	Q99497 PARK7_HUMAN	Protein DJ-1 (Oncogene DJ1) (Parkinson disease protein 7) - Homo sapiens (Human)
177	2.0	14.8	Q99497 PARK7_HUMAN	Protein DJ-1 (Oncogene DJ1) (Parkinson disease protein 7) - Homo sapiens (Human)
120	9.6	28.6	Q99497 PARK7_HUMAN	Protein DJ-1 (Oncogene DJ1) (Parkinson disease protein 7) - Homo sapiens (Human)
358	2.0	11.4	Q9BRA2 TXNL5_HUMAN	Thioredoxin-like protein 5 (14 kDa thioredoxin-related protein) (TRP14) (Protein 42-9-9) - Homo sapiens (Human)
307	4.0	19.5	Q9BRA2 TXNL5_HUMAN	Thioredoxin-like protein 5 (14 kDa thioredoxin-related protein) (TRP14) (Protein 42-9-9) - Homo sapiens (Human)

340	2.0	49.5	O9H299 SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1) - Homo sapiens (Human)
176	2.0	20.4	O9H299 SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1) - Homo sapiens (Human)
213	6.0	31.2	O9H299 SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1) - Homo sapiens (Human)
118	6.4	26.1	O9NUV9 GIMA4_HUMAN	GPase IMAP family member 4 (Immunity-associated protein 4) (Immunity-associated nucleotide 1 protein) (hIAN1) - Homo sapiens (Human)
213	1.3	23.1	O9NUV9 GIMA4_HUMAN	GPase IMAP family member 4 (Immunity-associated protein 4) (Immunity-associated nucleotide 1 protein) (hIAN1) - Homo sapiens (Human)
105	10.4	24.9	O9NUV9 GIMA4_HUMAN	GPase IMAP family member 4 (Immunity-associated protein 4) (Immunity-associated nucleotide 1 protein) (hIAN1) - Homo sapiens (Human)
171	4.0	11.9	O9NY33 DPP3_HUMAN	Dipeptidyl-peptidase 3 (EC 3.4.14.4) (Dipeptidyl-peptidase III) (DPP III) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) - Homo sapiens (Human)
170	2.0	6.1	O9NY33 DPP3_HUMAN	Dipeptidyl-peptidase 3 (EC 3.4.14.4) (Dipeptidyl-peptidase III) (DPP III) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) - Homo sapiens (Human)
185	6.2	15.7	O9NY33 DPP3_HUMAN	Dipeptidyl-peptidase 3 (EC 3.4.14.4) (Dipeptidyl-peptidase III) (DPP III) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) - Homo sapiens (Human)
330	2.0	11.6	O9NYL9 TMOD3_HUMAN	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod) - Homo sapiens (Human)
305	4.0	7.1	O9NYL9 TMOD3_HUMAN	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod) - Homo sapiens (Human)
211	3.2	10.5	O9P258 RCC2_HUMAN	Protein RCC2 (Telophase disk protein of 60 kDa) (RCC1-like protein TD-60) - Homo sapiens (Human)
273	4.1	8.2	O9P258 RCC2_HUMAN	Protein RCC2 (Telophase disk protein of 60 kDa) (RCC1-like protein TD-60) - Homo sapiens (Human)
113	6.8	38.9	O9UBR2 CATZ_HUMAN	Cathepsin Z precursor (EC 3.4.22.-) (Cathepsin X) (Cathepsin P) - Homo sapiens (Human)
99	3.7	11.6	O9UBR2 CATZ_HUMAN	Cathepsin Z precursor (EC 3.4.22.-) (Cathepsin X) (Cathepsin P) - Homo sapiens (Human)
145	8.0	24.8	O9UBR2 CATZ_HUMAN	Cathepsin Z precursor (EC 3.4.22.-) (Cathepsin X) (Cathepsin P) - Homo sapiens (Human)
223	3.0	17.0	O9UJU6 DBNL_HUMAN	Drebrin-like protein (SH3 domain-containing protein 7) (Drebrin-F) (Cervical SH3P7) (HPK1-interacting protein of 55 kDa) (HIP-55) (Cervical mucin-associated protein) - Homo sapiens (Human)
248	4.7	22.6	O9UJU6 DBNL_HUMAN	Drebrin-like protein (SH3 domain-containing protein 7) (Drebrin-F) (Cervical SH3P7) (HPK1-interacting protein of 55 kDa) (HIP-55) (Cervical mucin-associated protein) - Homo sapiens (Human)
95	8.1	26.4	O9UL46 PSME2_HUMAN	Proteasome activator complex subunit 2 (Proteasome activator 28-subunit beta) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex subunit beta) (REG-beta) - Homo sapiens (Human)
163	2.0	16.3	O9UL46 PSME2_HUMAN	Proteasome activator complex subunit 2 (Proteasome activator 28-subunit beta) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex subunit beta) (REG-beta) - Homo sapiens (Human)
182	6.2	26.4	O9UL46 PSME2_HUMAN	Proteasome activator complex subunit 2 (Proteasome activator 28-subunit beta) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex subunit beta) (REG-beta) - Homo sapiens (Human)
198	4.0	14.6	O9ULV4 COR1C_HUMAN	Coronin-1C (Coronin-3) (hCRNN4) - Homo sapiens (Human)
200	1.8	17.3	O9ULV4 COR1C_HUMAN	Coronin-1C (Coronin-3) (hCRNN4) - Homo sapiens (Human)
223	6.0	18.1	O9ULV4 COR1C_HUMAN	Coronin-1C (Coronin-3) (hCRNN4) - Homo sapiens (Human)
288	2.0	6.3	O9UQ80 PA2G4_HUMAN	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (ErbB3-binding protein 1) - Homo sapiens (Human)
174	6.5	18.8	O9UQ80 PA2G4_HUMAN	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (ErbB3-binding protein 1) - Homo sapiens (Human)
75	9.8	7.6	O9Y490 TLN1_HUMAN	Talin-1 - Homo sapiens (Human)
67	14.8	8.8	O9Y490 TLN1_HUMAN	Talin-1 - Homo sapiens (Human)
328	2	27.0	O9Y5S9 RBM8A_HUMAN	RNA-binding protein 8A (RNA-binding motif protein 8A) (Ribonucleoprotein RBM8A) (RNA-binding protein Y14) (Binder of OVCA1-1) (BOV-1) - Homo sapiens (Human)
485	2	18.4	O9Y5S9 RBM8A_HUMAN	RNA-binding protein 8A (RNA-binding motif protein 8A) (Ribonucleoprotein RBM8A) (RNA-binding protein Y14) (Binder of OVCA1-1) (BOV-1) - Homo sapiens (Human)

ONLINE TABLE II

PEPTIDES IDENTIFIED IN THE CONDITIONED MEDIUM OF CFUs (n=3)

N	Unused	Total	% Cov	Contrib	Conf	Sequence	Prec MW	Prec m/z	Theor MW	Theor m/z
000299 CLIC1_HUMAN										
Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (Chloride channel ABP) (Regulatory nuclear chloride ion channe										
123.0	9.5	9.5	31.1	2.0	99.0	AEEQPOVELFVK	1457.7	1458.8	1457.7	1458.7
123.0	9.5	9.5	31.1	2.0	99.0	EFASTCPDDEEIELAVEGVAK	2572.1	2573.1	2573.1	2573.1
123.0	9.5	9.5	31.1	2.0	99.0	LAALNPESNTAGLDIFAK	1844.0	1845.0	1844.0	1845.0
123.0	9.5	9.5	31.1	1.4	96.0	GFTIPEAFR	1036.5	1037.5	1036.5	1037.5
123.0	9.5	9.5	31.1	1.2	94.0	YLSNAYAR	956.5	957.5	956.5	957.5
123.0	9.5	9.5	31.1	0.9	86.0	YRGTIPEAFR	1355.7	1356.7	1355.7	1356.7
69.0	4.9	4.9	30.3	2.0	99.0	LAALNPESNTAGLDIFAK	1844.0	1845.0	1844.0	1845.0
69.0	4.9	4.9	30.3	1.7	98.0	YRGTIPEAFR	1355.7	1356.7	1355.7	1356.7
69.0	4.9	4.9	30.3	1.2	93.0	GFTIPEAFR	1036.5	1037.5	1036.5	1037.5
108.0	7.3	8.2	20.7	2.0	99.0	EEQPOVELFVK	1328.7	1329.7	1328.7	1329.7
108.0	7.3	8.2	20.7	2.0	99.0	GFTIPEAFR	1036.5	1037.5	1036.5	1037.5
108.0	7.3	8.2	20.7	1.7	98.0	YRGTIPEAFR	1355.7	1356.7	1355.7	1356.7
108.0	7.3	8.2	20.7	1.2	93.0	IGNCPFSOR	1077.5	1078.5	1077.5	1078.5
108.0	7.3	8.2	20.7	0.5	65.0	YLSNAYAR	956.5	957.5	956.5	957.5
108.0	7.3	8.2	20.7	0.0	86.0	FSAYIK	727.4	728.4	727.4	728.4
000391 QSCN6_HUMAN										
Sulfhydryl oxidase 1 precursor (EC 1.8.3.2) (Quiescin Q6) (hSOX) - Homo sapiens (Human)										
201.0	6.0	6.0	12.2	2.0	99.0	LAGAPSEDPQPK	1355.7	1356.7	1355.7	1356.7
201.0	6.0	6.0	12.2	2.0	99.0	NNEEYLALIFEK	1481.8	1482.8	1481.7	1482.7
201.0	6.0	6.0	12.2	2.0	99.0	SFYTAYLR	1147.6	1148.6	1147.6	1148.6
160.0	2.0	2.0	11.1	2.0	99.0	NNEEYLALIFEK	1481.8	1482.8	1481.7	1482.7
000479 HMGN4_HUMAN										
High-mobility group nucleosome-binding domain-containing protein 4 (Nonhistone chromosomal protein HMG-17-like 3) (Non-histone chromosom										
285.0	4.0	4.0	44.4	2.0	99.0	LSAKPAPPKPEPR	1386.8	1387.8	1386.8	1387.8
285.0	4.0	4.0	44.4	2.0	99.0	LSAKPAPPKPEPRPK	1611.9	1613.0	1611.9	1613.0
338.0	2.0	2.0	51.1	2.0	98.0	LSAKPAPPKPEPRPK	1611.9	1613.0	1611.9	1613.0
014773 TPP1_HUMAN										
Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase 1) (TPP-1) (TPP-1) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insen										
490.0	2.0	2.0	4.6	2.0	99.0	LYQQHAGLFDVTR	1603.8	1604.8	1603.8	1604.8
138.0	2.1	2.1	14.9	2.0	99.0	LFGGNFAHQASVAR	1473.7	1474.7	1473.7	1474.8
138.0	2.1	2.1	14.9	0.1	26.0	LYQQHAGLFDVTR	1603.8	1604.8	1603.8	1604.8
189.0	4.0	4.0	5.0	2.0	99.0	LFGGNFAHQASVAR	1473.7	1474.8	1473.7	1474.8
189.0	4.0	4.0	5.0	2.0	99.0	LYQQHAGLFDVTR	1603.8	1604.8	1603.8	1604.8
014818 PSA7_HUMAN										
Proteasome subunit alpha type 7 (EC 3.4.25.1) (Proteasome subunit RC6-1) (Proteasome subunit XAPC7) - Homo sapiens (Human)										
177.0	6.5	6.5	17.3	2.0	99.0	KICALDDNVCMAFAGLTADAR	2311.1	2312.1	2311.1	2312.1
177.0	6.5	6.5	17.3	2.0	99.0	LYQTDPSGYHAWK	1665.8	1666.8	1665.8	1666.8
177.0	6.5	6.5	17.3	2.0	99.0	YIASLKOR	977.6	978.6	977.6	978.6
177.0	6.5	6.5	17.3	0.5	67.0	KICALDDNVCMAFAGLTADAR	2183.0	2184.0	2183.0	2184.0
202.0	3.7	3.7	11.7	2.0	99.0	KICALDDNVCMAFAGLTADAR	2311.1	2312.1	2311.1	2312.1
202.0	3.7	3.7	11.7	1.7	98.0	YIASLKOR	977.6	978.6	977.6	978.6
014979 HNRDL_HUMAN										
Heterogeneous nuclear ribonucleoprotein D-like (hnRPD-like protein) (hnHNRP-DL) (JKT41-binding protein) (AU-rich element RNA-binding factor)										
452.0	2.0	6.0	9.8	2.0	99.0	RGFCFTYDDEEVK	1989.0	1990.0	1989.0	1990.0
452.0	2.0	6.0	9.8	0.0	99.0	GFGVLFK	913.5	914.5	913.5	914.5
452.0	2.0	6.0	9.8	0.0	99.0	SRGFGVLFK	1156.6	1157.6	1156.6	1157.6
87.0	4.0	4.0	18.8	2.0	99.0	GFGVLFK	913.5	914.5	913.5	914.5
87.0	4.0	4.0	18.8	2.0	99.0	PSAPATLASR	1044.6	1045.6	1044.5	1045.5
278.0	2.1	2.1	19.5	2.0	99.0	GFGVLFK	913.5	914.5	913.5	914.5
015143 ARCB1_HUMAN										
Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC) - Homo sapiens (Human)										
152.0	8.0	8.0	17.7	2.0	99.0	CSQFCTTGMGGMSIWDVK	2164.9	2165.9	2164.9	2165.9
152.0	8.0	8.0	17.7	2.0	99.0	TWKPTLVLR	1225.8	1226.8	1225.8	1226.8
152.0	8.0	8.0	17.7	2.0	99.0	VHEIKHNGVGTGIDWAPESNR	2517.2	2518.2	2517.2	2518.2
152.0	8.0	8.0	17.7	2.0	99.0	WAPNENKFAVGSGR	1618.8	1619.8	1618.8	1619.8
152.0	8.0	8.0	17.7	0.0	99.0	CSQFCTTGMGGMSIWDVK	2179.9	2179.9	2179.9	2179.9
152.0	8.0	8.0	17.7	0.0	99.0	CSQFCTTGMGGMSIWDVK	2163.9	2163.9	2163.9	2163.9
128.0	2.3	2.3	24.7	2.0	99.0	CSQFCTTGMGGMSIWDVK	2161.9	2162.9	2161.9	2162.9
128.0	2.3	2.3	24.7	0.3	48.0	TWKPTLVLR	1225.8	1226.8	1225.8	1226.8
128.0	2.3	2.3	24.7	0.0	99.0	CSQFCTTGMGGMSIWDVK	2179.9	2179.9	2179.9	2179.9
85.0	8.9	8.9	22.3	2.0	99.0	AYHSFLVEPISSHAWNKDR	2371.1	2372.1	2371.1	2372.1
85.0	8.9	8.9	22.3	2.0	99.0	CSQFCTTGMGGMSIWDVK	2161.9	2162.9	2161.9	2162.9
85.0	8.9	8.9	22.3	2.0	99.0	EVEERPAPTPWGSK	1581.8	1582.8	1581.8	1582.8
85.0	8.9	8.9	22.3	2.0	99.0	WAPNENKFAVGSGR	1618.8	1619.8	1618.8	1619.8
85.0	8.9	8.9	22.3	0.9	86.0	FSAYIK	727.4	728.4	727.4	728.4
015144 ARPC2_HUMAN										
Actin-related protein 2/3 complex subunit 2 (ARP2/3 complex 34 kDa subunit) (p34-ARC) - Bos taurus (Bovine) ; Actin-related protein 2/3 comple										
172.0	6.7	6.7	20.7	2.0	99.0	DNTINLIHTFR	1342.7	1343.7	1342.7	1343.7
172.0	6.7	6.7	20.7	2.0	99.0	VFMQEFKEGR	1269.6	1270.6	1269.6	1270.6
172.0	6.7	6.7	20.7	2.0	99.0	YFQFQEEGKEGSR	1759.8	1760.8	1759.8	1760.8
172.0	6.7	6.7	20.7	0.7	79.0	MILLEVNRR	1100.6	1101.6	1100.6	1101.6
196.0	1.7	1.7	21.0	1.2	93.0	DNTINLIHTFR	1342.7	1343.7	1342.7	1343.7
196.0	1.7	1.7	21.0	0.5	71.0	YFQFQEEGKEGSR	1757.8	1758.8	1757.8	1760.8
151.0	4.7	4.7	11.7	2.0	99.0	DSIVHQAGMLKR	1353.7	1354.7	1353.7	1354.7
151.0	4.7	4.7	11.7	2.0	99.0	VFMQEFKEGR	1269.6	1270.6	1269.6	1270.6
151.0	4.7	4.7	11.7	0.7	79.0	VFMQEFK	927.5	928.5	927.5	928.5
015145 ARPC3_HUMAN										
Actin-related protein 2/3 complex subunit 3 (ARP2/3 complex 21 kDa subunit) (p21-ARC) - Bos taurus (Bovine) ; Actin-related protein 2/3 comple										
238.0	5.1	5.1	21.9	2.0	99.0	LIGNMALLPIR	1209.7	1210.7	1209.7	1210.7
238.0	5.1	5.1	21.9	1.7	98.0	AYLQQLR	890.5	891.5	890.5	891.5
238.0	5.1	5.1	21.9	1.4	96.0	SOFGPAPR	986.5	987.5	986.5	987.5
247.0	2.3	2.3	15.2	2.0	99.0	LIGNMALLPIR	1209.7	1210.7	1209.7	1210.7
247.0	2.3	2.3	15.2	0.3	47.0	AYLQQLR	890.5	891.5	890.5	891.5
247.0	2.3	2.3	15.2	0.0	31.0	AYLQQLR	890.5	891.5	890.5	891.5
015204 ADEC1_HUMAN										
ADAM DEC1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain-like protein decysin 1) (ADAM-like protein decysin 1) - Homo sap										
264.0	4.3	4.3	10.4	2.0	99.0	HLLGPDYETLYSPR	1760.9	1761.9	1760.9	1761.9
264.0	4.3	4.3	10.4	2.0	99.0	LKPGTDCGGDAPNHTE	1768.8	1769.8	1768.8	1769.8
264.0	4.3	4.3	10.4	0.3	44.0	GYFTHHHR	1181.5	1182.5	1181.5	1182.6
81.0	4.2	4.2	7.7	2.0	99.0	ECTNLCEALTCK	1657.7	1658.7	1657.7	1658.7
81.0	4.2	4.2	7.7	2.0	99.0	HLLGPDYETLYSPR	1760.9	1761.9	1760.9	1761.9
81.0	4.2	4.2	7.7	0.2	39.0	YLLSQKPK	975.6	976.6	975.6	976.6
216.0	3.2	3.2	8.5	2.0	99.0	LKPGTDCGGDAPNHTE	1768.8	1769.8	1768.8	1769.8
216.0	3.2	3.2	8.5	1.2	93.0	GYFTHHHR	1181.6	1182.6	1181.5	1182.6
043390 HNRPR_HUMAN										
Heterogeneous nuclear ribonucleoprotein R (hnRNP R) - Homo sapiens (Human)										
267.0	4.2	4.2	20.7	2.0	99.0	DLYEDELVPEK	1608.8	1609.8	1608.8	1609.8
267.0	4.2	4.2	20.7	2.0	99.0	LKDYAFVHFEDR	1538.8	1539.8	1538.8	1539.8
267.0	4.2	4.2	20.7	0.1	26.0	STAYEDYYHPPPR	1757.8	1758.8	1757.8	1758.8
166.0	4.3	4.3	14.5	2.0	99.0	LKDYAFVHFEDR	1538.8	1539.8	1538.8	1539.8
166.0	4.3	4.3	14.5	1.5	97.0	RGRAGYSOR	1130.5	1131.5	1130.5	1131.5
166.0	4.3	4.3	14.5	0.8	84.0	DLYEDELVPEK	1608.8	1609.8	1608.8	1609.8
043707 ACTN4_HUMAN										
Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross-linking protein) - Homo sapiens (Human)										
10.0	41.3	41.3	35.2	2.0	99.0	ASFNHFDDKHGGALGPEEFK	2199.0	2200.0	2202.0	2203.0
10.0	41.3	41.3	35.2	2.0	99.0	CQLEINFITLTK	1590.8	1591.8	1590.8	1591.8
10.0	41.3	41.3	35.2	2.0	99.0	DGLAFNALIHR	1225.6	1226.6	1225.7	1226.7
10.0	41.3	41.3	35.2	2.0	99.0	EGLLWVQK	1373.6	1374.6	1373.6	1374.6
10.0	41.3	41.3	35.2	2.0	99.0	GISEQMGQEFR	1351.6	1352.6	1351.6	1352.6
10.0	41.3	41.3	35.2	2.0	99.0	ICDOWDALGSLTHSR	1757.8	1758.8	1757.8	1758.8
10.0	41.3	41.3	35.2</							

10.0	41.3	41.3	35.2	1.0	89.0	HTNYTMEHIR	1300.6	1301.6	1300.6	1301.6
10.0	41.3	41.3	35.2	0.2	30.0	DAKGISEQEQOEFR	1665.8	1666.8	1665.8	1666.8
10.0	41.3	41.3	35.2	0.0	99.0	LEDFRDYRR	1268.6	1269.6	1268.6	1269.6
44.0	6.9	6.9	13.9	2.0	99.0	ELPPDOAEYCIAR	1560.7	1561.7	1560.7	1561.7
44.0	6.9	6.9	13.9	2.0	99.0	VGWEQLLTTIAR	1385.7	1386.8	1385.8	1386.8
44.0	6.9	6.9	13.9	1.7	99.0	LEDFRDYRR	1432.5	1433.5	1432.5	1433.5
44.0	6.9	6.9	13.9	0.9	88.0	LSNRPFAMPSSEK	1432.7	1433.7	1432.7	1433.7
44.0	6.9	6.9	13.9	0.3	44.0	LEDFRDYRR	1268.6	1269.6	1268.6	1269.6
44.0	6.9	6.9	13.9	0.0	84.0	ELPPDOAEYCIAR	1557.7	1558.7	1560.7	1561.7
44.0	6.9	6.9	13.9	0.0	95.0	LEDFRDYRR	1112.5	1113.6	1112.5	1113.5
22.0	22.9	22.9	32.3	2.0	99.0	ASFNFHFKDHGGALGPEEFK	2202.0	2203.0	2202.0	2203.0
22.0	22.9	22.9	32.3	2.0	99.0	EGLLLLWGOR	1173.6	1174.6	1173.6	1174.6
22.0	22.9	22.9	32.3	2.0	99.0	ELPPDOAEYCIAR	1560.7	1561.7	1560.7	1561.7
22.0	22.9	22.9	32.3	2.0	99.0	GISEQEQOEFR	1351.6	1352.6	1351.6	1352.6
22.0	22.9	22.9	32.3	2.0	99.0	HTNYTMEHIR	1300.6	1301.6	1300.6	1301.6
22.0	22.9	22.9	32.3	2.0	99.0	KTFATWCNSHLR	1519.7	1520.7	1519.7	1520.7
22.0	22.9	22.9	32.3	2.0	99.0	LEDFRDYRR	1112.5	1113.5	1112.5	1113.5
22.0	22.9	22.9	32.3	2.0	99.0	LSNRPFAMPSSEK	1432.7	1433.7	1432.7	1433.7
22.0	22.9	22.9	32.3	2.0	99.0	TINEVENQLTR	1428.8	1429.8	1428.8	1429.8
22.0	22.9	22.9	32.3	2.0	99.0	VLAGDKNFITAEELRR	1831.0	1832.0	1831.0	1832.0
22.0	22.9	22.9	32.3	1.7	98.0	LEDFRDYRR	1268.6	1269.6	1268.6	1269.6
22.0	22.9	22.9	32.3	0.8	85.0	KHEAFESDLAAHQDR	1752.8	1753.8	1752.8	1753.8
22.0	22.9	22.9	32.3	0.4	56.0	EALAIKAEQAR	1377.8	1378.8	1377.8	1378.8
22.0	22.9	22.9	32.3	0.0	99.0	ASFNFHFKDHGGALGPEEFK	2203.0	2204.0	2203.0	2204.0
22.0	22.9	22.9	32.3	0.0	20.0	ASFNFHFKDHGGALGPEEFK	2199.0	2200.0	2202.0	2203.0
22.0	22.9	22.9	32.3	0.0	97.0	LEDFRDYRR	1268.6	1269.6	1268.6	1269.6
O43776 SYNC_HUMAN Asparaginyl-tRNA synthetase, cytoplasmic (EC 6.1.1.22) (Asparagine--tRNA ligase) (AsnRS) - Homo sapiens (Human)										
212.0	6.0	6.0	9.3	2.0	99.0	EGIDPTPYWYTDOR	1902.8	1903.8	1902.8	1903.8
212.0	6.0	6.0	9.3	2.0	99.0	IFDSEELAGYKRR	1539.8	1540.8	1539.8	1540.8
212.0	6.0	6.0	9.3	2.0	99.0	NLMFLVLR	1004.6	1005.6	1004.6	1005.6
255.0	2.0	2.0	6.4	2.0	99.0	NLMFLVLR	1004.6	1005.6	1004.6	1005.6
O75083 WDR1_HUMAN WD repeat protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1) - Homo sapiens (Human)										
108.0	10.0	10.0	16.5	2.0	99.0	IKDIAWTEDESKR	1460.8	1461.8	1460.8	1461.8
108.0	10.0	10.0	16.5	2.0	99.0	MTVDESGLQISCSMDTVR	2142.9	2144.0	2142.9	2143.9
108.0	10.0	10.0	16.5	2.0	99.0	VFASLPQVER	1144.6	1145.6	1144.6	1145.6
108.0	10.0	10.0	16.5	2.0	99.0	YAPSGFYASGDVSGKLR	1887.0	1888.0	1887.0	1888.0
108.0	10.0	10.0	16.5	2.0	99.0	YEYOPFAGK	1101.5	1102.5	1101.5	1102.5
111.0	6.9	6.9	14.4	2.0	99.0	IKDIAWTEDESKR	1460.8	1461.8	1460.8	1461.8
111.0	6.9	6.9	14.4	2.0	99.0	YEYOPFAGK	1101.5	1102.5	1101.5	1102.5
111.0	6.9	6.9	14.4	1.3	95.0	VFASLPQVER	1144.6	1145.6	1144.6	1145.6
111.0	6.9	6.9	14.4	0.9	88.0	FTIGDHSR	931.5	932.5	931.5	932.5
111.0	6.9	6.9	14.4	0.5	65.0	LATGSDDNACAAFFEGPPFKFK	2318.1	2319.1	2318.1	2319.1
111.0	6.9	6.9	14.4	0.2	33.0	YAPSGFYASGDVSGKLR	1887.0	1888.0	1887.0	1888.0
O75368 SH3L1_HUMAN SH3 domain-binding glutamic acid-rich-like protein - Homo sapiens (Human)										
320.0	4.0	4.0	24.6	2.0	99.0	ENNAVVFGLTAPGSK	1847.9	1849.0	1847.9	1848.9
320.0	4.0	4.0	24.6	2.0	99.0	GDYDAFFEAR	1189.5	1190.6	1189.5	1190.5
373.0	2.0	2.0	8.8	2.0	99.0	GDYDAFFEAR	1189.5	1190.5	1189.5	1190.5
O75791 GRAP2_HUMAN GRB2-related adapter protein 2 (GADS protein) (Growth factor receptor-binding protein) (GRBLG) (Grf40 adapter protein) (Grf-40) (GRB-2-like pr										
553.0	2.0	2.0	3.3	2.0	99.0	YLOHHHFHOER	1530.7	1531.7	1530.7	1531.7
384.0	1.7	1.7	11.2	1.7	98.0	YLOHHHFHOER	1530.7	1531.7	1530.7	1531.7
P00338 LDHA_HUMAN L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH muscle subunit) (LDH-M) (Proliferation-inducing gene 19 protein) (Renal carcinoma										
129.0	9.1	11.3	30.4	2.0	99.0	GEMMDLHSGLSFLR	1632.8	1633.8	1632.8	1633.8
129.0	9.1	11.3	30.4	2.0	99.0	KSADTLWGQKELQF	1762.9	1763.9	1762.9	1763.9
129.0	9.1	11.3	30.4	2.0	99.0	SADTLWGQKELQF	1634.8	1635.8	1634.8	1635.8
129.0	9.1	11.3	30.4	1.5	99.0	SADTLWGQK	1117.6	1118.6	1117.6	1118.6
129.0	9.1	11.3	30.4	1.2	99.0	DLADELALVDVIEDK	1656.8	1657.8	1656.8	1657.9
129.0	9.1	11.3	30.4	0.2	43.0	RHPVSTMIK	1166.7	1167.7	1166.7	1167.7
129.0	9.1	11.3	30.4	0.1	25.0	FRYLMGER	1070.5	1071.5	1070.5	1071.5
129.0	9.1	11.3	30.4	0.0	26.0	QOEGESRLNLVOR	1555.8	1556.8	1555.8	1556.8
129.0	9.1	11.3	30.4	0.0	83.0	VIGSGCNLSAR	1247.6	1248.6	1247.6	1248.6
156.0	2.0	4.0	11.1	2.0	99.0	SADTLWGQKELQF	1634.8	1635.9	1634.8	1635.8
156.0	2.0	4.0	11.1	0.0	99.0	SADTLWGQK	1117.6	1118.6	1117.6	1118.6
P00491 PNPH_HUMAN Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine phosphorylase) (PNP) - Homo sapiens (Human)										
166.0	7.0	7.0	32.9	2.0	99.0	FGDRFPAMSDAYDR	1646.7	1647.7	1646.7	1647.7
166.0	7.0	7.0	32.9	2.0	99.0	FHMVEGYPLWK	1467.7	1470.7	1467.7	1470.7
166.0	7.0	7.0	32.9	2.0	99.0	LGADAVGMISTVPEVIVAR	1784.0	1785.0	1784.0	1785.0
166.0	7.0	7.0	32.9	1.0	89.0	FEVGDMLLR	1192.6	1192.6	1192.6	1192.6
141.0	5.7	5.7	29.1	2.0	99.0	FEVGDMLLR	1191.6	1192.6	1191.6	1192.6
141.0	5.7	5.7	29.1	2.0	99.0	FHMVEGYPLWK	1467.7	1470.7	1467.7	1470.7
141.0	5.7	5.7	29.1	1.7	98.0	FGDRFPAMSDAYDR	1646.7	1647.7	1646.7	1647.7
P00558 PGK1_HUMAN Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2) (Cell migration-inducing gene 10 protein) - Homo sapiens (Human)										
22.0	28.0	28.0	53.0	2.0	99.0	ACANPAAGSVILLENLR	1767.9	1768.9	1767.9	1768.9
22.0	28.0	28.0	53.0	2.0	99.0	AEPAKIEAFR	1130.6	1131.6	1130.6	1131.6
22.0	28.0	28.0	53.0	2.0	99.0	AHSSMVGYNLPQK	1366.7	1367.7	1366.7	1367.7
22.0	28.0	28.0	53.0	2.0	99.0	ELNYFAK	883.4	884.5	883.4	884.5
22.0	28.0	28.0	53.0	2.0	99.0	FHVVEEGKGDASGNKVK	1958.0	1959.0	1958.0	1959.0
22.0	28.0	28.0	53.0	2.0	99.0	GCITIGGGDTATCCAK	1753.8	1754.8	1753.8	1754.8
22.0	28.0	28.0	53.0	2.0	99.0	ITLPVDFVTADKFDENAK	2022.0	2023.0	2022.0	2023.0
22.0	28.0	28.0	53.0	2.0	99.0	LGDVYVNDAFGTADR	1633.8	1634.8	1633.8	1634.8
22.0	28.0	28.0	53.0	2.0	99.0	TGOATVASSGIPAGWMLDCGPESK	2476.1	2477.1	2476.1	2477.1
22.0	28.0	28.0	53.0	2.0	99.0	TGOATVASSGIPAGWMLDCGPESKSK	2605.2	2606.2	2605.2	2606.2
22.0	28.0	28.0	53.0	2.0	99.0	VDFNVPKMNQITNNQR	2031.0	2032.0	2031.0	2032.0
22.0	28.0	28.0	53.0	2.0	99.0	VKAEPAKIEAFR	1357.8	1358.8	1357.8	1358.8
22.0	28.0	28.0	53.0	2.0	99.0	VLNMMIEGTSLFDEEGAK	1965.9	1966.9	1965.9	1966.9
22.0	28.0	28.0	53.0	2.0	99.0	WNTEDKSHVSTGGGASLELLEK	2513.2	2514.2	2513.2	2514.2
22.0	28.0	28.0	53.0	0.0	99.0	AEPAKIEAFR	1130.6	1131.6	1130.6	1131.6
22.0	28.0	28.0	53.0	0.0	99.0	AHSSMVGYNLPQK	1366.7	1367.7	1366.7	1367.7
22.0	28.0	28.0	53.0	0.0	99.0	LGDVYVNDAFGTADR	1634.8	1635.8	1634.8	1635.8
76.0	4.6	4.6	30.5	2.0	99.0	ITLPVDFVTADKFDENAK	2022.0	2023.0	2022.0	2023.0
76.0	4.6	4.6	30.5	2.0	99.0	LGDVYVNDAFGTADR	1633.8	1634.8	1633.8	1634.8
76.0	4.6	4.6	30.5	0.3	53.0	VDFNVPKMNQITNNQR	2031.0	2032.0	2031.0	2032.0
76.0	4.6	4.6	30.5	0.2	39.0	VLNMMIEGTSLFDEEGAK	1965.9	1966.9	1965.9	1966.9
30.0	20.8	20.8	45.6	2.0	99.0	ACANPAAGSVILLENLR	1919.9	1920.9	1919.9	1920.9
30.0	20.8	20.8	45.6	2.0	99.0	AEPAKIEAFR	1130.6	1131.6	1130.6	1131.6
30.0	20.8	20.8	45.6	2.0	99.0	AHSSMVGYNLPQK	1366.7	1367.7	1366.7	1367.7
30.0	20.8	20.8	45.6	2.0	99.0	ALESPEPFLAILGGAK	1768.0	1769.0	1768.0	1769.0
30.0	20.8	20.8	45.6	2.0	99.0	FHVVEEGKGDASGNKVK	1958.0	1959.0	1958.0	1959.0
30.0	20.8	20.8	45.6	2.0	99.0	GCITIGGGDTATCCAK	1753.8	1754.8	1753.8	1754.8
30.0	20.8	20.8	45.6	2.0	99.0	ITLPVDFVTADKFDENAK	2022.0	2023.0	2022.0	2023.0
30.0	20.8	20.8	45.6	2.0	99.0	LGDVYVNDAFGTADR	1633.8	1634.8	1633.8	1634.8
30.0	20.8	20.8	45.6	2.0	99.0	SLLGKDLVFLKDCVGPVEEK	2245.2	2246.2	2245.2	2246.2
30.0	20.8	20.8	45.6	2.0	99.0	VDFNVPKMNQITNNQR	2031.0	2032.0	2031.0	2032.0
30.0	20.8	20.8	45.6	0.7	78.0	ELNYFAK	883.5	884.5	883.5	884.5
30.0	20.8	20.8	45.6	0.0	93.0	ACANPAAGSVILLENLR	1767.9	1768.9	1767.9	1768.9
30.0	20.8	20.8	45.6	0.0	99.0	LGDVYVNDAFGTADR	1634.8	1635.8	1634.8	1635.8
30.0	20.8	20.8	45.6	0.0	99.0	VDFNVPKMNQITNNQR	2031.0	2032.0	2031.0	2032.0
P01023 AZMG_HUMAN Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Human)										
65.0	15.3	15.3	11.9	2.0	99.0	AIGVNTGYOR	1310.7	1311.7	1310.7	1311.7
65.0	15.3	15.3	11.9	2.0	99.0	MVSGFILPKPTVK	1415.8	1416.8	1415.8	1416.8
65.0	15.3	15.3	11.9	2.0	99.0	NALFCLESAAWK	1323.6	1324.6	1323.6	1324.6
65.0	15.3	15.3	11.9	2.0	99.0	SGGRTEHPFTVEEFVLPK	2001.0	2002.0	2001.0	2002.0
65.0	15.3	15.3	11.9	2.0	99.0	VTAAPQSCALR	1301.7	1302.7	1301.7	1302.

16.0	16.5	16.5	18.1	0.6	73.0	YGAATFTR	1013.5	1014.5	1013.5	1014.5
16.0	16.5	16.5	18.1	0.4	60.0	ALLAYAFALAGNQDK	1606.8	1606.9	1606.9	1607.9
16.0	16.5	16.5	18.1	0.2	30.0	NOGNTWLTAFVLK	1635.7	1636.7	1635.7	1636.7
16.0	16.5	16.5	18.1	0.0	30.0	NALFCLESAWK	1475.6	1476.6	1475.6	1476.6
16.0	16.5	16.5	18.1	0.0	25.0	QTVSWAVTPK	1115.6	1116.6	1115.6	1116.6
18.0	26.1	26.1	17.1	2.0	99.0	AIGYLNLYQYQR	1310.7	1311.7	1310.7	1311.7
18.0	26.1	26.1	17.1	2.0	99.0	DNYSFLEDMGLK	1446.6	1447.6	1446.7	1447.7
18.0	26.1	26.1	17.1	2.0	99.0	GRNQGNTWLTAFVLK	1635.8	1636.8	1635.8	1636.8
18.0	26.1	26.1	17.1	2.0	99.0	HYDGSYSTFGERY	1538.7	1539.7	1538.7	1539.7
18.0	26.1	26.1	17.1	2.0	99.0	LPPNVVEESAR	1209.6	1210.6	1209.6	1210.6
18.0	26.1	26.1	17.1	2.0	99.0	NALFCLESAWK	1324.6	1325.6	1324.6	1325.6
18.0	26.1	26.1	17.1	2.0	99.0	QTVSWAVTPK	1098.5	1099.5	1098.6	1099.6
18.0	26.1	26.1	17.1	2.0	99.0	SGGRTEHPFTVEEFVLPK	2001.0	2002.0	2001.0	2002.0
18.0	26.1	26.1	17.1	2.0	99.0	SKAIGYLNLYQYQR	1525.8	1526.8	1525.8	1526.8
18.0	26.1	26.1	17.1	2.0	99.0	VTAAPOSVICALR	1301.7	1302.7	1301.7	1302.7
18.0	26.1	26.1	17.1	2.0	99.0	VYDYETDEFAIAEYNAPCSK	2506.0	2507.1	2506.1	2507.1
18.0	26.1	26.1	17.1	2.0	99.0	YGAATFTRTG	1043.5	1044.5	1043.5	1044.5
18.0	26.1	26.1	17.1	1.4	96.0	ALLAYAFALAGNQDK	1608.8	1609.8	1608.9	1609.9
18.0	26.1	26.1	17.1	0.5	70.0	KSGGRTEHPFTVEEFVLPK	2554.4	2555.4	2554.4	2555.4
18.0	26.1	26.1	17.1	0.2	33.0	FSGQLNSHGCFYQQVTK	2057.9	2058.9	2057.9	2058.9
18.0	26.1	26.1	17.1	0.0	99.0	NALFCLESAWK	1323.6	1324.6	1323.6	1324.6
18.0	26.1	26.1	17.1	0.0	99.0	NALFCLESAWK	1475.6	1476.6	1475.6	1476.6
P01033 TIMP1_HUMAN	Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid-potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases) (Fibroblast collag									
319.0	4.0	4.0	14.5	2.0	99.0	EPGLCTWQSLR	1345.6	1346.7	1345.6	1346.7
319.0	4.0	4.0	14.5	2.0	99.0	LOGSTHCLWTDQLLOGSEK	2200.0	2201.1	2200.1	2201.1
169.0	2.0	2.0	22.2	2.0	99.0	GFOALGDAADIR	1232.6	1233.6	1232.6	1233.6
195.0	4.0	4.0	13.0	2.0	99.0	EPGLCTWQSLR	1345.6	1346.7	1345.6	1346.7
195.0	4.0	4.0	13.0	2.0	99.0	FVYTPAMESVCGYFHR	1962.9	1963.9	1962.9	1963.9
P01034 CYTC_HUMAN	Cystatin-C precursor (Cystatin-3) (Neuroendocrine basic polypeptide) (Gamma-trace) (Post-gamma-globulin) - Homo sapiens (Human)									
302.0	4.0	4.0	25.3	2.0	99.0	ALDFAVGEYNK	1225.6	1226.6	1225.6	1226.6
302.0	4.0	4.0	25.3	2.0	99.0	LVGQPMWASVEEGRVRR	1909.9	1910.9	1909.9	1910.9
104.0	3.4	3.4	26.0	2.0	99.0	ALDFAVGEYNK	1225.6	1226.6	1225.6	1226.6
104.0	3.4	3.4	26.0	1.4	96.0	TOPMLDNCPPHDPHLK	2060.0	2061.0	2060.0	2061.0
355.0	2.0	2.0	13.7	2.0	99.0	ALDFAVGEYNK	1225.6	1226.6	1225.6	1226.6
P01834 KAC_HUMAN	Ig kappa chain C region - Homo sapiens (Human)									
260.0	4.5	4.5	37.7	2.0	99.0	ADYEKHVYACEVTHOGLSSPVTK	2746.3	2747.3	2746.3	2747.3
260.0	4.5	4.5	37.7	2.0	99.0	VYACEVTHOGLSSPVTK	1874.9	1875.9	1874.9	1875.9
260.0	4.5	4.5	37.7	0.4	64.0	SGTASVCLLNFPYR	1797.9	1798.9	1797.9	1798.9
188.0	4.0	4.0	31.1	2.0	99.0	SGTASVCLLNFPYR	1797.9	1798.9	1797.9	1798.9
188.0	4.0	4.0	31.1	2.0	99.0	VYACEVTHOGLSSPVTK	1874.9	1875.9	1874.9	1875.9
P01842 LAC_HUMAN	Ig lambda chain C regions - Homo sapiens (Human)									
332.0	3.7	3.7	39.0	2.0	99.0	YAASSYLSLTPEQW	1677.8	1678.8	1677.7	1678.7
332.0	3.7	3.7	39.0	1.5	97.0	SYSCQVTEGSTVEK	1710.8	1711.8	1710.8	1711.8
332.0	3.7	3.7	39.0	0.1	29.1	QPKAAPSVTLPF	1256.7	1257.7	1256.7	1257.7
64.0	5.3	5.3	19.0	2.0	99.0	YAASSYLSLTPEQW	1677.8	1678.8	1677.7	1678.7
64.0	5.3	5.3	19.0	2.0	99.0	YAASSYLSLTPEQWK	1742.9	1743.9	1742.9	1743.9
64.0	5.3	5.3	19.0	1.3	95.0	OSNNKYAASSYLSLTPEQWK	2314.1	2315.1	2314.1	2315.1
203.0	3.7	3.7	28.6	2.0	99.0	SYSCQVTEGSTVEK	1710.8	1711.8	1710.8	1711.8
203.0	3.7	3.7	28.6	1.7	98.0	YAASSYLSLTPEQWK	1742.9	1743.9	1742.9	1743.9
P01871 MUC_HUMAN	Ig mu chain C region - Homo sapiens (Human)									
570.0	1.7	1.7	1.8	1.7	98.0	QIQVSWLR	1011.5	1012.6	1011.6	1012.6
195.0	1.7	1.7	7.0	1.7	98.0	QIQVSWLR	1028.6	1029.6	1028.6	1029.6
108.0	7.6	7.6	17.2	2.0	99.0	ESDWLSQSMFTCR	1645.7	1646.7	1645.7	1646.7
106.0	7.6	7.6	17.2	2.0	99.0	GFPSVLR	774.4	775.4	774.4	775.4
106.0	7.6	7.6	17.2	2.0	99.0	GOPLSPEKYVTSAPMPEPQAPGR	2438.2	2439.2	2438.2	2439.2
106.0	7.6	7.6	17.2	1.5	97.0	QIQVSWLR	1011.5	1012.5	1011.6	1012.6
106.0	7.6	7.6	17.2	0.0	96.0	QIQVSWLR	1028.6	1029.6	1028.6	1029.6
P02746 C1QB_HUMAN	Complement C1q subcomponent subunit B precursor - Homo sapiens (Human)									
95.0	4.0	4.0	13.5	2.0	99.0	FDHVITNMINNVEPR	1862.8	1863.8	1862.8	1863.8
95.0	4.0	4.0	13.5	2.0	99.0	VPLGYFTYHASSR	1659.8	1660.8	1659.8	1660.8
337.0	2.0	2.0	14.3	2.0	99.0	VPLGYFTYHASSR	1659.8	1660.8	1659.8	1660.8
P02747 C1QC_HUMAN	Complement C1q subcomponent subunit C precursor - Homo sapiens (Human)									
386.0	2.4	2.4	14.7	1.7	98.0	QTHOPPAPNSLIR	1457.8	1458.8	1457.8	1458.8
386.0	2.4	2.4	14.7	0.7	81.0	FOSVFTVTR	1083.6	1084.6	1083.6	1084.6
190.0	2.0	2.0	3.7	2.0	99.0	FOSVFTVTR	1083.6	1084.6	1083.6	1084.6
354.0	2.0	2.0	10.2	2.0	99.0	QTHOPPAPNSLIR	1457.8	1458.8	1457.8	1458.8
P02751 F1NC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo sapiens (Human)									
584.0	1.4	1.4	1.1	1.4	96.0	YQCYCYGR	1168.4	1169.5	1168.4	1169.5
22.0	13.3	13.3	13.7	2.0	99.0	GEWTCIAVQSRLR	1482.7	1483.7	1482.7	1483.7
22.0	13.3	13.3	13.7	2.0	99.0	IGDOWDKQHDGMHMMR	1983.9	1984.9	1983.9	1984.9
22.0	13.3	13.3	13.7	2.0	99.0	LLCQCLGFGSGHFR	1650.8	1651.8	1650.8	1651.8
22.0	13.3	13.3	13.7	2.0	99.0	YQCYCYGR	1168.4	1169.5	1168.4	1169.5
22.0	13.3	13.3	13.7	1.7	98.0	IYLYTLNDNAR	1354.7	1355.7	1354.7	1355.7
22.0	13.3	13.3	13.7	1.5	97.0	ODGHLWCSTTSNVEQDOK	2195.9	2196.9	2195.9	2196.9
22.0	13.3	13.3	13.7	1.4	96.0	EYLGAIACSTCFGGQR	1877.8	1878.8	1877.8	1878.8
22.0	13.3	13.3	13.7	0.6	72.0	GATYNIIVEALKDOOR	1817.9	1818.9	1817.9	1818.9
22.0	13.3	13.3	13.7	0.1	11.0	IFYSCTTEGR	1220.5	1221.5	1220.5	1221.5
27.0	21.3	21.3	16.4	2.0	99.0	GATYNIIVEALKDQQR	1818.0	1819.0	1818.0	1819.0
27.0	21.3	21.3	16.4	2.0	99.0	GEWTCIAVQSRLR	1482.7	1483.7	1482.7	1483.7
27.0	21.3	21.3	16.4	2.0	99.0	HTSVQTTSSGSPFTDVR	1862.9	1863.9	1862.9	1863.9
27.0	21.3	21.3	16.4	2.0	99.0	HYQINQWVER	1400.7	1401.7	1400.7	1401.7
27.0	21.3	21.3	16.4	2.0	99.0	LLCQCLGFGSGHFR	1650.8	1651.8	1650.8	1651.8
27.0	21.3	21.3	16.4	2.0	99.0	TYLGNALVTCYGGSR	1790.8	1791.8	1790.8	1791.8
27.0	21.3	21.3	16.4	2.0	99.0	WCHDNGVNYK	1292.5	1293.5	1292.5	1293.5
27.0	21.3	21.3	16.4	2.0	99.0	WLPSSPVTYGR	1348.7	1349.7	1348.7	1349.7
27.0	21.3	21.3	16.4	2.0	99.0	WSRPQAPITGYR	1430.7	1431.7	1430.7	1431.7
27.0	21.3	21.3	16.4	2.0	99.0	YQCYCYGR	1168.4	1169.5	1168.4	1169.5
27.0	21.3	21.3	16.4	1.2	93.0	IGDQWDKQHDGMHMMR	1999.8	2000.9	1999.8	2000.9
27.0	21.3	21.3	16.4	0.0	99.0	YQCYCYGR	1171.5	1172.5	1171.5	1172.5
P02792 FRIL_HUMAN	Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)									
550.0	2.0	2.0	8.6	2.0	99.0	LGRPEALGLEYLFR	1606.8	1607.8	1606.8	1607.8
370.0	2.0	2.0	8.6	2.0	99.0	LGRPEALGLEYLFR	1606.8	1607.8	1606.8	1607.8
P02795 MT2_HUMAN	Metallothionein-2 (MT-2) (Metallothionein-1I) (MT-1I) (Metallothionein-2A) - Homo sapiens (Human)									
216.0	6.0	6.0	82.0	2.0	99.0	CAOQCICKGASDKCSCCA	2074.7	2075.7	2074.7	2075.7
216.0	6.0	6.0	82.0	2.0	99.0	MDPNCSCAAAGDSCCTCAGSCK	2249.8	2250.8	2249.8	2250.8
216.0	6.0	6.0	82.0	0.0	99.0	SCCSCCPVGCAK	1444.5	1445.5	1444.5	1445.5
216.0	6.0	6.0	82.0	0.0	99.0	MDPNCSCAAAGDSCCTCAGSCK	2252.8	2253.8	2252.8	2253.8
216.0	6.0	6.0	82.0	0.0	99.0	MDPNCSCAAAGDSCCTCAGSCK	2192.7	2193.7	2192.7	2193.7
216.0	6.0	6.0	82.0	0.0	99.0	MDPNCSCAAAGDSCCTCAGSCK	2253.8	2254.8	2253.7	2254.7
216.0	6.0	6.0	82.0	0.0	47.0	MDPNCSCAAAGDSCCTCAGSCK	2207.7	2208.7	2207.7	2208.7
216.0	6.0	6.0	82.0	0.0	99.0	SCCSCCPVGCAK	1447.5	1448.5	1447.5	1448.5
216.0	6.0	6.0	82.0	0.0	99.0	SCCSCCPVGCAK	1447.5	1448.5	1447.5	1448.5
114.0	6.7	6.7	62.3	2.0	99.0	KSCSCCPVGCCK	1573.6	1574.6	1573.6	1574.6
114.0	6.7	6.7	62.3	2.0	99.0	MDPNCSCAAAGDSCCTCAGSCK	2249.8	2250.8	2249.8	2250.8
114.0	6.7	6.7	62.3	2.0	99.0	SCCSCCPVGCAK	1444.5	1445.5	1444.5	1445.5
114.0	6.7	6.7	62.3	0.7	81.0	MDPNCSCAAAGDSCCTCAGSCKCKECK	2955.0	2956.0	2955.0	2956.0
114.0	6.7	6.7	62.3	0.0	99.0	MDPNCSCAAAGDSCCTCAGSCK	2250.7	2251.7	2250.7	2251.7
114.0	6.7	6.7	62.3	0.0	99.0	MDPNCSCAAAGDSCCTCAGSCK	2253.8	2254.8	2253.7	2254.7
114.0	6.7	6.7	62.3	0.0	97.0	MDPNCSCAAAGDSCCTCAGSCK	2265.8	2266.8	2265.8	2266.8
114.0	6.7	6.7	62.3	0.0	99.0	SCCSCCPVGCAK	1446.5	1447.5	1446.5	1447.5
114.0	6.7	6.7	62.3	0.0	99.0	SCCSCCPVGCAK	1446.5	1447.5	1446.5	1447.5
P04004 VTNC_HUMAN	Vitronectin precursor (Serum-spreading factor) (S-protein) (V75) [Contains: Vitronectin V65 subunit: Vitronectin V10 subunit: Somatomedin B] -									
482.0	2.0	2.0	6.1	2.0	99.0	DWVGIEGPIDAAFTR	1645.8	1646.8	1645.8	1646.8
119.0	2.5	2.5	12.3	2.0	99.0	DWVGIEGPIDAAFTR	1645.8	1646.8		

16.0	37.1	37.1	57.7	2.0	99.0	DGADFACWR	1064.5	1065.5	1064.5	1065.5
16.0	37.1	37.1	57.7	2.0	99.0	IGEHTPSALAIMENANVLR	2106.1	2107.1	2106.1	2107.1
16.0	37.1	37.1	57.7	2.0	99.0	IVAPGKGLAADESTGSIKRR	2053.1	2054.2	2053.2	2054.2
16.0	37.1	37.1	57.7	2.0	99.0	KELSDIAHR	1067.6	1068.6	1067.6	1068.6
16.0	37.1	37.1	57.7	2.0	99.0	LOSIGTENTENRR	1645.8	1646.8	1645.8	1646.8
16.0	37.1	37.1	57.7	2.0	99.0	PYQYPALTPKQK	1433.7	1434.7	1433.7	1434.7
16.0	37.1	37.1	57.7	2.0	99.0	PYQYPALTPKQK	1561.8	1562.8	1561.8	1562.8
16.0	37.1	37.1	57.7	2.0	99.0	PYQYPALTPKQKELSDIAHR	2483.3	2484.3	2483.3	2484.3
16.0	37.1	37.1	57.7	2.0	99.0	RLOSIGTENTENRR	1801.9	1802.9	1801.9	1802.9
16.0	37.1	37.1	57.7	2.0	99.0	YTPSGGAAAASESLFVSNHAY	2227.0	2228.0	2227.0	2228.0
16.0	37.1	37.1	57.7	1.7	98.0	YQYPALTPKQKELSDIAHR	2479.2	2480.2	2479.2	2480.2
16.0	37.1	37.1	57.7	1.4	96.0	KENLKAQEEYVVKR	1704.9	1705.9	1704.9	1705.9
16.0	37.1	37.1	57.7	0.7	82.0	ENLKAQEEYVVKR	1576.8	1577.8	1576.8	1577.8
16.0	37.1	37.1	57.7	0.5	70.0	VDKGVVPLAGTNGETTTQGLDGLSER	2614.3	2615.3	2614.3	2615.3
16.0	37.1	37.1	57.7	0.5	65.0	GVVPLAGTNGETTTQGLDGLSER	2272.1	2273.1	2272.1	2273.1
16.0	37.1	37.1	57.7	0.3	51.0	MPYQYPALTPKQKELSDIAHR	2495.3	2496.3	2495.3	2496.3
16.0	37.1	37.1	57.7	0.0	58.0	LOSIGTENTENRR	1648.8	1649.8	1648.8	1649.8
52.0	6.2	6.2	29.4	2.0	99.0	IGEHTPSALAIMENANVLR	2106.1	2107.1	2106.1	2107.1
52.0	6.2	6.2	29.4	2.0	99.0	PYQYPALTPKQK	1561.8	1562.8	1561.8	1562.8
52.0	6.2	6.2	29.4	1.5	97.0	LOSIGTENTENRR	1645.8	1646.8	1645.8	1646.8
52.0	6.2	6.2	29.4	0.6	75.0	YTPSGGAAAASESLFVSNHAY	2227.0	2228.0	2227.0	2228.0
52.0	6.2	6.2	29.4	0.1	15.0	FSHEEIAMATVTLARR	1830.9	1832.0	1830.9	1831.9
23.0	22.8	22.8	50.5	2.0	99.0	ADDGRPFQVIK	1341.7	1342.7	1341.7	1342.7
23.0	22.8	22.8	50.5	2.0	99.0	ALANSLACQK	1131.6	1132.6	1131.6	1132.6
23.0	22.8	22.8	50.5	2.0	99.0	AWGGKKNLKAQEEYVVKR	2204.2	2205.2	2204.2	2205.2
23.0	22.8	22.8	50.5	2.0	99.0	CAQYKKGADFAK	1483.7	1484.7	1483.7	1484.7
23.0	22.8	22.8	50.5	2.0	99.0	IGEHTPSALAIMENANVLR	2106.1	2107.1	2106.1	2107.1
23.0	22.8	22.8	50.5	2.0	99.0	KENLKAQEEYVVKR	1704.9	1705.9	1704.9	1705.9
23.0	22.8	22.8	50.5	2.0	99.0	LOSIGTENTENRR	1645.8	1646.8	1645.8	1646.8
23.0	22.8	22.8	50.5	2.0	99.0	PYQYPALTPKQK	1433.7	1434.7	1433.7	1434.7
23.0	22.8	22.8	50.5	2.0	99.0	PYQYPALTPKQK	1561.8	1562.8	1561.8	1562.8
23.0	22.8	22.8	50.5	2.0	99.0	PYQYPALTPKQKELSDIAHR	2483.3	2484.3	2483.3	2484.3
23.0	22.8	22.8	50.5	2.0	99.0	YTPSGGAAAASESLFVSNHAY	2227.0	2228.0	2227.0	2228.0
23.0	22.8	22.8	50.5	0.4	57.0	RLOSIGTENTENRR	1801.9	1802.9	1801.9	1802.9
23.0	22.8	22.8	50.5	0.3	55.0	GVVPLAGTNGETTTQGLDGLSER	2272.1	2273.1	2272.1	2273.1
23.0	22.8	22.8	50.5	0.0	99.0	IGEHTPSALAIMENANVLR	2107.1	2108.1	2107.1	2108.1
23.0	22.8	22.8	50.5	0.0	99.0	PYQYPALTPKQK	1564.8	1565.9	1564.8	1565.8
23.0	22.8	22.8	50.5	0.0	98.0	PYQYPALTPKQKELSDIAHR	2484.3	2485.3	2484.3	2484.3
P04080 CYTB_HUMAN						Cystatin-B (Stefin-B) (Liver thiol proteinase inhibitor) (CPI-B) - Homo sapiens (Human)				
318.0	4.0	4.0	36.7	2.0	99.0	MMCGAPSATOPATAETOHADQVR	2612.2	2613.2	2612.2	2613.2
318.0	4.0	4.0	36.7	2.0	99.0	VHVGDDEFVHLR	1421.7	1422.7	1421.7	1422.7
277.0	2.1	2.1	30.6	2.0	99.0	VHVGDDEFVHLR	1421.7	1422.7	1421.7	1422.7
P04406 G3P_HUMAN						Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) - Homo sapiens (Human)				
30.0	24.2	24.2	49.6	2.0	99.0	DGRGALONIPASTGAAK	1739.9	1739.9	1739.9	1739.9
30.0	24.2	24.2	49.6	2.0	99.0	GKVKVGVNGFGR	1217.7	1218.7	1217.7	1218.7
30.0	24.2	24.2	49.6	2.0	99.0	IISNASCTNCLAPLAK	1832.9	1833.9	1832.9	1833.9
30.0	24.2	24.2	49.6	2.0	99.0	IKWGDAGAEYVVESTGVFTTMEK	2517.2	2518.2	2517.2	2518.2
30.0	24.2	24.2	49.6	2.0	99.0	LEKPAKYDIKK	1446.8	1447.8	1446.8	1447.8
30.0	24.2	24.2	49.6	2.0	99.0	LISWYDNEFGYSNR	1762.8	1763.8	1762.8	1763.8
30.0	24.2	24.2	49.6	2.0	99.0	GVVNGFGR	805.4	806.4	805.4	806.4
30.0	24.2	24.2	49.6	2.0	99.0	VIIISAPSADAPMFVGMVNHKE	2212.1	2213.1	2212.1	2213.1
30.0	24.2	24.2	49.6	2.0	99.0	VIIISAPSADAPMFVGMVNHKEYDNSLK	2933.4	2933.4	2933.4	2933.4
30.0	24.2	24.2	49.6	2.0	99.0	VPTANVSVVDLTCR	1529.8	1530.8	1529.8	1530.8
30.0	24.2	24.2	49.6	2.0	99.0	IKWGDAGAEYVVESTGVFTTMEK	2277.1	2278.1	2277.0	2277.0
30.0	24.2	24.2	49.6	1.3	95.0	VIPENKLTGMFAFR	1645.9	1646.9	1645.9	1646.9
30.0	24.2	24.2	49.6	0.5	67.0	LTGMFAFR	794.4	795.4	794.4	795.4
30.0	24.2	24.2	49.6	0.4	60.0	LTGMFAFRVPTANVSVVDLTCR	2306.2	2307.2	2306.2	2307.2
30.0	24.2	24.2	49.6	0.0	97.0	GKVKVGVNGFGR	1217.7	1218.7	1217.7	1218.7
30.0	24.2	24.2	49.6	0.0	80.0	GKVKVGVNGFGR	1217.7	1218.7	1217.7	1218.7
30.0	24.2	24.2	49.6	0.0	99.0	LISWYDNEFGYSNR	1764.8	1765.8	1762.8	1763.8
30.0	24.2	24.2	49.6	0.0	99.0	LISWYDNEFGYSNR	1778.8	1779.8	1778.8	1779.8
30.0	24.2	24.2	49.6	0.0	80.0	LISWYDNEFGYSNR	1763.8	1764.8	1763.8	1764.8
74.0	4.7	4.7	25.4	2.0	99.0	LISWYDNEFGYSNR	1762.8	1763.8	1762.8	1763.8
74.0	4.7	4.7	25.4	2.0	99.0	VPTANVSVVDLTCR	1529.8	1530.8	1529.8	1530.8
74.0	4.7	4.7	25.4	0.5	65.0	VIIISAPSADAPMFVGMVNHKE	2212.1	2213.1	2212.1	2213.1
74.0	4.7	4.7	25.4	0.3	44.0	PELNKLTGMFAFR	1465.8	1466.8	1465.7	1466.7
74.0	4.7	4.7	25.4	0.0	60.0	LISWYDNEFGYSNR	1778.8	1779.8	1778.8	1779.8
74.0	4.7	4.7	25.4	0.0	43.0	LISWYDNEFGYSNR	1754.7	1755.7	1762.8	1763.8
34.0	19.3	19.3	40.3	2.0	99.0	GALONIPASTGAAK	1410.8	1411.8	1410.8	1411.8
34.0	19.3	19.3	40.3	2.0	99.0	IISNASCTNCLAPLAK	1832.9	1833.9	1832.9	1833.9
34.0	19.3	19.3	40.3	2.0	99.0	IKWGDAGAEYVVESTGVFTTMEK	2517.2	2518.2	2517.2	2518.2
34.0	19.3	19.3	40.3	2.0	99.0	LEKPAKYDIKK	1446.8	1447.8	1446.8	1447.8
34.0	19.3	19.3	40.3	2.0	99.0	LISWYDNEFGYSNR	1762.8	1763.8	1762.8	1763.8
34.0	19.3	19.3	40.3	2.0	99.0	VPTANVSVVDLTCR	1529.8	1530.8	1529.8	1530.8
34.0	19.3	19.3	40.3	2.0	99.0	VVDLMAHMASKE	1329.6	1330.7	1329.6	1330.6
34.0	19.3	19.3	40.3	2.0	99.0	IKWGDAGAEYVVESTGVFTTMEK	2277.0	2278.0	2277.0	2277.0
34.0	19.3	19.3	40.3	1.4	96.0	VIIISAPSADAPMFVGMVNHKE	2212.1	2213.1	2212.1	2213.1
34.0	19.3	19.3	40.3	1.2	94.0	LEKPAKYDIKK	1318.7	1319.7	1318.7	1319.7
34.0	19.3	19.3	40.3	0.7	80.0	LTGMFAFR	794.4	795.4	794.4	795.4
34.0	19.3	19.3	40.3	0.0	60.0	LISWYDNEFGYSNR	1763.8	1764.8	1763.8	1764.8
34.0	19.3	19.3	40.3	0.0	99.0	LISWYDNEFGYSNR	1778.8	1779.8	1778.8	1779.8
34.0	19.3	19.3	40.3	0.0	99.0	LISWYDNEFGYSNR	1794.8	1795.8	1794.8	1795.8
P05109 S10A8_HUMAN						Protein S100-A8 (S100 calcium-binding protein A8) (Calgranulin-A) (Migration inhibitory factor-related protein 8) (MRP-8) (Cystic fibrosis antigen)				
317.0	4.0	4.0	25.8	2.0	99.0	GNFHAYRDDLK	1561.8	1562.8	1561.8	1562.8
317.0	4.0	4.0	25.8	2.0	99.0	LLETECPQYIR	1420.7	1421.7	1420.7	1421.7
161.0	4.4	4.4	25.8	2.0	99.0	GNFHAYRDDLK	1561.8	1562.8	1561.8	1562.8
161.0	4.4	4.4	25.8	2.0	99.0	LLETECPQYIR	1420.7	1421.7	1420.7	1421.7
161.0	4.4	4.4	25.8	0.4	63.0	GNFHAYR	962.5	963.5	962.5	963.5
161.0	4.4	4.4	25.8	0.0	33.0	GNFHAYRDDLK	1561.8	1562.8	1561.8	1562.8
P05120 PAI2_HUMAN						Plasminogen activator inhibitor 2 precursor (PAI-2) (Placental plasminogen activator inhibitor) (Monocyte Arg-serpin) (Urokinase inhibitor) - Hon				
114.0	10.0	10.0	13.5	2.0	99.0	ITNCLFFGR	1239.6	1240.6	1239.6	1240.7
114.0	10.0	10.0	13.5	2.0	99.0	LEEHYELR	1087.5	1088.5	1087.5	1088.5
114.0	10.0	10.0	13.5	2.0	99.0	SASFREYIR	1256.6	1257.6	1256.6	1257.6
114.0	10.0	10.0	13.5	2.0	99.0	TPVOMMYLR	1137.6	1138.6	1137.6	1138.6
114.0	10.0	10.0	13.5	2.0	99.0	YYSSEPAQVDFLECAEEAR	2263.0	2264.0	2263.0	2264.0
114.0	10.0	10.0	13.5	0.0	99.0	SASFREYIR	1256.6	1257.6	1256.6	1257.6
38.0	8.1	8.1	21.2	2.0	99.0	AIIQAQAADKIHSSFR	1754.9	1755.9	1754.9	1756.0
38.0	8.1	8.1	21.2	2.0	99.0	SASFREYIR	1256.6	1257.6	1256.6	1257.6
38.0	8.1	8.1	21.2	2.0	99.0	TPVOMMYLR	1137.6	1138.6	1137.6	1138.6
38.0	8.1	8.1	21.2	2.0	99.0	YYSSEPAQVDFLECAEEAR	2263.0	2264.0	2263.0	2264.0
17.0	26.4	26.4	37.3	2.0	99.0	AIIQAQAADKIHSSFR	1754.9	1755.9	1754.9	1756.0
17.0	26.4	26.4	37.3	2.0	99.0	GKYPNLLPEGSVDGTR	1766.9	1767.9	1766.9	1767.9
17.0	26.4	26.4	37.3	2.0	99.0	GKYPNLLPEGSVDGTR	1766.9	1767.9	1766.9	1767.9
17.0	26.4	26.4	37.3	2.0	99.0	GSYPDAILQAQAADKIHSSFR	2274.1	2275.1	2274.1	2275.1
17.0	26.4	26.4	37.3	2.0	99.0	ITNCLFFGR	1239.6	1240.6	1239.6	1240.7
17.0	26.4	26.4	37.3	2.0	99.0	KKINSWVK	1001.5	1002.5	1001.5	1002.5
17.0	26.4	26.4	37.3	2.0	99.0	LEEHYELR	1087.5	1088.5	1087.5	1088.5
17.0	26.4	26.4	37.3	2.0	99.0	MAEDEVEYIPOFK	1696.8	1697.8	1696.8	1697.8
17.0	26.4									

51.0	17.4	17.4	38.3	2.0	99.0	LCGTFLGGKPPQR	1526.8	1527.8	1526.8	1527.8
51.0	17.4	17.4	38.3	2.0	99.0	LPASFDAR	875.5	876.5	875.5	876.5
51.0	17.4	17.4	38.3	2.0	99.0	SGVYQHVTGEMGGHAIR	1928.9	1929.9	1928.9	1929.9
51.0	17.4	17.4	38.3	2.0	99.0	VMFTEDLKLPAFDAR	1838.9	1839.9	1838.9	1839.9
51.0	17.4	17.4	38.3	1.5	97.0	EQWPCPTIK	1285.6	1286.6	1285.6	1286.6
51.0	17.4	17.4	38.3	1.2	94.0	ILRGDQHCGIESEVAVGIPR	2205.1	2206.1	2205.1	2206.1
51.0	17.4	17.4	38.3	0.5	67.0	DQSGSCSOWAFGAVEAISDR	2171.9	2172.9	2171.9	2172.9
51.0	17.4	17.4	38.3	0.1	26.0	RLCGTFLGGKPPQR	1682.9	1683.9	1682.9	1683.9
71.0	4.9	4.9	28.0	2.0	99.0	EQWPCPTIK	1683.8	1684.8	1683.8	1684.8
71.0	4.9	4.9	28.0	2.0	99.0	SGVYQHVTGEMGGHAIR	1928.9	1929.9	1928.9	1929.9
71.0	4.9	4.9	28.0	0.9	86.0	EQWPCPTIK	1285.6	1286.6	1285.6	1286.6
48.0	15.7	15.7	34.2	2.0	99.0	DQSGSCSOWAFGAVEAISDR	2171.9	2172.9	2171.9	2172.9
48.0	15.7	15.7	34.2	2.0	99.0	EQWPCPTIK	1683.8	1684.8	1683.8	1684.8
48.0	15.7	15.7	34.2	2.0	99.0	ICEPGYSPYTKQDK	1684.8	1685.8	1684.8	1685.8
48.0	15.7	15.7	34.2	2.0	99.0	ILRGDQHCGIESEVAVGIPR	2205.1	2206.1	2205.1	2206.1
48.0	15.7	15.7	34.2	2.0	99.0	LPASFDAR	875.5	876.5	875.5	876.5
48.0	15.7	15.7	34.2	2.0	99.0	SGVYQHVTGEMGGHAIR	1928.9	1929.9	1928.9	1929.9
48.0	15.7	15.7	34.2	2.0	99.0	VMFTEDLKLPAFDAR	1838.9	1839.9	1838.9	1839.9
48.0	15.7	15.7	34.2	1.7	88.0	EQWPCPTIK	1285.6	1286.6	1285.6	1286.6
P07900 HS90A_HUMAN Heat shock protein HSP 90-alpha (HSP 86) (Renal carcinoma antigen NY-REN-38) - Homo sapiens (Human)										
75.0	4.7	4.7	23.5	2.0	99.0	HIYYITGETK	1223.6	1224.6	1223.6	1224.6
75.0	4.7	4.7	23.5	2.0	99.0	SLTNDWEDHLAVK	1526.7	1527.7	1526.7	1527.7
75.0	4.7	4.7	23.5	0.6	73.0	RAPFDLFENR	1263.6	1264.7	1263.6	1264.6
75.0	4.7	4.7	23.5	0.1	23.0	KHLEINPDHSIETLR	1914.0	1915.0	1914.0	1915.0
20.0	29.4	29.4	29.9	2.0	99.0	ALLFVPR	814.5	815.5	814.5	815.5
20.0	29.4	29.4	29.9	2.0	99.0	AQALRDNSTMGYMAAK	1726.8	1727.8	1726.8	1727.8
20.0	29.4	29.4	29.9	2.0	99.0	FYEQFSK	947.4	948.4	947.4	948.4
20.0	29.4	29.4	29.9	2.0	99.0	HFSVEGQLEFR	1347.7	1348.7	1347.7	1348.7
20.0	29.4	29.4	29.9	2.0	99.0	HIYYITGETK	1223.6	1224.6	1223.6	1224.6
20.0	29.4	29.4	29.9	2.0	99.0	HIYYITGETKEDQVANSVAFV	2442.2	2443.2	2442.2	2443.2
20.0	29.4	29.4	29.9	2.0	99.0	KHLEINPDHSIETLR	1914.0	1915.0	1914.0	1915.0
20.0	29.4	29.4	29.9	2.0	99.0	LVTSPCCIVTSTYGTWVANMER	2445.1	2446.1	2445.1	2446.1
20.0	29.4	29.4	29.9	2.0	99.0	NPDIDTNEYGEFYK	1833.8	1834.8	1833.8	1834.8
20.0	29.4	29.4	29.9	2.0	99.0	RAPFDLFENR	1263.6	1264.6	1263.6	1264.6
20.0	29.4	29.4	29.9	2.0	99.0	VILHLKEDQTEYLEER	2014.0	2015.0	2014.0	2015.0
20.0	29.4	29.4	29.9	2.0	99.0	YIDOEELNK	1150.6	1151.6	1150.6	1151.6
20.0	29.4	29.4	29.9	2.0	99.0	YIDOEELNKTKPIWTR	2033.1	2034.1	2033.1	2034.1
20.0	29.4	29.4	29.9	2.0	99.0	YYSASGDEMVLKDYCTR	2245.0	2246.0	2245.0	2246.0
20.0	29.4	29.4	29.9	1.4	96.0	AQALRDNSTMGYMAAKK	1854.9	1855.9	1854.9	1855.9
20.0	29.4	29.4	29.9	0.0	99.0	HIYYITGETK	1235.6	1236.6	1235.6	1236.6
20.0	29.4	29.4	29.9	0.0	99.0	YIDOEELNK	1152.5	1153.5	1152.5	1153.5
P07910 HNRPC_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1 / hnRNP C2) - Homo sapiens (Human)										
241.0	5.0	5.0	8.8	2.0	99.0	GFAFYVNER	1328.6	1329.7	1328.7	1329.7
241.0	5.0	5.0	8.8	2.0	99.0	SVPARVPPPIAR	1516.8	1517.9	1516.9	1517.9
241.0	5.0	5.0	8.8	0.6	72.0	MYSVAPRVPPPIAR	1811.0	1812.0	1811.0	1812.0
241.0	5.0	5.0	8.8	0.4	63.0	VPPPIAR	942.6	943.6	942.6	943.6
213.0	3.2	3.2	27.5	2.0	99.0	GFAFYVNER	1328.6	1329.6	1328.7	1329.7
213.0	3.2	3.2	27.5	1.2	93.0	VPPPIAR	942.6	943.6	942.6	943.6
P08107 HSP71_HUMAN Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2) - Homo sapiens (Human)										
127.0	9.2	14.3	29.2	2.0	99.0	FEELCSDLFR	1314.6	1315.6	1314.6	1315.6
127.0	9.2	14.3	29.2	2.0	99.0	LLQDFNDRDLNK	1579.8	1580.8	1579.8	1580.8
127.0	9.2	14.3	29.2	2.0	99.0	MVQEAKEYKADEVORER	2237.1	2238.1	2237.1	2238.1
127.0	9.2	14.3	29.2	1.7	98.0	ARFEELCSDLFR	1541.7	1542.7	1541.7	1542.7
127.0	9.2	14.3	29.2	1.2	99.0	ATAGDTHLGGEDFDNR	1674.7	1675.7	1674.7	1675.7
127.0	9.2	14.3	29.2	1.3	46.0	DAGYVAGLNVL	1196.7	1197.7	1196.7	1197.7
127.0	9.2	14.3	29.2	0.0	45.0	LDKAQIHDVLVGGSTR	1837.0	1838.0	1837.0	1838.0
127.0	9.2	14.3	29.2	0.0	99.0	TTPSYVAFDTER	1486.7	1487.7	1486.7	1487.7
127.0	9.2	14.3	29.2	0.0	99.0	VEIANDOGNR	1227.6	1228.6	1227.6	1228.6
126.0	2.3	5.0	23.2	1.5	97.0	AFYPEEISSMVLTK	1613.8	1614.8	1613.8	1614.8
126.0	2.3	5.0	23.2	0.5	80.0	IINEPTAAAIAYGLDR	1686.9	1687.9	1686.9	1687.9
126.0	2.3	5.0	23.2	0.2	43.0	FEELCSDLFR	1314.6	1315.6	1314.6	1315.6
126.0	2.3	5.0	23.2	0.0	47.0	ATAGDTHLGGEDFDNR	1690.7	1691.7	1690.7	1691.7
126.0	2.3	5.0	23.2	0.0	39.0	NALESYAFNMK	1302.6	1303.6	1302.6	1303.6
126.0	2.3	5.0	23.2	0.0	99.0	TTPSYVAFDTER	1486.7	1487.7	1486.7	1487.7
P08571 CD14_HUMAN Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein) [Contains: Monocyte differentiation antigen CD14] - Homo sapiens (Human)										
548.0	2.0	2.0	4.8	2.0	99.0	VLSIAQAHSFASCEQVR	1999.0	2000.0	1999.0	2000.0
145.0	2.1	2.1	16.3	2.0	99.0	VLSIAQAHSFASCEQVR	1999.0	2000.0	1999.0	2000.0
182.0	4.0	4.0	18.1	2.0	99.0	FPALTSLDSDNPLGLER	1972.0	1973.0	1972.0	1973.0
182.0	4.0	4.0	18.1	2.0	99.0	VLSIAQAHSFASCEQVR	1999.0	2000.0	1999.0	2000.0
P08575 CD45_HUMAN Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (T200) (CD45 antigen) - Homo sapiens (Human)										
250.0	4.7	4.7	3.7	2.0	99.0	FOLHDCQVEK	1403.7	1404.7	1403.7	1404.7
250.0	4.7	4.7	3.7	2.0	99.0	LFLAEFQSIPIR	1319.7	1320.7	1319.7	1320.7
250.0	4.7	4.7	3.7	0.7	80.0	TDFGSPGQIIFCR	1722.8	1723.8	1722.8	1723.8
323.0	2.0	2.0	6.7	2.0	99.0	LFLAEFQSIPIR	1319.7	1320.7	1319.7	1320.7
P08670 VIME_HUMAN Vimentin - Homo sapiens (Human)										
3.0	63.4	63.4	70.0	2.0	99.0	EEAENTLOSFRQVDNASLAR	2392.1	2393.1	2392.1	2393.1
3.0	63.4	63.4	70.0	2.0	99.0	EKLOEEMLOREAEENTLQFSR	2607.2	2608.3	2607.3	2608.3
3.0	63.4	63.4	70.0	2.0	99.0	EMEEENFAVEAANYQDTIGR	2186.0	2187.0	2186.0	2187.0
3.0	63.4	63.4	70.0	2.0	99.0	FADLSEAAANRNNDALR	1775.9	1776.9	1775.9	1776.9
3.0	63.4	63.4	70.0	2.0	99.0	FANVYDKVR	1125.6	1126.6	1125.6	1126.6
3.0	63.4	63.4	70.0	2.0	99.0	FSLADAINTEFK	1355.7	1356.7	1355.7	1356.7
3.0	63.4	63.4	70.0	2.0	99.0	FSLADAINTEFKNTR	1725.9	1726.9	1725.9	1726.9
3.0	63.4	63.4	70.0	2.0	99.0	HLREYDGLNVK	1526.8	1527.8	1526.8	1527.8
3.0	63.4	63.4	70.0	2.0	99.0	KLHEEIEIQLOAQIQEQHVQID	2684.3	2685.3	2684.3	2685.3
3.0	63.4	63.4	70.0	2.0	99.0	KVESLOEEIAFLK	1532.8	1533.8	1532.8	1533.9
3.0	63.4	63.4	70.0	2.0	99.0	KVESLOEEIAFLKK	1660.9	1662.0	1660.9	1661.9
3.0	63.4	63.4	70.0	2.0	99.0	LGDLYEEMR	1253.6	1254.6	1253.6	1254.6
3.0	63.4	63.4	70.0	2.0	99.0	LGDLYEEMRELRR	1651.8	1652.8	1651.8	1652.8
3.0	63.4	63.4	70.0	2.0	99.0	LGDLYEEMRELRR	1807.9	1808.9	1807.9	1808.9
3.0	63.4	63.4	70.0	2.0	99.0	LHEEIEIQLOAQIQEQHVQID	2556.2	2557.2	2556.2	2557.3
3.0	63.4	63.4	70.0	2.0	99.0	LODEIQNKKEEMAR	1733.8	1734.8	1733.8	1734.8
3.0	63.4	63.4	70.0	2.0	99.0	LOEEMLOREAEENTLQFSR	2350.1	2351.1	2350.1	2351.1
3.0	63.4	63.4	70.0	2.0	99.0	MFGGPGTASRPSSSR	1493.7	1494.7	1493.7	1494.7
3.0	63.4	63.4	70.0	2.0	99.0	NLOEAEWYK	1308.6	1309.6	1308.6	1309.6
3.0	63.4	63.4	70.0	2.0	99.0	NLOEAEWYKSK	1523.7	1524.7	1523.7	1524.7
3.0	63.4	63.4	70.0	2.0	99.0	QVDLTDNPKAR	1269.6	1270.6	1269.6	1270.6
3.0	63.4	63.4	70.0	2.0	99.0	QVQSLTCEVDALKGTNESLER	2359.1	2360.1	2359.1	2360.1
3.0	63.4	63.4	70.0	2.0	99.0	ROVDLTDNPKAR	1442.8	1443.8	1442.8	1443.8
3.0	63.4	63.4	70.0	2.0	99.0	SLYASSPGVYATR	1427.7	1428.7	1427.7	1428.7
3.0	63.4	63.4	70.0	2.0	99.0	SRLGDLYEEMRELRR	2051.0	2052.0	2051.0	2052.0
3.0	63.4	63.4	70.0	2.0	99.0	TNEKVELOELNDR	1586.8	1587.8	1586.8	1587.8
3.0	63.4	63.4	70.0	2.0	99.0	TVETRDGGVINETSQHDDLE	2423.1	2424.1	2423.1	2424.1
3.0	63.4	63.4	70.0	2.0	99.0	VELOELNDR	1114.6	1115.6	1114.6	1115.6
3.0	63.4	63.4	70.0	2.0	99.0	VELOELNDR	1404.7	1405.8	1404.8	1405.8
3.0	63.4	63.4	70.0	2.0	99.0	VEVERDNLAEDIMR	1687.8	1688.8	1687.8	1688.8
3.0	63.4	63.4	70.0	1.5	97.0	EYVDLLNVK	1120.6	1121.6	1120.6	1121.6
3.0	63.4	63.4	70.0	1.2	94.0	FADLSEAAANR	1092.5	1093.5	1092.5	1093.5
3.0	63.4	63.4	70.0	0.5	65.0	LOEEMLQR	1045.5	1046.5	1045.5	1046.5
3.0	63.4	63.4	70.0	0.2	37.0	EEAENTLQFSR	1322.6	1323.6	1322.6	1323.6
3.0	63.4	63.4	70.0	0.0	99.0	EMEEENFAVEAANYQDTIGR	2191.0	2192.0	2191.0	2192.0
3.0	63.4	63.4	70.0	0.0	99.0	QVQSLTCEVDALKGTNESLER	2377.2	2378.2	2377.2	2378.2
3.0	63.4	63.4	70.0	0.0	95.0	TNEKVELOELNDR	1586.8	1587.8		

8.0	22.8	22.8	70.6	0.1	28.0	HLREYDOLLNVK	1526.8	1527.8	1526.8	1527.8
8.0	22.8	22.8	70.6	0.1	18.0	FANYIDKVR	1124.6	1125.6	1125.6	1125.6
8.0	22.8	22.8	70.6	0.0	95.0	QVQSLTCEVDALKGTNESLER	2376.2	2377.2	2376.2	2377.2
8.0	22.8	22.8	70.6	0.0	56.0	TNEKVELQELNDR	1586.8	1587.8	1586.8	1587.8
8.0	44.3	44.3	62.2	2.0	99.0	DGQVINETSQHHDDLE	1835.8	1836.8	1835.8	1836.8
8.0	44.3	44.3	62.2	2.0	99.0	EEAFLQSDRQDVNDASLAR	2392.1	2393.1	2392.1	2393.1
8.0	44.3	44.3	62.2	2.0	99.0	EKLOEMLQR	1302.7	1303.7	1302.7	1303.7
8.0	44.3	44.3	62.2	2.0	99.0	EKLOEEMLOREAEANTLOSFR	2607.3	2608.3	2607.3	2608.3
8.0	44.3	44.3	62.2	2.0	99.0	EMENFAVEAANYODTIGR	2185.9	2186.9	2185.9	2187.0
8.0	44.3	44.3	62.2	2.0	99.0	FADLSEANRNNDALR	1775.9	1776.9	1775.9	1776.9
8.0	44.3	44.3	62.2	2.0	99.0	FANYIDKVR	1124.6	1125.6	1124.6	1125.6
8.0	44.3	44.3	62.2	2.0	99.0	FSLADANTEFK	1354.7	1355.7	1354.7	1355.7
8.0	44.3	44.3	62.2	2.0	99.0	FSLADANTEFKNTR	1725.9	1726.9	1725.9	1726.9
8.0	44.3	44.3	62.2	2.0	99.0	HLREYDOLLNVK	1526.8	1527.8	1526.8	1527.8
8.0	44.3	44.3	62.2	2.0	99.0	LGDLYEEMR	1253.6	1254.6	1253.6	1254.6
8.0	44.3	44.3	62.2	2.0	99.0	LGDLYEEMRELRR	1807.9	1808.9	1807.9	1808.9
8.0	44.3	44.3	62.2	2.0	99.0	LODEIQNMKEEMAR	1733.8	1734.8	1733.8	1734.8
8.0	44.3	44.3	62.2	2.0	99.0	LOEEMLQR	1045.5	1046.5	1045.5	1046.5
8.0	44.3	44.3	62.2	2.0	99.0	NLQEAEEVYWK	1308.6	1309.6	1308.6	1309.6
8.0	44.3	44.3	62.2	2.0	99.0	QVQSLTCEVDALKGTNESLER	2351.1	2352.1	2351.1	2352.1
8.0	44.3	44.3	62.2	2.0	99.0	RQVDLQNTDKAR	1442.8	1443.8	1442.8	1443.8
8.0	44.3	44.3	62.2	2.0	99.0	TNEKVELQELNDR	1586.8	1587.8	1586.8	1587.8
8.0	44.3	44.3	62.2	2.0	99.0	TVETRDGQVINETSQHHDDLE	2423.1	2424.1	2423.1	2424.1
8.0	44.3	44.3	62.2	2.0	99.0	VEVERDNLAEDIMR	1687.8	1688.8	1687.8	1688.8
8.0	44.3	44.3	62.2	1.7	98.0	EYQDOLLNVK	1120.6	1121.6	1120.6	1121.6
8.0	44.3	44.3	62.2	1.2	93.0	VELQELNDR	1114.6	1115.6	1114.6	1115.6
8.0	44.3	44.3	62.2	0.9	87.0	KVESLQEEIAFLK	1532.8	1533.8	1532.8	1533.9
8.0	44.3	44.3	62.2	0.3	46.0	EEAENTLQSFPR	1322.6	1323.6	1322.6	1323.6
8.0	44.3	44.3	62.2	0.2	42.0	QVDQLTNDKAR	1286.7	1287.7	1286.7	1287.7
8.0	44.3	44.3	62.2	0.0	99.0	FADLSEANRNNDALR	1775.9	1776.9	1775.9	1776.9
8.0	44.3	44.3	62.2	0.0	42.0	FSLADANTEFK	1354.7	1355.7	1354.7	1355.7
8.0	44.3	44.3	62.2	0.0	32.0	QVDQLTNDKAR	1270.6	1271.6	1270.6	1271.6
8.0	44.3	44.3	62.2	0.0	99.0	QVQSLTCEVDALKGTNESLER	2371.1	2372.1	2371.1	2372.1
8.0	44.3	44.3	62.2	0.0	94.0	TNEKVELQELNDR	1586.8	1587.8	1586.8	1587.8
8.0	44.3	44.3	62.2	0.0	22.0	TVETRDGQVINETSQHHDDLE	2422.1	2423.1	2422.1	2423.1
P09211 GSTP1_HUMAN Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1) - Homo sapiens (Human)										
96.0	11.7	11.7	37.6	2.0	99.0	AFLASPEYVNLPIPINGNGKO	2033.0	2034.0	2033.0	2034.0
96.0	11.7	11.7	37.6	2.0	99.0	ALPGQLKPFETLLSONQGGK	2125.2	2126.2	2125.2	2126.2
96.0	11.7	11.7	37.6	2.0	99.0	FODGDLTLYQSNTILR	1882.9	1883.9	1882.9	1883.9
96.0	11.7	11.7	37.6	2.0	99.0	MLLADQGSQWK	1275.7	1276.7	1275.6	1276.6
96.0	11.7	11.7	37.6	2.0	99.0	PPYTVVYFVPR	1336.7	1337.7	1336.7	1337.7
96.0	11.7	11.7	37.6	1.7	98.0	PPYTVVYFVPR	1549.8	1550.8	1549.8	1550.8
96.0	11.7	11.7	37.6	0.0	47.0	PPYTVVYFVPR	1553.8	1554.8	1553.8	1554.8
47.0	6.6	6.6	23.3	2.0	99.0	ALPGQLKPFETLLSONQGGK	2125.2	2126.2	2125.2	2126.2
47.0	6.6	6.6	23.3	2.0	99.0	PPYTVVYFVPR	1336.7	1337.7	1336.7	1337.7
47.0	6.6	6.6	23.3	2.0	99.0	PPYTVVYFVPR	1549.8	1550.8	1549.8	1550.8
47.0	6.6	6.6	23.3	0.6	72.0	FODGDLTLYQSNTILR	1882.9	1883.9	1882.9	1883.9
99.0	8.0	8.0	18.6	2.0	99.0	ASCLYGLPK	1136.6	1137.6	1136.6	1137.6
99.0	8.0	8.0	18.6	2.0	99.0	FODGDLTLYQSNTILR	1882.9	1883.9	1882.9	1883.9
99.0	8.0	8.0	18.6	2.0	99.0	PPYTVVYFVPR	1336.7	1337.7	1336.7	1337.7
99.0	8.0	8.0	18.6	2.0	99.0	PPYTVVYFVPR	1549.8	1550.8	1549.8	1550.8
P09382 LEG1_HUMAN Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-1) (Lactose-binding lectin 1) (S-Lac lectin 1) (Galapin) (14)										
99.0	11.2	11.2	61.5	2.0	99.0	ACGLVASNLNPKGCECLR	2013.0	2014.0	2013.0	2014.0
99.0	11.2	11.2	61.5	2.0	99.0	DSNNLCLHFNPR	1485.7	1486.7	1485.7	1486.7
99.0	11.2	11.2	61.5	2.0	99.0	FNAHGDAINTVCSNK	1646.8	1647.8	1646.7	1647.8
99.0	11.2	11.2	61.5	2.0	99.0	LNLEAINVMAADGDFK	1783.8	1784.9	1783.8	1784.9
99.0	11.2	11.2	61.5	2.0	99.0	LPDGYEFKFPNR	1481.7	1482.7	1481.7	1482.7
99.0	11.2	11.2	61.5	1.2	94.0	DGGAWGTEGR	1075.5	1076.5	1075.5	1076.5
99.0	11.2	11.2	61.5	0.0	71.0	LPDGYEFKFPNR	1480.7	1481.7	1480.7	1481.7
68.0	4.9	4.9	61.5	2.0	99.0	ACGLVASNLNPKGCECLR	2013.0	2014.0	2013.0	2014.0
68.0	4.9	4.9	61.5	2.0	99.0	DSNNLCLHFNPR	1485.7	1486.7	1485.7	1486.7
68.0	4.9	4.9	61.5	0.7	81.0	FNAHGDAINTVCSNK	1646.8	1647.8	1646.7	1647.8
68.0	4.9	4.9	61.5	0.2	38.0	LPDGYEFKFPNR	1481.7	1482.7	1481.7	1482.7
142.0	5.7	5.7	29.6	2.0	99.0	ACGLVASNLNPKGCECLR	2013.0	2014.0	2013.0	2014.0
142.0	5.7	5.7	29.6	2.0	99.0	LPDGYEFKFPNR	1481.7	1482.7	1481.7	1482.7
142.0	5.7	5.7	29.6	1.7	98.0	DGGAWGTEGR	1075.5	1076.5	1075.5	1076.5
P09429 HMG1_HUMAN High mobility group protein B1 (High mobility group protein 1) (HMG-1) - Homo sapiens (Human)										
42.0	20.0	20.0	45.6	2.0	99.0	GKMSSYAFFVQTCR	1680.8	1681.8	1680.8	1681.8
42.0	20.0	20.0	45.6	2.0	99.0	GKMSSYAFFVQTCR	2332.1	2333.1	2332.1	2333.1
42.0	20.0	20.0	45.6	2.0	99.0	KHPDASVNFSEFSKK	1719.9	1720.9	1719.9	1720.9
42.0	20.0	20.0	45.6	2.0	99.0	KLGEWNNNTAADDKOPYEK	2237.0	2238.0	2237.0	2238.0
42.0	20.0	20.0	45.6	2.0	99.0	LGEMWNNNTAADDKOPYEK	2109.0	2110.0	2109.0	2110.0
42.0	20.0	20.0	45.6	2.0	99.0	LGEMWNNNTAADDKOPYEK	2237.0	2238.0	2237.0	2238.0
42.0	20.0	20.0	45.6	2.0	99.0	LKEKYEKIDIAAYR	1625.9	1626.9	1625.9	1626.9
42.0	20.0	20.0	45.6	2.0	99.0	MSSYAFFVQTCR	1495.7	1496.7	1495.7	1496.7
42.0	20.0	20.0	45.6	2.0	99.0	MSSYAFFVQTCR	2147.0	2148.0	2147.0	2148.0
42.0	20.0	20.0	45.6	0.0	99.0	YEKIDIAAYR	1127.6	1128.6	1127.6	1128.6
42.0	20.0	20.0	45.6	0.0	99.0	MSSYAFFVQTCR	1495.7	1496.7	1495.7	1496.7
40.0	7.5	7.5	33.5	2.0	99.0	LKEKYEKIDIAAYR	1625.9	1626.9	1625.9	1626.9
40.0	7.5	7.5	33.5	2.0	99.0	MSSYAFFVQTCR	1495.7	1496.7	1495.7	1496.7
40.0	7.5	7.5	33.5	2.0	99.0	MSSYAFFVQTCR	2147.0	2148.0	2147.0	2148.0
40.0	7.5	7.5	33.5	1.3	95.0	KLGEWNNNTAADDKOPYEK	2237.0	2238.0	2237.0	2238.0
40.0	7.5	7.5	33.5	0.2	40.0	YEKIDIAAYR	1127.6	1128.6	1127.6	1128.6
73.0	10.0	10.0	53.5	2.0	99.0	GKMSSYAFFVQTCR	1680.8	1681.8	1680.8	1681.8
73.0	10.0	10.0	53.5	2.0	99.0	IKGEHPGLSIGDVAK	1519.8	1520.8	1519.8	1520.8
73.0	10.0	10.0	53.5	2.0	99.0	LKEKYEKIDIAAYR	1625.9	1626.9	1625.9	1626.9
73.0	10.0	10.0	53.5	2.0	99.0	RPPSAFFLFCSEYRPK	2001.0	2002.0	2001.0	2002.0
73.0	10.0	10.0	53.5	2.0	99.0	YEKIDIAAYR	1127.6	1128.6	1127.6	1128.6
73.0	10.0	10.0	53.5	0.0	35.0	LKEKYEKIDIAAYR	1622.8	1623.8	1622.8	1623.8
P09496 CLCA_HUMAN Clathrin light chain A (Lca) - Homo sapiens (Human)										
315.0	4.0	4.0	12.9	2.0	99.0	AEEAFVNDIDESSPGTEWER	2351.0	2352.0	2351.0	2352.0
315.0	4.0	4.0	12.9	2.0	99.0	AIKELEEWYAR	1406.7	1407.7	1406.7	1407.7
203.0	1.5	1.5	11.3	1.5	97.0	AIKELEEWYAR	1406.7	1407.7	1406.7	1407.7
P09651 ROA1_HUMAN Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) - Homo sapiens (Human)										
32.0	23.7	28.6	63.4	2.0	99.0	ALSKOEMASASSSORGR	1820.9	1821.9	1820.9	1821.9
32.0	23.7	28.6	63.4	2.0	99.0	AVSREDSORPGAHLTVKK	1978.1	1979.1	1978.1	1979.1
32.0	23.7	28.6	63.4	2.0	99.0	EDSORPGAHLTVK	1436.7	1437.7	1436.7	1437.7
32.0	23.7	28.6	63.4	2.0	99.0	GFAFVTFDDHSDVKIVIOK	2280.1	2281.1	2280.1	2281.1
32.0	23.7	28.6	63.4	2.0	99.0	KALSKOEMASASSSORGR	1949.0	1950.0	1949.0	1950.0
32.0	23.7	28.6	63.4	2.0	99.0	NOGGYGGSSSSSYGSGR	1693.7	1694.7	1693.7	1694.7
32.0	23.7	28.6	63.4	2.0	99.0	RAVSREDSORPGAHLTVKK	2134.2	2135.2	2134.2	2135.2
32.0	23.7	28.6	63.4	2.0	99.0	SHEEQWGLTDCVVMRDPNTR	2677.3	2678.3	2677.2	2678.2
32.0	23.7	28.6	63.4	2.0	99.0	SSGPGYGGGQYFAKPR	1627.8	1628.8	1627.8	1628.8
32.0	23.7	28.6	63.4	2.0	99.0	YHTVNGHNCVPR	1484.7	1485.7	1484.7	1485.7
32.0	23.7	28.6	63.4	1.7	98.0	IEVIEIMTR	1217.6	1218.6	1217.6	1218.6
32.0	23.7	28.6	63.4	1.2	99.0	LFIGGLSFETTESLDR	1783.9	1784.9	1783.9	1784.9
32.0	23.7	28.6	63.4	0.4	59.0	KLFIGGLSFETTESLDR	1912.0	1913.0	1912.0	1913.0
32.0	23.7	28.6	63.4	0.3	44.7	SKSESPKEPEQLRK	1683.9	1684.9	1683.9	1684.9
32.0	23.7	28.6	63.4	0.1	20.0	AVSREDSORPGAHLTVK	1850.0	1851.0	1850.0	1851.0
32.0	23.7	28.6	63.4	0.0	99.0	IFVGGIKEDTEEHLR	1879.0	1880.0	1879.0	1880.0
32.0	23.7	28.6	63.4</							

65.0	11.9	13.9	51.1	0.0	99.0	IFVGKIKEDTEEHHLR	1878.9	1880.0	1879.0	1880.0
65.0	11.9	13.9	51.1	0.0	99.0	IFVGKIKEDTEEHHLR	1879.0	1880.0	1879.0	1880.0
P09874 PARP1_HUMAN Poly [ADP-ribose] polymerase 1 (EC 2.4.2.30) (PARP-1) (ADPRT) (NAD(+)-ADP-ribosyltransferase 1) (Poly[ADP-ribose] synthetase 1) - Homo sapiens (Human)										
125.0	9.4	9.4	16.2	2.0	99.0	NREELGRFPEYSASOLK	2023.0	2024.0	2023.0	2024.0
125.0	9.4	9.4	16.2	2.0	99.0	SDAYTCGDTAWTK	1736.8	1737.8	1736.7	1737.7
125.0	9.4	9.4	16.2	2.0	99.0	VGSIRHPDVEVDGFSLELR	2149.2	2149.2	2149.1	2149.1
125.0	9.4	9.4	16.2	2.0	99.0	WYHRCFCVK	1192.5	1193.6	1192.5	1193.6
125.0	9.4	9.4	16.2	0.7	79.0	MVDPEKPOLGMIDR	1627.8	1628.8	1627.8	1628.8
125.0	9.4	9.4	16.2	0.6	77.0	LLWHGSR	867.5	868.5	867.5	868.5
224.0	2.9	2.9	3.9	1.5	97.0	WYHRCFCVK	1192.5	1193.6	1192.5	1193.6
224.0	2.9	2.9	3.9	1.4	96.0	MAESSDKLYR	1214.6	1215.6	1214.6	1215.6
P09960 LKHA4_HUMAN Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase) (Leukotriene A(4) hydrolase) - Homo sapiens (Human)										
342.0	2.0	2.0	5.1	2.0	99.0	MQEVYFNAINNSEIR	1940.9	1941.9	1940.9	1941.9
115.0	9.9	9.9	14.1	2.0	99.0	HFNALGGWGLONSVK	1755.9	1756.9	1755.9	1756.9
115.0	9.9	9.9	14.1	2.0	99.0	MQEVYFNAINNSEIR	1940.9	1941.9	1940.9	1941.9
115.0	9.9	9.9	14.1	2.0	99.0	PEIVDTCSLSPASVCR	1860.9	1861.9	1860.9	1861.9
115.0	9.9	9.9	14.1	2.0	99.0	TLTGTAALTVSQEDNLR	1917.0	1918.0	1917.0	1918.0
115.0	9.9	9.9	14.1	1.7	98.0	APLPLGHKRR	1100.7	1101.7	1100.7	1101.7
115.0	9.9	9.9	14.1	0.2	34.0	MKFTFRPLFK	1166.7	1167.7	1166.7	1167.7
P10124 PGSG_HUMAN Secretory granule proteoglycan core protein precursor (Platelet proteoglycan core protein) (P.PG) (Hematopoietic proteoglycan core protein) (Ser)										
179.0	6.4	6.4	39.2	2.0	99.0	GMPELLPAGESNKIPR	1783.9	1784.9	1783.9	1784.9
179.0	6.4	6.4	39.2	2.0	99.0	NLPSSDSDLGOHGLEEDFML	2244.0	2245.0	2244.0	2245.0
179.0	6.4	6.4	39.2	2.0	99.0	YQLVDESDFHNDLNR	1820.8	1821.8	1820.8	1821.8
179.0	6.4	6.4	39.2	0.4	61.0	ARYQWVR	977.5	978.5	977.5	978.5
179.0	6.4	6.4	39.2	0.0	99.0	YQLVDESDFHNDLNR	1820.8	1821.8	1820.8	1821.8
48.0	6.5	6.5	39.2	2.0	99.0	GMPELLPAGESNKIPR	1783.9	1784.9	1783.9	1784.9
48.0	6.5	6.5	39.2	2.0	99.0	NLPSSDSDLGOHGLEEDFML	2244.0	2245.0	2244.0	2245.0
48.0	6.5	6.5	39.2	1.5	97.0	YQLVDESDFHNDLNR	1820.8	1821.8	1820.8	1821.8
48.0	6.5	6.5	39.2	0.9	86.0	ARYQWVR	977.5	978.5	977.5	978.5
48.0	6.5	6.5	39.2	0.1	23.0	YQWVR	751.4	752.4	751.4	752.4
82.0	9.0	9.0	39.2	2.0	99.0	GMPELLPAGESNKIPR	1783.9	1784.9	1783.9	1784.9
82.0	9.0	9.0	39.2	2.0	99.0	NLPSSDSDLGOHGLEEDFML	2244.0	2245.0	2244.0	2245.0
82.0	9.0	9.0	39.2	2.0	99.0	SLDRNLPSSDSDLGOHGLEEDFML	2715.3	2716.3	2715.2	2716.3
82.0	9.0	9.0	39.2	2.0	99.0	YQLVDESDFHNDLNR	1820.8	1821.8	1820.8	1821.8
82.0	9.0	9.0	39.2	0.5	69.0	YQWVR	751.4	752.4	751.4	752.4
82.0	9.0	9.0	39.2	0.5	65.0	ARYQWVR	977.5	978.5	977.5	978.5
82.0	9.0	9.0	39.2	0.0	99.0	YQLVDESDFHNDLNR	1820.8	1821.8	1820.8	1821.8
P10145 IL8_HUMAN Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-activat										
133.0	8.4	8.4	49.5	2.0	99.0	ELCLDPKENWVQR	1685.8	1686.8	1685.8	1686.8
133.0	8.4	8.4	49.5	2.0	99.0	LSDGRELLDLPKENWVQR	2214.1	2215.1	2214.1	2215.1
133.0	8.4	8.4	49.5	2.0	99.0	TSYKPFHPK	1103.6	1104.6	1103.6	1104.6
133.0	8.4	8.4	49.5	2.0	99.0	VIESGPHCANTEIIVK	1765.9	1766.9	1765.9	1766.9
133.0	8.4	8.4	49.5	0.2	40.0	ENWVQR	830.4	831.4	830.4	831.4
133.0	8.4	8.4	49.5	0.1	27.0	FIKELR	804.5	805.5	804.5	805.5
133.0	8.4	8.4	49.5	0.0	99.0	VIESGPHCANTEIIVK	1765.9	1766.9	1765.9	1766.9
133.0	8.4	8.4	49.5	0.0	99.0	VIESGPHCANTEIIVK	1917.9	1918.9	1917.9	1918.9
133.0	8.4	8.4	49.5	0.0	99.0	VIESGPHCANTEIIVK	1767.9	1768.9	1767.9	1768.9
73.0	4.8	4.8	43.4	2.0	99.0	LSDGRELLDLPKENWVQR	2214.1	2215.1	2214.1	2215.1
73.0	4.8	4.8	43.4	2.0	99.0	VIESGPHCANTEIIVK	1765.9	1766.9	1765.9	1766.9
73.0	4.8	4.8	43.4	0.6	74.0	ELCLDPKENWVQR	1685.8	1686.8	1685.8	1686.8
73.0	4.8	4.8	43.4	0.2	36.0	TSYKPFHPK	1103.6	1104.6	1103.6	1104.6
73.0	4.8	4.8	43.4	0.0	24.0	VIESGPHCANTEIIVK	1765.9	1766.9	1765.9	1766.9
105.0	7.7	7.7	56.6	2.0	99.0	ELCLDPKENWVQR	1685.8	1686.8	1685.8	1686.8
105.0	7.7	7.7	56.6	2.0	99.0	LSDGRELLDLPKENWVQR	2214.1	2215.1	2214.1	2215.1
105.0	7.7	7.7	56.6	2.0	99.0	VIESGPHCANTEIIVK	1765.9	1766.9	1765.9	1766.9
105.0	7.7	7.7	56.6	1.4	96.0	TSYKPFHPK	1103.6	1104.6	1103.6	1104.6
105.0	7.7	7.7	56.6	0.3	47.0	FIKELR	804.5	805.5	804.5	805.5
105.0	7.7	7.7	56.6	0.0	99.0	VIESGPHCANTEIIVK	1765.9	1766.9	1765.9	1766.9
P10319 IB58_HUMAN HLA class I histocompatibility antigen, B-58 alpha chain precursor (MHC class I antigen B*58) (Bw-58) - Homo sapiens (Human)										
107.0	3.2	3.2	41.7	2.0	99.0	WAAVVVPSGEEOR	1426.7	1427.7	1426.7	1427.7
107.0	3.2	3.2	41.7	0.7	79.0	AYLEGLCVEWLR	1507.8	1508.8	1507.7	1508.8
107.0	3.2	3.2	41.7	0.3	55.0	APWIEQGEPEYWDGETR	2061.9	2062.9	2061.9	2062.9
107.0	3.2	3.2	41.7	0.1	22.0	YFYTAMSRGRGEPTR	1786.8	1787.8	1786.9	1787.9
160.0	7.4	12.3	40.6	2.0	99.0	APWIEQGEPEYWDGETR	2061.9	2062.9	2061.9	2062.9
160.0	7.4	12.3	40.6	2.0	99.0	DGEDDTQDTELVEVTRPAGDRITFOK	2735.3	2736.3	2735.3	2736.3
160.0	7.4	12.3	40.6	2.0	99.0	YTCVGHGLPKPLT	1778.9	1779.9	1778.9	1779.9
160.0	7.4	12.3	40.6	1.2	99.0	MNGDVLGPDGR	1225.5	1226.5	1225.5	1226.5
160.0	7.4	12.3	40.6	0.2	38.0	AYLEGLCVEWLR	1507.8	1508.8	1507.7	1508.8
160.0	7.4	12.3	40.6	0.0	99.0	FIAVGVDDTQFVVR	1628.8	1629.8	1628.8	1629.8
160.0	7.4	12.3	40.6	0.0	99.0	WAAVVVPSGEEOR	1426.7	1427.7	1426.7	1427.7
P10412 H14_HUMAN Histone H1.4 (Histone H1b) - Homo sapiens (Human)										
74.0	14.0	14.0	18.3	2.0	99.0	ALAAAGYDVEKNNSR	1577.8	1578.8	1577.8	1578.8
74.0	14.0	14.0	18.3	2.0	99.0	KALAAAGYDVEKNNSR	1705.9	1706.9	1705.9	1706.9
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAEK	1519.8	1520.8	1519.8	1520.8
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAEKTPVK	1945.0	1946.0	1945.0	1946.0
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAEKTPVKK	2073.1	2074.1	2073.1	2074.1
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAEKTPVKKK	2201.2	2202.2	2201.2	2202.2
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAEKTPVKKKAR	2428.4	2429.4	2428.3	2429.4
74.0	14.0	14.0	18.3	0.0	99.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
74.0	14.0	14.0	18.3	0.0	20.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
160.0	4.4	7.7	24.2	2.0	99.0	SETAPAAPAAPAEKTPVKK	2073.1	2074.1	2073.1	2074.1
160.0	4.4	7.7	24.2	1.2	99.0	SETAPAAPAAPAEKTPVK	1945.0	1946.0	1945.0	1946.0
160.0	4.4	7.7	24.2	1.2	99.0	SETAPAAPAAPAEKTPVKKK	2201.2	2202.2	2201.2	2202.2
160.0	4.4	7.7	24.2	0.0	98.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
160.0	4.4	7.7	24.2	0.0	98.0	ALAAAGYDVEKNNSR	1577.8	1578.8	1577.8	1578.8
P10599 THIO_HUMAN Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphhydryl protein) (SASP) - Homo sapiens (Human)										
113.0	10.0	10.0	42.9	2.0	99.0	CMPTFOFFK	1187.5	1188.5	1187.5	1188.6
113.0	10.0	10.0	42.9	2.0	99.0	CMPTFOFFKK	1332.6	1333.6	1332.6	1333.6
113.0	10.0	10.0	42.9	2.0	99.0	CMPTFOFFKGGK	1628.8	1629.8	1628.8	1629.8
113.0	10.0	10.0	42.9	2.0	99.0	MIKPFHLSSEK	1462.8	1463.8	1462.8	1463.8
113.0	10.0	10.0	42.9	2.0	99.0	VGEFSGANKLEATINELV	2147.1	2148.1	2147.1	2148.1
113.0	10.0	10.0	42.9	0.0	99.0	CMPTFOFFK	1204.5	1205.5	1204.5	1205.5
113.0	10.0	10.0	42.9	0.0	85.0	CMPTFOFFK	1187.6	1188.6	1187.6	1188.6
113.0	10.0	10.0	42.9	0.0	63.0	CMPTFOFFKK	1315.6	1316.6	1315.6	1316.6
80.0	4.3	4.3	33.3	2.0	99.0	CMPTFOFFK	1159.5	1160.5	1159.5	1160.5
80.0	4.3	4.3	33.3	2.0	99.0	MIKPFHLSSEK	1462.8	1463.8	1462.8	1463.8
80.0	4.3	4.3	33.3	0.3	51.0	CMPTFOFFKK	1315.6	1316.6	1315.6	1316.6
80.0	4.3	4.3	33.3	0.0	99.0	CMPTFOFFK	1204.5	1205.5	1204.5	1205.5
80.0	4.3	4.3	33.3	0.0	99.0	CMPTFOFFK	1187.5	1188.5	1187.5	1188.6
80.0	4.3	4.3	33.3	0.0	79.0	CMPTFOFFK	1203.5	1204.5	1203.5	1204.5
80.0	4.3	4.3	33.3	0.0	41.0	CMPTFOFFK	1220.5	1221.5	1220.5	1221.5
81.0	9.1	9.1	42.9	2.0	99.0	CMPTFOFFK	1187.5	1188.5	1187.5	1188.6
81.0	9.1	9.1	42.9	2.0	99.0	CMPTFOFFKGGK	1628.8	1629.8	1628.8	1629.8
81.0	9.1	9.1	42.9	2.0	99.0	MIKPFHLSSEK	1478.8	1479.8	1478.8	1479.8
81.0	9.1	9.1	42.9	2.0	99.0	VGEFSGANKLEATINELV	2147.1	2148.1	2147.1	2148.1
81.0	9.1	9.1	42.9	1.1	92.0	CMPTFOFFKK	1315.6	1316.6	1315.6	1316.6
81.0	9.1	9.1	42.9	0.0	99.0	CMPTFOFFK	1204.5	1205.5	1204.5	1205.5
81.0	9.1	9.1	42.9	0.0	99.0	CMPTFOFFK	1189.5	1190.5	1189.5	1190.6
81.0	9.1	9.1	42.9	0.0	99.0	MIKPFHLSSEK	1462.8	1463.8	1462.8	1463.8
P11021 GRP78_HUMAN 78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP) (Endopl										
104.0	10.4	13.3	22.3	2.0	99.0	IEIESFYEGEDFSETLTR	2164.0	2165.0	2164.0	2165.0
104.0										

83.0	9.0	10.6	15.3	1.0	92.0	FEELNMDLFR	1312.6	1313.6	1312.6	1313.6
83.0	9.0	10.6	15.3	0.0	36.0	FEELNMDLFR	1252.6	1253.6	1252.6	1253.6
83.0	9.0	10.6	15.3	0.0	96.0	VEIANDQGNR	1227.6	1228.6	1227.6	1228.6
P11142 HSP7C_HUMAN Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) - Homo sapiens (Human)										
9.0	43.1	43.1	46.0	2.0	99.0	ARFELNADLFR	1479.7	1480.8	1479.7	1480.8
9.0	43.1	43.1	46.0	2.0	99.0	ATVDEKLGKINDEDEKQK	2229.1	2230.2	2229.1	2230.2
9.0	43.1	43.1	46.0	2.0	99.0	FEELNADLFR	1252.6	1253.6	1252.6	1253.6
9.0	43.1	43.1	46.0	2.0	99.0	HWPFMVHNDVGRPK	1652.8	1653.8	1652.8	1653.8
9.0	43.1	43.1	46.0	2.0	99.0	LDKSIQHDIVLVGGSTR	1837.0	1838.0	1837.0	1838.0
9.0	43.1	43.1	46.0	2.0	99.0	LLQDFGFKELNK	1565.8	1566.8	1565.8	1566.8
9.0	43.1	43.1	46.0	2.0	99.0	MVNHFAIEFK	1234.6	1235.6	1234.6	1235.6
9.0	43.1	43.1	46.0	2.0	99.0	MVNHFAIEFKR	1390.7	1391.7	1390.7	1391.7
9.0	43.1	43.1	46.0	2.0	99.0	MVQAEKYKAEDEKOR	1980.0	1981.0	1980.0	1981.0
9.0	43.1	43.1	46.0	2.0	99.0	MVQAEKYKAEDEKORVKVSSK	2625.3	2626.3	2625.3	2626.3
9.0	43.1	43.1	46.0	2.0	99.0	NOVAMPNTVFDAR	1648.8	1649.8	1648.8	1649.8
9.0	43.1	43.1	46.0	2.0	99.0	NOVAMPNTVFDADR	1805.0	1806.0	1804.9	1805.9
9.0	43.1	43.1	46.0	2.0	99.0	NSLESYAFNMK	1302.6	1303.6	1302.6	1303.6
9.0	43.1	43.1	46.0	2.0	99.0	SFYPEEVSMSVLTK	1615.8	1616.8	1615.8	1616.8
9.0	43.1	43.1	46.0	2.0	99.0	SQIHDIVLVGGSTR	1480.8	1481.8	1480.8	1481.8
9.0	43.1	43.1	46.0	2.0	99.0	STAGDTHLGGDFDNR	1690.7	1691.7	1690.7	1691.7
9.0	43.1	43.1	46.0	2.0	99.0	TTPSYVAFTDTER	1486.7	1487.7	1486.7	1487.7
9.0	43.1	43.1	46.0	2.0	99.0	TVTNAVITVPAYFNDSOR	1981.0	1982.0	1981.0	1982.0
9.0	43.1	43.1	46.0	2.0	99.0	VEIANDQGNR	1227.6	1228.6	1227.6	1228.6
9.0	43.1	43.1	46.0	2.0	99.0	VQVEYKGETK	1179.6	1180.6	1179.6	1180.6
9.0	43.1	43.1	46.0	1.7	98.0	RFDDAVQSDMK	1409.7	1410.7	1409.7	1410.7
9.0	43.1	43.1	46.0	1.3	95.0	MVQAEKYKAEDEKORDK	2224.1	2225.1	2224.1	2225.1
9.0	43.1	43.1	46.0	0.0	79.0	MVQAEKYKAEDEKOR	1981.0	1982.0	1981.0	1982.0
9.0	43.1	43.1	46.0	0.0	99.0	STAGDTHLGGDFDNR	1693.8	1694.8	1693.8	1694.8
15.0	16.6	16.6	32.5	2.0	99.0	IINEPTAAAIAVGLDKK	1787.0	1788.0	1787.0	1788.0
15.0	16.6	16.6	32.5	2.0	99.0	MVNHFAIEFK	1390.7	1391.7	1390.7	1391.7
15.0	16.6	16.6	32.5	2.0	99.0	MVNHFAIEFKR	1390.7	1391.7	1390.7	1391.7
15.0	16.6	16.6	32.5	2.0	99.0	SFYPEEVSMSVLTK	1615.7	1616.7	1615.8	1616.8
15.0	16.6	16.6	32.5	2.0	99.0	STAGDTHLGGDFDNR	1690.7	1691.7	1690.7	1691.7
15.0	16.6	16.6	32.5	2.0	99.0	TTPSYVAFTDTER	1486.7	1487.7	1486.7	1487.7
15.0	16.6	16.6	32.5	1.4	96.0	TVTNAVITVPAYFNDSOR	1981.0	1982.0	1981.0	1982.0
15.0	16.6	16.6	32.5	1.2	93.0	NOVAMPNTVFDAR	1804.9	1805.9	1804.9	1805.9
15.0	16.6	16.6	32.5	1.0	91.0	MVQAEKYKAEDEKOR	1981.0	1982.0	1981.0	1982.0
15.0	16.6	16.6	32.5	0.7	82.0	NSLESYAFNMK	1302.6	1303.6	1302.6	1303.6
15.0	16.6	16.6	32.5	0.2	34.0	DAGTIAGLNVLRL	1199.7	1199.7	1199.7	1199.7
26.0	21.5	21.5	28.8	2.0	99.0	DAGTIAGLNVLRL	1199.7	1199.7	1199.7	1199.7
26.0	21.5	21.5	28.8	2.0	99.0	LDKSIQHDIVLVGGSTR	1837.0	1838.0	1837.0	1838.0
26.0	21.5	21.5	28.8	2.0	99.0	MVNHFAIEFK	1234.6	1235.6	1234.6	1235.6
26.0	21.5	21.5	28.8	2.0	99.0	NOVAMPNTVFDAR	1805.8	1806.8	1805.8	1806.8
26.0	21.5	21.5	28.8	2.0	99.0	OATKADAGTIAGLNVLRL	1609.9	1610.9	1609.9	1610.9
26.0	21.5	21.5	28.8	2.0	99.0	SFYPEEVSMSVLTK	1615.8	1616.8	1615.8	1616.8
26.0	21.5	21.5	28.8	2.0	99.0	STAGDTHLGGDFDNR	1690.7	1691.7	1690.7	1691.7
26.0	21.5	21.5	28.8	2.0	99.0	TTPSYVAFTDTER	1486.7	1487.7	1486.7	1487.7
26.0	21.5	21.5	28.8	2.0	99.0	TVTNAVITVPAYFNDSOR	1981.0	1982.0	1981.0	1982.0
26.0	21.5	21.5	28.8	1.4	96.0	VEIANDQGNR	1227.6	1228.6	1227.6	1228.6
26.0	21.5	21.5	28.8	1.1	92.0	FEELNADLFR	1252.6	1253.6	1252.6	1253.6
26.0	21.5	21.5	28.8	0.9	88.0	MVNHFAIEFKR	1390.7	1391.7	1390.7	1391.7
26.0	21.5	21.5	28.8	0.0	99.0	STAGDTHLGGDFDNR	1693.8	1694.8	1690.7	1691.7
26.0	21.5	21.5	28.8	0.0	99.0	STAGDTHLGGDFDNR	1689.7	1689.7	1690.7	1691.7
P11413 G6PD_HUMAN Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD) - Homo sapiens (Human)										
100.0	11.1	11.1	20.8	2.0	99.0	DGLLEPTIFVGVYR	1663.9	1664.9	1663.9	1664.9
100.0	11.1	11.1	20.8	2.0	99.0	LKLEDFAR	1137.6	1138.6	1137.6	1138.6
100.0	11.1	11.1	20.8	2.0	99.0	LNSHMNALHLGSOANR	1761.9	1762.9	1761.9	1762.9
100.0	11.1	11.1	20.8	2.0	99.0	NIHESCMSIQGWNR	1730.8	1731.8	1730.8	1731.8
100.0	11.1	11.1	20.8	2.0	99.0	NSYVAGVYDDAASYOR	1806.8	1807.8	1806.8	1807.8
100.0	11.1	11.1	20.8	0.6	74.0	WDGVFPILR	1101.6	1102.6	1101.6	1102.6
100.0	11.1	11.1	20.8	0.5	69.0	LOFHDVAGDIFHQCKR	2098.0	2099.0	2098.0	2099.0
205.0	1.5	1.5	6.8	1.0	89.0	LKLEDFAR	1137.6	1138.6	1137.6	1138.6
205.0	1.5	1.5	6.8	0.5	70.0	LOFHDVAGDIFHQCKR	2098.0	2099.0	2098.0	2099.0
101.0	7.7	7.7	22.9	2.0	98.0	LKLEDFAR	1137.6	1138.6	1137.6	1138.6
101.0	7.7	7.7	22.9	2.0	98.0	LOFHDVAGDIFHQCKR	1941.9	1942.9	1941.9	1942.9
101.0	7.7	7.7	22.9	2.0	98.0	NSYVAGVYDDAASYOR	1806.8	1807.8	1806.8	1807.8
101.0	7.7	7.7	22.9	1.7	98.0	DGLLEPTIFVGVYR	1663.9	1664.9	1663.9	1664.9
101.0	7.7	7.7	22.9	0.0	98.0	NSYVAGVYDDAASYOR	1807.8	1808.8	1807.8	1808.8
P11717 MPRI_HUMAN Cation-independent mannose-6-phosphate receptor precursor (CI Man-6-P receptor) (CI-MPR) (M6PR) (Insulin-like growth factor 2 receptor) (Igf2R) - Homo sapiens (Human)										
201.0	1.5	1.5	6.2	1.5	97.0	GHOAFDVGOQR	1210.6	1211.6	1210.6	1211.6
322.0	2.0	2.0	2.5	2.0	99.0	GHOAFDVGOQR	1210.6	1211.6	1210.6	1211.6
P11940 PABP1_HUMAN Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) - Homo sapiens (Human)										
6.0	6.0	6.0	21.2	2.0	99.0	GFGVSEFR	1044.5	1045.5	1044.5	1045.5
194.0	6.0	6.0	21.2	2.0	99.0	QAHLTNOVMOR	1371.6	1372.6	1371.6	1372.6
194.0	6.0	6.0	21.2	2.0	99.0	SLGYAYVNFQOPADAER	1927.9	1928.9	1927.9	1928.9
194.0	6.0	6.0	21.2	0.0	99.0	QAHLTNOVMOR	1388.7	1389.7	1388.7	1389.7
117.0	2.6	2.6	18.4	1.4	96.0	SLGYAYVNFQOPADAER	1927.9	1928.9	1927.9	1928.9
117.0	2.6	2.6	18.4	1.2	94.0	GFGVSEFR	1044.5	1045.5	1044.5	1045.5
199.0	3.7	3.7	11.9	2.0	98.0	GFGVSEFR	1044.5	1045.5	1044.5	1045.5
199.0	3.7	3.7	11.9	1.7	98.0	GFGVSEFR	1738.8	1739.8	1738.8	1739.8
P12955 PEPD_HUMAN Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptidase) (Proline dipeptidase) (Prolidase) (Imidodipeptidase) - Homo sapiens (Human)										
572.0	1.5	1.5	3.4	1.5	97.0	AFTPSEPK	950.5	951.5	950.5	951.5
367.0	2.0	2.0	2.0	2.0	99.0	VPLALFNLR	1112.7	1113.7	1112.7	1113.7
P12956 KU70_HUMAN ATP-dependent DNA helicase 2 subunit 1 (ATP-dependent DNA helicase II 70 kDa subunit) (Lupus Ku autoantigen protein p70) (Ku70) (70 kDa subunit) - Homo sapiens (Human)										
49.0	18.0	18.0	20.2	2.0	99.0	DTGIFLDMHLK	1401.7	1402.7	1401.7	1402.7
49.0	18.0	18.0	20.2	2.0	99.0	GGFDISLFYR	1173.6	1174.6	1173.6	1174.6
49.0	18.0	18.0	20.2	2.0	99.0	ILEDQFKGOOGQKR	1787.0	1788.0	1787.0	1788.0
49.0	18.0	18.0	20.2	2.0	99.0	IMATPEQVQK	1072.6	1073.6	1072.6	1073.6
49.0	18.0	18.0	20.2	2.0	99.0	IMLFNEDNPHGNSDAK	1901.9	1902.9	1901.9	1902.9
49.0	18.0	18.0	20.2	2.0	99.0	NIVLQELDNPAKR	1729.9	1730.9	1729.9	1730.9
49.0	18.0	18.0	20.2	2.0	99.0	SDSFENPVLQOHFR	1702.8	1703.8	1702.8	1703.8
49.0	18.0	18.0	20.2	2.0	99.0	SGWESYK	1060.5	1061.5	1060.5	1061.5
49.0	18.0	18.0	20.2	2.0	99.0	VHFESKLEDLR	1700.9	1701.9	1700.9	1701.9
49.0	18.0	18.0	20.2	0.0	99.0	SDSFENPVLQOHFR	1705.8	1706.8	1702.8	1703.8
227.0	2.9	2.9	11.8	2.0	99.0	GGFDISLFYR	1173.6	1174.6	1173.6	1174.6
227.0	2.9	2.9	11.8	0.9	87.0	KPGGDISLFYR	1398.7	1399.7	1398.7	1399.7
P13284 GILT_HUMAN Gamma-interferon-inducible lysosomal thiol reductase precursor (Gamma-interferon-inducible protein IP-30) - Homo sapiens (Human)										
545.0	2.0	2.0	4.2	2.0	99.0	GMQLMHANAQR	1255.6	1256.6	1255.6	1256.6
545.0	2.0	2.0	4.2	0.0	99.0	GMQLMHANAQR	1256.6	1257.6	1256.6	1257.6
545.0	2.0	2.0	4.2	0.0	99.0	GMQLMHANAQR	1256.6	1257.6	1256.6	1257.6
183.0	2.0	2.0	8.8	2.0	99.0	GMQLMHANAQR	1255.6	1256.6	1255.6	1256.6
366.0	2.0	2.0	4.2	2.0	98.0	GMQLMHANAQR	1256.6	1257.6	1256.6	1257.6
366.0	2.0	2.0	4.2	0.0	98.0	GMQLMHANAQR	1271.6	1272.6	1271.6	1272.6
366.0	2.0	2.0	4.2	0.0	98.0	GMQLMHANAQR	1256.6	1257.6	1256.6	1257.6
366.0	2.0	2.0	4.2	0.0	98.0	GMQLMHANAQR	1256.6	1257.6	1256.6	1257.6
P13489 RINI_HUMAN Ribonuclease inhibitor (Ribonuclease/angiogenin inhibitor 1) (RAI) (Placental ribonuclease inhibitor) (RNase inhibitor) (RI) - Homo sapiens (Human)										
232.0	5.3	5.3	15.0	2.0	99.0	SLDIQSLDICEELSDAR	2133.0	2134.0	2133.0	2134.0
232.0	5.3	5.3	15.0	2.0	99.0	TLWIECCGITAK	1477.8	1478.8	1477.8	1478.8
232.0	5.3	5.3	15.0	1.3	95.0	LDDCGLTEAR	1148.5	1149.5	1148.5	1149.5
300.0	2.0	2.0	6.9	2.0	99.0	SCSFTAACCSHFSSVLAQNR	2289.0	2290.0	2289.0	2290.0
P13639 EF2_HUMAN Elongation factor 2 (EF-2) - Homo sapiens (Human)										
35.0	22.8	22.8	20.3	2.0	99.0	ARPPDGLAEDIKGEVSAR	2142.1	2143.1	2142.1	2143.1
35.0	22.8	22.8	20.3	2.0	99.0	AYLPVNESFGFTAD				

33.0	9.8	9.8	18.4	2.0	99.0	CLYASVLTQAPR	1377.7	1378.7	1377.7	1378.7
33.0	9.8	9.8	18.4	2.0	99.0	GHVFEESVAGTTPMFVVK	1961.0	1962.0	1961.0	1962.0
33.0	9.8	9.8	18.4	2.0	99.0	YLAEKYVDVAEAR	1741.8	1742.8	1741.8	1742.8
33.0	9.8	9.8	18.4	1.3	95.0	YEWVDAEAR	1137.5	1138.5	1137.5	1138.5
33.0	9.8	9.8	18.4	0.2	42.0	FSVSPVVR	889.5	890.5	889.5	890.5
33.0	9.8	9.8	18.4	0.2	97.0	CELLVEGPPDDEAAMGK	1999.9	1999.9	1999.9	1999.9
51.0	15.4	15.4	27.2	2.0	98.0	CLYASVLTQAPR	1367.0	1367.1	1367.0	1367.1
51.0	15.4	15.4	27.2	2.0	98.0	GHVFEESVAGTTPMFVVK	1961.0	1962.0	1961.0	1962.0
51.0	15.4	15.4	27.2	2.0	98.0	IMGPNYTPGKEDLYLKPIQR	2460.3	2461.3	2460.3	2461.3
51.0	15.4	15.4	27.2	2.0	98.0	VNFTVDQIR	1090.6	1091.6	1090.6	1091.6
51.0	15.4	15.4	27.2	2.0	98.0	YEWVDAEAR	1137.5	1138.5	1137.5	1138.5
51.0	15.4	15.4	27.2	2.0	98.0	YLAEKYVDVAEAR	1741.8	1742.8	1741.8	1742.8
51.0	15.4	15.4	27.2	1.7	98.0	AYLPVNESFGFTADLR	1798.9	1799.9	1798.9	1799.9
51.0	15.4	15.4	27.2	1.1	92.0	FYAFGR	759.4	760.4	759.4	760.4
51.0	15.4	15.4	27.2	0.3	49.0	ANIRNMSVIAHVDHGK	1763.8	1764.8	1763.8	1764.8
51.0	15.4	15.4	27.2	0.2	30.0	FAAKGEGQLGPAER	1429.7	1430.7	1429.7	1430.7
51.0	15.4	15.4	27.2	0.1	22.0	GGGQIIPARR	1124.6	1125.6	1124.6	1125.6
P13640 MT1G_HUMAN Metallothionein-1G (MT-1G) (Metallothionein-1G) (Metallothionein-1K) (MT-1K) - Homo sapiens (Human)										
460.0	2.0	4.0	53.2	2.0	99.0	MDPNCSCAAAGVSTCASSCK	2334.8	2335.8	2334.8	2335.9
460.0	2.0	4.0	53.2	0.0	99.0	SCCSCCPVGCCK	1444.5	1445.5	1444.5	1445.5
460.0	2.0	4.0	53.2	0.0	99.0	SCCSCCPVGCCK	1447.5	1448.5	1444.5	1445.5
460.0	2.0	4.0	53.2	0.0	99.0	SCCSCCPVGCCK	1447.5	1448.5	1444.5	1445.5
182.0	2.0	2.0	53.2	2.0	99.0	SCCSCCPVGCCK	1444.5	1445.5	1444.5	1445.5
305.0	2.0	6.0	54.8	2.0	98.0	MDPNCSCAAAGVSTCASSCK	2334.8	2335.9	2334.8	2335.9
305.0	2.0	6.0	54.8	0.0	98.0	KSCCSCCPVGCCK	1573.6	1574.6	1573.6	1573.6
305.0	2.0	6.0	54.8	0.0	98.0	MDPNCSCAAAGVSTCASSCK	2338.8	2339.9	2338.8	2339.8
305.0	2.0	6.0	54.8	0.0	98.0	SCCSCCPVGCCK	1444.5	1445.5	1444.5	1445.5
305.0	2.0	6.0	54.8	0.0	98.0	SCCSCCPVGCCK	1446.5	1447.5	1444.5	1445.5
305.0	2.0	6.0	54.8	0.0	98.0	SCCSCCPVGCCK	1446.5	1447.5	1444.5	1445.5
P13686 PPA5_HUMAN Tartrate-resistant acid phosphatase type-5 precursor (EC 3.1.3.2) (TR-AP) (Tartrate-resistant acid ATPase) (TrATPase) (Acid phosphatase 5, tartr										
247.0	4.9	4.9	12.3	2.0	99.0	FOETFEDVFSDR	1518.7	1519.7	1518.7	1519.7
247.0	4.9	4.9	12.3	2.0	99.0	FVAVGDWGGVNPAPFHTR	1997.0	1998.0	1997.0	1998.0
247.0	4.9	4.9	12.3	0.9	86.0	WNFSPFVR	1212.6	1213.6	1212.6	1213.6
144.0	2.1	2.1	15.7	2.0	99.0	FVAVGDWGGVNPAPFHTR	1997.0	1998.0	1997.0	1998.0
299.0	2.0	2.0	6.5	2.0	98.0	FOETFEDVFSDR	1518.7	1519.7	1518.7	1519.7
P13796 PLSL_HUMAN Plastin-2 (L-plastin) (Lymphocyte cytosolic protein 1) (LCP-1) (LC64P) - Homo sapiens (Human)										
26.0	26.0	26.0	32.2	2.0	99.0	AECMLQOAEI	1234.5	1235.6	1234.5	1235.6
25.0	26.0	26.0	32.2	2.0	99.0	FSLVGGIGDQLNEGNR	1674.8	1675.8	1674.8	1675.8
25.0	26.0	26.0	32.2	2.0	99.0	GDEEGVPAVIDMSGRL	1742.9	1743.9	1742.9	1743.9
25.0	26.0	26.0	32.2	2.0	99.0	IKVPVDWNR	1125.6	1126.6	1125.6	1126.6
25.0	26.0	26.0	32.2	2.0	99.0	KLENCNYAVELGKNOAK	1978.0	1979.0	1978.0	1979.0
25.0	26.0	26.0	32.2	2.0	99.0	LENCNYAVELGKNOAK	1849.9	1850.9	1849.9	1850.9
25.0	26.0	26.0	32.2	2.0	99.0	MINLSVPDITIDER	1501.7	1502.8	1501.7	1502.8
25.0	26.0	26.0	32.2	2.0	99.0	QFVATDQVVR	1134.6	1135.6	1134.6	1135.6
25.0	26.0	26.0	32.2	2.0	99.0	VNDDIIVNWNENLTLR	1798.9	1799.9	1798.9	1799.9
25.0	26.0	26.0	32.2	2.0	99.0	VYALPEDLVEVNPCK	1584.8	1585.8	1584.8	1585.8
25.0	26.0	26.0	32.2	2.0	99.0	YAFVNWINK	1153.6	1154.6	1153.6	1154.6
25.0	26.0	26.0	32.2	2.0	99.0	YTLNILEIEGGQK	1533.8	1534.8	1533.8	1534.8
25.0	26.0	26.0	32.2	1.4	96.0	VNKPPYK	941.5	942.5	941.5	942.5
25.0	26.0	26.0	32.2	0.6	75.0	TFRNWNMSLGVNPR	1690.8	1691.8	1690.8	1691.8
25.0	26.0	26.0	32.2	0.0	99.0	KLENCNYAVELGKNOAK	1978.0	1979.0	1978.0	1979.0
25.0	26.0	26.0	32.2	0.0	97.0	YAFVNWINK	1155.6	1156.6	1155.6	1156.6
18.0	14.2	14.2	31.4	2.0	99.0	FSLVGGIGDQLNEGNR	1674.8	1675.8	1674.8	1675.8
18.0	14.2	14.2	31.4	2.0	99.0	GDEEGVPAVIDMSGRL	1742.9	1743.9	1742.9	1743.9
18.0	14.2	14.2	31.4	2.0	99.0	IKVPVDWNR	1125.6	1126.6	1125.6	1126.6
18.0	14.2	14.2	31.4	2.0	99.0	KLENCNYAVELGKNOAK	1978.0	1979.0	1977.9	1979.0
18.0	14.2	14.2	31.4	2.0	99.0	NWNMSLGVNPR	1286.6	1287.6	1286.6	1287.6
18.0	14.2	14.2	31.4	2.0	99.0	VYALPEDLVEVNPCK	1584.8	1585.8	1584.8	1585.8
18.0	14.2	14.2	31.4	1.0	91.0	QFVATDQVVR	1134.6	1135.6	1134.6	1135.6
18.0	14.2	14.2	31.4	0.6	72.0	VNDDIIVNWNENLTLR	1798.9	1799.9	1798.9	1799.9
18.0	14.2	14.2	31.4	0.3	45.0	YAFVNWINK	1153.6	1154.6	1153.6	1154.6
18.0	14.2	14.2	31.4	0.1	27.0	MINLSVPDITIDER	1501.7	1502.8	1501.7	1502.8
18.0	14.2	14.2	31.4	0.1	23.0	QFVATDQVVRGNPK	1530.8	1531.8	1530.8	1531.8
18.0	14.2	14.2	31.4	0.1	21.2	DLKTEINLNDDEK	1562.7	1563.7	1562.7	1563.7
18.0	14.2	14.2	31.4	0.0	83.0	KLENCNYAVELGKNOAK	1978.0	1979.0	1978.0	1979.0
18.0	14.2	14.2	31.4	0.0	83.0	QFVATDQVVR	1130.6	1131.6	1130.6	1131.6
24.0	22.6	22.6	37.5	2.0	98.0	AECMLQOAEI	1234.5	1235.6	1234.5	1235.6
24.0	22.6	22.6	37.5	2.0	98.0	FSLVGGIGDQLNEGNR	1674.8	1675.8	1674.8	1675.8
24.0	22.6	22.6	37.5	2.0	98.0	GDEEGVPAVIDMSGRL	1742.8	1743.9	1742.9	1743.9
24.0	22.6	22.6	37.5	2.0	98.0	IKVPVDWNR	1125.6	1126.6	1125.6	1126.6
24.0	22.6	22.6	37.5	2.0	98.0	KLENCNYAVELGKNOAK	1978.0	1979.0	1978.0	1979.0
24.0	22.6	22.6	37.5	2.0	98.0	QFVATDQVVR	1134.6	1135.6	1134.6	1135.6
24.0	22.6	22.6	37.5	2.0	98.0	TFRNWNMSLGVNPR	1690.8	1691.8	1690.8	1691.8
24.0	22.6	22.6	37.5	2.0	98.0	VNDDIIVNWNENLTLR	1798.9	1799.9	1798.9	1799.9
24.0	22.6	22.6	37.5	2.0	98.0	VYALPEDLVEVNPCK	1584.8	1585.8	1584.8	1585.8
24.0	22.6	22.6	37.5	2.0	98.0	YAFVNWINK	1153.6	1154.6	1153.6	1154.6
24.0	22.6	22.6	37.5	1.7	88.0	EGICAGGTSEQSSVGTQHSYSEEEK	2769.2	2770.2	2769.2	2770.2
24.0	22.6	22.6	37.5	0.8	84.0	YTLNILEIEGGQK	1533.8	1534.8	1533.8	1534.8
24.0	22.6	22.6	37.5	0.1	23.0	RYTLNILEIEGGQK	1689.9	1690.9	1689.9	1690.9
24.0	22.6	22.6	37.5	0.0	98.0	QFVATDQVVR	1117.6	1118.6	1117.6	1118.6
P14174 MI_F_HUMAN Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) - Homo sapiens (
193.0	6.0	6.0	22.6	2.0	99.0	LLCGLLAEI	1043.6	1044.6	1043.6	1044.6
193.0	6.0	6.0	22.6	2.0	99.0	PMFVNTNPR	1286.7	1287.7	1286.7	1287.7
193.0	6.0	6.0	22.6	2.0	99.0	SYSKLLCGLLAEI	1508.8	1509.8	1508.8	1509.8
193.0	6.0	6.0	22.6	0.0	99.0	PMFVNTNPR	1298.7	1299.7	1298.7	1299.7
193.0	6.0	6.0	22.6	0.0	92.0	PMFVNTNPR	1289.7	1290.7	1286.7	1287.7
193.0	6.0	6.0	22.6	0.0	90.0	PMFVNTNPR	1314.7	1315.7	1314.7	1315.7
94.0	4.0	4.0	17.4	2.0	99.0	LLCGLLAEI	1043.6	1044.6	1043.6	1044.6
94.0	4.0	4.0	17.4	2.0	99.0	PMFVNTNPR	1286.7	1287.7	1286.7	1287.7
94.0	4.0	4.0	17.4	0.0	99.0	PMFVNTNPR	1298.7	1299.7	1298.7	1299.7
94.0	4.0	4.0	17.4	0.0	98.0	PMFVNTNPR	1287.7	1288.7	1286.7	1287.7
94.0	4.0	4.0	17.4	0.0	75.0	PMFVNTNPR	1289.7	1290.7	1287.7	1288.7
194.0	4.0	4.0	17.4	2.0	98.0	LLCGLLAEI	1043.6	1044.6	1043.6	1044.6
194.0	4.0	4.0	17.4	2.0	98.0	PMFVNTNPR	1286.7	1287.7	1286.7	1287.7
194.0	4.0	4.0	17.4	0.0	98.0	PMFVNTNPR	1287.7	1288.7	1287.7	1288.7
P14317 HCLS1_HUMAN Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75) - Homo sapiens (Human)										
130.0	8.7	8.7	13.8	2.0	99.0	EHPVPLPPI	1169.7	1170.7	1169.7	1170.7
130.0	8.7	8.7	13.8	2.0	99.0	FGGGOYGIQK	1053.5	1054.5	1053.5	1054.5
130.0	8.7	8.7	13.8	2.0	99.0	RSPEAPQPIVAMEEPAVPAPLPK	2423.3	2424.3	2423.3	2424.3
130.0	8.7	8.7	13.8	2.0	99.0	TEHINHQLR	1259.7	1260.7	1259.7	1260.7
130.0	8.7	8.7	13.8	0.5	71.0	TIEGSGRTEHINHQLR	1960.0	1961.0	1960.0	1961.0
130.0	8.7	8.7	13.8	0.2	36.0	FGGGOYGIQKDR	1324.7	1325.7	1324.7	1325.7
130.0	8.7	8.7	13.8	0.0	99.0	TEHINHQLR	1259.7	1260.7	1259.7	1260.7
137.0	2.1	2.1	30.0	2.0	99.0	FGGGOYGIQK	1053.5	1054.5	1053.5	1054.5
153.0	4.6	4.6	17.9	2.0	98.0	EHPVPLPPI	1169.7	1170.7	1169.7	1170.7
153.0	4.6	4.6	17.9	2.0	98.0	TEHINHQLR	1259.7	1260.7	1259.7	1260.7
153.0	4.6	4.6	17.9	0.5	68.0	ASHGYGRRFGVER	1391.7	1392.7	1391.7	1392.7
153.0	4.6	4.6	17.9	0.1	29.0	FGGGOYGIQKDRVCK	1666.8	1667.8	1666.8	1667.8
P14618 KPYM_HUMAN Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase muscle isozyme) (Pyruvate Kinase 2/3) (Cytosolic thyroid hormone-binding prot										
14.0	38.4	38.4	54.6	2.0	99.0	APIAVTRNPQIAR	1506.9	1507.9	1506.9	1507.9
14.0	38.4	38.4	54.6	2.0	99.0	CDENILWLDYK	1450			

14.0	38.4	38.4	54.6	1.7	98.0	MQHLIAR	867.5	868.5	867.5	868.5
14.0	38.4	38.4	54.6	1.0	91.0	SGRSAHOVAR	1070.6	1071.6	1070.6	1071.6
14.0	38.4	38.4	54.6	0.7	81.0	YRPRAPIAVTR	1411.8	1412.8	1411.8	1412.8
14.0	38.4	38.4	54.6	0.6	72.0	EAEAAYIHLQFLFELRR	2088.1	2088.1	2088.1	2088.1
14.0	38.4	38.4	54.6	0.3	55.0	TATESFASDPILYRPAVALDTKGPEIR	3016.6	3017.6	3016.6	3017.6
14.0	38.4	38.4	54.6	0.0	99.0	CDENILWLDYK	1467.7	1468.7	1467.7	1468.7
14.0	38.4	38.4	54.6	0.0	99.0	CDENILWLDYKNICK	1965.9	1966.9	1965.9	1966.9
14.0	38.4	38.4	54.6	0.0	99.0	LAPITSDPTEATAVGAVEASF	2174.1	2175.1	2174.1	2175.1
14.0	38.4	38.4	54.6	0.0	58.0	LAPITSDPTEATAVGAVEASF	2170.2	2171.2	2170.2	2171.2
49.0	6.4	6.4	37.1	2.0	99.0	LNFSHGTHEYHAETIK	1882.8	1883.8	1882.9	1883.9
49.0	6.4	6.4	37.1	1.5	97.0	CDENILWLDYK	1467.7	1468.7	1467.7	1468.7
49.0	6.4	6.4	37.1	1.4	96.0	GDGLGIEPAEKVFLAQK	1827.0	1828.0	1827.0	1828.0
49.0	6.4	6.4	37.1	1.2	94.0	LAPITSDPTEATAVGAVEASF	2174.1	2175.1	2174.1	2175.1
49.0	6.4	6.4	37.1	0.2	32.0	HISKIENHEGVR	1393.8	1394.8	1393.8	1394.8
16.0	27.4	27.4	51.2	2.0	99.0	APIAVTRNPOTAR	1506.9	1507.9	1506.9	1507.9
16.0	27.4	27.4	51.2	2.0	99.0	CDENILWLDYK	1450.6	1451.6	1450.6	1451.7
16.0	27.4	27.4	51.2	2.0	99.0	CDENILWLDYKNICK	1965.9	1966.9	1965.9	1966.9
16.0	27.4	27.4	51.2	2.0	99.0	EAEAAYIHLQFLFELRR	1931.0	1932.0	1931.0	1932.0
16.0	27.4	27.4	51.2	2.0	99.0	FGVEQDQDMVWFASFIR	1858.9	1859.9	1858.9	1859.9
16.0	27.4	27.4	51.2	2.0	99.0	IISKIENHEGVR	1393.8	1394.8	1393.8	1394.8
16.0	27.4	27.4	51.2	2.0	99.0	LAPITSDPTEATAVGAVEASF	2174.1	2175.1	2174.1	2175.1
16.0	27.4	27.4	51.2	2.0	99.0	LDIDSPPTAR	1196.6	1197.6	1196.6	1197.6
16.0	27.4	27.4	51.2	2.0	99.0	LNFSHGTHEYHAETIK	1882.9	1883.9	1882.9	1883.9
16.0	27.4	27.4	51.2	2.0	99.0	LNFSHGTHEYHAETIKNVR	2252.1	2253.1	2252.1	2253.1
16.0	27.4	27.4	51.2	2.0	99.0	NTGIICIGPASR	1358.7	1359.7	1358.7	1359.7
16.0	27.4	27.4	51.2	2.0	99.0	RFDEILEASDGMVAR	1820.9	1821.9	1820.9	1821.9
16.0	27.4	27.4	51.2	1.1	92.0	GDGLGIEPAEKVFLAQK	1827.0	1828.0	1827.0	1828.0
16.0	27.4	27.4	51.2	1.0	91.0	MQHLIAR	867.5	868.5	867.5	868.5
16.0	27.4	27.4	51.2	0.7	81.0	FDEILEASDGMVAR	1664.8	1665.8	1664.8	1665.8
16.0	27.4	27.4	51.2	0.5	68.0	TATESFASDPILYRPAVALDTK	2463.3	2464.3	2463.3	2464.3
16.0	27.4	27.4	51.2	0.0	99.0	NTGIICIGPASR	1358.7	1359.7	1358.7	1359.7
16.0	27.4	27.4	51.2	0.0	99.0	RFDEILEASDGMVAR	1818.9	1819.9	1818.9	1819.9
P14625]ENPL_HUMAN						Endoplasmic precursor (Heat shock protein 90 kDa beta member 1) (94 kDa glucose-regulated protein) (GRP94) (gp96 homolog) (Tumor rejection)				
467.0	2.0	2.0	5.5	2.0	99.0	FQAOEVNRR	1080.5	1081.5	1080.5	1081.5
316.0	2.0	2.0	8.8	2.0	99.0	FQAOEVNRR	1080.5	1081.5	1080.5	1081.5
P14780]MMP9_HUMAN						Matrix metalloproteinase-9 precursor (EC 3.4.24.35) (MMP-9) (92 kDa type I collagenase) (92 kDa gelatinase) (Gelatinase B) (GELB) [Contains:				
8.0	44.0	44.0	50.2	2.0	99.0	AFALWSAVTPLTFTTR	1679.9	1680.9	1679.9	1680.9
8.0	44.0	44.0	50.2	2.0	99.0	AVIDDAFAR	976.5	977.5	976.5	977.5
8.0	44.0	44.0	50.2	2.0	99.0	FGFCPSER	998.4	999.4	998.4	999.4
8.0	44.0	44.0	50.2	2.0	99.0	FGNADGAACHFFPFIFEGR	2011.9	2012.9	2011.9	2012.9
8.0	44.0	44.0	50.2	2.0	99.0	FTEGPPHKKDDVNGIR	1794.9	1795.9	1794.9	1795.9
8.0	44.0	44.0	50.2	2.0	99.0	GDGRLWCATTSNFDSDDK	2055.9	2056.9	2055.9	2056.9
8.0	44.0	44.0	50.2	2.0	99.0	GKMLLFSGR	1007.6	1008.6	1007.6	1008.6
8.0	44.0	44.0	50.2	2.0	99.0	GSRPQGPFLIADKWPALPR	2105.1	2106.2	2105.2	2106.2
8.0	44.0	44.0	50.2	2.0	99.0	KLFFFSGR	1000.5	1001.6	1000.5	1001.6
8.0	44.0	44.0	50.2	2.0	99.0	LWCATTSNFDSDDK	1671.8	1672.8	1671.8	1672.8
8.0	44.0	44.0	50.2	2.0	99.0	MFGPVPDLTHDVFQYREK	2150.0	2151.0	2150.0	2151.0
8.0	44.0	44.0	50.2	2.0	99.0	QLAEELYR	1166.6	1167.6	1166.6	1167.6
8.0	44.0	44.0	50.2	2.0	99.0	QLSLPETGELDSATLK	1700.9	1701.9	1700.9	1701.9
8.0	44.0	44.0	50.2	2.0	99.0	OSSLVLPFGDLR	1327.7	1328.7	1327.7	1328.7
8.0	44.0	44.0	50.2	2.0	99.0	QVWVYTGASVGLPR	1531.8	1532.8	1531.8	1532.8
8.0	44.0	44.0	50.2	2.0	99.0	SDGLPWCSTTANYDTDDR	2072.8	2073.8	2072.8	2073.8
8.0	44.0	44.0	50.2	2.0	99.0	SLGPALLLLOK	1151.7	1152.7	1151.7	1152.7
8.0	44.0	44.0	50.2	2.0	99.0	WCATTANYDRDKLFGFCPTR	2478.1	2479.1	2478.1	2479.1
8.0	44.0	44.0	50.2	1.4	96.0	OQSTLVLPFGDLR	1611.9	1612.9	1611.9	1612.9
8.0	44.0	44.0	50.2	1.2	94.0	MLLFSGR	822.4	823.4	822.4	823.4
8.0	44.0	44.0	50.2	1.2	93.0	DGNADGKPCQFFIFGQSQSACTTDGR	3123.3	3124.3	3123.3	3124.4
8.0	44.0	44.0	50.2	1.2	93.0	LFGFCPTR	996.5	997.5	996.5	997.5
8.0	44.0	44.0	50.2	0.8	83.0	LLFFFSGR	872.5	873.5	872.5	873.5
8.0	44.0	44.0	50.2	0.7	81.0	WCATTANYDRDK	1499.6	1500.7	1499.6	1500.7
8.0	44.0	44.0	50.2	0.6	76.0	RLDKLGLGADVAQVTGALR	1952.0	1953.1	1952.0	1953.1
8.0	44.0	44.0	50.2	0.5	69.0	CGVPDLGR	872.4	873.4	872.4	873.4
8.0	44.0	44.0	50.2	0.1	28.8	ONVSEDLPR	1273.5	1274.5	1273.5	1274.5
8.0	44.0	44.0	50.2	0.1	27.0	AYFCODRFYWR	1610.7	1611.7	1610.7	1611.7
8.0	44.0	44.0	50.2	0.1	27.0	FVWVPTTR	726.4	727.4	726.4	727.4
8.0	44.0	44.0	50.2	0.0	99.0	FGNADGAACHFFPFIFEGR	2012.9	2013.9	2011.9	2012.9
8.0	44.0	44.0	50.2	0.0	99.0	QLAEELYR	1183.6	1184.6	1183.6	1184.6
8.0	44.0	44.0	50.2	0.0	43.0	QLAEELYR	1166.6	1167.6	1166.6	1167.6
8.0	44.0	44.0	50.2	0.0	99.0	QLSLPETGELDSATLK	1683.9	1684.9	1683.9	1684.9
8.0	44.0	44.0	50.2	0.0	96.0	QVWVYTGASVGLPR	1514.8	1515.8	1514.8	1515.8
6.0	31.5	31.5	42.9	2.0	99.0	AVIDDAFAR	976.5	977.5	976.5	977.5
6.0	31.5	31.5	42.9	2.0	99.0	FGNADGAACHFFPFIFEGR	2014.9	2015.9	2011.9	2012.9
6.0	31.5	31.5	42.9	2.0	99.0	FOTFEGDLK	1083.5	1084.5	1083.5	1084.5
6.0	31.5	31.5	42.9	2.0	99.0	FTEGPPHKKDDVNGIR	1794.9	1795.9	1794.9	1795.9
6.0	31.5	31.5	42.9	2.0	99.0	GKMLLFSGR	1007.6	1008.6	1007.6	1008.6
6.0	31.5	31.5	42.9	2.0	99.0	GSRPQGPFLIADKWPALPR	2105.2	2106.2	2105.2	2106.2
6.0	31.5	31.5	42.9	2.0	99.0	KLFFFSGR	1000.5	1001.6	1000.5	1001.6
6.0	31.5	31.5	42.9	2.0	99.0	LFGFCPTR	996.5	997.5	996.5	997.5
6.0	31.5	31.5	42.9	2.0	99.0	LWCATTSNFDSDDK	1671.7	1672.7	1671.8	1672.8
6.0	31.5	31.5	42.9	2.0	99.0	QLAEELYR	1166.6	1167.6	1166.6	1167.6
6.0	31.5	31.5	42.9	2.0	99.0	OSSLVLPFGDLR	1327.7	1328.7	1327.7	1328.7
6.0	31.5	31.5	42.9	2.0	99.0	QVWVYTGASVGLPR	1531.8	1532.8	1531.8	1532.8
6.0	31.5	31.5	42.9	2.0	99.0	SDGLPWCSTTANYDTDDR	2068.9	2069.9	2072.8	2073.8
6.0	31.5	31.5	42.9	2.0	99.0	SLGPALLLLOK	1151.7	1152.7	1151.7	1152.7
6.0	31.5	31.5	42.9	1.2	93.0	LLFFFSGR	872.5	873.5	872.5	873.5
6.0	31.5	31.5	42.9	1.1	92.0	FGFCPSER	998.4	999.4	998.4	999.4
6.0	31.5	31.5	42.9	0.6	74.0	QLSLPETGELDSATLK	1700.9	1701.9	1700.9	1701.9
6.0	31.5	31.5	42.9	0.5	70.0	MLLFSGR	822.5	823.5	822.4	823.4
6.0	31.5	31.5	42.9	0.1	24.0	AFALWSAVTPLTFTTR	1679.9	1680.9	1679.9	1680.9
6.0	31.5	31.5	42.9	0.0	99.0	AVIDDAFAR	976.5	977.5	976.5	977.5
6.0	31.5	31.5	42.9	0.0	99.0	FGNADGAACHFFPFIFEGR	2011.9	2012.9	2011.9	2012.9
6.0	31.5	31.5	42.9	0.0	99.0	FTEGPPHKKDDVNGIR	1793.9	1794.9	1793.9	1794.9
6.0	31.5	31.5	42.9	0.0	89.0	FTEGPPHKKDDVNGIR	1794.9	1795.9	1794.9	1795.9
6.0	31.5	31.5	42.9	0.0	99.0	QLAEELYR	1183.6	1184.6	1183.6	1184.6
6.0	31.5	31.5	42.9	0.0	20.0	QLAEELYR	1166.6	1167.6	1166.6	1167.6
6.0	31.5	31.5	42.9	0.0	97.0	OSSLVLPFGDLR	1327.7	1328.7	1327.7	1328.7
6.0	31.5	31.5	42.9	0.0	45.0	OSSLVLPFGDLR	1341.7	1342.7	1341.7	1342.7
6.0	31.5	31.5	42.9	0.0	97.0	QVWVYTGASVGLPR	1514.8	1515.8	1514.8	1515.8
6.0	31.5	31.5	42.9	0.0	99.0	SDGLPWCSTTANYDTDDR	2072.8	2073.8	2072.8	2073.8
6.0	46.9	46.9	48.9	2.0	99.0	AVIDDAFAR	976.5	977.5	976.5	977.5
6.0	46.9	46.9	48.9	2.0	99.0	EKAYFCQDR	1215.5	1216.5	1215.5	1216.5
6.0	46.9	46.9	48.9	2.0	99.0	FGNADGAACHFFPFIFEGR	2012.9	2013.9	2011.9	2012.9
6.0	46.9	46.9	48.9	2.0	99.0	FOTFEGDLK	1083.5	1084.5	1083.5	1084.5
6.0	46.9	46.9	48.9	2.0	99.0	FTEGPPHKKDDVNGIR	1794.9	1795.9	1794.9	1795.9
6.0	46.9	46.9	48.9	2.0	99.0	GSRPQGPFLIADKWPALPR	2105.1	2106.2	2105.2	2106.2
6.0	46.9	46.9	48.9	2.0	99.0	KLDSVFEELSKK	1518.8	1519.8	1518.8	1519.8
6.0	46.9	46.9	48.9	2.0	99.0	LFGFCPTR	996.5	997.5	996.5	997.5
6.0	46.9	46.9	48.9	2.0	99.0	LGLGADVAQVTGALR	1438.8	1440.8	1438.8	1440.8
6.0	46.9	46.9	48.9	2.0	99.0	LWCATTSNFDSDDK	1671.8	1672.8	1671.8	1672.8
6.0	46.9	46.9	48.9	2.0	99.0	MFGPVPDL				

6.0	46.9	46.9	48.9	0.0	99.0	FGNADGAACHFFPFIFEGR	2011.9	2012.9	2011.9	2012.9
6.0	46.9	46.9	48.9	0.0	89.0	FGNADGAACHFFPFIFEGR	2013.9	2014.9	2013.9	2014.9
6.0	46.9	46.9	48.9	0.0	99.0	QLAEELYLR	1166.6	1167.6	1166.6	1167.6
6.0	46.9	46.9	48.9	0.0	70.0	QLSLPETGSDSATLK	1682.9	1683.9	1682.9	1683.9
6.0	46.9	46.9	48.9	0.0	99.0	QSTLVLPFGDLR	1327.7	1328.7	1327.7	1328.7
6.0	46.9	46.9	48.9	0.0	99.0	QVWVYFVAVLSPR	1531.8	1532.8	1531.8	1532.8
P14854	CX6B1_HUMAN		Cytochrome c oxidase subunit VI b isoform 1 (EC 1.9.3.1) (COX VIb-1) - Homo sapiens (Human)							
344.0	3.4	3.4	31.4	2.0	99.0	GGDISVCEVYQR	1468.6	1469.6	1468.6	1469.6
344.0	3.4	3.4	31.4	1.4	96.0	TAPFDSRFPNQOTR	1777.8	1778.8	1777.8	1778.8
155.0	4.6	4.6	65.1	2.0	99.0	GGDISVCEVYQR	1468.6	1468.6	1468.6	1469.6
155.0	4.6	4.6	65.1	2.0	99.0	VYQSLCPTSVWTDWDEQR	2269.0	2270.0	2269.0	2270.0
155.0	4.6	4.6	65.1	0.4	57.0	FPNQNTQR	1052.4	1053.4	1052.5	1053.5
155.0	4.6	4.6	65.1	0.3	44.0	TAPFDSRFPNQNTQR	1777.9	1778.9	1777.8	1778.9
P15153	RAC2_HUMAN		Ras-related C3 botulinum toxin substrate 2 precursor (p21-Rac2) (Small G protein) (GX) - Homo sapiens (Human)							
304.0	4.0	4.0	9.4	2.0	99.0	AKWFPEVR	1031.6	1032.6	1031.6	1032.6
304.0	4.0	4.0	9.4	2.0	99.0	YLECSALTQR	1239.6	1240.6	1239.6	1240.6
356.0	2.0	2.0	5.2	2.0	99.0	YLECSALTQR	1239.6	1240.6	1239.6	1240.6
P15311	EZRI_HUMAN		Ezrin (p81) (Cytovillin) (Villin-2) - Homo sapiens (Human)							
46.0	19.0	27.2	41.1	2.0	99.0	EVWVFLGHVYDVK	1668.8	1669.8	1668.8	1669.8
46.0	19.0	27.2	41.1	2.0	99.0	IAQDLEMVGINVFEIK	1946.0	1947.0	1945.9	1947.0
46.0	19.0	27.2	41.1	2.0	99.0	KENPLOKFR	1305.7	1306.7	1305.7	1306.7
46.0	19.0	27.2	41.1	2.0	99.0	QLLTLSSLSOAR	1427.8	1428.8	1427.8	1428.8
46.0	19.0	27.2	41.1	2.0	99.0	RKDEVEEWOHR	1639.8	1640.8	1639.8	1640.8
46.0	19.0	27.2	41.1	2.0	99.0	RRKDEVEEWOHR	1795.9	1796.9	1795.9	1796.9
46.0	19.0	27.2	41.1	2.0	99.0	THNDIHNENMR	1492.7	1493.7	1492.7	1493.7
46.0	19.0	27.2	41.1	2.0	99.0	VMDQHLKTR	1126.6	1127.6	1126.6	1127.6
46.0	19.0	27.2	41.1	1.4	99.0	IQVWHAHR	1174.6	1175.6	1174.6	1175.6
46.0	19.0	27.2	41.1	1.4	96.0	DQWEDRIQVWHAHR	2003.9	2004.9	2003.9	2004.9
46.0	19.0	27.2	41.1	0.1	26.0	RTEAEKNERVQR	1670.9	1671.9	1670.9	1671.9
46.0	19.0	27.2	41.1	0.0	99.0	APDFVYAPR	1181.6	1182.6	1181.6	1182.6
46.0	19.0	27.2	41.1	0.0	99.0	IGFPWSEIR	1103.6	1104.6	1103.6	1104.6
46.0	19.0	27.2	41.1	0.0	99.0	IQVWHAHR	1174.6	1175.6	1174.6	1175.6
46.0	19.0	27.2	41.1	0.0	99.0	KAPDFVYAPR	1309.7	1310.7	1309.7	1310.7
46.0	19.0	27.2	41.1	0.0	97.0	LFVLQVK	893.5	894.5	893.5	894.5
46.0	19.0	27.2	41.1	0.0	97.0	RKDEVEEWOHR	1639.8	1640.8	1639.8	1640.8
127.0	2.3	10.3	24.9	2.0	99.0	THNDIHNENMR	1492.7	1493.7	1492.7	1493.7
127.0	2.3	10.3	24.9	0.1	31.0	FGDYNKEVHK	1235.6	1236.6	1235.6	1236.6
127.0	2.3	10.3	24.9	0.1	26.0	IQVWHAHR	1174.6	1175.6	1174.6	1175.6
127.0	2.3	10.3	24.9	0.0	99.0	APDFVYAPR	1181.6	1182.6	1181.6	1182.6
127.0	2.3	10.3	24.9	0.0	99.0	IGFPWSEIR	1103.6	1104.6	1103.6	1104.6
127.0	2.3	10.3	24.9	0.0	99.0	IGFPWSEIR	1101.6	1102.6	1103.6	1104.6
127.0	2.3	10.3	24.9	0.0	99.0	KAPDFVYAPR	1310.7	1309.7	1310.7	1310.7
127.0	2.3	10.3	24.9	0.0	99.0	LFVLQVK	893.5	894.5	893.5	894.5
67.0	11.1	23.1	38.4	2.0	99.0	DQWEDRIQVWHAHR	2003.9	2005.0	2003.9	2004.9
67.0	11.1	23.1	38.4	2.0	99.0	FGDYNKEVHKSGLSSER	2115.0	2116.0	2115.0	2116.0
67.0	11.1	23.1	38.4	2.0	99.0	IQVWHAHR	1174.6	1175.6	1174.6	1175.6
67.0	11.1	23.1	38.4	2.0	99.0	RKDEVEEWOHR	1639.8	1640.8	1639.8	1640.8
67.0	11.1	23.1	38.4	2.0	99.0	THNDIHNENMR	1492.7	1493.7	1492.7	1493.7
67.0	11.1	23.1	38.4	0.9	90.0	FGDYNKEVHK	1235.6	1236.6	1235.6	1236.6
67.0	11.1	23.1	38.4	0.1	23.0	KEDEVEEWOHR	1483.7	1484.7	1483.7	1484.7
67.0	11.1	23.1	38.4	0.1	20.0	IAQDLEMVGINVFEIK	1946.0	1947.0	1945.9	1947.0
67.0	11.1	23.1	38.4	0.0	24.0	AKFVPEDVAELIQDITQK	2280.0	2281.0	2281.0	2281.1
67.0	11.1	23.1	38.4	0.0	99.0	APDFVYAPR	1181.6	1182.6	1181.6	1182.6
67.0	11.1	23.1	38.4	0.0	99.0	IGFPWSEIR	1103.6	1104.6	1103.6	1104.6
67.0	11.1	23.1	38.4	0.0	99.0	IQVWHAHR	1174.6	1175.6	1174.6	1175.6
67.0	11.1	23.1	38.4	0.0	99.0	KAPDFVYAPR	1309.7	1310.7	1309.7	1310.7
67.0	11.1	23.1	38.4	0.0	98.0	LFVLQVK	893.5	894.5	893.5	894.5
67.0	11.1	23.1	38.4	0.0	99.0	RKPDTEVQOMK	1471.8	1472.8	1471.8	1472.8
67.0	11.1	23.1	38.4	0.0	99.0	RRKPDTEVQOMK	1627.9	1628.9	1627.9	1628.9
67.0	11.1	23.1	38.4	0.0	78.0	RRKPDTEVQOMK	1627.9	1628.9	1627.9	1628.9
P16070	CD44_HUMAN		CD44 antigen precursor (Phagocytic glycoprotein 1) (PGP-1) (HUTCH-1) (Extracellular matrix receptor-111) (ECMR-111) (GP90 lymphocyte homing,							
346.0	3.3	3.3	4.0	2.0	99.0	YGFIEGHVIVPR	1385.7	1386.8	1385.7	1386.8
346.0	3.3	3.3	4.0	1.3	95.0	ALSIQFETCR	1152.6	1153.6	1152.6	1153.6
109.0	3.2	3.2	6.9	2.0	99.0	YGFIEGHVIVPR	1385.7	1386.7	1385.7	1386.8
109.0	3.2	3.2	6.9	1.2	93.0	ALSIQFETCR	1152.6	1153.6	1152.6	1153.6
156.0	4.6	4.6	7.5	2.0	99.0	YGFIEGHVIVPR	1385.7	1386.7	1385.7	1386.8
156.0	4.6	4.6	7.5	1.3	95.0	ALSIQFETCR	1152.6	1153.6	1152.6	1153.6
156.0	4.6	4.6	7.5	1.3	95.0	FAGVHVEK	1032.5	1033.5	1032.5	1033.5
P16152	CBR1_HUMAN		Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) (Prostaglandin-E(2) 9-reductase) (EC 1.1.1.189) (Prosta							
329.0	3.7	3.7	13.4	2.0	99.0	GQAAVQQLQAEGLSPR	1651.9	1652.9	1651.9	1652.9
329.0	3.7	3.7	13.4	1.7	98.0	KEYGGLDLVLVNAGIAFKVAD	2224.1	2225.1	2224.1	2225.1
193.0	4.0	4.0	13.4	2.0	99.0	GQAAVQQLQAEGLSPR	1651.9	1652.9	1651.9	1652.9
193.0	4.0	4.0	13.4	2.0	99.0	KEYGGLDLVLVNAGIAFKVAD	2210.1	2211.1	2210.1	2211.1
193.0	4.0	4.0	13.4	0.0	93.0	KEYGGLDLVLVNAGIAFKVAD	2224.1	2225.1	2224.1	2225.1
P16401	H15_HUMAN		Histone H1.5 (Histone H1a) - Homo sapiens (Human)							
235.0	5.2	6.0	23.5	2.0	99.0	SETAPAEATATPAPVEKSPAK	2023.0	2024.0	2023.0	2024.0
235.0	5.2	6.0	23.5	2.0	99.0	SETAPAEATATPAPVEKSPAKK	2151.1	2152.1	2151.1	2152.1
235.0	5.2	6.0	23.5	1.2	99.0	ALAAAGYDVEKNNSR	1563.8	1564.8	1563.8	1564.8
246.0	2.3	2.3	22.6	2.0	99.0	SETAPAEATATPAPVEKSPAK	2023.0	2024.0	2023.0	2024.0
246.0	2.3	2.3	22.6	0.3	49.0	ALAAAGYDVEKNNSR	1563.8	1564.8	1563.8	1564.8
P16402	H13_HUMAN		Histone H1.3 (Histone H1c) - Homo sapiens (Human)							
451.0	2.0	6.0	23.5	2.0	99.0	SETAPLAPITPAPAEKTPVKKK	2315.3	2316.3	2315.3	2316.3
451.0	2.0	6.0	23.5	0.0	99.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
451.0	2.0	6.0	23.5	0.0	99.0	ALAAAGYDVEKNNSR	1577.8	1578.8	1577.8	1578.8
451.0	2.0	6.0	23.5	0.0	20.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
451.0	2.0	6.0	23.5	0.0	99.0	KALAAAGYDVEKNNSR	1705.9	1706.9	1705.9	1706.9
309.0	2.0	3.7	30.3	2.0	99.0	SETAPLAPITPAPAEKTPVKKK	2315.3	2316.3	2315.3	2316.3
309.0	2.0	3.7	30.3	0.0	98.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
309.0	2.0	3.7	30.3	0.0	98.0	ALAAAGYDVEKNNSR	1577.8	1578.8	1577.8	1578.8
P16403	H12_HUMAN		Histone H1.2 (Histone H1d) - Homo sapiens (Human)							
227.0	5.4	11.4	22.1	2.0	99.0	SETAPAAAAPAEKAPVKK	2043.1	2044.1	2043.1	2044.1
227.0	5.4	11.4	22.1	2.0	99.0	SETAPAAAAPAEKAPVKKK	2171.2	2172.2	2171.2	2172.2
227.0	5.4	11.4	22.1	1.4	96.0	SETAPAAAAPAEKAPVK	1915.0	1916.0	1915.0	1916.0
227.0	5.4	11.4	22.1	0.0	99.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
227.0	5.4	11.4	22.1	0.0	99.0	ALAAAGYDVEKNNSR	1577.8	1578.8	1577.8	1578.8
227.0	5.4	11.4	22.1	0.0	20.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
227.0	5.4	11.4	22.1	0.0	99.0	KALAAAGYDVEKNNSR	1705.9	1706.9	1705.9	1706.9
227.0	5.4	11.4	22.1	0.0	99.0	SETAPAAAAPAEKAPVKK	1519.8	1520.8	1519.8	1520.8
102.0	7.7	7.7	23.5	2.0	99.0	SETAPAAAAPAEKAPVKK	1915.0	1916.0	1915.0	1916.0
102.0	7.7	7.7	23.5	2.0	99.0	SETAPAAAAPAEKAPVKKK	2043.1	2044.1	2043.1	2044.1
102.0	7.7	7.7	23.5	2.0	99.0	SETAPAAAAPAEKAPVKKK	2171.2	2172.2	2171.2	2172.2
102.0	7.7	7.7	23.5	1.7	98.0	ALAAAGYDVEKNNSR	1577.8	1578.8	1577.8	1578.8
102.0	7.7	7.7	23.5	0.0	98.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
P16949	STMN1_HUMAN		Stathmin - Bos taurus (Bovine) - Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia-associated phosphoprotein p18) (pp							
243.0	4.9	4.9	27.5	2.0	99.0	ASGQAFELILSPR	1387.7	1388.8	1387.7	1388.8
243.0	4.9	4.9	27.5	2.0	99.0	LREKDKHIEEVRK	1679.0	1680.0	1678.9	1680.0
243.0	4.9	4.9	27.5	0.9	88.0	RASGOAFELILSPR	1543.9	1544.9	1543.8	1544.9
149.0	2.0	2.0	12.8	2.0	99.0	ASGQAFELILSPR	1387.7	1388.8	1387.7	1388.8
297.0	2.0	2.0	21.5	2.0	99.0	ASGQAFELILSPR	138			

160.0	7.4	12.3	40.6	0.0	99.0	WAAVVVPSGEEOR	1426.7	1427.7	1426.7	1427.7
40.0	20.6	20.6	61.0	2.0	99.0	AAAYKLVLR	1087.7	1088.7	1087.7	1088.7
40.0	20.6	20.6	61.0	2.0	99.0	ALPFWNEEIVPOIK	1682.9	1683.9	1682.9	1683.9
40.0	20.6	20.6	61.0	2.0	99.0	FSGWYDADLSPAGHEEAK	1978.9	1979.9	1978.9	1979.9
40.0	20.6	20.6	61.0	2.0	99.0	FSGWYDADLSPAGHEEAKR	2135.0	2136.0	2135.0	2136.0
40.0	20.6	20.6	61.0	2.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
40.0	20.6	20.6	61.0	2.0	99.0	HYGGLTGLNK	1058.6	1059.6	1058.6	1059.6
40.0	20.6	20.6	61.0	2.0	99.0	HYGGLTGLNKAETAAK	1629.8	1630.8	1629.8	1630.9
40.0	20.6	20.6	61.0	2.0	99.0	SYDVPPPPMEPDHPFYNSISK	2416.1	2417.1	2416.1	2417.1
40.0	20.6	20.6	61.0	2.0	99.0	VLIAAHGNSLR	1149.7	1150.7	1149.7	1150.7
40.0	20.6	20.6	61.0	2.0	99.0	YADLTEDOLPSCESLKDITARI	2424.1	2425.1	2424.1	2425.2
40.0	20.6	20.6	61.0	0.5	68.0	ALPFWNEEIVPOIKEGKR	2153.2	2154.2	2153.2	2154.2
40.0	20.6	20.6	61.0	0.1	20.0	TWRLNER	973.5	974.5	973.5	974.5
40.0	20.6	20.6	61.0	0.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
40.0	20.6	20.6	61.0	0.0	99.0	HGESAWNLENR	1323.6	1324.6	1323.6	1324.6
40.0	20.6	20.6	61.0	0.0	99.0	HYGGLTGLNKAETAAK	1629.8	1630.8	1629.8	1630.9
36.0	8.6	8.6	38.6	2.0	99.0	ALPFWNEEIVPOIK	1682.9	1683.9	1682.9	1683.9
36.0	8.6	8.6	38.6	2.0	99.0	FSGWYDADLSPAGHEEAK	1978.9	1979.9	1978.9	1979.9
36.0	8.6	8.6	38.6	2.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
36.0	8.6	8.6	38.6	2.0	99.0	YADLTEDOLPSCESLKDITARI	2424.2	2425.2	2424.2	2425.2
36.0	8.6	8.6	38.6	0.5	67.0	FSGWYDADLSPAGHEEAKR	2135.0	2136.0	2135.0	2136.0
53.0	14.0	14.0	42.9	2.0	99.0	ALPFWNEEIVPOIK	1682.9	1683.9	1682.9	1683.9
53.0	14.0	14.0	42.9	2.0	99.0	FSGWYDADLSPAGHEEAK	1978.9	1979.9	1978.9	1979.9
53.0	14.0	14.0	42.9	2.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
53.0	14.0	14.0	42.9	2.0	99.0	HYGGLTGLNK	1058.6	1059.6	1058.6	1059.6
53.0	14.0	14.0	42.9	2.0	99.0	HYGGLTGLNKAETAAK	1629.8	1630.8	1629.8	1630.9
53.0	14.0	14.0	42.9	2.0	99.0	VLIAAHGNSLR	1149.7	1150.7	1149.7	1150.7
53.0	14.0	14.0	42.9	2.0	99.0	YADLTEDOLPSCESLKDITARI	2424.1	2425.1	2424.1	2425.2
53.0	14.0	14.0	42.9	0.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
53.0	14.0	14.0	42.9	0.0	99.0	HGESAWNLENR	1323.6	1324.6	1323.6	1324.6
53.0	14.0	14.0	42.9	0.0	64.0	VLIAAHGNSLR	1150.6	1151.7	1150.6	1151.7
P18669 PGAM1_HUMAN Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1) - H										
40.0	20.6	20.6	61.0	2.0	99.0	AAAYKLVLR	1087.7	1088.7	1087.7	1088.7
40.0	20.6	20.6	61.0	2.0	99.0	ALPFWNEEIVPOIK	1682.9	1683.9	1682.9	1683.9
40.0	20.6	20.6	61.0	2.0	99.0	FSGWYDADLSPAGHEEAK	1978.9	1979.9	1978.9	1979.9
40.0	20.6	20.6	61.0	2.0	99.0	FSGWYDADLSPAGHEEAKR	2135.0	2136.0	2135.0	2136.0
40.0	20.6	20.6	61.0	2.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
40.0	20.6	20.6	61.0	2.0	99.0	HYGGLTGLNK	1058.6	1059.6	1058.6	1059.6
40.0	20.6	20.6	61.0	2.0	99.0	HYGGLTGLNKAETAAK	1629.8	1630.8	1629.8	1630.9
40.0	20.6	20.6	61.0	2.0	99.0	SYDVPPPPMEPDHPFYNSISK	2416.1	2417.1	2416.1	2417.1
40.0	20.6	20.6	61.0	2.0	99.0	VLIAAHGNSLR	1149.7	1150.7	1149.7	1150.7
40.0	20.6	20.6	61.0	2.0	99.0	YADLTEDOLPSCESLKDITARI	2424.1	2425.1	2424.1	2425.2
40.0	20.6	20.6	61.0	0.5	68.0	ALPFWNEEIVPOIKEGKR	2153.2	2154.2	2153.2	2154.2
40.0	20.6	20.6	61.0	0.1	20.0	TWRLNER	973.5	974.5	973.5	974.5
40.0	20.6	20.6	61.0	0.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
40.0	20.6	20.6	61.0	0.0	99.0	HGESAWNLENR	1323.6	1324.6	1323.6	1324.6
40.0	20.6	20.6	61.0	0.0	99.0	HYGGLTGLNKAETAAK	1629.8	1630.8	1629.8	1630.9
36.0	8.6	8.6	38.6	2.0	99.0	ALPFWNEEIVPOIK	1682.9	1683.9	1682.9	1683.9
36.0	8.6	8.6	38.6	2.0	99.0	FSGWYDADLSPAGHEEAK	1978.9	1979.9	1978.9	1979.9
36.0	8.6	8.6	38.6	2.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
36.0	8.6	8.6	38.6	2.0	99.0	YADLTEDOLPSCESLKDITARI	2424.2	2425.2	2424.2	2425.2
36.0	8.6	8.6	38.6	0.5	67.0	FSGWYDADLSPAGHEEAKR	2135.0	2136.0	2135.0	2136.0
53.0	14.0	14.0	42.9	2.0	99.0	ALPFWNEEIVPOIK	1682.9	1683.9	1682.9	1683.9
53.0	14.0	14.0	42.9	2.0	99.0	FSGWYDADLSPAGHEEAK	1978.9	1979.9	1978.9	1979.9
53.0	14.0	14.0	42.9	2.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
53.0	14.0	14.0	42.9	2.0	99.0	HYGGLTGLNK	1058.6	1059.6	1058.6	1059.6
53.0	14.0	14.0	42.9	2.0	99.0	HYGGLTGLNKAETAAK	1629.8	1630.8	1629.8	1630.9
53.0	14.0	14.0	42.9	2.0	99.0	VLIAAHGNSLR	1149.7	1150.7	1149.7	1150.7
53.0	14.0	14.0	42.9	2.0	99.0	YADLTEDOLPSCESLKDITARI	2424.1	2425.1	2424.1	2425.2
53.0	14.0	14.0	42.9	0.0	99.0	HGESAWNLENR	1311.6	1312.6	1311.6	1312.6
53.0	14.0	14.0	42.9	0.0	99.0	HGESAWNLENR	1323.6	1324.6	1323.6	1324.6
53.0	14.0	14.0	42.9	0.0	64.0	VLIAAHGNSLR	1150.6	1151.7	1150.6	1151.7
P19105 MLRM_HUMAN Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC) - Homo sapiens (Human)										
128.0	6.0	6.0	33.9	2.0	99.0	ELLTMDGRFTDEEVDLYR	2431.2	2432.2	2431.1	2432.1
128.0	6.0	6.0	33.9	2.0	99.0	GNFNIEYFR	1259.6	1260.6	1259.6	1260.6
128.0	6.0	6.0	33.9	2.0	99.0	NAFACFDEEATGTIQEDYLR	2349.0	2350.0	2349.0	2350.0
151.0	8.0	8.0	29.1	2.0	99.0	ELLTMDGRFTDEEVDLYR	2431.1	2432.1	2431.1	2432.1
151.0	8.0	8.0	29.1	2.0	99.0	FTDEEVDLYR	1414.6	1415.6	1414.6	1415.6
151.0	8.0	8.0	29.1	2.0	99.0	GNFNIEYFR	1259.6	1260.6	1259.6	1260.6
151.0	8.0	8.0	29.1	2.0	99.0	NAFACFDEEATGTIQEDYLR	2349.0	2350.0	2349.0	2350.0
146.0	2.1	2.1	17.4	2.0	99.0	GNFNIEYFR	1259.6	1260.6	1259.6	1260.6
P19823 ITI1H2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin inhibitor ch										
55.0	16.9	16.9	13.4	2.0	99.0	AHVSFKPTVAQQR	1465.8	1466.8	1465.8	1466.8
55.0	16.9	16.9	13.4	2.0	99.0	FYNOVSTPLLR	1336.7	1337.7	1336.7	1337.7
55.0	16.9	16.9	13.4	2.0	99.0	IOPSGGTNINEALLR	1581.8	1582.8	1581.8	1582.9
55.0	16.9	16.9	13.4	2.0	99.0	IYGNQDTSOLKK	1492.8	1493.8	1492.8	1493.8
55.0	16.9	16.9	13.4	2.0	99.0	KFYNOVSTPLLR	1464.8	1465.8	1464.8	1465.8
55.0	16.9	16.9	13.4	2.0	99.0	VOFELHYOEYK	1418.7	1419.7	1418.7	1419.7
55.0	16.9	16.9	13.4	2.0	99.0	VOFELHYOEYKWR	1760.9	1761.9	1760.9	1761.9
55.0	16.9	16.9	13.4	2.0	99.0	VVNSPQPQNVFVQIQPK	2144.1	2145.1	2144.1	2145.1
55.0	16.9	16.9	13.4	0.9	88.0	VIEPQGLR	924.5	925.5	924.5	925.5
55.0	16.9	16.9	13.4	0.0	33.0	FYNOVSTPLLR	1335.7	1336.7	1335.7	1336.7
31.0	10.0	10.0	12.4	2.0	99.0	FYNOVSTPLLR	1336.7	1337.7	1336.7	1337.7
31.0	10.0	10.0	12.4	2.0	99.0	IOPSGGTNINEALLR	1581.8	1582.8	1581.8	1582.9
31.0	10.0	10.0	12.4	2.0	99.0	VOFELHYOEYK	1418.7	1419.7	1418.7	1419.7
31.0	10.0	10.0	12.4	2.0	99.0	VVNSPQPQNVFVQIQPK	2144.1	2145.1	2144.1	2145.1
31.0	10.0	10.0	12.4	1.5	97.0	VOFELHYOEYKWR	1760.9	1761.9	1760.9	1761.9
31.0	10.0	10.0	12.4	0.3	47.0	AEDHFSVIDFNQINR	1814.8	1815.8	1814.8	1815.8
31.0	10.0	10.0	12.4	0.1	29.0	KFYNOVSTPLLR	1464.8	1465.8	1464.8	1465.8
31.0	10.0	10.0	12.4	0.0	99.0	VOFELHYOEYK	1419.7	1420.7	1418.7	1419.7
20.0	23.9	23.9	20.3	2.0	99.0	AHVSFKPTVAQQR	1465.8	1466.8	1465.8	1466.8
20.0	23.9	23.9	20.3	2.0	99.0	FYNOVSTPLLR	1336.7	1337.7	1336.7	1337.7
20.0	23.9	23.9	20.3	2.0	99.0	GOQKAHVSKPTVAQQR	1876.0	1877.0	1876.0	1877.0
20.0	23.9	23.9	20.3	2.0	99.0	IOPSGGTNINEALLR	1581.8	1582.8	1581.8	1582.9
20.0	23.9	23.9	20.3	2.0	99.0	IYGNQDTSOLKK	1364.7	1365.7	1364.7	1365.7
20.0	23.9	23.9	20.3	2.0	99.0	IYGNQDTSOLKK	1492.8	1493.8	1492.8	1493.8
20.0	23.9	23.9	20.3	2.0	99.0	KFYNOVSTPLLR	1464.8	1465.8	1464.8	1465.8
20.0	23.9	23.9	20.3	2.0	99.0	TWRNLSATK	1289.7	1290.7	1289.7	1290.7
20.0	23.9	23.9	20.3	2.0	99.0	VOFELHYOEYK	1418.7	1419.7	1418.7	1419.7
20.0	23.9	23.9	20.3	2.0	99.0	VOFELHYOEYKWR	1760.9	1761.9	1760.9	1761.9
20.0	23.9	23.9	20.3	2.0	99.0	VVNSPQPQNVFVQIQPK	2144.1	2145.1	2144.1	2145.1
20.0	23.9	23.9	20.3	1.7	98.0	AEDHFSVIDFNQINR	1814.8	1815.8	1814.8	1815.9
20.0	23.9	23.9	20.3	0.1	28.4	VIEPQGLR	924.5	925.5	924.5	925.5
20.0	23.9	23.9	20.3	0.0	98.0	AHVSFKPTVAQQR	1465.8	1466.8	1465.8	1466.8
20.0	23.9	23.9	20.3	0.0	98.0	FYNOVSTPLLR	1337.7	1338.7	1337.7	1338.7
20.0	23.9	23.9	20.3	0.0	94.0	FYNOVSTPLLR	1336.7	1337.7	1336.7	1337.7
P19971 TYPH_HUMAN Thymidine phosphorylase precursor (EC 2.4.2.4) (TdRase) (TP) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (Gliostatin) - Homo s										
416.0	2.1	2.1	8.9	2.0	99.0	FGGAAVFPNQEQR	1490.7	1491.7	1490.7	1491.7
107.0	7.5	7.5	23.0	2.0	99.0	AREQEELLAPADGTVELVR	2095.1	2096.1	2095.1	2096.1
107.0	7.5	7.5	23.0	2.0	99.0	FGGAAVFPNQEQR				

100.0	7.8	7.8	27.6	2.0	99.0	COSLTEDLEFR	1379.6	1380.6	1379.6	1380.6
100.0	7.8	7.8	27.6	2.0	99.0	COSLTEDLEFRK	1507.7	1508.7	1507.7	1508.8
100.0	7.8	7.8	27.6	2.0	99.0	LOEKEELRELNDR	1670.9	1671.9	1670.9	1671.9
100.0	7.8	7.8	27.6	0.9	88.0	LYKEELEQTYHAK	1650.8	1651.8	1650.8	1651.8
100.0	7.8	7.8	27.6	0.8	84.0	LREYEALANSK	1292.7	1293.7	1292.7	1293.7
P20742 PZP_HUMAN	Pregnancy zone protein precursor - Homo sapiens (Human)									
358.0	3.1	7.7	8.4	2.0	99.0	DLFHCVSFTLPR	1490.7	1491.7	1490.7	1491.7
358.0	3.1	7.7	8.4	1.0	99.0	QONACQGSFSTQDTVVALHALSR	2503.2	2504.2	2503.2	2504.2
358.0	3.1	7.7	8.4	0.0	99.0	MVSGFPLPKPTVK	1415.8	1416.8	1415.8	1416.8
358.0	3.1	7.7	8.4	0.0	97.0	NGOINTWLTAFVLK	1635.7	1636.7	1635.7	1636.7
358.0	3.1	7.7	8.4	0.0	24.0	YGAATFR	1013.5	1014.5	1013.5	1014.5
214.0	3.2	5.2	7.8	2.0	99.0	DLFHCVSFTLPR	1490.7	1491.7	1490.7	1491.7
214.0	3.2	5.2	7.8	1.0	91.0	FEIENCLANK	1275.6	1276.6	1275.6	1276.6
214.0	3.2	5.2	7.8	0.0	99.0	GRNOGNTWLTAFVLK	1635.8	1636.8	1635.8	1636.8
P21291 CSR1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP1) - Bos taurus (Bovine) ; Cysteine and glycine-rich protein 1 (Cysteine-rich prot									
527.0	2.0	2.0	7.8	2.0	99.0	GFGFGGGAGALVHSE	1432.7	1433.7	1432.7	1433.7
360.0	2.0	2.0	7.8	2.0	99.0	GFGFGGGAGALVHSE	1432.7	1433.7	1432.7	1433.7
P21333 FLNA_HUMAN	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin) - Homo sapi									
24.0	27.7	27.7	14.3	2.0	99.0	AEAGVPAEFSIWTR	1532.8	1533.8	1532.8	1533.8
24.0	27.7	27.7	14.3	2.0	99.0	AFGPGLOGGSAGSPAR	1428.7	1429.7	1428.7	1429.7
24.0	27.7	27.7	14.3	2.0	99.0	ATCAPOHGAPGPGPADASK	1788.8	1789.8	1788.8	1789.8
24.0	27.7	27.7	14.3	2.0	99.0	DAPQDFHPDRVK	1423.7	1424.7	1423.7	1424.7
24.0	27.7	27.7	14.3	2.0	99.0	EATTEFSVDAR	1224.6	1225.6	1224.6	1225.6
24.0	27.7	27.7	14.3	2.0	99.0	LSPFMADIR	1048.5	1049.5	1048.5	1049.5
24.0	27.7	27.7	14.3	2.0	99.0	VANPSGNLTETVQDR	1762.9	1763.9	1762.8	1763.9
24.0	27.7	27.7	14.3	2.0	99.0	VHGPIOSGTTNKPNKFTVETR	2367.2	2368.2	2367.2	2368.2
24.0	27.7	27.7	14.3	2.0	99.0	VHSPSGALEECYVTEIDODKYAVR	2765.3	2766.3	2765.3	2766.3
24.0	27.7	27.7	14.3	2.0	99.0	WGDEHIGPSYR	1412.6	1413.6	1412.6	1413.7
24.0	27.7	27.7	14.3	2.0	99.0	YGGQVPNFPFSK	1289.6	1290.6	1289.6	1290.6
24.0	27.7	27.7	14.3	2.0	99.0	YNECIVPSSFTFAR	1601.8	1602.8	1601.8	1602.8
24.0	27.7	27.7	14.3	1.5	97.0	YGGDEIFPSPYRVR	1654.8	1655.8	1654.8	1655.8
24.0	27.7	27.7	14.3	1.4	96.0	IQQNTFR	1006.5	1007.5	1006.5	1007.5
24.0	27.7	27.7	14.3	0.7	81.0	GAPLRLKLNPKKAR	1445.9	1446.9	1445.9	1446.9
29.0	10.2	10.2	7.9	2.0	99.0	AEAGVPAEFSIWTR	1532.8	1533.8	1532.8	1533.8
29.0	10.2	10.2	7.9	2.0	99.0	AFGPGLOGGSAGSPAR	1428.7	1429.7	1428.7	1429.7
29.0	10.2	10.2	7.9	2.0	99.0	AGNNMLLVGVHGR	1433.7	1434.7	1433.8	1434.8
29.0	10.2	10.2	7.9	2.0	99.0	LSPFMADIR	1048.5	1049.5	1048.5	1049.5
29.0	10.2	10.2	7.9	1.7	98.0	WGDEHIGPSYR	1412.6	1413.7	1412.6	1413.7
29.0	10.2	10.2	7.9	0.3	46.0	VANPSGNLTETVQDR	1762.9	1763.9	1762.8	1763.9
29.0	10.2	10.2	7.9	0.1	27.0	LOVEPAVDTSGVQCYGPIEGGQVFR	2763.3	2764.3	2762.3	2763.3
36.0	18.9	18.9	13.4	2.0	99.0	AEAGVPAEFSIWTR	1532.8	1533.8	1532.8	1533.8
36.0	18.9	18.9	13.4	2.0	99.0	AFGPGLOGGSAGSPAR	1428.7	1429.7	1428.7	1429.7
36.0	18.9	18.9	13.4	2.0	99.0	ATCAPOHGAPGPGPADASK	1788.8	1789.8	1788.8	1789.8
36.0	18.9	18.9	13.4	2.0	99.0	AWGPGLEGVIVGK	1225.6	1226.6	1225.6	1226.7
36.0	18.9	18.9	13.4	2.0	99.0	WGDEHIGPSYR	1412.7	1413.7	1412.6	1413.7
36.0	18.9	18.9	13.4	2.0	99.0	YGGPYHIGGSPFK	1378.7	1379.7	1378.7	1379.7
36.0	18.9	18.9	13.4	2.0	99.0	YGGQVPNFPFSK	1289.6	1290.6	1289.6	1290.6
36.0	18.9	18.9	13.4	1.5	97.0	DAPQDFHPDRVK	1423.7	1424.7	1423.7	1424.7
36.0	18.9	18.9	13.4	1.5	97.0	VANPSGNLTETVQDR	1762.9	1763.9	1762.8	1763.9
36.0	18.9	18.9	13.4	1.2	93.0	LOVEPAVDTSGVQCYGPIEGGQVFR	2763.3	2764.3	2762.3	2763.3
36.0	18.9	18.9	13.4	0.7	80.0	TGVAIVNKPAEFTVDAK	1645.9	1646.9	1645.9	1646.9
36.0	18.9	18.9	13.4	0.0	56.0	AEAGVPAEFSIWTR	1528.8	1529.8	1528.8	1529.8
P22314 UBE1_HUMAN	Ubiquitin-activating enzyme E1 (A1S9 protein) - Homo sapiens (Human)									
226.0	5.4	5.4	5.3	2.0	99.0	NEEDAELVALAQAVNAR	1882.9	1883.9	1882.9	1883.9
226.0	5.4	5.4	5.3	2.0	99.0	QLVYLCEAMIKR	1426.7	1427.7	1426.7	1427.7
226.0	5.4	5.4	5.3	1.2	94.0	VGEFCHNR	1017.5	1018.5	1017.4	1018.5
226.0	5.4	5.4	5.3	0.2	30.0	OFLFRPWDTVK	1435.8	1436.8	1435.8	1436.8
261.0	2.2	2.2	9.4	2.0	99.0	NEEDAELVALAQAVNAR	1882.9	1883.9	1882.9	1883.9
261.0	2.2	2.2	9.4	0.2	30.0	ALPAVQNNLDELIR	1806.8	1807.8	1806.9	1807.9
P22392 NDBK_HUMAN	Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B) (nm23-H2) (C-myc purine-binding transcription factor PUF) - Homo sapiens									
140.0	8.0	8.0	48.7	2.0	99.0	GDFCQVGR	1050.5	1051.5	1050.5	1051.5
140.0	8.0	8.0	48.7	2.0	99.0	SAEKEISLWFKPEELVDYK	2310.2	2311.2	2310.2	2311.2
140.0	8.0	8.0	48.7	2.0	99.0	TFIAIKPQGVOR	1343.8	1344.8	1343.8	1344.8
140.0	8.0	8.0	48.7	2.0	99.0	VMLGETNPADSKPGTIR	1784.9	1785.9	1784.9	1785.9
131.0	6.0	6.0	44.7	2.0	99.0	GDFCQVGR	1050.5	1051.5	1050.5	1051.5
131.0	6.0	6.0	44.7	2.0	99.0	TFIAIKPQGVOR	1343.7	1344.8	1343.8	1344.8
131.0	6.0	6.0	44.7	2.0	99.0	VMLGETNPADSKPGTIR	1784.9	1785.9	1784.9	1785.9
P27695 APEX1_HUMAN	DNA (apurinic or pyrimidinic site) lyase (EC 4.2.99.18) (AP endonuclease 1) (APEX nuclease) (APEXN) (Protein REF-1) - Homo sapiens (Human)									
158.0	7.6	7.6	24.8	2.0	99.0	GLDWVKEAPDILCLQETK	2243.1	2244.1	2243.1	2244.1
158.0	7.6	7.6	24.8	2.0	99.0	ICSWNVNVDGLR	1218.6	1219.6	1218.6	1219.6
158.0	7.6	7.6	24.8	2.0	99.0	QRWDEAFRK	1234.6	1235.6	1234.6	1235.6
158.0	7.6	7.6	24.8	0.7	78.0	VSYGIGDEEHDQGR	1689.7	1690.7	1689.7	1690.7
158.0	7.6	7.6	24.8	0.6	74.0	NAGFTPOER	1018.5	1019.5	1018.5	1019.5
158.0	7.6	7.6	24.8	0.2	39.0	WDEAFRK	950.5	951.5	950.5	951.5
158.0	7.6	7.6	24.8	0.1	21.0	OGFGLLOAVPLDSFR	1846.9	1848.0	1847.0	1848.0
158.0	7.6	7.6	24.8	0.0	88.0	QRWDEAFRK	1234.6	1235.6	1234.6	1235.6
159.0	2.0	2.0	28.9	2.0	99.0	ICSWNVNVDGLR	1218.6	1219.6	1218.6	1219.6
P23246 SFPO_HUMAN	Splicing factor, proline- and glutamine-rich (Polyypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF									
52.0	17.2	17.2	23.6	2.0	99.0	FAOHGTFEYYSQR	1761.8	1762.8	1761.8	1762.8
52.0	17.2	17.2	23.6	2.0	99.0	FGGQGGAGPVGQGGPR	1342.7	1343.7	1342.7	1343.7
52.0	17.2	17.2	23.6	2.0	99.0	GIVEFASKPAAR	1244.7	1245.7	1244.7	1245.7
52.0	17.2	17.2	23.6	2.0	99.0	LFVGNLPADITDEFKRR	1963.0	1964.0	1963.0	1964.0
52.0	17.2	17.2	23.6	2.0	99.0	OHPHPYHOHHGQGGPGGGR	2385.1	2386.1	2385.1	2386.1
52.0	17.2	17.2	23.6	2.0	99.0	RMEELHNOEMOKR	1727.8	1728.8	1727.8	1728.8
52.0	17.2	17.2	23.6	2.0	99.0	TERFGGGAGPVGQGGPR	1726.9	1727.9	1726.9	1727.9
52.0	17.2	17.2	23.6	1.2	94.0	GGROHPPYHOHHGQGGPGGGR	2672.2	2673.2	2672.3	2673.3
52.0	17.2	17.2	23.6	1.1	92.0	RREEEMMIR	1248.6	1249.6	1248.6	1249.6
52.0	17.2	17.2	23.6	0.8	85.0	GMGPGTPAGYGR	1119.5	1120.5	1119.5	1120.5
212.0	1.3	1.3	16.4	1.3	95.0	FAOHGTFEYYSQR	1761.8	1762.8	1761.8	1762.8
134.0	6.0	6.0	25.2	2.0	99.0	FAOHGTFEYYSQR	1761.8	1762.8	1761.8	1762.8
134.0	6.0	6.0	25.2	2.0	99.0	YGERCVFNKGK	1437.7	1438.7	1437.7	1437.7
134.0	6.0	6.0	25.2	1.0	91.0	FGGGAGPVGQGGPR	1342.7	1343.7	1342.7	1343.7
134.0	6.0	6.0	25.2	0.4	61.0	RPGEKTYTRQR	1582.7	1583.7	1582.8	1583.8
134.0	6.0	6.0	25.2	0.4	56.0	GMGPGTPAGYGR	1119.5	1120.5	1119.5	1120.5
134.0	6.0	6.0	25.2	0.1	28.0	RMEELHNOEMOKR	1727.8	1728.8	1727.8	1728.8
P23284 PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1) - Homo sapien									
142.0	2.1	2.1	6.7	2.0	99.0	VIFGLFKG	879.5	880.5	879.5	880.5
248.0	2.3	2.3	10.1	2.0	99.0	SIYGERPPDENFKLK	1841.9	1842.9	1841.9	1842.9
248.0	2.3	2.3	10.1	0.3	47.0	VYFDLR	859.4	860.4	859.4	860.4
248.0	2.3	2.3	10.1	0.0	34.0	VYFDLR	811.4	812.4	811.4	812.4
248.0	2.3	2.3	10.1	0.0	27.0	VYFDLR	843.4	844.4	843.4	844.4
P23381 SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TrpRS) (IFP53) (HWR5) - Homo sapiens (Human)									
43.0	19.9	19.9	32.9	2.0	99.0	ATGQRPHFLR	1318.7	1319.7	1318.7	1319.7
43.0	19.9	19.9	32.9	2.0	99.0	ATGQRPHFLR	1478.8	1479.8	1478.8	1479.8
43.0	19.9	19.9	32.9	2.0	99.0	EVTDIEVKFMTPR	1692.8	1693.8	1692.8	1693.8
43.0	19.9	19.9	32.9	2.0	99.0	GIDYDKLIVR	1190.7	1191.7	1190.7	1191.7
43.0	19.9	19.9	32.9	2.0	99.0	HAFSGGRDTIEEHR	1610.8	1611.8	1610.8	1611.8
43.0	19.9	19.9	32.9	2.0	99.0	MSASDPNSSIFLDTAK	1783.8	1784.8	1783.8	1784.8
43.0	19.9	19.9	32.9	2.0	99.0	RKEVTDIEVKFMTPR	1977.0	1978.0	1977.0	1978.0
43.0	19.9	19.9	32.9	2.0	99.0	TDIQCPLCAIDQDPYFR	2224.0	2225.0	2224.0	2225.0
43.0	19.9	19.9	32.9	2.0	99.0	VNKHAFSGGRDTIEEHR	1952.0	1953.0	1952.0	1953.0
43.0	19.9	19.9	32.9	1.4	96.0	ALIEVLOPLIAEHOAR	1800.0	1801.0	1800	

38.0	18.5	18.5	32.7	0.9	86.0	ATGORPHFLRR	1474.8	1475.8	1474.8	1475.8
38.0	18.5	18.5	32.7	0.7	80.0	ATGORPHFLRR	1318.7	1318.7	1318.7	1319.7
38.0	18.5	18.5	32.7	0.4	56.0	IDKELINR	999.6	1000.6	999.6	1000.6
38.0	18.5	18.5	32.7	0.0	68.0	ATGORPHFLRR	1474.8	1474.8	1474.8	1475.8
P23528 COF1_HUMAN										
Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) - Homo sapiens (Human)										
42.0	7.2	7.2	29.5	2.0	99.0	ASGVAVSDGVKVFNDMK	1871.9	1878.9	1871.9	1879.0
42.0	7.2	7.2	29.5	2.0	99.0	KLTKIKHELOANCYEEVKDR	2430.2	2431.2	2430.2	2431.2
42.0	7.2	7.2	29.5	2.0	99.0	LTGKIKHELOANCYEEVKDR	2302.1	2303.1	2302.1	2303.1
42.0	7.2	7.2	29.5	1.2	94.0	YALYDATYETK	1336.6	1337.6	1336.6	1337.6
37.0	22.3	22.3	51.8	2.0	99.0	ASGVAVSDGVK	1143.6	1144.6	1143.6	1144.6
22.3	22.3	22.3	51.8	2.0	99.0	ASGVAVSDGVKVFNDMK	1877.9	1879.0	1877.9	1879.0
37.0	22.3	22.3	51.8	2.0	99.0	ASGVAVSDGVKVFNDMKVRR	2133.1	2134.1	2133.1	2134.1
37.0	22.3	22.3	51.8	2.0	99.0	ESKKEDLVFIFWAPESAPLK	2333.2	2334.2	2333.2	2334.2
37.0	22.3	22.3	51.8	2.0	99.0	ESKKEDLVFIFWAPESAPLKS	2548.4	2549.4	2548.4	2549.4
37.0	22.3	22.3	51.8	2.0	99.0	HELOANCYEEVKDR	1789.8	1790.8	1789.8	1790.8
37.0	22.3	22.3	51.8	2.0	99.0	KEDLVFIFWAPESAPLK	1989.1	1990.1	1989.1	1990.1
37.0	22.3	22.3	51.8	2.0	99.0	KLTKIKHELOANCYEEVKDR	2430.2	2431.2	2430.2	2431.2
37.0	22.3	22.3	51.8	2.0	99.0	LTGKIKHELOANCYEEVKDR	2302.1	2303.1	2302.1	2303.1
37.0	22.3	22.3	51.8	2.0	99.0	VFNDMKVRR	1007.5	1008.5	1007.5	1008.5
37.0	22.3	22.3	51.8	2.0	99.0	YALYDATYETK	1336.6	1337.6	1336.6	1337.6
37.0	22.3	22.3	51.8	0.3	50.0	MLPDKDCR	1033.5	1034.5	1033.5	1034.5
54.0	13.7	13.7	60.2	2.0	99.0	ESKKEDLVFIFWAPESAPLK	2333.2	2334.2	2333.2	2334.2
54.0	13.7	13.7	60.2	2.0	99.0	HELOANCYEEVKDR	1789.8	1790.8	1789.8	1790.8
54.0	13.7	13.7	60.2	2.0	99.0	KLTKIKHELOANCYEEVKDR	2431.2	2432.2	2431.2	2432.2
54.0	13.7	13.7	60.2	2.0	99.0	LTGKIKHELOANCYEEVKDR	2302.1	2303.1	2302.1	2303.1
54.0	13.7	13.7	60.2	2.0	99.0	MIYASSDKAIKK	1353.7	1354.7	1353.7	1354.7
54.0	13.7	13.7	60.2	2.0	99.0	YALYDATYETK	1336.6	1337.6	1336.6	1337.6
54.0	13.7	13.7	60.2	1.7	98.0	ASGVAVSDGVKVFNDMKVRR	2133.1	2134.1	2133.1	2134.1
54.0	13.7	13.7	60.2	0.0	99.0	LTGKIKHELOANCYEEVKDR	2303.1	2304.1	2303.1	2304.1
P25774 CAT5_HUMAN										
Cathepsin S precursor (EC 3.4.22.27) - Homo sapiens (Human)										
139.0	8.1	8.1	20.5	2.0	99.0	HPSFLYR	1065.5	1066.5	1065.5	1066.5
139.0	8.1	8.1	20.5	2.0	99.0	NKGNHCGIASFPSYPEI	1889.9	1890.9	1889.9	1890.9
139.0	8.1	8.1	20.5	2.0	99.0	NSWGHNFGEEGYIR	1664.7	1665.7	1664.7	1665.7
139.0	8.1	8.1	20.5	2.0	99.0	YTELPYGREVDLK	1581.8	1582.8	1581.8	1582.8
139.0	8.1	8.1	20.5	0.1	22.0	YTELPYGR	997.5	998.5	997.5	998.5
139.0	8.1	8.1	20.5	0.0	99.0	NSWGHNFGEEGYIR	1665.7	1666.7	1665.7	1666.7
39.0	8.0	8.0	30.2	2.0	99.0	HPSFLYR	1065.5	1066.5	1065.5	1066.5
39.0	8.0	8.0	30.2	2.0	99.0	NKGNHCGIASFPSYPEI	1889.9	1890.9	1889.9	1890.9
39.0	8.0	8.0	30.2	2.0	99.0	NSWGHNFGEEGYIR	1664.7	1665.7	1664.7	1665.7
39.0	8.0	8.0	30.2	2.0	99.0	YTELPYGREVDLK	1581.8	1582.8	1581.8	1582.8
58.0	13.0	13.0	23.3	2.0	99.0	EAVANKGPVSVGVDR	1567.8	1568.8	1567.8	1568.8
58.0	13.0	13.0	23.3	2.0	99.0	HPSFLYR	1065.5	1066.5	1065.5	1066.5
58.0	13.0	13.0	23.3	2.0	99.0	LPDSVDWR	986.5	987.5	986.5	987.5
58.0	13.0	13.0	23.3	2.0	99.0	LPDSVDWREK	1243.6	1244.6	1243.6	1244.6
58.0	13.0	13.0	23.3	2.0	99.0	NSWGHNFGEEGYIR	1664.7	1665.7	1664.7	1665.7
58.0	13.0	13.0	23.3	2.0	99.0	YTELPYGREVDLK	1581.8	1582.8	1581.8	1582.8
58.0	13.0	13.0	23.3	0.9	87.0	GIDSDASYPPKAMDQK	1803.8	1804.8	1803.8	1804.8
58.0	13.0	13.0	23.3	0.1	25.0	YTELPYGR	997.5	998.5	997.5	998.5
58.0	13.0	13.0	23.3	0.0	98.0	HPSFLYR	1077.5	1078.5	1077.5	1078.5
58.0	13.0	13.0	23.3	0.0	99.0	NSWGHNFGEEGYIR	1665.7	1666.7	1665.7	1666.7
58.0	13.0	13.0	23.3	0.0	99.0	NSWGHNFGEEGYIR	1677.8	1678.8	1677.8	1677.8
P25781 PSA1_HUMAN										
Proteasome subunit alpha type 1 (EC 3.4.25.1) (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit										
135.0	2.2	2.2	13.7	2.0	99.0	NGYDNDVTWVSPQGR	1777.8	1778.8	1777.8	1778.8
135.0	2.2	2.2	13.7	0.2	94.0	FVFDRLPLVSR	1332.7	1333.7	1332.7	1332.7
118.0	9.7	9.7	26.2	2.0	99.0	AQPAQPADEPAEKADPEMEH	2159.9	2160.9	2159.9	2160.9
118.0	9.7	9.7	26.2	2.0	99.0	HMSEFMENCLNELVK	1879.8	1880.8	1879.8	1880.8
118.0	9.7	9.7	26.2	2.0	99.0	LLCNFMR	952.5	953.5	952.5	953.5
118.0	9.7	9.7	26.2	2.0	99.0	NGYDNDVTWVSPQGR	1777.8	1778.8	1777.8	1778.8
118.0	9.7	9.7	26.2	1.7	98.0	FVFDRLPLVSR	1331.7	1332.7	1331.7	1332.7
144.0	5.3	5.3	26.2	2.0	99.0	AQPAQPADEPAEKADPEMEH	2159.9	2160.9	2159.9	2161.0
144.0	5.3	5.3	26.2	2.0	99.0	IHQIYAMEAVK	1430.7	1431.7	1430.7	1431.7
144.0	5.3	5.3	26.2	0.8	84.0	NGYDNDVTWVSPQGR	1778.8	1779.8	1778.8	1779.8
144.0	5.3	5.3	26.2	0.5	65.0	FVFDRLPLVSR	1331.7	1332.7	1331.7	1332.7
P25782 PSA2_HUMAN										
Proteasome subunit alpha type 2 (EC 3.4.25.1) (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit										
435.0	2.0	2.0	18.4	2.0	99.0	HIGLVYSGMGPDYR	1563.7	1564.7	1563.8	1564.8
187.0	2.0	2.0	6.0	2.0	99.0	HIGLVYSGMGPDYR	1563.8	1564.8	1563.8	1564.8
279.0	2.1	2.1	17.9	2.0	99.0	HIGLVYSGMGPDYR	1563.8	1564.8	1563.8	1564.8
P25789 PSA4_HUMAN										
Proteasome subunit alpha type 4 (EC 3.4.25.1) (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex subunit										
524.0	2.0	2.0	3.8	2.0	99.0	LLDEVFSEK	1225.6	1226.6	1225.6	1226.6
147.0	2.0	2.0	12.6	2.0	99.0	LLDEVFSEK	1225.6	1226.6	1225.6	1226.6
359.0	2.0	2.0	3.8	2.0	99.0	LLDEVFSEK	1225.6	1226.6	1225.6	1226.6
P26038 MOES_HUMAN										
Moesin (Membrane-organizing extension spike protein) - Homo sapiens (Human)										
5.0	53.4	53.4	55.3	2.0	99.0	AKFYPEDEVSEELIQDITOR	2280.1	2281.1	2280.1	2281.1
5.0	53.4	53.4	55.3	2.0	99.0	APDFVYAPR	1181.6	1182.6	1181.6	1182.6
5.0	53.4	53.4	55.3	2.0	99.0	AQMVOEDLEKTR	1446.7	1447.7	1446.7	1447.7
5.0	53.4	53.4	55.3	2.0	99.0	AQMVOEDLEKTRAEK	1888.0	1889.0	1888.0	1889.0
5.0	53.4	53.4	55.3	2.0	99.0	ESEAVEWQK	1232.6	1233.6	1232.6	1233.6
5.0	53.4	53.4	55.3	2.0	99.0	ESPLLFKFR	1135.6	1136.6	1135.6	1136.6
5.0	53.4	53.4	55.3	2.0	99.0	EVWFFGLOYDQTK	1659.8	1660.8	1659.8	1660.8
5.0	53.4	53.4	55.3	2.0	99.0	FYQEDVSEELIQDITOR	2081.0	2082.0	2081.0	2082.0
5.0	53.4	53.4	55.3	2.0	99.0	IGFPWSEIR	1103.6	1104.6	1103.6	1104.6
5.0	53.4	53.4	55.3	2.0	99.0	ILALCMGNHELYMR	1719.8	1720.8	1719.8	1720.8
5.0	53.4	53.4	55.3	2.0	99.0	IQVWHEEHR	1232.6	1233.6	1232.6	1233.6
5.0	53.4	53.4	55.3	2.0	99.0	ISOLEMAR	946.5	947.5	946.5	947.5
5.0	53.4	53.4	55.3	2.0	99.0	KAPDFVYAPR	1309.7	1310.7	1309.7	1310.7
5.0	53.4	53.4	55.3	2.0	99.0	KAQOELEEQTRR	1514.8	1515.8	1514.8	1515.8
5.0	53.4	53.4	55.3	2.0	99.0	KTANDMIHAENMR	1529.7	1530.7	1529.7	1530.7
5.0	53.4	53.4	55.3	2.0	99.0	OKKESAVEWQK	1616.8	1617.8	1616.8	1617.8
5.0	53.4	53.4	55.3	2.0	99.0	ORIDEFEM	1136.5	1137.5	1136.5	1137.5
5.0	53.4	53.4	55.3	2.0	99.0	SGYLAGDKLLPOR	1416.8	1417.8	1416.8	1417.8
5.0	53.4	53.4	55.3	2.0	99.0	TAMSTPHVAEPAENEQEQDENGAEASADLR	3312.4	3313.4	3312.4	3313.4
5.0	53.4	53.4	55.3	2.0	99.0	TANDMIHAENMR	1401.6	1402.6	1401.6	1402.6
5.0	53.4	53.4	55.3	2.0	99.0	TOEQLALEMAELTAR	1702.9	1703.9	1702.9	1703.9
5.0	53.4	53.4	55.3	2.0	99.0	VLEQHKLNKQDWEER	1951.0	1952.0	1951.0	1952.0
5.0	53.4	53.4	55.3	2.0	99.0	YGFNKEVHK	1235.6	1236.6	1235.6	1236.6
5.0	53.4	53.4	55.3	1.7	98.0	GMLREDAVLEYLK	1535.8	1536.8	1535.8	1536.8
5.0	53.4	53.4	55.3	1.5	97.0	LEQVQK	893.5	894.5	893.5	894.5
5.0	53.4	53.4	55.3	1.4	96.0	DESKTANDMIHAENMR	1989.9	1990.9	1989.9	1990.9
5.0	53.4	53.4	55.3	1.0	89.0	AQOELEEQTRR	1230.6	1231.6	1230.6	1231.6
5.0	53.4	53.4	55.3	0.9	86.0	LKQIEEQTK	1243.7	1244.7	1243.7	1244.7
5.0	53.4	53.4	55.3	0.7	80.0	RALELEQER	1142.6	1143.6	1142.6	1143.6
5.0	53.4	53.4	55.3	0.0	99.0	IQVWHEEHR	1232.6	1233.6	1232.6	1233.6
5.0	53.4	53.4	55.3	0.0	99.0	VLEQHKLNKQDWEER	1951.0	1952.0	1951.0	1952.0
5.0	53.4	53.4	55.3	0.0	99.0	YGFNKEVHK	1235.6	1236.6	1235.6	1236.6
11.0	20.7	20.7	37.1	2.0	99.0	APDFVYAPR	1181.6	1182.6	1181.6	1182.6
11.0	20.7	20.7	37.1	2.0	99.0	EVWFFGLOYDQTK	1659.8	1660.8	1659.8	1660.8
11.0	20.7	20.7	37.1	2.0	99.0	IAQDLEMVGNVFSIK	1889.9	1890.9	1889.9	1890.9
11.0	20.7	20.7	37.1	2.0	99.0	IGFPWSEIR	1101.6	1102.6	1101.6	1102.6
11.0	20.7	20.7	37.1	2.0	99.0	IQVWHEEHR	1232.6	1233.6	1232.6	1233.6
11.0	20.7	20.7	37.1	2.0	99.0	KAPDFVYAPR	1309.7</			

7.0	44.9	44.9	56.7	2.0	99.0	KAPDFVFFYAPR	1309.7	1310.7	1309.7	1310.7
7.0	44.9	44.9	56.7	2.0	99.0	KTANDMIHAENMR	1529.7	1530.7	1530.7	1530.7
7.0	44.9	44.9	56.7	2.0	99.0	RKPDTEIVQQMK	1471.8	1472.8	1471.8	1472.8
7.0	44.9	44.9	56.7	2.0	99.0	RRKPTDTEIVQQMK	1627.9	1628.9	1627.9	1628.9
7.0	44.9	44.9	56.7	2.0	99.0	SGYLAGDKLLPQR	1416.8	1417.8	1416.8	1417.8
7.0	44.9	44.9	56.7	2.0	99.0	TANDMIHAENMR	1402.6	1403.6	1402.6	1403.6
7.0	44.9	44.9	56.7	2.0	99.0	TQEQALALEMELTAR	1702.8	1703.8	1702.8	1703.8
7.0	44.9	44.9	56.7	2.0	99.0	VLEQHKLNKDQWEER	1951.0	1952.0	1951.0	1952.0
7.0	44.9	44.9	56.7	2.0	99.0	YGFNFKVHK	1236.6	1237.6	1236.6	1237.6
7.0	44.9	44.9	56.7	1.7	98.0	LFLLQVK	893.5	894.5	893.5	894.5
7.0	44.9	44.9	56.7	1.5	97.0	QRIDEFESM	1136.5	1137.5	1136.5	1137.5
7.0	44.9	44.9	56.7	1.4	96.0	FYPEDVSEELIQDITQR	2081.0	2082.0	2081.0	2082.0
7.0	44.9	44.9	56.7	1.2	94.0	ESPLLFKFR	1136.6	1137.6	1136.6	1137.6
7.0	44.9	44.9	56.7	1.0	89.0	LLPQRVLEQHK	1419.7	1420.7	1419.8	1420.8
7.0	44.9	44.9	56.7	0.8	83.0	DESKKTANDMIHAENMR	1988.9	1989.9	1988.9	1989.9
7.0	44.9	44.9	56.7	0.5	70.0	ALTSANANAR	1044.6	1045.6	1044.6	1045.6
7.0	44.9	44.9	56.7	0.4	60.0	RALELEQER	1142.6	1143.6	1142.6	1143.6
7.0	44.9	44.9	56.7	0.2	30.0	KAQOQLELEOTRR	1514.8	1515.8	1514.8	1515.8
7.0	44.9	44.9	56.7	0.1	27.0	EWVFFGLQYQDTK	1659.8	1660.8	1659.8	1660.8
7.0	44.9	44.9	56.7	0.0	99.0	IQVWHEEHR	1232.6	1233.6	1232.6	1233.6
7.0	44.9	44.9	56.7	0.0	46.0	IQVWHEEHR	1248.6	1249.6	1248.6	1249.6
7.0	44.9	44.9	56.7	0.0	33.0	IQVWHEEHR	1286.5	1287.5	1286.5	1287.5
7.0	44.9	44.9	56.7	0.0	78.0	RRKPDTEIVQQMK	1627.9	1628.9	1627.9	1628.9
7.0	44.9	44.9	56.7	0.0	99.0	VLEQHKLNKDQWEER	1951.0	1952.0	1951.0	1952.0
P26447 S10A4_HUMAN	Protein S100-A4 (S100 calcium-binding protein A4) (Metastasin) (Protein Mts1) (Placental calcium-binding protein) (Calvasculin) - Homo sapiens									
499.0	2.0	2.0	19.8	2.0	99.0	ELPSFLGKR	1045.6	1046.6	1045.6	1046.6
181.0	2.0	2.0	19.8	2.0	99.0	ELPSFLGKR	1045.6	1046.6	1045.6	1046.6
268.0	2.1	2.1	20.8	2.0	99.0	ELPSFLGKR	1045.6	1046.6	1045.6	1046.6
268.0	2.1	2.1	20.8	0.1	21.0	LNKSELKELLTR	1538.8	1539.8	1538.8	1539.8
P26583 HMG2_HUMAN	High mobility group protein B2 (High mobility group protein 2) (HMG-2) - Bos taurus (Bovine) ; High mobility group protein B2 (High mobility gro									
288.0	4.0	16.0	50.7	2.0	99.0	IKSEHPLESGDTAK	1551.8	1552.8	1551.8	1552.8
288.0	4.0	16.0	50.7	2.0	99.0	LGMWSEQSAKDKOPYEQK	2281.1	2282.1	2281.1	2282.1
288.0	4.0	16.0	50.7	0.0	99.0	GKMSSYAFFVOTCR	1680.8	1681.8	1680.8	1681.8
288.0	4.0	16.0	50.7	0.0	99.0	GKMSSYAFFVOTCRREEKK	2332.1	2333.1	2332.1	2333.1
288.0	4.0	16.0	50.7	0.0	99.0	LKEKYEDIAAYR	1625.9	1626.9	1625.9	1626.9
288.0	4.0	16.0	50.7	0.0	99.0	MSSYAFFVOTCR	1498.7	1499.7	1498.7	1499.7
288.0	4.0	16.0	50.7	0.0	99.0	MSSYAFFVOTCR	1495.7	1496.7	1495.7	1496.7
288.0	4.0	16.0	50.7	0.0	99.0	MSSYAFFVOTCRREEKK	2147.0	2148.0	2147.0	2148.0
288.0	4.0	16.0	50.7	0.0	99.0	YEKIDIAAYR	1127.6	1128.6	1127.6	1128.6
264.0	2.1	8.2	39.7	2.0	99.00	KLGEWVSEQSAKDKOPYEQK	2409.1	2410.1	2409.1	2410.1
264.0	2.1	8.2	39.7	0.1	25.00	IKSEHPLESGDTAK	1551.8	1552.8	1551.8	1552.8
264.0	2.1	8.2	39.7	0.0	99.00	GKMSSYAFFVOTCR	1680.8	1681.8	1680.8	1681.8
264.0	2.1	8.2	39.7	0.0	99.00	LKEKYEDIAAYR	1625.9	1626.9	1625.9	1626.9
264.0	2.1	8.2	39.7	0.0	35.00	LKEKYEDIAAYR	1622.8	1623.8	1622.8	1623.8
264.0	2.1	8.2	39.7	0.0	99.00	YEKIDIAAYR	1127.6	1128.6	1127.6	1128.6
P27695 APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP endonuclease 1) (APEX nuclease) (APEN) (Protein REF-1) - Homo sapiens (Human)									
158.0	7.6	7.6	24.8	2.0	99.0	GLDWVKEAPDILCLOETK	2243.1	2244.1	2243.1	2244.1
158.0	7.6	7.6	24.8	2.0	99.0	ICSWNVDGLR	1218.6	1219.6	1218.6	1219.6
158.0	7.6	7.6	24.8	2.0	99.0	QRWDEAFRK	1234.6	1235.6	1234.6	1235.6
158.0	7.6	7.6	24.8	0.7	78.0	VSYGIGDEEHDDEGR	1689.7	1690.7	1689.7	1690.7
158.0	7.6	7.6	24.8	0.6	74.0	NAGFTPOER	1018.5	1019.5	1018.5	1019.5
158.0	7.6	7.6	24.8	0.2	39.0	WDEAFRK	950.5	951.5	950.5	951.5
158.0	7.6	7.6	24.8	0.1	21.0	QGFGLLOAVPLADFSR	1846.9	1848.0	1847.0	1848.0
158.0	7.6	7.6	24.8	0.0	88.0	QRWDEAFRK	1234.6	1235.6	1234.6	1235.6
159.0	2.0	2.0	28.9	2.0	99.0	ICSWNVDGLR	1218.6	1219.6	1218.6	1219.6
P27797 CALR_HUMAN	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60) (grp60) - Homo sapiens (Human)									
86.0	12.2	12.2	25.4	2.0	99.0	EPAVYKEQFLDGGDWTSR	2244.0	2245.0	2244.0	2245.1
86.0	12.2	12.2	25.4	2.0	99.0	EQFLDGGDWTSR	1409.6	1410.6	1409.6	1410.6
86.0	12.2	12.2	25.4	2.0	99.0	FVLSGKFGYDEEKKGLQTSODAR	2804.3	2805.4	2804.4	2805.4
86.0	12.2	12.2	25.4	2.0	99.0	FYGDDEKDKGLQTSODAR	2086.0	2087.0	2086.0	2087.0
86.0	12.2	12.2	25.4	2.0	99.0	HEQNDICGGGYVK	1475.7	1476.7	1475.6	1476.7
86.0	12.2	12.2	25.4	2.0	99.0	IKDPDASKPEDWDER	1799.8	1800.8	1799.8	1800.8
86.0	12.2	12.2	25.4	0.2	38.1	AVYFKEQFLDGGDWTSR	2018.0	2019.0	2018.0	2019.0
86.0	12.2	12.2	25.4	0.0	99.0	IKDPDASKPEDWDER	1799.8	1800.8	1799.8	1800.8
123.0	6.0	6.0	13.9	2.0	99.0	FYGDDEKDKGLQTSODAR	2086.0	2087.0	2086.0	2087.0
123.0	6.0	6.0	13.9	2.0	99.0	IKDPDASKPEDWDER	1799.8	1800.8	1799.8	1800.8
123.0	6.0	6.0	13.9	1.7	98.0	EQFLDGGDWTSR	1409.6	1410.6	1409.6	1410.6
123.0	6.0	6.0	13.9	0.3	54.0	HEQNDICGGGYVK	1475.7	1476.7	1475.6	1476.7
123.0	6.0	6.0	13.9	0.0	87.0	IKDPDASKPEDWDER	1799.8	1800.8	1799.8	1800.8
P28062 PSBB_HUMAN	Proteasome subunit beta type 8 precursor (EC 3.4.25.1) (Proteasome component C13) (Macropain subunit C13) (Multicatalytic endopeptidase cor									
149.0	8.0	8.0	21.7	2.0	99.0	FOHGVIAAVDSR	1298.7	1299.7	1298.7	1299.7
149.0	8.0	8.0	21.7	2.0	99.0	GMGLSMGSMICGWDK	1628.7	1629.7	1628.7	1629.7
149.0	8.0	8.0	21.7	2.0	99.0	KGPGLYVDEHGTR	1590.8	1591.8	1590.8	1591.8
149.0	8.0	8.0	21.7	2.0	99.0	LLSNMCCOYR	1314.6	1315.6	1314.6	1315.6
149.0	8.0	8.0	21.7	0.0	99.0	KGPGLYVDEHGTR	1590.8	1591.8	1590.8	1591.8
131.0	2.2	2.2	13.0	2.0	99.0	FOHGVIAAVDSR	1298.7	1299.7	1298.7	1299.7
131.0	2.2	2.2	13.0	0.2	35.0	LLSNMCCOYR	1314.6	1315.6	1314.6	1315.6
120.0	6.2	6.2	21.4	2.0	99.0	FOHGVIAAVDSR	1298.7	1299.7	1298.7	1299.7
120.0	6.2	6.2	21.4	2.0	99.0	GNGLSMGSMICGWDK	1628.7	1629.7	1628.7	1629.7
120.0	6.2	6.2	21.4	2.0	99.0	EQFLDGGDWTSR	1409.6	1410.6	1409.6	1410.6
120.0	6.2	6.2	21.4	0.1	26.0	KGPGLYVDEHGTR	1590.8	1591.8	1590.8	1591.8
120.0	6.2	6.2	21.4	0.1	21.0	ECRLYYLR	1142.6	1143.6	1142.6	1143.6
P28062 PSAA5_HUMAN	Proteasome subunit alpha type 5 (EC 3.4.25.1) (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain)									
169.0	6.7	6.7	26.6	2.0	99.0	AIGSASEGASLSQEVYHK	1960.9	1961.9	1960.9	1962.0
169.0	6.7	6.7	26.6	2.0	99.0	GWNTFSPEGR	1062.5	1063.5	1062.5	1063.5
169.0	6.7	6.7	26.6	2.0	99.0	SEYDRGVNTFSPEGR	1712.8	1713.8	1712.8	1713.8
169.0	6.7	6.7	26.6	0.7	81.0	LFOVEYIAEIK	1422.8	1423.8	1422.8	1423.8
169.0	6.7	6.7	26.6	0.0	99.0	AIGSASEGASLSQEVYHK	1958.9	1959.9	1960.9	1962.0
169.0	6.7	6.7	26.6	0.0	99.0	SEYDRGVNTFSPEGR	1712.8	1713.8	1712.8	1713.8
190.0	4.0	4.0	14.1	2.0	99.0	AIGSASEGASLSQEVYHK	1958.9	1959.9	1960.9	1962.0
190.0	4.0	4.0	14.1	2.0	99.0	SEYDRGVNTFSPEGR	1712.8	1713.8	1712.8	1713.8
P28070 PSB4_HUMAN	Proteasome subunit beta type 4 precursor (EC 3.4.25.1) (Proteasome beta chain) (Macropain beta chain) (Multicatalytic endopeptidase complex b									
281.0	4.0	4.0	24.2	2.0	99.0	AIHSWLTR	982.5	983.5	982.5	983.5
281.0	4.0	4.0	24.2	2.0	99.0	EVLEKOPVLSQTEAR	1725.9	1726.9	1725.9	1726.9
136.0	2.2	2.2	22.3	2.0	99.0	AIHSWLTR	982.5	983.5	982.5	983.5
136.0	2.2	2.2	22.3	0.2	31.0	EVLEKOPVLSQTEAR	1725.9	1726.9	1725.9	1726.9
P28482 MKO1_HUMAN	Mitogen-activated protein kinase 1 (EC 2.7.11.24) (Extracellular signal-regulated kinase 2) (ERK-2) (Mitogen-activated protein kinase 2) (MAP kir									
167.0	2.0	2.0	15.0	2.0	99.0	LKELFEETAR	1347.7	1348.7	1347.7	1348.7
175.0	4.0	4.0	11.9	2.0	99.0	QGVFDVGR	973.5	974.5	973.5	974.5
175.0	4.0	4.0	11.9	2.0	99.0	LKELFEETAR	1347.7	1348.7	1347.7	1348.7
P28799 GRN_HUMAN	Granulins precursor (Proepithelin) (PEPI) [Contains: Acrogranin; Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3 (Grar									
368.0	2.9	2.9	10.1	2.0	99.0	QHCCPAGYTCNVK	1593.7	1594.7	1593.6	1594.7
368.0	2.9	2.9	10.1	0.9	86.0	QGWACCPYR	1179.5	1180.5	1179.5	1180.5
229.0	2.8	2.8	13.2	1.5	97.0	QHCCPAGYTCNVK	1576.6	1577.6	1576.6	1577.6
229.0	2.8	2.8	13.2	0.6	73.0	CDMEVSCPDGYTCR	1907.6	1908.6	1907.6	1908.7
229.0	2.8	2.8	13.2	0.4	60.0	QGWACCPYR	1179.5	1180.5	1179.5	1180.5
229.0	2.8	2.8	13.2	0.3	51.0	DVEGEGHFCHDNQTCR	2278.8	2280.8	2278.8	2280.8
229.0	2.8	2.8	13.2	0.0	21.0	QGWACCPYR	1196.5	1197.5	1196.5	1197.5
P28838 AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Leucine aminopeptidase 3) (Proline aminopeptid									
44.0	19.5	19.5	30.1	2.0	99.0	AAGIDQENWHEGKENIR	2095.0	2096.0	2095.0	2096.0
44.0	19.5	19.5	30.1	2.0	99.0	EKEDDVPOFTSAGENFDKLLGAK	2537.2	2538.2	2537.2	2538.2
44.0	19.5	19.5	30							

32.0	20.0	20.0	37.2	2.0	99.0	LYGSGDQEAQWQK	1380.6	1381.6	1380.6	1381.6
32.0	20.0	20.0	37.2	2.0	99.0	LYGSGDQEAQWQKGVLFASQGNLAR	2594.3	2594.3	2594.3	2595.3
32.0	20.0	20.0	37.2	2.0	99.0	MPLFEHYTR	1192.6	1193.6	1192.6	1193.6
32.0	20.0	20.0	37.2	2.0	99.0	QLMETPANEMTPTTR	1600.7	1601.7	1600.7	1601.7
32.0	20.0	20.0	37.2	2.0	99.0	QVVDQCLADVNNIGKYR	1991.0	1992.0	1991.0	1992.0
32.0	20.0	20.0	37.2	2.0	99.0	SWIEQAMGSLVAK	1781.9	1782.9	1781.9	1782.9
32.0	20.0	20.0	37.2	1.3	95.0	FAEIEK	848.5	848.5	848.5	849.5
32.0	20.0	20.0	37.2	0.6	72.0	TLIEFLLR	1003.6	1004.6	1003.6	1004.6
32.0	20.0	20.0	37.2	0.0	99.0	AAGIDEQENWHEGKENIR	2095.0	2096.0	2095.0	2096.0
32.0	20.0	20.0	37.2	0.0	99.0	KAGIDEQENWHEGKENIR	2223.1	2224.1	2223.1	2224.1
P29350	PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 (EC 3.1.3.48) (Protein-tyrosine phosphatase 1C) (PTP-1C) (Hematopoietic cell protein-tyrosine)								
128.0	9.2	9.2	25.0	2.0	99.0	AGFWEEFESLQK	1469.7	1470.7	1469.7	1470.7
128.0	9.2	9.2	25.0	2.0	99.0	AGFWEEFESLQKQEVK	1953.9	1953.9	1953.9	1955.0
128.0	9.2	9.2	25.0	2.0	99.0	YKNILPFDHSR	1388.7	1389.7	1388.7	1389.7
128.0	9.2	9.2	25.0	1.3	95.0	AYGPPSYVINGEHDTEYKLR	2461.1	2461.1	2461.1	2461.1
128.0	9.2	9.2	25.0	1.0	89.0	DLISGLDAETLLK	1303.7	1304.7	1303.7	1304.7
128.0	9.2	9.2	25.0	0.7	82.0	VGSDVTHIR	1023.5	1024.6	1023.5	1024.6
128.0	9.2	9.2	25.0	0.1	26.0	NKCVYVWPEVGMQR	1762.8	1763.9	1762.8	1763.8
287.0	2.0	2.0	74.4	2.0	99.0	YKNILPFDHSR	1388.7	1389.7	1388.7	1389.7
P29401	TKT_HUMAN	Transketolase (EC 2.2.1.1) (TK) - Homo sapiens (Human)								
53.0	17.1	17.1	30.0	2.0	99.0	GITGVEDKESWHGKPLPK	1977.0	1978.0	1977.0	1978.0
53.0	17.1	17.1	30.0	2.0	99.0	ILATPPQEDAPSVDIANIR	2019.1	2020.1	2019.1	2020.1
53.0	17.1	17.1	30.0	2.0	99.0	LGOSDPAPLQHQMDIYOK	2068.0	2069.0	2068.0	2069.0
53.0	17.1	17.1	30.0	2.0	99.0	MESYHKPQQK	1431.6	1432.7	1431.6	1432.7
53.0	17.1	17.1	30.0	2.0	99.0	MFGIDRAIAQAVR	1561.8	1562.8	1561.8	1562.8
53.0	17.1	17.1	30.0	2.0	99.0	SVPTSTVFYPSDGVATEK	1884.9	1884.9	1884.9	1884.9
53.0	17.1	17.1	30.0	2.0	99.0	TSRPNENAIYNNDFQVGOAK	2507.2	2508.2	2507.2	2508.2
53.0	17.1	17.1	30.0	2.0	99.0	VLDPFITKPLDR	1412.8	1413.8	1412.8	1413.8
53.0	17.1	17.1	30.0	0.4	64.0	YFDKASVY	1048.5	1049.5	1048.5	1049.5
53.0	17.1	17.1	30.0	0.4	61.0	GICFIR	764.4	765.4	764.4	765.4
53.0	17.1	17.1	30.0	0.1	29.0	VLDPFITKPLDRK	1540.9	1541.9	1540.9	1541.9
62.0	5.6	5.6	23.4	2.0	99.0	ILATPPQEDAPSVDIANIR	2019.1	2020.1	2019.1	2020.1
62.0	5.6	5.6	23.4	2.0	99.0	VLDPFITKPLDR	1412.8	1413.8	1412.8	1413.8
62.0	5.6	5.6	23.4	1.2	94.0	TSRPNENAIYNNDFQVGOAK	2507.2	2508.2	2507.2	2508.2
62.0	5.6	5.6	23.4	0.2	34.0	GICFIR	764.4	765.4	764.4	765.4
62.0	5.6	5.6	23.4	0.1	28.0	MFGIDRAIAQAVR	1561.8	1562.8	1561.8	1562.8
66.0	11.8	11.8	22.8	2.0	99.0	GITGVEDKESWHGKPLPK	1977.0	1978.0	1977.0	1978.0
66.0	11.8	11.8	22.8	2.0	99.0	ILATPPQEDAPSVDIANIR	2019.1	2020.1	2019.1	2020.1
66.0	11.8	11.8	22.8	2.0	99.0	KKILATPPQEDAPSVDIANIR	2275.2	2276.3	2275.2	2276.3
66.0	11.8	11.8	22.8	2.0	99.0	TSRPNENAIYNNDFQVGOAK	2507.2	2508.2	2507.2	2508.2
66.0	11.8	11.8	22.8	2.0	99.0	VLDPFITKPLDR	1412.8	1413.8	1412.8	1413.8
66.0	11.8	11.8	22.8	1.7	98.0	MFGIDRAIAQAVR	1561.8	1562.8	1561.8	1562.8
P30041	PRDX6_HUMAN	Peroxiredoxin-6 (EC 1.1.1.15) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys Prx) (Acidic calcium-independent phospholipase A2) (EC 3.1)								
561.0	1.7	1.7	12.9	1.7	98.0	LAPEFAKR	930.5	931.5	930.5	931.5
215.0	3.2	3.2	18.3	2.0	99.0	PGGILLGDVAPNFANNTVGR	2097.1	2098.1	2097.1	2098.1
215.0	3.2	3.2	18.3	1.2	93.0	DFTPVCTTELGR	1394.7	1395.7	1394.7	1395.7
P30046	DOPD_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II) - Homo sapiens (Human)								
542.0	2.0	2.0	9.3	2.0	99.0	FFPLESWIQIK	1350.7	1351.7	1350.7	1351.7
365.0	2.0	2.0	9.3	2.0	99.0	FFPLESWIQIK	1350.7	1351.7	1350.7	1351.7
P30050	RL12_HUMAN	60S ribosomal protein L12 - Homo sapiens (Human)								
411.0	2.2	2.2	19.4	2.0	99.0	HSGNITFDEIVNIAR	1684.9	1685.9	1684.9	1685.9
411.0	2.2	2.2	19.4	0.2	43.0	ELSGTIK	803.4	804.4	803.4	804.4
331.0	2.0	2.0	17.0	2.0	99.0	HSGNITFDEIVNIAR	1684.9	1685.9	1684.9	1685.9
P30086	PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (hPBP) (Neuropeptide h3) (Raf kinase inhibitor protein)								
102.0	10.6	10.6	55.1	2.0	99.0	APVAGCYQAEWDDYVPK	2069.9	2069.9	2069.9	2069.9
102.0	10.6	10.6	55.1	2.0	99.0	GNDISSGTVLSDYVSGPPKGTGLHR	2570.2	2571.2	2570.2	2571.3
102.0	10.6	10.6	55.1	2.0	99.0	LYEQLSGK	936.5	937.5	936.5	937.5
102.0	10.6	10.6	55.1	2.0	99.0	YVWLVEQDRPLK	1707.9	1708.9	1707.9	1708.9
102.0	10.6	10.6	55.1	1.4	96.0	NRPTSIWVDGLDSGK	1631.8	1632.8	1631.8	1632.8
102.0	10.6	10.6	55.1	1.2	94.0	YVWLVEQDRPLKDEPILSNR	2792.4	2793.4	2792.4	2793.4
184.0	4.0	4.0	31.0	2.0	99.0	APVAGCYQAEWDDYVPK	2069.9	2069.9	2069.9	2069.9
184.0	4.0	4.0	31.0	2.0	99.0	GNDISSGTVLSDYVSGPPKGTGLHR	2571.3	2572.3	2571.3	2571.3
P30101	PDI A3_HUMAN	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57) (58 kDa g)								
63.0	15.7	15.7	23.6	2.0	99.0	AASNLRDNYR	1178.6	1179.6	1178.6	1179.6
63.0	15.7	15.7	23.6	2.0	99.0	ELSDFISYLQR	1369.7	1370.7	1369.7	1370.7
63.0	15.7	15.7	23.6	2.0	99.0	FVMQEEFSR	1171.5	1172.5	1171.5	1172.5
63.0	15.7	15.7	23.6	2.0	99.0	GFPTIVYSQANK	1341.7	1342.7	1341.7	1341.7
63.0	15.7	15.7	23.6	2.0	99.0	IFRDGEEAGAYDGR	1651.8	1652.8	1651.8	1652.8
63.0	15.7	15.7	23.6	2.0	99.0	LAPEYEAATR	1190.6	1191.6	1190.6	1191.6
63.0	15.7	15.7	23.6	2.0	99.0	MDATANDVPSPYEVR	1663.7	1664.8	1663.7	1664.8
63.0	15.7	15.7	23.6	1.7	98.0	FVMQEEFSR	1471.7	1472.7	1471.7	1472.7
63.0	15.7	15.7	23.6	0.0	78.0	IFRDGEEAGAYDGR	1651.8	1652.8	1651.8	1652.8
61.0	5.8	5.8	17.8	1.7	98.0	ELSDFISYLQR	1369.7	1370.7	1369.7	1370.7
61.0	5.8	5.8	17.8	1.7	98.0	FLODYFDGNLKR	1514.8	1515.8	1514.8	1515.8
61.0	5.8	5.8	17.8	1.7	98.0	FVMQEEFSR	1171.5	1172.5	1171.5	1172.5
61.0	5.8	5.8	17.8	0.7	78.0	MDATANDVPSPYEVR	1663.7	1664.8	1663.7	1664.8
97.0	8.0	8.0	16.4	2.0	99.0	ELSDFISYLQR	1369.7	1370.7	1369.7	1370.7
97.0	8.0	8.0	16.4	2.0	99.0	FLODYFDGNLKR	1514.7	1515.8	1514.8	1515.8
97.0	8.0	8.0	16.4	2.0	99.0	FVMQEEFSR	1171.5	1172.5	1171.5	1172.5
97.0	8.0	8.0	16.4	2.0	99.0	IFRDGEEAGAYDGR	1651.8	1652.8	1651.8	1652.8
P30508	1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain precursor (MHC class I antigen Cw*12) - Homo sapiens (Human)								
59.0	16.6	16.6	48.9	2.0	99.0	AEPKTHVTHHPVSDHEATLR	2398.2	2399.2	2398.2	2399.2
59.0	16.6	16.6	48.9	2.0	99.0	APWVEQGEPEYWDRETQK	2247.0	2248.0	2247.0	2248.0
59.0	16.6	16.6	48.9	2.0	99.0	AYLEGTVCVEWLR	1495.7	1496.7	1495.7	1496.7
59.0	16.6	16.6	48.9	2.0	99.0	DGEDOTDDELVELTRPAGDGTFOK	2636.2	2637.2	2636.2	2637.2
59.0	16.6	16.6	48.9	2.0	99.0	FIAVGYVDDTQFVR	1628.8	1629.8	1628.8	1629.8
59.0	16.6	16.6	48.9	2.0	99.0	THVTHHPVSDHEATLR	1835.9	1836.9	1835.9	1836.9
59.0	16.6	16.6	48.9	2.0	99.0	WAAVVVPSGEEQR	1426.7	1427.7	1426.7	1427.7
59.0	16.6	16.6	48.9	2.0	99.0	YFYTAVSRPRGEP	1754.9	1755.9	1754.9	1755.9
59.0	16.6	16.6	48.9	0.3	46.0	MYGCDLGPDPGR	1239.5	1240.5	1239.5	1240.5
59.0	16.6	16.6	48.9	0.1	26.0	ROAQADR	844.4	845.4	844.4	845.4
59.0	16.6	16.6	48.9	0.1	23.0	APWVEQGEPEYWDRETQK	1760.8	1761.8	1760.8	1761.8
270.0	2.1	7.4	30.9	2.0	99.0	APWVEQGEPEYWDRETQK	2247.0	2248.0	2247.0	2248.0
270.0	2.1	7.4	30.9	0.0	99.0	FIAVGYVDDTQFVR	1628.8	1629.8	1628.8	1629.8
270.0	2.1	7.4	30.9	0.0	99.0	WAAVVVPSGEEQR	1426.7	1427.7	1426.7	1427.7
270.0	2.1	7.4	30.9	0.0	94.0	YLENGKETLQR	1350.7	1351.7	1350.7	1351.7
P30740	IIEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Serpin B1) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI) - Homo sapiens (Human)								
155.0	7.7	7.7	14.0	2.0	99.0	FKLEESYTLNSDLAR	1784.9	1785.9	1784.9	1785.9
155.0	7.7	7.7	14.0	2.0	99.0	TFHFNTEVEVHSR	1601.8	1602.8	1601.8	1602.8
155.0	7.7	7.7	14.0	2.0	99.0	TYNFLPEFLVSTQK	1685.9	1686.9	1685.9	1686.9
155.0	7.7	7.7	14.0	1.7	98.0	FOSLNADINVKR	1304.7	1305.7	1304.7	1305.7
272.0	2.1	2.1	11.3	2.0	99.0	TFHFNTEVEVHSR	1601.8	1602.8	1601.8	1602.8
P31146	COR1A_HUMAN	Coronin-1A (Coronin-like protein p57) (Coronin-like protein A) (Clipin-A) (Tryptophan aspartate-containing coat protein) (TACO) - Homo sapiens (Human)								
26.0	25.9	25.9	41.2	2.0	99.0	CEPIAMTVPR	1156.6	1156.6	1156.6	1156.6
26.0	25.9	25.9	41.2	2.0	99.0	FRHVFQPAK	1186.6	1186.6	1186.6	1186.6
26.0	25.9	25.9	41.2	2.0	99.0	FRHVFQPAKADQCIEDVR	2322.1	2323.1	2322.1	2323.1
26.0	25.9	25.9	41.2	2.0	99.0	FYKLHER	991.5	992.5	991.5	992.5
26.0	25.9	25.9	41.2	2.0	99.0	HVFQPAKADQCIEDVR	2018.9	2019.9	2018.9	2019.9
26.0	25.9	25.9	41.2	2.0	99.0	ILTTGFSR	893.5	894.5	893.5	894.5
26.0	25.9	25.9	41.2	2.0	99.0	LDRLEETVOAK	1300.7	1301.7	1300.7	1301.7
26.0	25.9	25.9	41.2	2.0	99.0	LOATVQELQKR	1312.7	1313.7	1312.7	1313.8
26.0	25.9	25.9	41.2	2.0	99.0	RCEPI				

20.0	13.9	13.9	28.2	1.5	97.0	FRHVFQPAK	1185.6	1186.6	1185.6	1186.6
20.0	13.9	13.9	28.2	1.4	96.0	KLOATVQELQKR	1440.8	1441.9	1440.8	1441.8
20.0	13.9	13.9	28.2	1.2	93.0	CEPIAMTVPR	1155.5	1156.6	1155.6	1156.6
20.0	13.9	13.9	28.2	0.1	23.0	GTVVAEKDRPHEGTRPVR	2089.1	2090.1	2089.1	2090.1
20.0	13.9	13.9	28.2	0.0	44.0	FRHVFQPAK	1187.7	1188.7	1185.6	1186.6
25.0	21.5	21.5	32.8	2.0	98.0	FRHVFQPAK	1185.6	1186.6	1185.6	1186.6
25.0	21.5	21.5	32.8	2.0	98.0	FYKLER	991.5	992.5	991.5	992.5
25.0	21.5	21.5	32.8	2.0	99.0	HVFQPAKADQCYEDVR	2018.9	2019.9	2018.9	2019.9
25.0	21.5	21.5	32.8	2.0	99.0	KGTVVAEKDRPHEGTRPVR	2131.2	2132.2	2131.2	2132.2
25.0	21.5	21.5	32.8	2.0	99.0	KLOATVQELQKR	1440.8	1441.9	1440.8	1441.8
25.0	21.5	21.5	32.8	2.0	99.0	RCEPIAMTVPR	1328.7	1329.7	1328.7	1329.7
25.0	21.5	21.5	32.8	2.0	99.0	RGLVNVKCEIAR	1443.8	1444.8	1443.8	1444.8
25.0	21.5	21.5	32.8	1.7	98.0	LOATVQELQKR	1312.8	1313.8	1312.7	1313.8
25.0	21.5	21.5	32.8	1.5	97.0	CEPIAMTVPR	1155.5	1156.6	1155.6	1156.6
25.0	21.5	21.5	32.8	1.4	96.0	QVALWDTK	942.5	943.5	942.5	943.5
25.0	21.5	21.5	32.8	0.9	88.0	DGGLICTSCR	1137.5	1138.5	1137.5	1138.5
25.0	21.5	21.5	32.8	0.6	75.0	ILITGFSR	891.5	892.5	891.5	892.5
25.0	21.5	21.5	32.8	0.6	75.0	VSQTTWDSGFCVAVNPK	1795.8	1796.8	1795.8	1796.8
25.0	21.5	21.5	32.8	0.6	73.0	RDLRLEETVQAK	1458.8	1459.8	1458.8	1459.8
25.0	21.5	21.5	32.8	0.1	20.0	FYKLER	1147.6	1148.6	1147.6	1148.6
25.0	21.5	21.5	32.8	0.0	95.0	FRHVFQPAK	1185.6	1186.6	1185.6	1186.6
25.0	21.5	21.5	32.8	0.0	95.0	FYKLER	991.5	992.5	991.5	992.5
25.0	21.5	21.5	32.8	0.0	42.0	RCEPIAMTVPR	1344.7	1345.7	1344.7	1345.7
P31153	METK2_HUMAN	S-adenosylmethionine synthetase isoform type-2 (EC 2.5.1.6) (Methionine adenosyltransferase 2) (AdoMet synthetase 2) (Methionine adenosyltra								
239.0	5.0	5.0	18.7	2.0	99.0	DLDDKKPIYOR	1387.8	1388.8	1387.8	1388.8
239.0	5.0	5.0	18.7	2.0	99.0	YLDEDTIYHLOPSGR	1805.9	1806.9	1805.9	1806.9
239.0	5.0	5.0	18.7	0.9	87.0	TOVTVQYMODR	1367.7	1368.7	1367.7	1368.7
239.0	5.0	5.0	18.7	0.1	25.0	FVIGGPGDAGLTGR	1443.7	1444.7	1443.7	1444.8
177.0	4.0	4.0	12.2	2.0	99.0	FVIGGPGDAGLTGR	1443.7	1444.8	1443.7	1444.8
177.0	4.0	4.0	12.2	2.0	99.0	TOVTVQYMODR	1367.7	1368.7	1367.7	1368.7
P31949	S10AB_HUMAN	Protein S100-A11 (S100 calcium-binding protein A11) (Protein S100C) (Calgizzarin) (CALN170) - Homo sapiens (Human)								
210.0	6.0	6.0	46.7	2.0	99.0	CIESLIAVFK	1306.7	1307.7	1306.7	1307.7
210.0	6.0	6.0	46.7	2.0	99.0	TEFLSFMMTELAFTK	1848.9	1849.9	1848.9	1849.9
210.0	6.0	6.0	46.7	2.0	99.0	YAGKDGNYTLSK	1478.7	1479.7	1478.7	1479.7
189.0	2.0	2.0	10.5	2.0	99.0	CIESLIAVFK	1306.7	1307.7	1306.7	1307.7
310.0	2.0	2.4	37.1	2.0	99.0	YAGKDGNYTLSK	1478.7	1479.7	1478.7	1479.7
310.0	2.0	2.4	37.1	0.0	59.0	TEFLSFMMTELAFTK	1848.9	1849.9	1848.9	1849.9
P32455	GBP1_HUMAN	Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1) (Guanine nucleotide-binding protein 1) (GBP-1) (HuGBP-1) - Homo sapien								
54.0	17.0	17.0	27.2	2.0	99.0	AIAYEQMGGQK	1402.7	1403.7	1402.7	1403.7
54.0	17.0	17.0	27.2	2.0	99.0	ASEIHMTGPMCLIENTNGR	2173.0	2174.0	2173.0	2174.0
54.0	17.0	17.0	27.2	2.0	99.0	GIOAEILOTLYK	1504.8	1505.8	1504.8	1505.8
54.0	17.0	17.0	27.2	2.0	99.0	IMKNEIDLOLYK	1459.8	1460.8	1459.8	1460.8
54.0	17.0	17.0	27.2	2.0	99.0	KGIOAEILOTLYK	1633.9	1634.9	1633.9	1634.9
54.0	17.0	17.0	27.2	2.0	99.0	SKESMTDAILDQDTLTKETEKEIEVER	3151.5	3152.5	3151.5	3152.5
54.0	17.0	17.0	27.2	2.0	99.0	TLSGGIQQVNGPR	1197.7	1198.7	1197.6	1198.7
54.0	17.0	17.0	27.2	1.7	98.0	AGIYKPGGYR	1167.6	1168.6	1167.6	1168.6
54.0	17.0	17.0	27.2	0.8	85.0	CFVDFRPHR	1331.7	1332.7	1331.7	1332.7
54.0	17.0	17.0	27.2	0.4	62.0	MLQEMGR	934.4	935.4	934.4	935.4
42.0	17.7	17.7	37.7	2.0	99.0	AGIYKPGGYR	1167.6	1168.6	1167.6	1168.6
42.0	17.7	17.7	37.7	2.0	99.0	AIAYEQMGGQK	1402.7	1403.7	1402.7	1403.7
42.0	17.7	17.7	37.7	2.0	99.0	ASEIHMTGPMCLIENTNGR	2173.0	2174.0	2173.0	2174.0
42.0	17.7	17.7	37.7	2.0	99.0	EAIKVFIR	975.5	976.5	975.5	976.5
42.0	17.7	17.7	37.7	2.0	99.0	GTSQKDETFNLPR	1491.7	1492.7	1491.7	1492.7
42.0	17.7	17.7	37.7	2.0	99.0	KGIOAEILOTLYK	1633.9	1634.9	1633.9	1634.9
42.0	17.7	17.7	37.7	2.0	99.0	KGTSQKDETFNLPR	1620.8	1621.8	1620.8	1621.8
42.0	17.7	17.7	37.7	2.0	99.0	MENDRQLLKEQER	1786.9	1787.9	1786.9	1787.9
42.0	17.7	17.7	37.7	1.7	98.0	SYOEHKLOTKE	1502.8	1503.8	1502.8	1503.8
P32456	GBP2_HUMAN	Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2) (Guanine nucleotide-binding protein 2) (GBP-2) (HuGBP-2) - Homo sapien								
234.0	5.3	7.3	9.6	2.0	99.0	DIWDIQMR	1075.5	1076.5	1075.5	1076.5
234.0	5.3	7.3	9.6	2.0	99.0	NSFKVDVDMFOR	1513.7	1514.7	1513.7	1514.7
234.0	5.3	7.3	9.6	1.2	94.0	CFVDFRPHR	1248.6	1249.6	1248.6	1249.6
234.0	5.3	7.3	9.6	0.0	99.0	AIAYEQMGGQK	1402.7	1403.7	1402.7	1403.7
222.0	3.0	5.0	14.9	2.0	99.0	DIWDIQMR	1075.5	1076.5	1075.5	1076.5
222.0	3.0	5.0	14.9	1.0	90.0	LLKEGFENESKR	1448.8	1449.8	1448.8	1449.8
222.0	3.0	5.0	14.9	0.0	99.0	AIAYEQMGGQK	1402.7	1403.7	1402.7	1403.7
P33241	LSP1_HUMAN	Lymphocyte-specific protein 1 (Protein pp25) (52 kDa phosphoprotein) (Lymphocyte-specific antigen WVP34) (47 kDa actin-binding protein) - Hort								
84.0	12.3	12.3	35.7	2.0	99.0	IDVLEIQTDAIAGR	2021.0	2022.0	2021.0	2022.0
84.0	12.3	12.3	35.7	2.0	99.0	QOHEGAGALDSCPEPQCR	2064.9	2065.9	2064.9	2065.9
84.0	12.3	12.3	35.7	2.0	99.0	WETGEVQAQSAK	1403.7	1404.7	1403.7	1404.7
84.0	12.3	12.3	35.7	2.0	99.0	YKFVATGHGK	1106.6	1107.6	1106.6	1107.6
84.0	12.3	12.3	35.7	1.7	98.0	LIDRTESLNR	1215.7	1216.7	1215.7	1216.7
84.0	12.3	12.3	35.7	1.4	96.0	QLQADDEGGGHVPERPK	1974.0	1975.0	1974.0	1975.0
84.0	12.3	12.3	35.7	1.2	94.0	LKPSEAPLDEDEFGDWSORPEQR	2914.4	2915.4	2914.3	2915.3
168.0	4.2	4.2	21.5	2.0	99.0	WETGEVQAQSAK	1403.7	1404.7	1403.7	1404.7
168.0	4.2	4.2	21.5	2.0	99.0	YKFVATGHGKYEK	1526.8	1527.8	1526.8	1527.8
168.0	4.2	4.2	21.5	0.2	36.0	LIDRTESLNR	1215.7	1216.7	1215.7	1216.7
P35579	MYH9_HUMAN	Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle 11a) (Nonmuscle myosin heavy chain 11a) (NMHC-11a) (NMHC-11A) (Cellular								
17.0	36.9	36.9	25.6	2.0	99.0	ALEEAMEGKAALER	1645.8	1646.8	1645.8	1646.8
17.0	36.9	36.9	25.6	2.0	99.0	ANLQDQINTDLNER	1870.0	1871.0	1870.0	1871.0
17.0	36.9	36.9	25.6	2.0	99.0	DFSALESQLODTEQELLEENR	2492.2	2493.2	2492.2	2493.2
17.0	36.9	36.9	25.6	2.0	99.0	IAEFTTNLTTEEEKSK	1867.9	1868.9	1867.9	1868.9
17.0	36.9	36.9	25.6	2.0	99.0	IAQLEEELEEFGNTLINDR	2471.1	2472.1	2471.2	2472.2
17.0	36.9	36.9	25.6	2.0	99.0	IAQLEEDDNKTKER	1814.9	1815.9	1814.9	1815.9
17.0	36.9	36.9	25.6	2.0	99.0	IMPPEEQMGLLR	1614.8	1615.8	1614.8	1615.8
17.0	36.9	36.9	25.6	2.0	99.0	KTLEEEAKTHEAQIOEMR	2171.1	2172.1	2171.1	2172.1
17.0	36.9	36.9	25.6	2.0	99.0	LOQELDLLVDLHDOR	1949.0	1950.0	1949.0	1950.0
17.0	36.9	36.9	25.6	2.0	99.0	LTEMETLOSQMAEK	1750.8	1751.8	1750.8	1751.9
17.0	36.9	36.9	25.6	2.0	99.0	MQONIQLLEQLLEEEESAR	2332.0	2333.0	2332.0	2333.1
17.0	36.9	36.9	25.6	2.0	99.0	NAEQYKDOADKASTR	1723.8	1724.8	1723.8	1724.8
17.0	36.9	36.9	25.6	2.0	99.0	QLLOANPILEAFNGAK	1708.9	1709.9	1708.9	1709.9
17.0	36.9	36.9	25.6	2.0	99.0	OTLENERGELANEVK	1729.9	1730.9	1729.9	1730.9
17.0	36.9	36.9	25.6	2.0	99.0	RGDLPVVPVR	1154.7	1155.7	1154.7	1155.7
17.0	36.9	36.9	25.6	2.0	99.0	SMEAEMIQLOELAAAER	2047.9	2048.9	2047.0	2048.0
17.0	36.9	36.9	25.6	2.0	99.0	VSHLLGINVDFTR	1570.8	1571.8	1570.8	1571.9
17.0	36.9	36.9	25.6	1.2	93.0	LOAQMKDCMR	1279.6	1280.6	1279.6	1280.6
17.0	36.9	36.9	25.6	0.7	78.0	ASREEILAAQAKENEK	1714.9	1715.9	1714.9	1715.9
17.0	36.9	36.9	25.6	0.4	57.0	NWQWWR	974.4	975.4	974.5	975.5
17.0	36.9	36.9	25.6	0.2	37.0	ALEQOVEEMK	1203.6	1204.6	1203.6	1204.6
17.0	36.9	36.9	25.6	0.2	30.0	KLOAQMKDCMR	1407.7	1408.7	1407.7	1408.7
17.0	36.9	36.9	25.6	0.1	25.0	VKLOEMEGTVK	1260.7	1261.7	1260.7	1261.7
17.0	36.9	36.9	25.6	0.1	22.0	VEEEEEERCOHLOAEK	1912.8	1913.8	1912.9	1913.9
17.0	36.9	36.9	25.6	0.0	99.0	IAQLEEELEEFGNTLINDR	2471.1	2472.1	2471.2	2472.2
35.0	18.9	18.9	31.7	2.0	99.0	ANLQDQINTDLNER	1869.0	1870.0	1869.0	1870.0
35.0	18.9	18.9	31.7	2.0	99.0	ELSEIQSELQELLESER	2034.0	2035.0	2034.0	2035.0
35.0	18.9	18.9	31.7	2.0	99.0	IMPPEEQMGLLR	1614.8	1615.8	1614.8	1615.8
35.0	18.9	18.9	31.7	2.0	99.0	NAEQYKDOADKASTR	1723.8	1724.8	1723.8	1724.8
35.0	18.9	18.9	31.7	2.0	99.0	QLLOANPILEAFNGAK	1708.9	1709.9	1708.9	1709.9
35.0	18.9	18.9	31.7	1.7	98.0	SMEAEMIQLOELAAAER	2047.0	2048.0	2047.0	2048.0
35.0	18.9	18.9	31.7	1.5	97.0	KLOAQMKDCMR	1407.7	1408.7	1407.7	

38.0	22.0	22.0	43.9	1.5	97.0	ILGOVPPYATKGNQWVGYDDQESVK	2822.4	2823.4	2822.4	2823.4
38.0	22.0	22.0	43.9	0.4	63.0	GOEDASPDPRFSNTDYAVGYMLR	2491.1	2492.1	2491.1	2492.1
38.0	22.0	22.0	43.9	0.0	99.0	EAGTLAYYEICDFLR	1801.8	1802.9	1801.8	1802.8
38.0	22.0	22.0	43.9	0.0	99.0	GTGHHSPLFR	1208.6	1209.6	1208.6	1209.6
38.0	22.0	22.0	43.9	0.0	99.0	ILGOVPPYATK	1216.7	1217.7	1216.7	1217.7
38.0	22.0	22.0	43.9	0.0	76.0	LVMGIFTFGR	1091.6	1092.6	1091.6	1092.6
168.0	2.0	2.0	15.7	2.0	99.0	LVMGIFTFGR	1089.6	1090.6	1089.6	1090.6
104.0	7.7	7.7	18.3	2.0	99.0	EAGTLAYYEICDFLR	1819.8	1820.8	1819.8	1820.9
104.0	7.7	7.7	18.3	2.0	99.0	GTGHHSPLFR	1208.6	1209.6	1208.6	1209.6
104.0	7.7	7.7	18.3	2.0	99.0	TLLSVGGVWFGSOR	1520.8	1521.8	1520.8	1521.8
104.0	7.7	7.7	18.3	1.7	98.0	GNQWVGYDDQESVSKS	1838.9	1839.9	1838.9	1839.9
104.0	7.7	7.7	18.3	0.0	70.0	EAGTLAYYEICDFLR	1801.8	1802.8	1801.8	1802.8
104.0	7.7	7.7	18.3	0.0	99.0	GTGHHSPLFR	1208.6	1209.6	1208.6	1209.6
P37802 TAGL2_HUMAN Transgelin-2 (SM22-alpha homolog) - Homo sapiens (Human)										
66.0	14.8	14.8	61.3	2.0	99.0	ANRGPAYGLSR	1202.6	1203.6	1202.6	1203.6
66.0	14.8	14.8	61.3	2.0	99.0	DDGLFSGDPNWFPPK	1593.8	1594.8	1593.7	1594.7
66.0	14.8	14.8	61.3	2.0	99.0	GASQAQMTGYGMPPR	1382.6	1383.6	1382.6	1383.6
66.0	14.8	14.8	61.3	2.0	99.0	NFSDNQLQCEKNIWGLQMGTMNR	2462.2	2463.2	2462.2	2463.2
66.0	14.8	14.8	61.3	2.0	99.0	QMEIQSFLQAAER	1660.8	1661.8	1660.8	1661.8
66.0	14.8	14.8	61.3	2.0	99.0	TLMNLGGLAVAR	1214.7	1215.7	1214.7	1215.7
66.0	14.8	14.8	61.3	2.0	99.0	YGINTTDFOTVDLWEGK	2099.0	2100.0	2099.0	2100.0
66.0	14.8	14.8	61.3	0.8	85.0	DDGLFSGDPNWFPPK	1721.8	1722.8	1721.8	1722.8
66.0	14.8	14.8	61.3	0.0	99.0	QMEIQSFLQAAER	1677.8	1678.8	1677.8	1678.8
97.0	3.8	3.8	32.7	2.0	99.0	GASQAQMTGYGMPPR	1384.6	1385.6	1384.6	1385.6
97.0	3.8	3.8	32.7	1.4	96.0	DDGLFSGDPNWFPPK	1721.8	1722.8	1721.8	1722.8
97.0	3.8	3.8	32.7	0.4	61.0	QMEIQSFLQAAER	1660.8	1661.8	1660.8	1661.8
143.0	5.4	5.4	51.8	2.0	99.0	GASQAQMTGYGMPPR	1382.6	1383.6	1382.6	1383.6
143.0	5.4	5.4	51.8	2.0	99.0	QMEIQSFLQAAER	1660.8	1661.8	1660.8	1661.8
143.0	5.4	5.4	51.8	1.4	96.0	ANRGPAYGLSR	1202.6	1203.6	1202.6	1203.6
143.0	5.4	5.4	51.8	0.0	99.0	QMEIQSFLQAAER	1677.8	1678.8	1677.8	1678.8
P37837 TALDO_HUMAN Transglutase (EC 2.2.1.2) - Homo sapiens (Human)										
219.0	5.9	5.9	11.9	2.0	99.0	LSFDKDMVAAR	1251.6	1252.6	1251.6	1252.6
219.0	5.9	5.9	11.9	2.0	99.0	WLHNEQDQMAVEK	1498.7	1499.7	1498.7	1499.7
219.0	5.9	5.9	11.9	1.3	95.0	IYNYK	990.5	991.5	990.5	991.5
219.0	5.9	5.9	11.9	0.6	75.0	FAADAVKLER	1118.6	1119.6	1118.6	1119.6
209.0	1.4	1.4	6.8	1.4	96.0	WLHNEQDQMAVEK	1498.7	1499.7	1498.7	1499.7
220.0	3.1	3.1	18.4	2.0	99.0	WLHNEQDQMAVEK	1498.7	1499.7	1498.7	1499.7
220.0	3.1	3.1	18.4	1.0	90.0	LVPVLSAK	825.5	826.5	825.5	826.5
P38159 HNRPG_HUMAN Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein, X chromosome) (Glycoprotein p43) - Homo sapiens (Human)										
107.0	10.1	10.1	32.5	2.0	99.0	AIKVEQATKPSFESGR	1746.9	1747.9	1746.9	1747.9
107.0	10.1	10.1	32.5	2.0	99.0	ALEAVFGKYGR	1209.6	1210.7	1209.7	1210.7
107.0	10.1	10.1	32.5	2.0	99.0	DSYGGPDRRPLPSRR	1839.0	1840.0	1838.9	1840.0
107.0	10.1	10.1	32.5	2.0	99.0	GFAFVTFESPADAK	1485.7	1486.7	1485.7	1486.7
107.0	10.1	10.1	32.5	2.0	99.0	GFAFVTFESPADAKDAAR	1898.9	1899.9	1898.9	1899.9
151.0	2.0	2.0	33.2	2.0	99.0	AIKVEQATKPSFESGR	1746.9	1747.9	1746.9	1747.9
294.0	2.0	2.0	39.4	2.0	99.0	GFAFVTFESPADAKDAAR	1898.9	1899.9	1898.9	1899.9
P60842 IF4A1_HUMAN Eukaryotic initiation factor 4A-I (EC 3.6.1.-) (ATP-dependent RNA helicase eIF4A-1) (eIF4A-1) (eIF-4A-1) - Homo sapiens (Human)										
428.0	2.1	2.1	10.8	2.0	99.0	GIYAYGFEKPSAIQQR	1826.9	1827.9	1826.9	1827.9
231.0	2.7	2.7	12.3	2.0	99.0	GIYAYGFEKPSAIQQR	1826.9	1827.9	1826.9	1827.9
231.0	2.7	2.7	12.3	0.7	81.0	DFTVSAMHGDMQKER	1865.8	1866.8	1865.8	1866.8
P40121 CAPG_HUMAN Macrophage-capping protein (Actin-regulatory protein CAP-G) - Homo sapiens (Human)										
181.0	6.4	6.4	19.3	2.0	99.0	EVQGNESDLFMSYFPR	1917.9	1918.9	1917.9	1918.9
181.0	6.4	6.4	19.3	2.0	99.0	MOYAPNTOVEILPOGR	1843.9	1844.9	1843.9	1844.9
181.0	6.4	6.4	19.3	2.0	99.0	QALQVAEGFISR	1371.7	1372.7	1371.7	1372.7
181.0	6.4	6.4	19.3	0.3	54.0	OFFKDWK	980.5	981.5	980.5	981.5
181.0	6.4	6.4	19.3	0.0	98.0	QALQVAEGFISR	1388.7	1389.7	1388.7	1389.7
30.0	10.0	10.0	23.0	2.0	99.0	EVQGNESDLFMSYFPR	1917.9	1918.9	1917.9	1918.9
30.0	10.0	10.0	23.0	2.0	99.0	MOYAPNTOVEILPOGR	1843.9	1844.9	1843.9	1844.9
30.0	10.0	10.0	23.0	2.0	99.0	QALQVAEGFISR	1371.7	1372.7	1371.7	1372.7
30.0	10.0	10.0	23.0	2.0	99.0	OFFKDWK	997.5	998.5	997.5	998.5
30.0	10.0	10.0	23.0	2.0	99.0	YQEGGVSAFHK	1350.6	1351.6	1350.6	1351.6
30.0	10.0	10.0	23.0	0.0	94.0	EVQGNESDLFMSYFPR	1916.9	1918.0	1916.9	1917.9
30.0	10.0	10.0	23.0	0.0	99.0	QALQVAEGFISR	1388.7	1389.7	1388.7	1389.7
30.0	10.0	10.0	23.0	0.0	55.0	OFFKDWK	980.5	981.5	980.5	981.5
72.0	10.1	10.1	30.2	2.0	99.0	DLALAIRDSR	1257.7	1258.7	1257.7	1258.7
72.0	10.1	10.1	30.2	2.0	99.0	EVQGNESDLFMSYFPR	1917.9	1918.9	1917.9	1918.9
72.0	10.1	10.1	30.2	2.0	99.0	MOYAPNTOVEILPOGR	1843.9	1844.9	1843.9	1844.9
72.0	10.1	10.1	30.2	2.0	99.0	QALQVAEGFISR	1371.7	1372.7	1371.7	1372.7
72.0	10.1	10.1	30.2	2.0	99.0	YQEGGVSAFHK	1350.6	1351.6	1350.6	1351.6
72.0	10.1	10.1	30.2	0.0	56.0	EVQGNESDLFMSYFPR	1933.9	1934.9	1933.9	1934.9
72.0	10.1	10.1	30.2	0.0	99.0	QALQVAEGFISR	1388.7	1389.7	1388.7	1389.7
P40925 MDHC_HUMAN Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) - Homo sapiens (Human)										
90.0	12.0	12.0	31.4	2.0	99.0	EVGYEALKDSDSWLK	1750.9	1751.9	1750.9	1751.9
90.0	12.0	12.0	31.4	2.0	99.0	FVEGLPINDFSR	1392.7	1393.7	1392.7	1393.7
90.0	12.0	12.0	31.4	2.0	99.0	GEFVTTVOQR	1163.6	1164.6	1163.6	1164.6
90.0	12.0	12.0	31.4	2.0	99.0	NVIWGNHSSSTQYPDVNHAK	2279.1	2280.1	2279.1	2280.1
90.0	12.0	12.0	31.4	2.0	99.0	SAPSIPKENFSCLTR	1705.8	1706.9	1705.8	1706.9
90.0	12.0	12.0	31.4	2.0	99.0	VIVVGNPANTINCLTASK	1756.9	1757.9	1756.9	1757.9
90.0	12.0	12.0	31.4	2.0	99.0	FVEGLPINDFSR	1392.7	1393.7	1392.7	1393.7
58.0	6.0	6.0	12.9	2.0	99.0	ELTEEKESAFELSSA	1815.8	1816.8	1815.8	1816.8
58.0	6.0	6.0	12.9	2.0	99.0	FVEGLPINDFSR	1392.7	1393.7	1392.7	1393.7
58.0	6.0	6.0	12.9	2.0	99.0	SAPSIPKENFSCLTR	1705.8	1706.8	1705.8	1706.9
63.0	12.0	12.0	26.3	2.0	99.0	ELTEEKESAFELSSA	1815.8	1816.8	1815.8	1816.8
63.0	12.0	12.0	26.3	2.0	99.0	EVGYEALKDSDSWLK	1750.9	1751.9	1750.9	1751.9
63.0	12.0	12.0	26.3	2.0	99.0	FVEGLPINDFSR	1392.7	1393.7	1392.7	1393.7
63.0	12.0	12.0	26.3	2.0	99.0	GEFVTTVOQR	1163.6	1164.6	1163.6	1164.6
63.0	12.0	12.0	26.3	2.0	99.0	NVIWGNHSSSTQYPDVNHAK	2279.1	2280.1	2279.1	2280.1
63.0	12.0	12.0	26.3	2.0	99.0	SAPSIPKENFSCLTR	1705.8	1706.9	1705.8	1706.9
P40926 MDHM_HUMAN Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Homo sapiens (Human)										
71.0	14.1	14.1	42.6	2.0	99.0	AGAGSATLSMAYAGAR	1453.7	1454.7	1453.7	1454.7
71.0	14.1	14.1	42.6	2.0	99.0	GVLPEQLDPLCK	1489.7	1490.7	1489.7	1490.7
71.0	14.1	14.1	42.6	2.0	99.0	IFGVITLDIVR	1232.7	1233.7	1232.7	1233.7
71.0	14.1	14.1	42.6	2.0	99.0	LTYLDIAHPGVAADLSHIETK	2364.2	2365.3	2364.2	2365.2
71.0	14.1	14.1	42.6	2.0	99.0	SOETECTYFSTPLLLGKK	2101.0	2102.1	2101.0	2102.0
71.0	14.1	14.1	42.6	2.0	99.0	THIPLISQTPK	1369.8	1370.8	1369.8	1370.8
71.0	14.1	14.1	42.6	2.0	99.0	VDFPODQLTALTGR	1559.8	1560.8	1559.8	1560.8
280.0	2.1	2.1	17.2	2.0	99.0	HGVYNNPKIFGVITLDIVR	2142.1	2143.2	2142.2	2143.2
P42224 STAT1_HUMAN Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84) - Homo sapiens (Human)										
58.0	16.7	16.7	19.1	2.0	99.0	EGAITFTWVER	1307.7	1308.7	1307.7	1308.7
58.0	16.7	16.7	19.1	2.0	99.0	ELSAVTFPDIR	1359.7	1360.7	1359.7	1360.7
58.0	16.7	16.7	19.1	2.0	99.0	FHLLSLLDDQYSR	1735.8	1736.8	1735.8	1736.8
58.0	16.7	16.7	19.1	2.0	99.0	ODWEHAANDVSFATIR	1841.8	1842.9	1841.8	1842.8
58.0	16.7	16.7	19.1	2.0	99.0	OYLQWLEK	1160.6	1161.6	1160.6	1161.6
58.0	16.7	16.7	19.1	2.0	99.0	SLEDLQDEYDFK	1501.7	1502.7	1501.7	1502.7
58.0	16.7	16.7	19.1	2.0	99.0	SQWYELQLQDSK	1565.7	1566.7	1565.7	1566.7
58.0	16.7	16.7	19.1	2.0	99.0	YLYPNIQKDHAFGK	1679.8	1680.8	1679.8	1680.8
58.0	16.7	16.7	19.1	0.7	80.0	GLNVDLQNLMLGK	1429.7	1430.7	1429.7	1430.7
58.0	16.7	16.7	19.1	0.0	99.0	ODWEHAANDVSFATIR	1858.9	1859.9	1858.9	1859.9
83.0	4.1	4.1	11.2	2.0	99.0	FHLLSLLDDQYSR	1735.8	1736.8	1735.8	1736.8
83.0	4.1	4.1	11.2	2.0	99.0	SQWYELQLQDSK	1565.7	1566.7	1565.7	1566.7
83.0	4.1	4.1	11.2	0.1	21.0	ODWEHAANDVSFATIR	1858.9	1859.9	1858.9	1859.9
60.0	12.8	12.8	19.9	2.0	99.0	FHLLSLLDDQYSR	1735.8	1736.8	1735.8	

55.0	13.4	13.4	20.2	2.0	99.0	LLPPYLRL	870.5	871.5	870.5	871.5
55.0	13.4	13.4	20.2	2.0	99.0	MNPAAAEAFNILLATDSYK	2139.0	2140.0	2139.0	2140.0
55.0	13.4	13.4	20.2	2.0	99.0	SYSFDEIRK	1143.6	1144.6	1143.6	1144.6
55.0	13.4	13.4	20.2	2.0	99.0	VYSYFECR	1122.5	1123.5	1122.5	1123.5
55.0	13.4	13.4	20.2	1.4	96.0	IWGEDLRL	887.5	888.5	887.5	888.5
55.0	13.4	13.4	20.2	0.0	97.0	LHDFSYRL	906.5	907.5	906.5	907.4
P46777 RL5_HUMAN 60S ribosomal protein L5 - Homo sapiens (Human)										
79.0	13.3	13.3	35.0	2.0	99.0	DIICQIAYAR	1221.6	1222.6	1221.6	1222.6
79.0	13.3	13.3	35.0	2.0	99.0	HIMGQNVADYMR	1433.6	1434.7	1433.7	1434.7
79.0	13.3	13.3	35.0	2.0	99.0	KAHAAIRENPVYKPKK	1978.1	1979.1	1978.1	1979.1
79.0	13.3	13.3	35.0	2.0	99.0	NSVTPDMMEEMYYK	1701.7	1702.8	1701.7	1702.7
79.0	13.3	13.3	35.0	2.0	99.0	RFPQYDSEKFEFNAEVHRK	2295.1	2296.1	2295.1	2296.1
79.0	13.3	13.3	35.0	1.7	98.0	YLMEDEDAVYKOFSOYIK	2427.1	2428.1	2427.1	2428.1
79.0	13.3	13.3	35.0	1.5	97.0	AHAAIRENPVYK	1496.8	1497.8	1496.8	1497.8
79.0	13.3	13.3	35.0	0.1	20.0	AHAAIRENPVYKPKK	1850.0	1851.0	1850.0	1851.0
244.0	2.3	2.3	24.9	2.0	99.0	HIMGQNVADYMR	1433.6	1434.7	1433.7	1434.7
244.0	2.3	2.3	24.9	0.2	39.0	AHAAIRENPVYK	1496.8	1497.8	1496.8	1497.8
P46781 RS9_HUMAN 40S ribosomal protein S9 - Homo sapiens (Human)										
220.0	5.8	5.8	28.4	2.0	99.0	RLQTOVFK	1018.6	1019.6	1018.6	1019.6
220.0	5.8	5.8	28.4	1.7	98.0	QVWNIPSFIVR	1253.7	1254.7	1253.7	1254.7
220.0	5.8	5.8	28.4	1.3	95.0	LIGEYGLR	919.5	920.5	919.5	920.5
220.0	5.8	5.8	28.4	0.7	81.0	KNAKKGQGGAGAGDDEE	1613.8	1614.8	1613.7	1614.7
220.0	5.8	5.8	28.4	0.0	98.0	QVWNIPSFIVR	1270.7	1271.7	1270.7	1271.7
210.0	3.3	3.3	47.9	1.2	93.0	KQVWNIPSFIVR	1398.8	1399.8	1398.8	1399.8
210.0	3.3	3.3	47.9	1.0	89.0	HIDFSLR	886.5	887.5	886.5	887.5
210.0	3.3	3.3	47.9	0.6	77.0	LIGEYGLR	919.5	920.5	919.5	920.5
210.0	3.3	3.3	47.9	0.3	46.0	QVWNIPSFIVR	1270.7	1271.7	1270.7	1271.7
210.0	3.3	3.3	47.9	0.2	35.0	ELLTLDKDPDR	1483.8	1484.8	1483.8	1484.8
P46940 IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 (p195) - Homo sapiens (Human)										
180.0	6.4	6.4	6.8	2.0	99.0	ATFYGEQVDYK	1482.7	1483.7	1482.7	1483.7
180.0	6.4	6.4	6.8	2.0	99.0	IFYPETTDIDYRK	1659.8	1660.8	1659.8	1660.8
180.0	6.4	6.4	6.8	2.0	99.0	QNVAYEYLCHLEEAKR	2022.0	2023.0	2022.0	2023.0
180.0	6.4	6.4	6.8	0.4	59.0	MREVEITLIR	1258.7	1259.7	1258.7	1259.7
162.0	4.4	4.4	11.2	2.0	99.0	ATFYGEQVDYK	1482.7	1483.7	1482.7	1483.7
162.0	4.4	4.4	11.2	1.7	98.0	IFYPETTDIDYRK	1659.8	1660.8	1659.8	1660.8
162.0	4.4	4.4	11.2	0.5	66.0	YKATGLHFR	1091.6	1092.6	1091.6	1092.6
162.0	4.4	4.4	11.2	0.1	27.0	QLLSDKQQR	1275.6	1276.6	1275.6	1276.6
P48739 PINB_HUMAN Phosphatidylinositol transfer protein beta isoform (PtdIns transfer protein beta) (PtdInsTP) (PI-TP-beta) - Homo sapiens (Human)										
473.0	2.0	2.0	14.4	2.0	99.0	FKWWGLOSK	1178.6	1179.6	1178.6	1179.6
329.0	2.0	2.0	10.3	2.0	99.0	AWNAYPYCR	1199.5	1200.5	1199.5	1200.5
P49368 TCPG_HUMAN T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRIC5) - Homo sapiens (Human)										
87.0	12.2	12.2	23.9	2.0	99.0	AMTGVCEQVYR	1336.6	1337.6	1336.6	1337.6
87.0	12.2	12.2	23.9	2.0	99.0	GISDLAQHYLMR	1402.7	1403.7	1402.7	1403.7
87.0	12.2	12.2	23.9	2.0	99.0	GVMINKDVTHPR	1365.7	1366.7	1365.7	1366.7
87.0	12.2	12.2	23.9	2.0	99.0	KIGDEYFTITDCCKDPK	2076.0	2077.0	2076.0	2077.0
87.0	12.2	12.2	23.9	2.0	99.0	NLQDAMOVCR	1233.6	1234.6	1233.6	1234.6
87.0	12.2	12.2	23.9	0.9	86.0	MLLDPMGGIVMTNDGNAILR	2130.0	2131.0	2130.1	2131.1
87.0	12.2	12.2	23.9	0.8	84.0	TLIONCGASTIR	1332.7	1333.7	1332.7	1333.7
87.0	12.2	12.2	23.9	0.5	69.0	TAVETAALLLR	1184.7	1185.7	1184.7	1185.7
285.0	2.0	2.0	14.7	2.0	99.0	GVMINKDVTHPR	1365.7	1366.7	1365.7	1366.7
P50395 GDI2_HUMAN Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2) - Homo sapiens (Human)										
75.0	13.8	13.8	25.4	2.0	99.0	DLGTESIQIFSR	1364.7	1365.7	1364.7	1365.7
75.0	13.8	13.8	25.4	2.0	99.0	GRDWNVDLIPK	1311.7	1312.7	1311.7	1312.7
75.0	13.8	13.8	25.4	2.0	99.0	MTGSEDFEEMKR	1605.7	1606.7	1605.7	1606.7
75.0	13.8	13.8	25.4	2.0	99.0	NPYGGESASITPLEDYLR	2272.1	2273.1	2272.1	2273.1
75.0	13.8	13.8	25.4	2.0	99.0	TDDYLDQPCYETINR	1901.8	1902.8	1901.8	1902.8
75.0	13.8	13.8	25.4	2.0	99.0	TYDATTFHETCCDDIKNIYKR	2592.2	2593.2	2592.2	2593.2
75.0	13.8	13.8	25.4	1.2	93.0	LYSESLAR	937.5	938.5	937.5	938.5
75.0	13.8	13.8	25.4	0.7	79.0	FKIPGSPPEMGR	1401.7	1402.7	1401.7	1402.7
54.0	6.1	6.1	16.0	2.0	99.0	DLGTESIQIFSR	1364.7	1365.7	1364.7	1365.7
54.0	6.1	6.1	16.0	2.0	99.0	MTGSEDFEEMKR	1605.7	1606.7	1605.7	1606.7
54.0	6.1	6.1	16.0	2.0	99.0	TDDYLDQPCYETINR	1901.8	1902.8	1901.8	1902.8
54.0	6.1	6.1	16.0	0.1	24.0	GRDWNVDLIPK	1311.7	1312.7	1311.7	1312.7
91.0	8.1	8.1	20.4	2.0	99.0	DLGTESIQIFSR	1364.7	1365.7	1364.7	1365.7
91.0	8.1	8.1	20.4	2.0	99.0	TDDYLDQPCYETINR	1901.8	1902.8	1901.8	1902.8
91.0	8.1	8.1	20.4	2.0	99.0	TYDATTFHETCCDDIK	1916.8	1917.8	1916.8	1917.8
91.0	8.1	8.1	20.4	1.5	97.0	MTGSEDFEEMKR	1605.7	1606.7	1605.7	1606.7
91.0	8.1	8.1	20.4	0.6	75.0	LYSESLAR	937.5	938.5	937.5	938.5
P50453 SPB9_HUMAN Serpin B9 (Cytoplasmic antiprotease 3) (CAP-3) (CAP3) (Protease inhibitor 9) - Homo sapiens (Human)										
209.0	6.0	6.0	14.9	2.0	99.0	ANSILFCGR	1036.5	1037.5	1036.5	1037.5
209.0	6.0	6.0	14.9	2.0	99.0	AQLLELPYAR	1172.7	1173.7	1172.7	1173.7
209.0	6.0	6.0	14.9	2.0	99.0	GKWNEPFDETYTR	1641.7	1642.7	1641.7	1642.7
379.0	1.7	1.7	12.2	1.7	98.0	AQLLELPYAR	1172.7	1173.7	1172.7	1173.7
P50522 VASP_HUMAN Vasodilator-stimulated phosphoprotein (VASP) - Homo sapiens (Human)										
83.0	12.7	12.7	31.8	2.0	99.0	GVKYNQATPNFHQWR	1844.9	1845.9	1844.9	1845.9
83.0	12.7	12.7	31.8	2.0	99.0	SGGGGLMEEMNMLAR	1622.7	1623.7	1622.7	1623.7
83.0	12.7	12.7	31.8	2.0	99.0	SSSSVTITSETQPCPSSSDYDLQR	2706.2	2707.2	2706.2	2707.2
83.0	12.7	12.7	31.8	2.0	99.0	YNQATPNFHQWR	1560.7	1561.7	1560.7	1561.7
83.0	12.7	12.7	31.8	0.8	83.0	WLPATGQPAFSR	1387.7	1388.7	1387.7	1388.7
83.0	12.7	12.7	31.8	0.7	80.0	VOIYHNPTANSFR	1545.8	1546.8	1545.8	1546.8
83.0	12.7	12.7	31.8	0.7	78.0	VPAQSESVRRPWEK	1667.9	1668.9	1667.9	1668.9
83.0	12.7	12.7	31.8	0.4	56.0	MKSSSVTITSETQPCPSSSDYDLQR	2965.3	2966.3	2965.3	2966.3
83.0	12.7	12.7	31.8	0.2	41.0	QQPQSPHER	1259.6	1260.6	1259.6	1260.6
138.0	5.8	5.8	21.1	2.0	99.0	ATVMLYDDGNKR	1381.7	1382.7	1381.7	1382.7
138.0	5.8	5.8	21.1	2.0	99.0	YNQATPNFHQWR	1560.7	1561.7	1560.7	1561.7
138.0	5.8	5.8	21.1	1.7	98.0	VOIYHNPTANSFR	1545.8	1546.8	1545.8	1546.8
P50990 TCPO_HUMAN T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Renal carcinoma antigen NY-REN-15) - Homo sapiens (Human)										
208.0	6.0	6.0	6.4	2.0	99.0	FAEFAEAIPLR	1149.6	1150.6	1149.6	1150.6
208.0	6.0	6.0	6.4	2.0	99.0	HFGGLEAAVYR	1306.6	1307.6	1306.6	1307.6
208.0	6.0	6.0	6.4	2.0	99.0	KFAEFAEAIPLR	1277.7	1278.7	1277.7	1278.7
208.0	6.0	6.0	6.4	0.0	0.0	FAEFAEAIPLR	1149.6	1149.6	1149.6	1150.6
113.0	2.9	2.9	7.3	2.0	99.0	FAEFAEAIPLR	1149.6	1150.6	1149.6	1150.6
113.0	2.9	2.9	7.3	0.9	88.0	HFGGLEAAVYR	1306.6	1307.6	1306.6	1307.6
P51149 RAB7A_HUMAN Ras-related protein Rab-7a - Homo sapiens (Human)										
362.0	3.0	3.0	20.3	2.0	99.0	EAINVEQAFQTIAR	1588.8	1589.8	1588.8	1589.8
362.0	3.0	3.0	20.3	1.0	90.0	FQSLGVAFYR	1186.6	1187.6	1186.6	1187.6
209.0	3.4	3.4	11.6	2.0	99.0	FQSLGVAFYR	1186.6	1187.6	1186.6	1187.6
209.0	3.4	3.4	11.6	1.4	96.0	EAINVEQAFQTIAR	1588.8	1589.8	1588.8	1589.8
P51991 ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3) - Homo sapiens (Human)										
162.0	7.3	7.4	39.7	2.0	99.0	MEVKPPGRPQPSGR	1788.9	1789.9	1788.9	1789.9
162.0	7.3	7.4	39.7	2.0	99.0	YGKIETIEVMEDR	1581.8	1582.8	1581.8	1582.8
162.0	7.3	7.4	39.7	2.0	99.0	YHTINGHNCVVK	1599.7	1600.7	1599.7	1600.8
162.0	7.3	7.4	39.7	1.3	95.0	SSGSPYGGYGGGGGGYGR	1909.8	1910.8	1909.8	1910.8
162.0	7.3	7.4	39.7	0.0	94.0	YHTINGHNCVVK	1537.8	1538.8	1537.8	1538.8
208.0	3.4	3.7	29.6	2.0	99.0	YGKIETIEVMEDR	1581.8	1582.8	1581.8	1582.8
208.0	3.4	3.7	29.6	0.9	88.0	SSGSPYGGYGGGGGGYGR	1909.8	1910.8	1909.8	1910.8
208.0	3.4	3.7	29.6	0.5	67.0	YHTINGHNCVVK	1599.7	1600.7	1599.7	1600.8
208.0	3.4	3.7	29.6	0.0	39.0	DYFEKYGK	1048.5	1049.5	1048.5	1049.5
P52209 6PGD_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) - Homo sapiens (Human)										
414.0	2.2	2.2	13.5	2.0	99.0	VTGEPCCDWWGDEGAGHFVK	2276.0	2277.0	2276.0	2277.0
414.0	2.2	2.2	13.5	0.1	27.0	GILFVGSVSGGEGAR	1590.8	1591.8	1590.8	1591.8
121.0	2.4	2.4	10.8	2.0	99.0	GILFVGSVSGGEGAR	1590.8	1591.8	1590.8	1591.8
121.0	2.4	2.4	10.8	0.4	58.0	VTGEPCCDWWGDEGAGHFVK	2276.0	2277.0	2276.0	2277.0
50.0	15.5	15.5	26.3	2.0	99.0	FQDITDQKHLIPK	1397.7	1398.7	1397.7	1398.7
50.0	15.5	15.5	26.3	2.0	99.0	GILFVGSVSGGEGAR	1590.8	1591.8	1590.8	1591.8
50.0										

28.0	24.6	24.6	49.0	2.0	99.0	KYKEALLGR	1076.6	1077.6	1076.6	1077.6
28.0	24.6	24.6	49.0	2.0	99.0	OSFVLKGEVEYR	1453.8	1454.8	1453.8	1454.8
28.0	24.6	24.6	49.0	2.0	99.0	SIOEIQELDKDDESLR	1914.9	1915.9	1916.9	1917.9
28.0	24.6	24.6	49.0	2.0	99.0	SIOEIQELDKDDESLRK	2045.0	2046.0	2045.0	2046.0
28.0	24.6	24.6	49.0	2.0	99.0	YIQHLYR	979.5	980.5	979.5	980.5
28.0	24.6	24.6	49.0	2.0	99.0	YIQHLYRK	1108.6	1107.6	1108.6	1108.6
28.0	24.6	24.6	49.0	2.0	99.0	YKEALLGR	948.5	949.5	948.5	949.5
28.0	24.6	24.6	49.0	1.7	98.0	AEEYFELTPVEEAPKGMGLAR	2281.1	2282.1	2279.1	2280.1
28.0	24.6	24.6	49.0	0.9	88.0	VNREIVSGMK	1131.6	1132.6	1131.6	1132.6
28.0	24.6	24.6	49.0	0.0	95.0	AEEYFELTPVEEAPKGMGLAR	2279.1	2280.1	2279.1	2280.1
28.0	24.6	24.6	49.0	0.0	99.0	SIOEIQELDKDDESLR	1916.9	1917.9	1916.9	1917.9
82.0	4.1	4.1	26.0	2.0	99.0	AEEYFELTPVEEAPKGMGLAR	2280.1	2281.1	2279.1	2280.1
82.0	4.1	4.1	26.0	2.0	99.0	GVKIDKTDYVMVGSYGPR	1884.9	1885.9	1884.9	1885.9
86.0	8.8	8.8	51.0	2.0	99.0	AEEYFELTPVEEAPKGMGLAR	2279.1	2280.1	2279.1	2280.1
86.0	8.8	8.8	51.0	2.0	99.0	IKKTDYVMVGSYGPR	1600.8	1601.8	1600.8	1601.8
86.0	8.8	8.8	51.0	2.0	99.0	SIOEIQELDKDDESLR	1916.9	1917.9	1916.9	1917.9
86.0	8.8	8.8	51.0	2.0	99.0	YKEALLGR	948.5	949.5	948.5	949.5
86.0	8.8	8.8	51.0	0.5	69.0	KYKEALLGR	1076.6	1077.6	1076.6	1077.6
86.0	8.8	8.8	51.0	0.2	34.0	KOSFVLKGEVEYR	1650.8	1651.8	1650.8	1651.8
P52566 GDIS_HUMAN Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI) - Homo sapiens (Human)										
101.0	11.1	12.0	49.8	2.0	99.0	ATFMVGSYPRPEEYFELTPVEEAPK	2943.4	2944.4	2943.4	2944.4
101.0	11.1	12.0	49.8	2.0	99.0	ETIVLKEGSEYR	1422.7	1423.8	1422.7	1423.7
101.0	11.1	12.0	49.8	2.0	99.0	IHFKNR	912.5	913.5	912.5	913.5
101.0	11.1	12.0	49.8	2.0	99.0	SLKLEOEMDKDDESLIK	2020.0	2021.0	2020.0	2021.0
101.0	11.1	12.0	49.8	1.5	97.0	APNVVWTR	854.5	855.5	854.5	855.5
101.0	11.1	12.0	49.8	1.0	99.0	YVOHTYR	965.5	966.5	965.5	966.5
101.0	11.1	12.0	49.8	0.5	66.0	TLLGDGPVWTDKAPNVVWTR	2147.2	2148.2	2147.2	2148.2
269.0	2.1	2.1	49.3	2.0	99.0	IHFKNR	912.5	913.5	912.5	913.5
269.0	2.1	2.1	49.3	0.0	98.0	IHFKNR	912.5	913.5	912.5	913.5
P52597 HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo sapiens (Human)										
334.0	3.6	6.0	20.7	2.0	99.0	HSGPNADSANDGFVR	1629.7	1630.7	1629.7	1630.7
334.0	3.6	6.0	20.7	1.5	99.0	ITGEAFVQFASOELAEK	1866.9	1867.9	1866.9	1867.9
334.0	3.6	6.0	20.7	0.0	99.0	ATENDIYVFFSPLNPVR	1996.0	1997.0	1996.0	1997.0
230.0	2.7	2.7	12.3	1.5	97.0	ITGEAFVQFASOELAEK	1866.9	1867.9	1866.9	1867.9
230.0	2.7	2.7	12.3	1.2	94.0	HSGPNADSANDGFVR	1629.7	1630.7	1629.7	1630.7
P52907 CAZ1_HUMAN F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human)										
233.0	5.3	5.3	19.9	2.0	99.0	FITHAPPGFEFVFNVDNR	2088.0	2089.0	2088.0	2089.0
233.0	5.3	5.3	19.9	2.0	99.0	TIDGQOITACIESHOFQPK	2313.2	2314.2	2313.1	2314.1
233.0	5.3	5.3	19.9	1.3	95.0	LLLLNNDNLLR	1196.7	1197.7	1196.7	1197.7
166.0	2.0	2.0	19.2	2.0	99.0	FITHAPPGFEFVFNVDNR	2088.0	2089.0	2088.0	2089.0
282.0	2.1	2.1	15.4	2.0	99.0	TIDGQOITACIESHOFQPK	2313.2	2314.2	2313.1	2314.1
P53634 CATC_HUMAN Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP1) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase) [Con										
101.0	3.5	3.5	11.9	2.0	99.0	NVHGIVFVSPVR	1337.7	1338.7	1337.7	1338.7
101.0	3.5	3.5	11.9	1.4	96.0	WFAFFK	844.4	845.4	844.4	845.4
101.0	3.5	3.5	11.9	0.1	22.0	NWACFTGKK	1110.5	1111.6	1110.5	1111.5
311.0	2.0	2.0	3.7	2.0	99.0	NVHGIVFVSPVR	1337.7	1338.7	1337.7	1338.7
P54819 KAD2_HUMAN Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo sapiens (Human)										
189.0	6.1	6.1	34.7	2.0	99.0	LAENFCVCHLATGDMRLR	2005.9	2006.9	2005.9	2006.9
189.0	6.1	6.1	34.7	2.0	99.0	LOAYHTQTTPLEIYR	1996.0	1997.0	1996.0	1997.0
189.0	6.1	6.1	34.7	2.0	99.0	NGFLLDGFPR	1136.6	1137.6	1136.6	1137.6
189.0	6.1	6.1	34.7	0.0	86.0	NGFLLDGFPR	1134.6	1135.6	1134.6	1135.6
118.0	2.6	2.6	30.5	2.0	99.0	NGFLLDGFPR	1134.6	1135.6	1134.6	1135.6
118.0	2.6	2.6	30.5	0.6	74.0	LOAYHTQTTPLEIYR	1996.0	1997.0	1996.0	1997.0
126.0	6.0	6.0	28.9	2.0	99.0	LAENFCVCHLATGDMRLR	2005.9	2006.9	2005.9	2006.9
126.0	6.0	6.0	28.9	2.0	99.0	LOAYHTQTTPLEIYR	1996.0	1997.0	1996.0	1997.0
126.0	6.0	6.0	28.9	2.0	99.0	NGFLLDGFPR	1136.6	1137.6	1136.6	1137.6
126.0	6.0	6.0	28.9	0.0	99.0	LOAYHTQTTPLEIYR	1997.0	1998.0	1997.0	1998.0
P55072 TERA_HUMAN Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP) - Homo sapiens (H										
45.0	19.1	19.1	25.3	2.0	99.0	ELQELVQYVPEHPDKFLK	2211.1	2212.1	2211.1	2212.1
45.0	19.1	19.1	25.3	2.0	99.0	GILLYPPGTGK	1171.7	1172.7	1171.7	1172.7
45.0	19.1	19.1	25.3	2.0	99.0	GPELLTMWFGESEANVR	1950.9	1951.9	1950.9	1951.9
45.0	19.1	19.1	25.3	2.0	99.0	KYEMFAQTLQOSR	1628.8	1629.8	1628.8	1629.8
45.0	19.1	19.1	25.3	2.0	99.0	MDELQLFR	1050.5	1051.5	1050.5	1051.5
45.0	19.1	19.1	25.3	2.0	99.0	MTNGFSGADLTEICQR	1799.8	1800.8	1799.8	1800.8
45.0	19.1	19.1	25.3	2.0	99.0	QAAPCVLFFDELDSIAK	1923.0	1924.0	1923.0	1924.0
45.0	19.1	19.1	25.3	2.0	99.0	YEMFAQTLQOSR	1500.7	1501.7	1500.7	1501.7
45.0	19.1	19.1	25.3	1.7	93.0	WALSQSNPSALR	1329.7	1330.7	1329.7	1330.7
45.0	19.1	19.1	25.3	1.2	94.0	RDFHEEAMR	1189.5	1190.5	1189.5	1190.5
61.0	12.8	12.8	18.7	2.0	99.0	KYEMFAQTLQOSR	1628.8	1629.8	1628.8	1629.8
61.0	12.8	12.8	18.7	2.0	99.0	MDELQLFR	1050.5	1051.5	1050.5	1051.5
61.0	12.8	12.8	18.7	2.0	99.0	MDELQLFRGDTVLLK	1776.9	1778.0	1776.9	1778.0
61.0	12.8	12.8	18.7	2.0	99.0	MTNGFSGADLTEICQR	1799.8	1800.8	1799.8	1800.8
61.0	12.8	12.8	18.7	2.0	99.0	QAAPCVLFFDELDSIAK	1905.9	1906.9	1905.9	1906.9
61.0	12.8	12.8	18.7	2.0	99.0	RDFHEEAMR	1189.5	1190.5	1189.5	1190.5
61.0	12.8	12.8	18.7	0.5	71.0	NAPAIIFDELDAIAPKR	1966.1	1967.1	1966.1	1967.1
61.0	12.8	12.8	18.7	0.2	36.0	WALSQSNPSALR	1329.7	1330.7	1329.7	1330.7
61.0	12.8	12.8	18.7	0.0	80.0	RDFHEEAMR	1189.5	1190.5	1189.5	1190.5
P55209 NP1L1_HUMAN Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP) - Homo sapiens (Human)										
198.0	6.0	6.0	10.5	2.0	99.0	FYEVEHLDR	1336.6	1337.6	1336.6	1337.6
198.0	6.0	6.0	10.5	2.0	99.0	KYAVLYORLFDKDR	1639.9	1640.9	1639.9	1640.9
198.0	6.0	6.0	10.5	2.0	99.0	NVDLLSDMVQEHDEPILK	2094.0	2095.0	2094.0	2095.0
98.0	3.8	3.8	10.2	2.0	99.0	KYAVLYORLFDKDR	1639.9	1640.9	1639.9	1640.9
98.0	3.8	3.8	10.2	1.5	97.0	LDGLVETPTGYIESLPR	1859.0	1860.0	1859.0	1860.0
98.0	3.8	3.8	10.2	0.1	28.0	YAVLYORLFDKDR	1511.8	1512.8	1511.8	1512.8
187.0	4.0	4.0	10.0	2.0	99.0	FYEVEHLDR	1336.6	1337.6	1336.6	1337.6
187.0	4.0	4.0	10.0	2.0	99.0	LDGLVETPTGYIESLPR	1859.0	1860.0	1859.0	1860.0
P55786 PSA_HUMAN Puromycin-sensitive aminopeptidase (EC 3.4.11.-) (PSA) - Homo sapiens (Human)										
407.0	2.3	2.3	3.8	2.0	99.0	AFFESHAPSAER	1444.7	1445.7	1444.7	1445.7
407.0	2.3	2.3	3.8	0.2	36.0	YAAVTOFEATDAR	1441.7	1442.7	1441.7	1442.7
152.0	2.0	2.0	7.5	2.0	99.0	DAESIHQYLLOR	1471.7	1472.7	1471.7	1472.7
181.0	4.0	4.0	6.7	2.0	99.0	AFFESHAPSAER	1444.7	1445.7	1444.7	1445.7
181.0	4.0	4.0	6.7	2.0	99.0	DAESIHQYLLOR	1471.7	1472.7	1471.7	1472.7
P59998 ARPC4_HUMAN Actin-related protein 2/3 complex subunit 4 (ARP2/3 complex 20 kDa subunit) (p20-ARC) - Homo sapiens (Human)										
197.0	6.0	6.0	29.8	2.0	99.0	AENFFILR	1008.5	1009.5	1008.5	1009.5
197.0	6.0	6.0	29.8	2.0	99.0	IVAEEFLK	947.5	948.5	947.5	948.5
197.0	6.0	6.0	29.8	2.0	99.0	TATLRPYLSAVR	1388.8	1389.8	1388.8	1389.8
197.0	6.0	6.0	29.8	0.0	21.0	AENFFILR	1010.5	1011.5	1010.5	1011.5
123.0	2.3	2.3	23.8	2.0	99.0	AENFFILR	1008.5	1009.5	1008.5	1009.5
123.0	2.3	2.3	23.8	0.3	53.0	TATLRPYLSAVR	1388.8	1389.8	1388.8	1389.8
327.0	2.0	2.0	19.0	2.0	99.0	AENFFILR	1008.5	1009.5	1008.5	1009.5
P60174 TPIS_HUMAN Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Homo sapiens (Human)										
23.0	28.0	28.0	61.0	2.0	99.0	DCGATWVVLGHSEK	1585.7	1586.7	1585.7	1586.7
23.0	28.0	28.0	61.0	2.0	99.0	FFVGGNWK	953.5	954.5	953.5	954.5
23.0	28.0	28.0	61.0	2.0	99.0	HVFGSEDELIGQK	1457.7	1458.7	1457.7	1458.7
23.0	28.0	28.0	61.0	2.0	99.0	IIVAACNYK	1136.6	1137.6	1136.6	1137.6
23.0	28.0	28.0	61.0	2.0	99.0	IYGGSVTGTACK	1325.7	1326.7	1325.7	1326.7
23.0	28.0	28.0	61.0	2.0	99.0	KFFVGGNWK	1081.6	1082.6	1081.6	1082.6
23.0	28.0	28.0	61.0	2.0	99.0	OSLGELIGLNAAK	1396.8	1397.8	1396.8	1397.8
23.0	28.0	28.0	61.0	2.0	99.0	RHFVGSDELIGQK	1613.8	1614.8	1613.8	1614.8
23.0	28.0	28.0	61.0	2.0	99.0	TATPQOAGEVHEK	1465.7	1466.7	1465.7	1466.7
23.0	28.0	28.0	61.0	2.0	99.0	TATPQOAGEVHEKLR	1734.9	1735.9	1734.9	1735.9
23.0	28.0	28.0	61.0	2.0	99.0	VPADTEVVCAPPTAYIDFAR	2191.1	2192.1	2191.1	2192.1
23.0	28.0	28.0	61.0	2.0	99.0	VTNGAFGTGEISPGMIK	1621.8	1622.8	1621.8	1622.

13.0	18.3	18.3	66.7	2.0	99.0	VIADNVKDWK	1273.6	1274.7	1273.7	1274.7
13.0	18.3	18.3	66.7	2.0	99.0	VPADTEVVCAPPTAYIDFAR	2191.1	2192.1	2191.1	2192.1
13.0	18.3	18.3	66.7	2.0	99.0	VVLAYEPVWAIQTGK	1601.9	1602.9	1601.9	1602.9
13.0	18.3	18.3	66.7	0.3	48.0	IAVAQNCYK	1136.6	1137.6	1136.6	1137.6
13.0	18.3	18.3	66.7	0.0	99.0	FFVGGNWK	985.5	986.5	985.5	986.5
13.0	18.3	18.3	66.7	0.0	99.0	VPADTEVVCAPPTAYIDFAR	2191.1	2191.1	2191.1	2192.1
40.0	18.1	18.1	57.0	2.0	98.0	DCGATWVVLGHSESR	1586.7	1586.7	1586.7	1586.7
40.0	18.1	18.1	57.0	2.0	98.0	FFVGGNWK	953.5	954.5	953.5	954.5
40.0	18.1	18.1	57.0	2.0	98.0	IYVGGVGTGATCK	1325.7	1326.7	1325.7	1326.7
40.0	18.1	18.1	57.0	2.0	98.0	KFFVGGNWK	1081.6	1082.6	1081.6	1082.6
40.0	18.1	18.1	57.0	2.0	98.0	TATPQQAQEVHEK	1465.7	1466.7	1465.7	1466.7
40.0	18.1	18.1	57.0	2.0	98.0	VAHALAAGLGVIAICGEK	1807.0	1808.0	1807.0	1808.0
40.0	18.1	18.1	57.0	2.0	98.0	VPADTEVVCAPPTAYIDFAR	2191.1	2191.1	2191.1	2192.1
40.0	18.1	18.1	57.0	2.0	98.0	VVLAYEPVWAIQTGK	1601.9	1602.9	1601.9	1602.9
40.0	18.1	18.1	57.0	1.5	97.0	DCGATWVVLGHSESR	1741.8	1742.8	1741.8	1742.8
40.0	18.1	18.1	57.0	0.5	70.0	LRGWLK	771.5	772.5	771.5	772.5
P60660 MYL6_HUMAN Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosin light chain alkali 6) (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3)										
112.0	10.0	10.0	50.3	2.0	99.0	ALGONPTNAEVLK	1353.7	1354.7	1353.7	1354.7
112.0	10.0	10.0	50.3	2.0	99.0	EAFOLFDR	1024.5	1025.5	1024.5	1025.5
112.0	10.0	10.0	50.3	2.0	99.0	ILYSQCGDVMR	1340.6	1341.6	1340.6	1341.6
112.0	10.0	10.0	50.3	2.0	99.0	MCDFTEDQTAEFKEAFLQFDR	2538.1	2539.1	2538.1	2539.1
112.0	10.0	10.0	50.3	2.0	99.0	NKDQGTEDYVEGLR	1785.8	1786.8	1785.8	1786.8
65.0	5.2	5.2	31.1	2.0	99.0	EAFOLFDR	1024.5	1025.5	1024.5	1025.5
65.0	5.2	5.2	31.1	1.5	97.0	ILYSQCGDVMR	1340.6	1341.6	1340.6	1341.6
65.0	5.2	5.2	31.1	1.4	96.0	NKDQGTEDYVEGLR	1785.8	1786.8	1785.8	1786.8
65.0	5.2	5.2	31.1	0.3	48.0	ALGONPTNAEVLK	1353.7	1354.7	1353.7	1354.7
122.0	6.1	6.1	50.3	2	99.00	ILYSQCGDVMR	1340.6	1341.6	1340.6	1341.6
122.0	6.1	6.1	50.3	2	99.00	NKDQGTEDYVEGLR	1785.8	1786.8	1785.8	1786.8
122.0	6.1	6.1	50.3	2	99.00	FKVQKNGTVMGAIR	1722.8	1723.8	1722.8	1723.8
P60709 ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin) - Homo sapiens (Human)										
449.0	2.0	54.1	69.9	0.0	99.0	DDIIVLDVNDGSGMCK	1821.8	1822.8	1821.8	1822.8
449.0	2.0	54.1	69.9	0.0	99.0	AGFAGDDAPR	975.4	976.4	975.4	976.4
449.0	2.0	54.1	69.9	0.0	99.0	AGFAGDDAPR	975.4	976.4	975.4	976.4
449.0	2.0	54.1	69.9	0.0	99.0	AVFPSIVGRPR	1041.6	1042.6	1041.6	1042.6
449.0	2.0	54.1	69.9	0.0	99.0	AVFPSIVGRPR	1197.7	1198.7	1197.7	1198.7
449.0	2.0	54.1	69.9	0.0	99.0	CYVALDFEDEMATAASSSSLEK	2549.0	2550.0	2549.0	2550.0
449.0	2.0	54.1	69.9	0.0	99.0	DDIIVLDVNDGSGMCK	1973.8	1974.8	1973.8	1974.8
449.0	2.0	54.1	69.9	0.0	99.0	DDIIVLDVNDGSGMCK	1821.8	1822.8	1821.8	1822.8
449.0	2.0	54.1	69.9	0.0	99.0	DDIIVLDVNDGSGMCK	1821.8	1822.8	1821.8	1822.8
449.0	2.0	54.1	69.9	0.0	99.0	DDIIVLDVNDGSGMCK	1821.8	1822.8	1821.8	1822.8
449.0	2.0	54.1	69.9	0.0	99.0	DDIIVLDVNDGSGMCK	1973.8	1974.8	1973.8	1974.8
449.0	2.0	54.1	69.9	0.0	99.0	DLYANTVLSGGTMYPGIADR	2214.0	2215.0	2214.0	2215.0
449.0	2.0	54.1	69.9	0.0	99.0	EITALAPSTMK	1160.6	1161.6	1160.6	1161.6
449.0	2.0	54.1	69.9	0.0	99.0	GYSFTTAEIR	1131.5	1132.5	1131.5	1132.5
449.0	2.0	54.1	69.9	0.0	98.0	GYSFTTAEIREIVR	1628.8	1629.8	1628.8	1629.8
449.0	2.0	54.1	69.9	0.0	99.0	GYSFTTAEIREIVRDIK	1985.1	1986.1	1985.0	1986.0
449.0	2.0	54.1	69.9	0.0	95.0	GYSFTTAEIREIVRDIKEK	2242.2	2243.2	2242.2	2243.2
449.0	2.0	54.1	69.9	0.0	86.0	GYSFTTAEIREIVRDIKEK	2243.2	2244.2	2243.2	2244.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQK	1171.6	1172.6	1171.6	1172.6
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQK	1186.6	1187.6	1186.6	1187.6
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQK	1182.6	1183.6	1182.6	1183.6
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQK	1172.6	1173.6	1172.6	1173.6
449.0	2.0	54.1	69.9	0.0	29.0	HQGMVGMGQK	1186.6	1187.6	1186.6	1187.6
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSK	2366.1	2367.1	2366.1	2367.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSK	2351.1	2352.1	2351.1	2352.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSK	2394.1	2395.1	2394.1	2395.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSK	2366.1	2367.1	2366.1	2367.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSK	2378.1	2379.1	2378.1	2379.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSKR	2522.2	2523.2	2522.2	2523.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSKR	2522.2	2523.2	2522.2	2523.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSKR	2506.2	2507.2	2506.2	2507.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSKR	2534.2	2535.2	2534.2	2535.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAOSKR	2518.2	2519.2	2518.2	2519.2
449.0	2.0	54.1	69.9	0.0	95.0	HQGMVGMGQKDSYVGEAOSKR	2538.2	2539.2	2538.2	2539.2
449.0	2.0	54.1	69.9	0.0	23.0	IAPPER	794.5	795.5	794.5	795.5
449.0	2.0	54.1	69.9	0.0	83.0	IAPPERK	922.6	923.6	922.6	923.6
449.0	2.0	54.1	69.9	0.0	99.0	IKIAPPER	1035.6	1036.6	1035.6	1036.6
449.0	2.0	54.1	69.9	0.0	99.0	IKIAPPER	1035.6	1036.6	1035.6	1036.6
449.0	2.0	54.1	69.9	0.0	86.0	IKIAPPERK	1163.7	1164.7	1163.7	1164.7
449.0	2.0	54.1	69.9	0.0	41.4	ISKQEVDESGPSIVHR	1843.9	1844.9	1843.9	1844.9
449.0	2.0	54.1	69.9	0.0	89.0	IWHHTFYNE	1245.5	1246.5	1245.5	1246.5
449.0	2.0	54.1	69.9	0.0	26.8	IWHHTFYNEL	1359.7	1360.7	1358.6	1359.6
449.0	2.0	54.1	69.9	0.0	99.0	IWHHTFYNELR	1515.7	1516.7	1515.7	1516.7
449.0	2.0	54.1	69.9	0.0	99.0	IWHHTFYNELR	1514.7	1515.7	1514.7	1515.7
449.0	2.0	54.1	69.9	0.0	99.0	IWHHTFYNELR	1516.7	1517.7	1516.7	1517.7
449.0	2.0	54.1	69.9	0.0	99.0	IWHHTFYNELR	1530.7	1531.7	1530.7	1531.7
449.0	2.0	54.1	69.9	0.0	99.0	IWHHTFYNELR	1546.7	1547.7	1546.7	1547.7
449.0	2.0	54.1	69.9	0.0	99.0	IWHHTFYNELR	1515.7	1516.7	1515.7	1516.7
449.0	2.0	54.1	69.9	0.0	56.0	IWHHTFYNELR	1499.7	1499.7	1499.7	1500.7
449.0	2.0	54.1	69.9	0.0	44.0	IWHHTFYNELR	1471.7	1471.7	1471.7	1471.7
449.0	2.0	54.1	69.9	0.0	99.0	KDLVANTVLSGGTMYPGIADR	2342.2	2343.2	2342.1	2343.1
449.0	2.0	54.1	69.9	0.0	21.0	LDLAGRDLTDYLMK	1622.8	1623.8	1622.8	1623.8
449.0	2.0	54.1	69.9	0.0	99.0	MOKETALAPSTMK	1547.8	1548.8	1547.8	1548.8
449.0	2.0	54.1	69.9	0.0	99.0	QEYDESGPSIVHR	1515.7	1516.7	1515.7	1516.7
449.0	2.0	54.1	69.9	0.0	99.0	QEYDESGPSIVHR	1498.7	1499.7	1498.7	1499.7
449.0	2.0	54.1	69.9	0.0	99.0	QEYDESGPSIVHRK	1643.8	1644.8	1643.8	1644.8
449.0	2.0	54.1	69.9	0.0	99.0	QEYDESGPSIVHRK	1626.8	1627.8	1626.8	1627.8
449.0	2.0	54.1	69.9	0.0	92.0	RGILTLK	799.5	800.5	799.5	800.5
449.0	2.0	54.1	69.9	0.0	28.4	SLSTFOQMWSK	1454.7	1455.7	1454.7	1455.7
449.0	2.0	54.1	69.9	0.0	99.0	SYELPDGQVITIGNER	1789.9	1790.9	1789.9	1790.9
449.0	2.0	54.1	69.9	0.0	99.0	SYELPDGQVITIGNER	1789.9	1790.9	1789.9	1790.9
449.0	2.0	54.1	69.9	0.0	99.0	SYELPDGQVITIGNER	1791.9	1792.9	1791.9	1792.9
449.0	2.0	54.1	69.9	0.0	95.0	SYELPDGQVITIGNER	1786.0	1787.0	1785.9	1786.9
449.0	2.0	54.1	69.9	0.0	96.0	SYELPDGQVITIGNERFR	2093.1	2094.1	2093.1	2094.1
449.0	2.0	54.1	69.9	0.0	99.0	VAPEEHPVLLTEAPLNPK	1953.0	1954.0	1953.0	1954.0
449.0	2.0	54.1	69.9	0.0	99.0	VAPEEHPVLLTEAPLNPKANR	2294.2	2295.2	2294.2	2295.2
449.0	2.0	54.1	69.9	0.0	94.0	VAPEEHPVLLTEAPLNPKANREK	2551.4	2552.4	2551.4	2552.4
449.0	2.0	54.1	69.9	0.0	99.0	YPIEHGIVTNWDDMEK	1959.9	1960.9	1959.9	1960.9
449.0	2.0	54.1	69.9	0.0	99.0	YPIEHGIVTNWDDMEK	1945.9	1946.9	1945.9	1946.9
5.0	31.5	31.5	66.4	2.0	99.0	AVFPSIVGRPR	1197.7	1198.7	1197.7	1198.7
5.0	31.5	31.5	66.4	2.0	99.0	DDIIVLDVNDGSGMCK	1821.8	1822.8	1821.8	1822.8
5.0	31.5	31.5	66.4	2.0	99.0	DLTDYLMK	997.5	998.5	997.5	998.5
5.0	31.5	31.5	66.4	2.0	99.0	DLYANTVLSGGTMYPGIADR	2214.0	2215.0	2214.0	2215.0
5.0	31.5	31.5	66.4	2.0	99.0	HQGMVGMGQK	1170.6	1171.6	1170.6	1171.6
5.0	31.5	31.5	66.4	2.0	99.0	HQGMVGMGQKDSYVGEAOSK	2350.1	2351.1	2350.1	2351.1
5.0	31.5	31.5	66.4	2.0	99.0	HQGMVGMGQKDSYVGEAOSKR	2506.2	2507.2	2506.2	2507.2
5.0	31.5	31.5	66.4	2.0	99.0	IWHHTFYNELR	1514.7	1515.7	1514.7	1515.7
5.0	31.5	31.5	66.4	2.0	99.0	LCYVALDFEDEMATAASSSSLEK	2549.0	2550.0	2549.0	2550.0
5.0	31.5	31.5	66.4	2.0	99.0					

45.0	16.3	16.3	68.2	0.0	52.0	RLGMDGYR	982.5	983.5	982.5	983.5
45.0	16.3	16.3	68.2	0.0	99.0	STDYGFQINSR	1400.7	1401.7	1400.7	1401.7
45.0	16.3	16.3	68.2	0.0	95.0	WESGYNTR	1011.4	1012.5	1011.4	1012.4
45.0	16.3	16.3	68.2	0.0	65.0	WESGYNTR	1021.4	1022.4	1021.4	1022.4
45.0	16.3	16.3	68.2	0.0	23.0	WESGYNTR	1027.4	1028.5	1027.4	1028.4
P61769 B2MG_HUMAN	Beta2-microglobulin precursor [Contains Beta-2-microglobulin variant pl 5.3] - Homo sapiens (Human)									
94.0	11.7	11.7	49.6	2.0	99.0	IEKVEHSDLFSFK	1517.8	1518.8	1517.8	1518.8
94.0	11.7	11.7	49.6	2.0	99.0	IQVYSRHPAENGK	1497.8	1498.8	1497.8	1498.8
94.0	11.7	11.7	49.6	2.0	99.0	IVKWDRDM	1061.5	1062.5	1061.5	1062.5
94.0	11.7	11.7	49.6	2.0	99.0	VNHVTLISOPK	1121.6	1122.6	1121.6	1122.6
94.0	11.7	11.7	49.6	2.0	99.0	YTEFTPEKDEYACR	1908.8	1909.8	1908.8	1909.8
94.0	11.7	11.7	49.6	1.2	94.0	IQVYSR	764.4	765.4	764.4	765.4
94.0	11.7	11.7	49.6	0.4	58.0	IVKWDR	815.5	816.5	815.5	816.5
94.0	11.7	11.7	49.6	0.0	99.0	IQVYSRHPAENGK	1498.8	1499.8	1498.8	1499.8
94.0	11.7	11.7	49.6	0.0	99.0	VNHVTLISOPK	1104.6	1105.6	1104.6	1105.6
53.0	6.1	6.1	26.1	2.0	99.0	IQVYSRHPAENGK	1498.8	1499.8	1498.8	1499.8
53.0	6.1	6.1	26.1	2.0	99.0	IVKWDRDM	1061.5	1062.5	1061.5	1062.5
53.0	6.1	6.1	26.1	2.0	99.0	VNHVTLISOPK	1121.6	1122.6	1121.6	1122.6
53.0	6.1	6.1	26.1	0.1	27.0	IVKWDR	815.5	816.5	815.5	816.5
53.0	6.1	6.1	26.1	0.0	89.0	IQVYSRHPAENGK	1497.8	1498.8	1497.8	1498.8
69.0	10.4	10.4	37.8	2.0	99.0	IEKVEHSDLFSFK	1517.8	1518.8	1517.8	1518.8
69.0	10.4	10.4	37.8	2.0	99.0	IQVYSR	764.4	765.4	764.4	765.4
69.0	10.4	10.4	37.8	2.0	99.0	IQVYSRHPAENGK	1498.8	1499.8	1498.8	1499.8
69.0	10.4	10.4	37.8	2.0	99.0	IVKWDRDM	1061.5	1062.5	1061.5	1062.5
69.0	10.4	10.4	37.8	2.0	99.0	VNHVTLISOPK	1121.6	1122.6	1121.6	1122.6
69.0	10.4	10.4	37.8	0.4	60.0	IVKWDR	815.5	816.5	815.5	816.5
69.0	10.4	10.4	37.8	0.0	97.0	IQVYSRHPAENGK	1497.8	1498.8	1497.8	1498.8
69.0	10.4	10.4	37.8	0.0	99.0	VNHVTLISOPK	1122.6	1123.6	1121.6	1122.6
69.0	10.4	10.4	37.8	0.0	99.0	VNHVTLISOPK	1104.6	1105.6	1104.6	1105.6
P61916 NPC2_HUMAN	Epilidymal secretory protein E1 precursor (Niemann-Pick disease type C2 protein) (hE1) - Homo sapiens (Human)									
534.0	2.0	2.0	10.6	2.0	99.0	EVSRGTGPGQLSK	1843.9	1843.9	1842.9	1843.9
386.0	1.7	1.7	10.6	1.7	98.0	EVNVPCTGPQQLSK	1842.9	1843.9	1842.9	1843.9
P62158 CALM_HUMAN	Calmodulin (CaM) - Homo sapiens (Human)									
237.0	5.2	5.2	36.9	2.0	99.0	ADQLTEQIAIEFK	1562.7	1563.7	1562.7	1563.8
237.0	5.2	5.2	36.9	2.0	99.0	EADIDGDGQVNYEEFVOMMTAK	2489.1	2490.1	2489.1	2490.1
237.0	5.2	5.2	36.9	1.2	94.0	HVMNTLGEKLTDEEVDEMIR	2400.2	2401.2	2400.2	2401.2
254.0	2.2	2.2	19.5	2.0	99.0	ADQLTEQIAIEFK	1562.7	1563.8	1562.7	1563.8
254.0	2.2	2.2	19.5	0.2	38.0	VFDKDGNGYISAAELR	1754.9	1755.9	1754.8	1755.9
P62241 RS8_HUMAN	40S ribosomal protein S8 - Homo sapiens (Human)									
106.0	10.1	10.1	52.4	2.0	99.0	ADGVVLEKGELEFYLR	1901.0	1902.0	1901.0	1902.0
106.0	10.1	10.1	52.4	2.0	99.0	ELEFYLR	968.5	968.5	968.5	969.5
106.0	10.1	10.1	52.4	2.0	99.0	IIDVYVNSNNELVLR	1717.9	1718.9	1717.9	1718.9
106.0	10.1	10.1	52.4	2.0	99.0	ISSLLEEFQDQK	1505.8	1506.8	1505.8	1506.8
106.0	10.1	10.1	52.4	2.0	99.0	QWYESHYALPLGR	1601.8	1602.8	1601.8	1602.8
106.0	10.1	10.1	52.4	0.1	26.0	LLACIASRPGQCGGR	1557.8	1558.8	1557.8	1558.8
106.0	10.1	10.1	52.4	0.0	78.0	QWYESHYALPLGR	1618.8	1619.8	1618.8	1619.8
169.0	4.1	4.1	52.9	2.0	99.0	ADGVVLEKGELEFYLR	1900.9	1902.0	1901.0	1902.0
169.0	4.1	4.1	52.9	2.0	99.0	QWYESHYALPLGR	1601.8	1602.8	1601.8	1602.8
169.0	4.1	4.1	52.9	0.0	99.0	QWYESHYALPLGR	1618.8	1619.8	1618.8	1619.8
P62244 RS15A_HUMAN	40S ribosomal protein S15a - Homo sapiens (Human)									
296.0	4.0	4.0	21.5	2.0	99.0	HGYGEFEIIDDHR	1699.8	1700.8	1699.8	1700.8
296.0	4.0	4.0	21.5	2.0	99.0	IVNLTGR	870.5	871.5	870.5	871.5
387.0	1.7	1.7	16.9	0.9	87.0	HGYGEFEIIDDHR	1699.8	1700.8	1699.8	1700.8
387.0	1.7	1.7	16.9	0.8	84.0	IVNLTGR	870.5	871.5	870.5	871.5
P62249 RS16_HUMAN	40S ribosomal protein S16 - Homo sapiens (Human)									
159.0	7.4	7.4	47.3	2.0	99.0	GGGHVAQIYAIR	1240.7	1241.7	1240.7	1241.7
159.0	7.4	7.4	47.3	2.0	99.0	LLEPVLGK	1093.7	1094.7	1093.7	1094.7
159.0	7.4	7.4	47.3	2.0	99.0	PSKGPLQSVQVFR	1498.8	1499.8	1498.8	1499.8
159.0	7.4	7.4	47.3	0.8	85.0	EIKDILIQYDR	1404.8	1405.8	1404.8	1405.8
159.0	7.4	7.4	47.3	0.6	75.0	VKGGGHVAQIYAIR	1467.8	1468.8	1467.8	1468.8
106.0	3.3	3.3	35.6	2.0	99.0	PSKGPLQSVQVFR	1498.8	1499.8	1498.8	1499.8
106.0	3.3	3.3	35.6	1.2	94.0	EIKDILIQYDR	1404.8	1405.8	1404.8	1405.8
68.0	10.9	10.9	52.1	2.0	99.0	EIKDILIQYDR	1404.8	1405.8	1404.8	1405.8
68.0	10.9	10.9	52.1	2.0	99.0	GGGHVAQIYAIR	1240.7	1241.7	1240.7	1241.7
68.0	10.9	10.9	52.1	2.0	99.0	PSKGPLQSVQVFR	1498.8	1499.8	1498.8	1499.8
68.0	10.9	10.9	52.1	2.0	99.0	VKGGGHVAQIYAIR	1467.8	1468.8	1467.8	1468.8
68.0	10.9	10.9	52.1	1.5	97.0	FAGVDIR	776.4	777.4	776.4	777.4
68.0	10.9	10.9	52.1	1.3	95.0	ALVAVYQK	954.5	955.5	954.5	955.5
P62258 1433E_HUMAN	14-3-3 protein epsilon (14-3-3E) - Homo sapiens (Human)									
109.0	10.0	12.0	37.3	2.0	99.0	IISSEIOKEENKGGDEKLLK	2144.1	2145.1	2144.1	2145.1
109.0	10.0	12.0	37.3	2.0	99.0	LAEOAERYDEMVMESMKK	2056.0	2057.0	2056.0	2057.0
109.0	10.0	12.0	37.3	2.0	99.0	MDDREDLVYQAK	1523.7	1524.7	1523.7	1524.7
109.0	10.0	12.0	37.3	2.0	99.0	YLAEFATGDRK	1383.7	1384.7	1383.7	1384.7
109.0	10.0	12.0	37.3	2.0	99.0	YLAEFATGDRKAAENSLVYVK	2559.2	2560.2	2559.2	2560.2
109.0	10.0	12.0	37.3	0.0	99.0	DSTLIMQLLR	1188.7	1189.7	1188.7	1189.7
256.0	2.2	3.5	18.8	2.0	99.0	MDDREDLVYQAK	1523.7	1524.7	1523.7	1524.7
256.0	2.2	3.5	18.8	0.2	36.0	YLAEFATGDRK	1383.7	1384.7	1383.7	1384.7
256.0	2.2	3.5	18.8	0.0	94.0	DSTLIMQLLR	1188.7	1189.7	1188.7	1189.7
P62269 RS18_HUMAN	40S ribosomal protein S18 (K6-3) (K63) - Homo sapiens (Human)									
164.0	7.2	7.2	34.9	2.0	99.0	IPDWFNLR	1059.5	1060.5	1059.5	1060.6
164.0	7.2	7.2	34.9	2.0	99.0	SLVIPEKFOHILR	1620.9	1621.9	1620.9	1621.9
164.0	7.2	7.2	34.9	2.0	99.0	VITIMONPR	1070.6	1071.6	1070.6	1071.6
164.0	7.2	7.2	34.9	0.5	71.0	YAHVLRK	984.6	985.6	984.6	985.6
164.0	7.2	7.2	34.9	0.4	59.0	YAHVLR	856.5	857.5	856.5	857.5
164.0	7.2	7.2	34.9	0.3	46.0	HFVGLR	814.4	815.4	814.4	815.4
164.0	7.2	7.2	34.9	0.0	70.0	VITIMONPR	1070.6	1071.6	1070.6	1071.6
164.0	7.2	7.2	34.9	0.0	45.0	VITIMONPR	1232.6	1233.6	1232.6	1233.7
135.0	5.9	5.9	37.5	2.0	99.0	IPDWFNLR	1059.5	1060.5	1059.5	1060.6
135.0	5.9	5.9	37.5	2.0	99.0	VITIMONPR	1070.6	1071.6	1070.6	1071.6
135.0	5.9	5.9	37.5	1.4	96.0	SLVIPEKFOHILR	1620.9	1621.9	1620.9	1621.9
135.0	5.9	5.9	37.5	0.3	50.0	HFVGLR	814.4	815.4	814.4	815.4
135.0	5.9	5.9	37.5	0.2	37.0	YAHVLR	856.5	857.5	856.5	857.5
P62273 RS29_HUMAN	40S ribosomal protein S29 - Homo sapiens (Human)									
379.0	2.6	2.6	33.9	2.0	99.0	GHQQLYWSHPR	1407.7	1408.7	1407.7	1408.7
379.0	2.6	2.6	33.9	0.6	73.0	YGLNMCR	912.4	913.4	912.4	913.4
379.0	2.6	2.6	33.9	0.0	99.0	GHQQLYWSHPR	1407.7	1408.7	1407.7	1408.7
240.0	2.4	2.4	33.9	2.0	99.0	GHQQLYWSHPR	1407.7	1408.7	1407.7	1408.7
240.0	2.4	2.4	33.9	0.3	49.0	YGLNMCR	912.4	913.4	912.4	913.4
240.0	2.4	2.4	33.9	0.0	99.0	GHQQLYWSHPR	1407.7	1408.7	1407.7	1408.7
P62280 RS11_HUMAN	40S ribosomal protein S11 - Bos taurus (Bovine) ; 40S ribosomal protein S11 - Rattus norvegicus (Rat) ; 40S ribosomal protein S11 - Mus musculus									
82.0	12.8	12.8	39.2	2.0	99.0	AYQKQPTIFONK	1464.8	1465.8	1464.8	1465.8
82.0	12.8	12.8	39.2	2.0	99.0	AYQKQPTIFONKKR	1749.0	1750.0	1749.0	1750.0
82.0	12.8	12.8	39.2	2.0	99.0	DYLVHYR	979.5	979.5	979.5	979.5
82.0	12.8	12.8	39.2	2.0	99.0	HKNMSVHLSPCFR	1611.8	1612.8	1611.8	1612.8
82.0	12.8	12.8	39.2	2.0	99.0	NMSVHLSPCFR	1346.6	1347.6	1346.6	1347.6
82.0	12.8	12.8	39.2	1.4	96.0	VLLGETGKCKLPR	1438.9	1439.9	1438.9	1439.9
82.0	12.8	12.8	39.2	1.1	92.0	RDYLVHYR	1134.6	1135.6	1134.6	1135.6
82.0	12.8	12.8	39.2	0.3	52.0	CPFTGNVSR	1132.5	1133.5	1132.5	1133.5
116.0	6.6	6.6	34.2	2.0	99.0	CPFTGNVSR	1132.5	1133.5	1132.5	1133.5
116.0	6.6	6.6	34.2	2.0	99.0	DYLVHYR	979.5	979.5	979.5	979.5
116.0	6.6	6.6	34.2	2.0	99.0	NMSVHLSPCFR	1346.6	1347.6	1346.6	1347.6
116.0	6.6	6.6	34.2	0.6	74.0	AYQKQPTIFONK	1464.8	1465.8	1464.8	1465.8
72.0	4.9	4.9	25.3	2.0	99.0	DYLVHYR	979.5	979.5	979.5	979.5
72.0	4.9	4.9	25.3	1.7	98.0	AYQKQPTIFONK	1464.8	1465.8	1464.8	1465.8
72.0	4.9	4.9	25.3	1.2	93.0	CPFTGNVSR	1132.5	1133.5	1132.5	1133.5
P62310 LSM3_HUMAN	U6 snRNA-associated Sm-like protein LSM3 - Homo sapiens (Human									

29.0	24.5	24.5	97.7	2.0	99.0	KTETQEKNLPLSKETIEOEKQAGES	2828.4	2829.4	2828.4	2829.4
29.0	24.5	24.5	97.7	2.0	99.0	LKKTETQEKNLPLSKETIEOEK	2597.4	2598.4	2597.4	2598.4
29.0	24.5	24.5	97.7	2.0	99.0	LKKTETQEKNLPLSKETIEOEKQAGES	3069.6	3070.6	3069.6	3070.6
29.0	24.5	24.5	97.7	2.0	99.0	NPLPSKETIEOEK	1511.8	1512.8	1511.8	1512.8
29.0	24.5	24.5	97.7	2.0	99.0	NPLPSKETIEOEKQAGES	1984.0	1985.0	1984.0	1985.0
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAIEIEKFDK	1493.8	1494.8	1493.8	1494.8
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAIEIEKFDKSK	1908.9	1909.9	1908.9	1909.9
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAIEIEKFDKSKLK	2150.1	2151.1	2150.1	2151.1
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAIEIEKFDKSKLKK	2278.2	2279.2	2278.2	2279.2
29.0	24.5	24.5	97.7	2.0	99.0	TETQEKNLPLSKETIEOEK	2228.1	2229.1	2228.1	2229.1
29.0	24.5	24.5	97.7	2.0	99.0	TETQEKNLPLSKETIEOEKQAGES	2700.3	2701.3	2700.3	2701.3
29.0	24.5	24.5	97.7	0.5	67.0	SDKPDMAIEIEK	1303.6	1304.6	1303.6	1304.6
29.0	24.5	24.5	97.7	0.0	91.0	LKKTETQEKNLPLSKETIEOEKQAGES	3069.6	3070.6	3069.6	3070.6
28.0	21.1	21.1	97.7	2.0	99.0	KTETQEKNLPLSKETIEOEK	2356.3	2357.3	2356.2	2357.2
28.0	21.1	21.1	97.7	2.0	99.0	KTETQEKNLPLSKETIEOEKQAGES	2828.4	2829.4	2828.4	2829.4
28.0	21.1	21.1	97.7	2.0	99.0	LKKTETQEKNLPLSKETIEOEK	2597.4	2598.4	2597.4	2598.4
28.0	21.1	21.1	97.7	2.0	99.0	NPLPSKETIEOEKQAGES	1984.0	1985.0	1984.0	1985.0
28.0	21.1	21.1	97.7	2.0	99.0	SDKPDMAIEIEK	1303.6	1304.6	1303.6	1304.6
28.0	21.1	21.1	97.7	2.0	99.0	SDKPDMAIEIEKFDK	1693.8	1694.8	1693.8	1694.8
28.0	21.1	21.1	97.7	2.0	99.0	SDKPDMAIEIEKFDKSK	1908.9	1909.9	1908.9	1909.9
28.0	21.1	21.1	97.7	2.0	99.0	SDKPDMAIEIEKFDKSKLK	2150.1	2151.1	2150.1	2151.1
28.0	21.1	21.1	97.7	2.0	99.0	TETQEKNLPLSKETIEOEK	2228.1	2229.1	2228.1	2229.1
28.0	21.1	21.1	97.7	2.0	99.0	TETQEKNLPLSKETIEOEKQAGES	2700.3	2701.3	2700.3	2701.3
28.0	21.1	21.1	97.7	1.1	92.0	LKKTETQEKNLPLSKETIEOEKQAGES	3070.6	3071.6	3070.6	3071.6
28.0	21.1	21.1	97.7	0.0	40.0	TETQEKNLPLSKETIEOEK	2228.1	2229.1	2228.1	2229.1
P62633 CNBP_HUMAN	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9) - Bos taurus (Bovine) ; Cellular nucleic acid-binding protein (CNBP) (Zinc finger)									
353.0	3.2	3.2	43.5	2.0	99.0	ECCYCNCGKPGHLAR	1848.8	1849.8	1848.8	1849.8
353.0	3.2	3.2	43.5	1.2	94.0	CGESGHLAKDCLQEDACYNCGR	2697.0	2698.0	2697.0	2698.0
179.0	2.0	2.0	16.5	2.0	99.0	ECCYCNCGKPGHLAR	1848.8	1849.8	1848.8	1849.8
P62701 RS4X_HUMAN	40S ribosomal protein S4, X isoform (Single copy abundant mRNA protein) (SCR10) - Homo sapiens (Human)									
93.0	8.1	8.1	28.1	2.0	99.0	ECLPIIFLR	1272.7	1273.7	1272.7	1273.7
93.0	8.1	8.1	28.1	2.0	99.0	FDTGNLNCMTGGANLGR	1781.8	1782.8	1781.8	1782.8
93.0	8.1	8.1	28.1	2.0	99.0	GIPHLVTHDAR	1214.7	1215.7	1214.7	1215.7
93.0	8.1	8.1	28.1	2.0	99.0	GKPKWISLPR	1166.7	1167.7	1166.7	1167.7
93.0	8.1	8.1	28.1	0.0	99.0	GIPHLVTHDAR	1214.7	1215.7	1214.7	1215.7
195.0	6.0	6.0	21.7	2.0	99.0	ECLPIIFLR	1272.7	1273.7	1272.7	1273.7
195.0	6.0	6.0	21.7	2.0	99.0	GIPHLVTHDAR	1214.7	1215.7	1214.7	1215.7
195.0	6.0	6.0	21.7	2.0	99.0	GKPKWISLPR	1166.7	1167.7	1166.7	1167.7
P62753 RS6_HUMAN	40S ribosomal protein S6 (Phosphoprotein NP33) - Homo sapiens (Human)									
192.0	6.0	6.0	27.3	2.0	99.0	ISGGNDKQGFPMKQGVLTGHR	2226.1	2227.1	2226.1	2227.1
192.0	6.0	6.0	27.3	2.0	99.0	MATEVAADALGEEWKGYYVVR	2194.1	2195.1	2194.1	2195.1
192.0	6.0	6.0	27.3	2.0	99.0	MKLNISFPATGCCQ	1593.8	1594.8	1593.8	1594.8
140.0	2.1	2.1	37.8	2.0	99.0	MATEVAADALGEEWKGYYVVR	2194.1	2195.1	2194.1	2195.1
140.0	2.1	2.1	37.8	0.1	25.0	MKLNISFPATGCCQ	1593.8	1594.8	1593.8	1594.8
291.0	2.0	2.0	24.9	2.0	99.0	MATEVAADALGEEWKGYYVVR	2194.1	2195.1	2194.1	2195.1
P62805 H4_HUMAN	Histone H4 - Homo sapiens (Human)									
64.0	15.6	15.6	82.5	2.0	99.0	DNIQGITKPAIR	1324.7	1325.8	1324.7	1325.8
64.0	15.6	15.6	82.5	2.0	99.0	DNIQGITKPAIRR	1480.8	1481.9	1480.8	1481.9
64.0	15.6	15.6	82.5	2.0	99.0	ISGLIYEETR	1179.6	1180.6	1179.6	1180.6
64.0	15.6	15.6	82.5	2.0	99.0	ISGLIYEETRGLVK	1576.9	1577.9	1576.9	1577.9
64.0	15.6	15.6	82.5	2.0	99.0	KVLRDNIQGITKPAIRR	2005.2	2006.2	2005.2	2006.2
64.0	15.6	15.6	82.5	2.0	99.0	TVTAMDVVYALKR	1465.8	1466.8	1465.8	1466.8
64.0	15.6	15.6	82.5	2.0	99.0	VFLENVIR	988.6	989.6	988.6	989.6
64.0	15.6	15.6	82.5	1.3	95.0	TLYGFGG	713.3	714.3	713.3	714.3
64.0	15.6	15.6	82.5	0.2	37.0	DAVYTEHAQR	1289.6	1290.6	1289.6	1290.6
64.0	15.6	15.6	82.5	0.1	28.0	RISGLIYEETR	1335.7	1336.7	1335.7	1336.7
64.0	15.6	15.6	82.5	0.0	80.0	DNIQGITKPAIRR	1480.9	1481.9	1480.9	1481.9
46.0	6.6	6.6	70.9	2.0	99.0	ISGLIYEETR	1179.6	1180.6	1179.6	1180.6
46.0	6.6	6.6	70.9	2.0	99.0	VFLENVIR	988.6	989.6	988.6	989.6
46.0	6.6	6.6	70.9	1.7	98.0	TVTAMDVVYALKR	1465.8	1466.8	1465.8	1466.8
46.0	6.6	6.6	70.9	0.6	73.0	KVLRDNIQGITKPAIRR	2005.2	2006.2	2005.2	2006.2
46.0	6.6	6.6	70.9	0.2	39.0	RISGLIYEETR	1335.7	1336.7	1335.7	1336.7
46.0	6.6	6.6	70.9	0.1	20.0	DNIQGITKPAIR	1324.8	1325.8	1324.7	1325.8
31.0	20.7	20.7	88.3	2.0	99.0	DNIQGITKPAIR	1324.7	1325.8	1324.7	1325.8
31.0	20.7	20.7	88.3	2.0	99.0	DNIQGITKPAIRR	1480.8	1481.9	1480.8	1481.9
31.0	20.7	20.7	88.3	2.0	99.0	ISGLIYEETR	1179.6	1180.6	1179.6	1180.6
31.0	20.7	20.7	88.3	2.0	99.0	KVLRDNIQGITKPAIR	1849.1	1850.1	1849.1	1850.1
31.0	20.7	20.7	88.3	2.0	99.0	KVLRDNIQGITKPAIRR	2005.2	2006.2	2005.2	2006.2
31.0	20.7	20.7	88.3	2.0	99.0	RISGLIYEETR	1335.7	1336.7	1335.7	1336.7
31.0	20.7	20.7	88.3	2.0	99.0	TLYGFGG	713.3	714.3	713.3	714.3
31.0	20.7	20.7	88.3	2.0	99.0	TVTAMDVVYALKR	1465.8	1466.8	1465.8	1466.8
31.0	20.7	20.7	88.3	2.0	99.0	VFLENVIR	988.6	989.6	988.6	989.6
31.0	20.7	20.7	88.3	1.5	97.0	DAVYTEHAQ	1133.5	1134.5	1133.5	1134.5
31.0	20.7	20.7	88.3	1.1	92.0	TVTAMDVVYALK	1309.7	1310.7	1309.7	1310.7
31.0	20.7	20.7	88.3	0.0	98.0	DNIQGITKPAIR	1324.8	1325.8	1324.7	1325.8
31.0	20.7	20.7	88.3	0.0	87.0	DNIQGITKPAIRR	1480.8	1481.9	1480.8	1481.9
P62826 RAN_HUMAN	GTP-binding nuclear protein Ran (GTPase Ran) - Bos taurus (Bovine) ; GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) (And)									
397.0	2.3	2.3	28.7	1.3	95.0	VCEMIPVLGKGVVDIKDRK	2369.3	2370.3	2370.3	2370.3
397.0	2.3	2.3	28.7	0.7	78.0	AAQGEFQVQFK	1243.6	1244.6	1243.6	1244.6
397.0	2.3	2.3	28.7	0.3	54.0	SIVFHR	757.4	758.4	757.4	758.4
90.0	4.0	4.0	22.2	2.0	99.0	GPIKFNWDTAGQEK	1688.9	1689.9	1688.9	1689.9
90.0	4.0	4.0	22.2	2.0	99.0	SNYNFEKFLWLAR	1783.9	1784.9	1783.9	1784.9
147.0	5.0	5.0	20.4	2.0	99.0	KKNLQYDISAK	1470.8	1471.8	1470.8	1471.8
147.0	5.0	5.0	20.4	1.7	98.0	SNYNFEKFLWLAR	1783.9	1784.9	1783.9	1784.9
147.0	5.0	5.0	20.4	1.2	94.0	NVPNWRH	921.5	922.5	921.5	922.5
147.0	5.0	5.0	20.4	0.1	24.1	AAQGEFQVQFK	1243.6	1244.6	1243.6	1244.6
P62854 RS26_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human)									
178.0	2.0	2.0	29.6	2.0	99.0	DISEASVFDAVYLPK	1652.8	1653.8	1652.8	1653.8
222.0	5.7	5.7	51.3	2.0	99.0	DISEASVFDAVYLPK	1652.8	1653.8	1652.8	1653.8
222.0	5.7	5.7	51.3	2.0	99.0	LHYVSVCAIHSK	1473.7	1474.7	1473.7	1474.7
222.0	5.7	5.7	51.3	1.7	98.0	NIVEAAMR	941.5	942.5	941.5	942.5
282.0	2.0	2.0	30.4	2.0	99.0	FRPAGAAPRPPPKPM	1589.9	1590.9	1589.9	1590.9
P62873 GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human)									
534.0	2.0	2.0	3.8	2.0	99.0	ELAGHTGYLSCCR	1522.7	1523.7	1522.7	1523.7
363.0	2.0	2.0	3.8	2.0	99.0	ELAGHTGYLSCCR	1522.7	1523.7	1522.7	1523.7
P62937 PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human)									
27.0	24.9	24.9	81.8	2.0	99.0	ALSTGEKGFQYK	1256.6	1257.6	1256.6	1257.6
24.9	24.9	24.9	81.8	2.0	99.0	ALSTGEKGFQYKSCFHR	2000.9	2002.0	2001.0	2002.0
27.0	24.9	24.9	81.8	2.0	99.0	EGMNI VEAMER	1277.6	1278.6	1277.6	1278.6
27.0	24.9	24.9	81.8	2.0	99.0	FEDENFILK	1153.6	1154.6	1153.6	1154.6
27.0	24.9	24.9	81.8	2.0	99.0	FGYKGSFCFHR	1314.6	1315.6	1314.6	1315.6
27.0	24.9	24.9	81.8	2.0	99.0	HTGPGHLSMANAGPNTNGSOFFICTAK	2791.3	2792.3	2791.3	2792.3
27.0	24.9	24.9	81.8	2.0	99.0	IIPGFMCCGGDFTR	1597.7	1598.7	1597.7	1598.7
27.0	24.9	24.9	81.8	2.0	99.0	IIPGFMCCGGDFTRHNGTGK	2250.0	2251.0	2250.0	2251.0
27.0	24.9	24.9	81.8	2.0	99.0	SIYGEKFEDENFILK	1830.9	1831.9	1830.9	1831.9
27.0	24.9	24.9	81.8	2.0	99.0	VKEGMNI VEAMER	1504.7	1505.7	1504.7	1505.7
27.0	24.9	24.9	81.8	2.0	99.0	VNPTVFDDIADVGEPLGR	1945.0	1946.0	1945.0	1946.0
27.0	24.9	24.9	81.8	2.0	99.0	VSFELFADKVPK	1378.7	1379.7	1378.7	1379.7
27.0	24.9	24.9	81.8	0.9	87.0	KITIIDCGQLE	1246.6	1247.6	1246.6	1247.6
27.0	24.9	24.9	81.8	0.0	99.0	FGYKGSFCFHR	1314.6	1315.6	1314.6	1315.6
27.0	24.9	24.9	81.8	0.0	83.0	FGYKGSFCFHR	1466.6	1467.6	1466.6	1467.6
27.0	24.9	24.9	81.8	0.0	99.0					

154.0	2.0	31.4	66.4	0.0	98.0	GYSFTTAAEREIVR	1628.8	1629.8	1628.8	1629.8
154.0	2.0	31.4	66.4	0.0	99.0	HQGMVMGMGQK	1170.6	1171.6	1170.6	1171.6
154.0	2.0	31.4	66.4	0.0	94.0	HQGMVMGMGQK	1171.6	1172.6	1170.6	1171.6
154.0	2.0	31.4	66.4	0.0	22.0	HQGMVMGMGQK	1186.6	1187.6	1186.6	1187.6
154.0	2.0	31.4	66.4	0.0	99.0	HQGMVMGMGQKDSYVGDEAOSK	2350.1	2351.1	2350.1	2351.1
154.0	2.0	31.4	66.4	0.0	99.0	HQGMVMGMGQKDSYVGDEAOSKR	2506.2	2507.2	2506.2	2507.2
154.0	2.0	31.4	66.4	0.0	96.0	HQGMVMGMGQKDSYVGDEAOSKR	2506.2	2507.2	2506.2	2507.2
154.0	2.0	31.4	66.4	0.0	89.0	IKIAPPER	1035.7	1036.7	1035.6	1036.7
154.0	2.0	31.4	66.4	0.0	99.0	IWHHTFYNELR	1514.7	1515.7	1514.7	1515.7
154.0	2.0	31.4	66.4	0.0	99.0	IWHHTFYNELR	1515.8	1516.8	1515.7	1516.7
154.0	2.0	31.4	66.4	0.0	98.0	IWHHTFYNELR	1546.7	1547.7	1546.7	1547.7
154.0	2.0	31.4	66.4	0.0	99.0	LCYVALDFEQEMATAASSSSLEK	2549.0	2550.0	2549.1	2550.1
154.0	2.0	31.4	66.4	0.0	36.0	QEYDESGPSIVHR	1496.7	1497.7	1496.7	1497.7
154.0	2.0	31.4	66.4	0.0	99.0	QEYDESGPSIVHRK	1643.8	1644.8	1643.8	1644.8
154.0	2.0	31.4	66.4	0.0	74.0	QEYDESGPSIVHRK	1626.8	1627.8	1626.8	1627.8
154.0	2.0	31.4	66.4	0.0	99.0	SYELPDGGVITIGNER	1789.9	1790.9	1789.9	1790.9
154.0	2.0	31.4	66.4	0.0	99.0	VAPEEHPVLLTEAPLNPK	1953.1	1954.1	1953.1	1954.1
154.0	2.0	31.4	66.4	0.0	64.0	VAPEEHPVLLTEAPLNPKANR	2294.2	2295.2	2294.2	2295.2
154.0	2.0	31.4	66.4	0.0	99.0	VAPEEHPVLLTEAPLNPKANREK	2551.4	2552.4	2551.4	2552.4
154.0	2.0	31.4	66.4	0.0	99.0	YPIEHGIVTNWDDMEK	1959.9	1960.9	1959.9	1960.9
5.0	50.7	50.7	69.1	2.0	99.0	AGFAGDDAPR	975.4	976.5	975.4	976.4
5.0	50.7	50.7	69.1	2.0	99.0	AVFPSIVGRPR	1197.7	1198.7	1197.7	1198.7
5.0	50.7	50.7	69.1	2.0	99.0	CYVALDFEQEMATAASSSSLEK	2549.0	2550.0	2549.0	2550.0
5.0	50.7	50.7	69.1	2.0	99.0	DLYANTVLSGGTMYPGIADR	2214.1	2215.1	2214.1	2215.1
5.0	50.7	50.7	69.1	2.0	99.0	EEEEAALVIDNGSGMCK	1877.8	1878.8	1877.8	1878.8
5.0	50.7	50.7	69.1	2.0	99.0	GILTLKYPHEGIVTNWDDMEK	2585.3	2586.3	2585.3	2586.3
5.0	50.7	50.7	69.1	2.0	99.0	GYSFTTAAER	1131.5	1132.5	1131.5	1132.5
5.0	50.7	50.7	69.1	2.0	99.0	GYSFTTAAEREIVR	1628.8	1629.8	1628.8	1629.8
5.0	50.7	50.7	69.1	2.0	99.0	GYSFTTAAEREIVRDIKEK	2242.2	2243.2	2242.2	2243.2
5.0	50.7	50.7	69.1	2.0	99.0	HQGMVMGMGQK	1170.6	1171.6	1170.6	1171.6
5.0	50.7	50.7	69.1	2.0	99.0	HQGMVMGMGQKDSYVGDEAOSK	2350.1	2351.1	2350.1	2351.1
5.0	50.7	50.7	69.1	2.0	98.0	HQGMVMGMGQKDSYVGDEAOSKR	2506.2	2507.2	2506.2	2507.2
5.0	50.7	50.7	69.1	2.0	99.0	IKIAPPER	1035.7	1036.7	1035.6	1036.7
5.0	50.7	50.7	69.1	2.0	99.0	IKIAPPERK	1163.7	1164.8	1163.7	1164.7
5.0	50.7	50.7	69.1	2.0	99.0	IWHHTFYNELR	1515.7	1516.7	1515.7	1516.7
5.0	50.7	50.7	69.1	2.0	99.0	KDLYANTVLSGGTMYPGIADR	2342.2	2343.2	2342.2	2343.2
5.0	50.7	50.7	69.1	2.0	99.0	MQKEITALPSTMK	1547.8	1548.8	1547.8	1548.8
5.0	50.7	50.7	69.1	2.0	99.0	QEYDESGPSIVHR	1515.7	1516.7	1515.7	1516.7
5.0	50.7	50.7	69.1	2.0	99.0	QEYDESGPSIVHRK	1626.8	1627.8	1626.8	1627.8
5.0	50.7	50.7	69.1	2.0	99.0	SYELPDGGVITIGNER	1789.9	1790.9	1789.9	1790.9
5.0	50.7	50.7	69.1	2.0	99.0	VAPEEHPVLLTEAPLNPK	1953.1	1954.1	1953.1	1954.1
5.0	50.7	50.7	69.1	2.0	99.0	VAPEEHPVLLTEAPLNPKANR	2294.2	2295.2	2294.2	2295.2
5.0	50.7	50.7	69.1	2.0	99.0	YPIEHGIVTNWDDMEK	1975.9	1976.9	1975.9	1976.9
5.0	50.7	50.7	69.1	1.5	97.0	LDLAGRDLTIDYLMK	1622.8	1623.8	1622.8	1623.8
5.0	50.7	50.7	69.1	1.3	95.0	IIAPPERK	922.6	923.6	922.6	923.6
5.0	50.7	50.7	69.1	0.7	81.0	RGILTLK	799.5	800.5	799.5	800.5
5.0	50.7	50.7	69.1	0.6	72.0	VAPEEHPVLLTEAPLNPKANREK	2551.4	2552.4	2551.4	2552.4
5.0	50.7	50.7	69.1	0.5	65.0	FRCPEALFQPS	1350.6	1351.7	1350.6	1351.6
5.0	50.7	50.7	69.1	0.2	30.0	DSYVGDEAOSKR	1353.6	1354.6	1353.6	1354.6
5.0	50.7	50.7	69.1	0.0	99.0	EEEEAALVIDNGSGMCK	1876.9	1877.9	1876.9	1877.9
5.0	50.7	50.7	69.1	0.0	94.0	EEEEAALVIDNGSGMCK	1875.8	1876.8	1875.8	1876.8
5.0	50.7	50.7	69.1	0.0	27.0	EEEEAALVIDNGSGMCK	1893.9	1894.9	1893.8	1894.8
5.0	50.7	50.7	69.1	0.0	99.0	HQGMVMGMGQK	1173.6	1174.6	1173.6	1174.6
5.0	50.7	50.7	69.1	0.0	99.0	HQGMVMGMGQK	1186.6	1187.6	1186.6	1187.6
5.0	50.7	50.7	69.1	0.0	99.0	HQGMVMGMGQK	1182.6	1183.6	1182.6	1183.6
5.0	50.7	50.7	69.1	0.0	99.0	HQGMVMGMGQKDSYVGDEAOSKR	2522.2	2523.2	2522.2	2523.2
5.0	50.7	50.7	69.1	0.0	99.0	HQGMVMGMGQKDSYVGDEAOSKR	2518.2	2519.2	2518.2	2519.2
5.0	50.7	50.7	69.1	0.0	96.0	HQGMVMGMGQKDSYVGDEAOSKR	2522.2	2523.2	2522.2	2523.2
5.0	50.7	50.7	69.1	0.0	99.0	IKIAPPER	1035.7	1036.7	1035.6	1036.7
5.0	50.7	50.7	69.1	0.0	95.0	IKIAPPERK	1163.7	1164.8	1163.7	1164.7
5.0	50.7	50.7	69.1	0.0	99.0	IWHHTFYNELR	1517.7	1518.7	1517.7	1518.7
5.0	50.7	50.7	69.1	0.0	99.0	IWHHTFYNELR	1546.7	1547.7	1546.7	1547.7
5.0	50.7	50.7	69.1	0.0	99.0	IWHHTFYNELR	1530.7	1531.7	1530.7	1531.7
5.0	50.7	50.7	69.1	0.0	99.0	IWHHTFYNELR	1514.7	1515.7	1514.7	1515.7
5.0	50.7	50.7	69.1	0.0	99.0	IWHHTFYNELR	1512.8	1513.8	1512.8	1513.8
5.0	50.7	50.7	69.1	0.0	97.0	IWHHTFYNELR	1515.7	1516.7	1515.7	1516.7
5.0	50.7	50.7	69.1	0.0	99.0	QEYDESGPSIVHR	1498.7	1499.7	1498.7	1499.7
5.0	50.7	50.7	69.1	0.0	97.0	QEYDESGPSIVHR	1498.7	1499.7	1498.7	1499.7
5.0	50.7	50.7	69.1	0.0	99.0	QEYDESGPSIVHRK	1643.8	1644.8	1643.8	1644.8
5.0	50.7	50.7	69.1	0.0	99.0	QEYDESGPSIVHRK	1643.8	1644.8	1643.8	1644.8
5.0	50.7	50.7	69.1	0.0	99.0	QEYDESGPSIVHRK	1626.8	1627.8	1626.8	1627.8
5.0	50.7	50.7	69.1	0.0	94.0	QEYDESGPSIVHRK	1642.8	1643.8	1642.8	1643.8
5.0	50.7	50.7	69.1	0.0	67.0	QEYDESGPSIVHRK	1644.8	1645.8	1644.8	1645.8
5.0	50.7	50.7	69.1	0.0	99.0	SYELPDGGVITIGNER	1789.9	1790.9	1789.9	1790.9
5.0	50.7	50.7	69.1	0.0	99.0	SYELPDGGVITIGNER	1789.9	1790.9	1789.9	1790.9
5.0	50.7	50.7	69.1	0.0	99.0	SYELPDGGVITIGNER	1802.9	1803.9	1802.9	1803.9
5.0	50.7	50.7	69.1	0.0	99.0	SYELPDGGVITIGNER	1791.9	1792.9	1791.9	1792.9
5.0	50.7	50.7	69.1	0.0	99.0	YPIEHGIVTNWDDMEK	1959.9	1960.9	1959.9	1960.9
P63279 UBC9_HUMAN						SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (SUMO-protein ligase) (Ubiquitin-conjugating enzyme E2 I) (Ubiquitin ca				
491.0	2.0	2.0	15.8	2.0	99.0	GTPWEGGLFK	1090.5	1091.6	1090.5	1091.6
173.0	2.0	2.0	15.8	2.0	99.0	GTPWEGGLFK	1090.5	1091.6	1090.5	1091.6
P67936 TPM4_HUMAN						Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p1) - Homo sapiens (Human)				
39.0	21.0	21.0	45.6	2.0	99.0	AMKDEKMEIQEMQLK	1979.9	1979.9	1979.9	1980.9
39.0	21.0	21.0	45.6	2.0	99.0	HIAEADRKYEEVAR	1814.9	1815.9	1814.9	1815.9
39.0	21.0	21.0	45.6	2.0	99.0	IOALQQQADEAEDR	1613.8	1614.8	1613.8	1614.8
39.0	21.0	21.0	45.6	2.0	99.0	IOALQQQADEAEDRAOGLR	2267.1	2268.1	2267.1	2268.1
39.0	21.0	21.0	45.6	2.0	99.0	IQLVEELDR	1242.6	1243.6	1242.6	1243.6
39.0	21.0	21.0	45.6	2.0	99.0	IQLVEEELDR	1726.9	1727.9	1726.9	1727.9
39.0	21.0	21.0	45.6	2.0	99.0	KIQALQQQADEAEDR	1741.9	1742.9	1741.9	1742.9
39.0	21.0	21.0	45.6	2.0	99.0	KIQALQQQADEAEDRAOGLR	2395.2	2396.2	2395.2	2396.2
39.0	21.0	21.0	45.6	2.0	99.0	LATALQKLEEAEDAESER	2201.1	2202.1	2201.1	2202.1
39.0	21.0	21.0	45.6	2.0	99.0	RIQLVEEELDR	1883.0	1884.0	1883.0	1884.0
39.0	21.0	21.0	45.6	1.0	89.0	LEEAEKAADESER	1475.7	1476.7	1475.7	1476.7
39.0	21.0	21.0	45.6	0.0	99.0	HIAEADRKYEEVAR	1826.9	1827.9	1826.9	1827.9
39.0	21.0	21.0	45.6	0.0	74.0	HIAEADRKYEEVAR	1814.9	1815.9	1814.9	1815.9
39.0	21.0	21.0	45.6	0.0	95.0	IOALQQQADEAEDR	1641.8	1642.8	1641.8	1642.8
39.0	21.0	21.0	45.6	0.0	99.0	KIQALQQQADEAEDR	1769.9	1770.9	1769.9	1770.9
39.0	21.0	21.0	45.6	0.0	99.0	KIQALQQQADEAEDR	1769.9	1770.9	1769.9	1770.9
78.0	4.5	4.5	44.4	2.0	99.0	IQLVEEELDR	1726.9	1727.9	1726.9	1727.9
78.0	4.5	4.5	44.4	2.0	99.0	KIQALQQQADEAEDR	1769.9	1770.9	1769.9	1770.9
78.0	4.5	4.5	44.4	0.5	67.0	LATALQKLEEAEDAESER	2201.1	2202.1	2201.1	2202.1
57.0	13.2	13.2	49.6	2.0	99.0	IQLVEEELDR	1726.9	1727.9	1726.9	1727.9
57.0	13.2	13.2	49.6	2.0	99.0	KIQALQQQADEAEDR	1741.9	1742.9	1741.9	1742.9
57.0	13.2	13.2	49.6	2.0	99.0	KIQALQQQADEAEDRAOGLR	2395.2	2396.2	2395.2	2396.2
57.0	13.2	13.2	49.6	2.0	99.0	LATALQKLEEAEDAESER	2201.1	2202.1	2201.1	2202.1
57.0	13.2	13.2	49.6	2.0	99.0	RIQLVEEELDR	1883.0	1884.0	1883.0	1884.0
57.0	13.2	13.2	49.6	1.1	92.0	RIQLVEEELDR	1398.7	1399.7	1398.7	1399.7
57.0	13.2	13.2	49.6	0.8	83.0	LEEAEKAADESER	1475.7	1476.7	1475.7	1476.7
57.0	13.2	13.2	49.6	0.8	83.0					

90.0	8.2	8.2	22.1	2.0	99.0	YYVTIDAPGHRDFIK	1907.0	1908.0	1907.0	1908.0
90.0	8.2	8.2	22.1	0.2	42.0	STTTGHLIVK	1119.6	1120.6	1119.6	1120.6
90.0	8.2	8.2	22.1	0.0	97.0	QTVAVGVIK	896.5	897.5	896.5	897.5
P68363 TBAK_HUMAN Tubulin alpha-ubiquitous chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) - Homo sapiens (Human)										
33.0	23.4	23.4	38.6	2.0	99.0	AVCMLSNTTAAIAEAWAR	1863.9	1864.9	1863.9	1864.9
33.0	23.4	23.4	38.6	2.0	99.0	AVFVDEPTVIDEVR	1702.9	1703.9	1702.9	1703.9
33.0	23.4	23.4	38.6	2.0	99.0	LDHKFDLMYAKR	1535.8	1536.8	1535.8	1536.8
33.0	23.4	23.4	38.6	2.0	99.0	QLFHPEQLITGK	1392.7	1393.8	1392.7	1393.7
33.0	23.4	23.4	38.6	2.0	99.0	QLFHPEQLITGKEDAANNYAR	2414.2	2415.2	2414.2	2415.2
33.0	23.4	23.4	38.6	2.0	99.0	TIGGGDDSFNTFFSETGAGK	2006.9	2007.9	2006.9	2007.9
33.0	23.4	23.4	38.6	2.0	99.0	TIGGGDDSFNTFFSETGAGKHVPR	2496.2	2497.2	2496.2	2497.1
33.0	23.4	23.4	38.6	2.0	99.0	VGINYOPTVVPVGGDLAK	1824.0	1825.0	1824.0	1825.0
33.0	23.4	23.4	38.6	2.0	99.0	YMACLLYR	1248.5	1249.5	1248.5	1249.5
33.0	23.4	23.4	38.6	2.0	99.0	YMACCLLYRQDVVVK	1843.9	1844.9	1843.9	1844.9
33.0	23.4	23.4	38.6	1.4	96.0	RSIOFVDWCPTGFK	1739.9	1740.9	1739.9	1740.9
33.0	23.4	23.4	38.6	1.3	95.0	AFVHWVVGEGMEGEFSEAR	2329.0	2330.0	2329.0	2330.0
33.0	23.4	23.4	38.6	0.7	78.0	EIIDLVLDR	1084.6	1085.6	1084.6	1085.6
33.0	23.4	23.4	38.6	0.0	98.0	QLFHPEQLITGK	1409.8	1410.8	1409.8	1410.8
33.0	23.4	23.4	38.6	0.0	94.0	QLFHPEQLITGKEDAANNYAR	2397.2	2398.2	2397.2	2398.2
49.0	15.5	15.5	29.9	2.0	99.0	AFVHWVVGEGMEGEFSEAR	2329.0	2330.0	2329.0	2330.0
49.0	15.5	15.5	29.9	2.0	99.0	AVCMLSNTTAAIAEAWAR	1863.9	1864.9	1863.9	1864.9
49.0	15.5	15.5	29.9	2.0	99.0	AVFVDEPTVIDEVR	1700.9	1701.9	1700.9	1701.9
49.0	15.5	15.5	29.9	2.0	99.0	LDHKFDLMYAKR	1535.8	1536.8	1535.8	1536.8
49.0	15.5	15.5	29.9	2.0	99.0	QLFHPEQLITGK	1392.7	1393.7	1392.7	1393.7
49.0	15.5	15.5	29.9	2.0	99.0	QLFHPEQLITGKEDAANNYAR	2397.2	2398.2	2397.2	2398.2
49.0	15.5	15.5	29.9	2.0	99.0	YMACLLYR	1248.5	1249.5	1248.5	1249.5
49.0	15.5	15.5	29.9	1.5	97.0	YMACCLLYRQDVVVK	1843.9	1844.9	1843.9	1844.9
49.0	15.5	15.5	29.9	0.0	99.0	QLFHPEQLITGKEDAANNYAR	2414.2	2415.2	2414.2	2415.2
P68431 H31_HUMAN Histone H3.1 (H3/a) (H3/b) (H3/c) (H3/d) (H3/f) (H3/g) (H3/h) (H3/i) (H3/j) (H3/k) (H3/l) - Homo sapiens (Human)										
154.0	7.9	7.9	41.2	2.0	99.0	EIAQDFKTDLR	1334.6	1335.6	1334.7	1335.7
154.0	7.9	7.9	41.2	2.0	99.0	KSAPATGGVKKPHR	1489.9	1489.9	1489.9	1489.9
154.0	7.9	7.9	41.2	2.0	99.0	STELLIR	830.5	831.5	830.5	831.5
154.0	7.9	7.9	41.2	1.5	97.0	YRPGTVALR	1031.6	1032.6	1031.6	1032.6
154.0	7.9	7.9	41.2	0.3	54.0	KQLATKAAR	1027.6	1028.6	1027.7	1028.7
154.0	7.9	7.9	41.2	0.0	99.0	EIAQDFKTDLR	1348.7	1349.7	1348.7	1349.7
154.0	7.9	7.9	41.2	0.0	99.0	KSAPATGGVKKPHR	1474.9	1475.9	1474.8	1475.8
112.0	6.9	6.9	37.5	2.0	99.0	EIAQDFKTDLR	1334.7	1335.7	1334.7	1335.7
112.0	6.9	6.9	37.5	2.0	99.0	KSAPATGGVKKPHR	1488.9	1489.9	1488.9	1489.9
112.0	6.9	6.9	37.5	2.0	99.0	YRPGTVALR	1031.6	1032.6	1031.6	1032.6
112.0	6.9	6.9	37.5	0.7	80.0	KLPFQR	787.5	788.5	787.5	788.5
112.0	6.9	6.9	37.5	0.1	23.0	STELLIR	830.5	831.5	830.5	831.5
112.0	6.9	6.9	37.5	0.0	99.0	EIAQDFKTDLR	1348.7	1349.7	1348.7	1349.7
112.0	6.9	6.9	37.5	0.0	53.0	EIAQDFKTDLR	1362.7	1363.7	1362.7	1363.7
112.0	6.9	6.9	37.5	0.0	41.0	KLPFQR	787.5	788.5	787.5	788.5
139.0	2.1	2.1	19.1	2.0	99.0	EIAQDFKTDLR	1334.6	1335.6	1334.7	1335.7
139.0	2.1	2.1	19.1	0.1	24.0	STELLIR	830.5	831.5	830.5	831.5
P78417 GSTO1_HUMAN Glutathione transferase omega-1 (EC 2.5.1.18) (GSTO 1-1) - Homo sapiens (Human)										
369.0	2.9	2.9	14.5	2.0	99.0	VPSLVGSFIR	1073.6	1074.6	1073.6	1074.6
369.0	2.9	2.9	14.5	0.6	75.0	SLGKGSAPPGPVPEGSIR	1704.9	1705.9	1704.9	1705.9
369.0	2.9	2.9	14.5	0.3	46.0	GSAPPGVPEGSIR	1319.7	1320.7	1319.7	1320.7
188.0	2.0	2.0	3.3	2.0	99.0	NKPEWFFK	1094.6	1095.6	1094.6	1095.6
146.0	5.1	5.1	28.6	2.0	99.0	SLGKGSAPPGPVPEGSIR	1704.9	1705.9	1704.9	1705.9
146.0	5.1	5.1	28.6	2.0	99.0	VPSLVGSFIR	1073.6	1074.6	1073.6	1074.6
146.0	5.1	5.1	28.6	0.7	78.0	NKPEWFFK	1094.6	1095.6	1094.6	1095.6
146.0	5.1	5.1	28.6	0.3	46.0	GIRHEVINNLK	1405.8	1406.8	1405.8	1406.8
146.0	5.1	5.1	28.6	0.1	23.0	GSAPPGVPEGSIR	1319.7	1320.7	1319.7	1320.7
P80295 MT11_HUMAN Metallothionein-11 (MT-11) (Metallothionein-11) - Homo sapiens (Human)										
459.0	2.0	4.0	52.5	2.0	99.0	MDPNCSCAAGVSCCTCAGSCK	2263.8	2264.8	2263.8	2264.8
459.0	2.0	4.0	52.5	0.0	99.0	MDPNCSCAAGVSCCTCAGSCK	2233.8	2234.8	2233.8	2234.8
459.0	2.0	4.0	52.5	0.0	99.0	SCCSCCPVGCAC	1444.5	1445.5	1444.5	1445.5
459.0	2.0	4.0	52.5	0.0	99.0	SCCSCCPVGCAC	1447.5	1448.5	1447.5	1448.5
459.0	2.0	4.0	52.5	0.0	99.0	SCCSCCPVGCAC	1447.5	1448.5	1447.5	1448.5
304.0	2.0	6.0	54.1	2.0	99.0	MDPNCSCAAGVSCCTCAGSCK	2263.8	2264.8	2263.8	2264.8
304.0	2.0	6.0	54.1	0.0	99.0	KSCCSCPVGCAC	1573.6	1574.6	1573.6	1574.6
304.0	2.0	6.0	54.1	0.0	99.0	SCCSCCPVGCAC	1444.5	1445.5	1444.5	1445.5
304.0	2.0	6.0	54.1	0.0	99.0	SCCSCCPVGCAC	1446.5	1447.5	1446.5	1447.5
304.0	2.0	6.0	54.1	0.0	99.0	SCCSCCPVGCAC	1447.5	1448.5	1447.5	1448.5
182.0	2.0	2.0	53.2	2.0	99.0	SCCSCCPVGCAC	1444.5	1445.5	1444.5	1445.5
P84103 SF3S3_HUMAN Splicing factor, arginine/serine-rich 3 - Bos taurus (Bovine) ; Splicing factor, arginine/serine-rich 3 (Pre-mRNA-splicing factor SRP20) - Homo sap										
279.0	4.0	4.0	37.8	2.0	99.0	AFGYGLR	1042.5	1043.5	1042.5	1043.5
279.0	4.0	4.0	37.8	2.0	99.0	NPPGFVFEEDPRDAADAVR	2319.1	2320.1	2319.1	2320.1
313.0	2.0	2.0	46.3	2.0	99.0	AFGYGLR	1042.5	1043.5	1042.5	1043.5
Q00610 CLH1_HUMAN Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)										
408.0	2.3	2.3	3.6	2.0	99.0	FLENPYYDSR	1458.7	1459.7	1458.7	1459.7
408.0	2.3	2.3	3.6	0.2	43.0	LLLPWLEAR	1109.7	1110.7	1109.7	1110.7
234.0	2.5	2.5	3.5	2.0	99.0	IHEGCEEPATHNALAK	1775.8	1776.8	1775.8	1776.8
234.0	2.5	2.5	3.5	0.5	68.0	NMRPSEPLQTR	1384.6	1385.7	1384.7	1385.7
Q00839 HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SFA-A) (p120) (pp120) - Homo sapiens (Human)										
93.0	11.9	11.9	23.1	2.0	99.0	CHGDFQPTQQQQPOOQR	2395.1	2396.1	2395.1	2396.1
93.0	11.9	11.9	23.1	2.0	99.0	GVEFYIEENKYSR	1696.8	1697.8	1696.8	1697.8
93.0	11.9	11.9	23.1	2.0	99.0	KMCLFAGFOR	1256.6	1257.6	1256.6	1257.6
93.0	11.9	11.9	23.1	2.0	99.0	MCLFAGFOR	1128.5	1129.5	1128.5	1129.5
93.0	11.9	11.9	23.1	2.0	99.0	SSGPTSLFVAVPPGAR	1713.9	1714.9	1713.9	1714.9
93.0	11.9	11.9	23.1	1.7	98.0	FIEIAAR	818.5	819.5	818.5	819.5
93.0	11.9	11.9	23.1	0.2	31.0	RGNMPPRGGGGGSGGIGYPYR	2303.1	2304.1	2303.1	2304.1
93.0	11.9	11.9	23.1	0.0	98.0	SSGPTSLFVAVPPGAR	1711.9	1712.9	1711.9	1712.9
140.0	5.7	5.7	20.6	2.0	99.0	FIEIAAR	818.5	819.5	818.5	819.5
140.0	5.7	5.7	20.6	2.0	99.0	MCLFAGFOR	1128.5	1129.5	1128.5	1129.5
140.0	5.7	5.7	20.6	1.7	98.0	GVEFYIEENKYSR	1696.8	1697.8	1696.8	1697.8
Q01082 SPTB2_HUMAN Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1) (Beta-II spectrin) (Fodrin beta chain) - Homo sapiens (Human)										
119.0	9.6	9.6	8.6	2.0	99.0	DLDDDFQVLSR	1381.6	1382.6	1381.6	1382.6
119.0	9.6	9.6	8.6	2.0	99.0	EVDDLEQWIAER	1501.7	1502.7	1501.7	1502.7
119.0	9.6	9.6	8.6	2.0	99.0	FMELEPLNER	1389.7	1390.7	1389.7	1390.7
119.0	9.6	9.6	8.6	1.7	98.0	FYHDAKEIFGR	1381.7	1382.7	1381.7	1382.7
119.0	9.6	9.6	8.6	1.2	94.0	DASVAEAWLLGOEYLSR	2091.0	2092.0	2091.0	2092.0
119.0	9.6	9.6	8.6	0.5	70.0	WVNSHLAR	981.5	982.5	981.5	982.5
119.0	9.6	9.6	8.6	0.1	27.0	LOAAAYAGDKADDIOKR	1761.9	1762.9	1761.9	1762.9
119.0	9.6	9.6	8.6	0.0	37.0	FYHDAKEIFGR	1381.7	1382.7	1381.7	1382.7
255.0	2.2	2.2	7.9	2.0	99.0	DASVAEAWLLGOEYLSR	2091.0	2092.1	2091.0	2092.0
255.0	2.2	2.2	7.9	0.2	35.0	AHERELALR	1262.6	1263.6	1262.6	1263.6
Q01105 SET_HUMAN Protein SET (Phosphatase 2A inhibitor 12PP2A) (-)2-PP2A) (Template-activating factor 1) (TAF-1) (HLA-DR-associated protein 11) (PHAPI1) (Inhibi										
61.0	16.1	16.1	15.2	2.0	99.0	IDFYFDENPYFENK	1839.8	1840.8	1839.8	1840.8
61.0	16.1	16.1	15.2	2.0	99.0	IDFYFDENPYFENKVLSK	2267.1	2268.1	2267.1	2268.1
61.0	16.1	16.1	15.2	2.0	99.0	SCVRIIDFYFDENPYFENK	2303.0	2304.1	2303.0	2304.0
61.0	16.1	16.1	15.2	2.0	99.0	VEVTEFEDIK	1208.6	1209.6	1208.6	1209.6
61.0	16.1	16.1	15.2	2.0	99.0	VEVTEFEDIKSGYR	1670.8	1671.8	1670.8	1671.8
61.0	16.1	16.1	15.2	2.0	99.0	YNKLRPFFOKR	1623.9	1624.9	1623.9	1624.9
61.0	16.1	16.1	15.2	1.5	97.0	LROPFFOKR	1218.7	1219.7	1218.7	1219.7
61.0	16.1	16.1	15.2	1.5	97.0	OPFFOKR	949.5	950.5	949.5	950.5
61.0	16.1	16.1	15.2	1.1	92.0	LROPFFOK	1062.6	1063.6	1062.6	1063.6
61.0	16.1	16.1	15.2	0.0	99.0	VEVTEFEDIK	1208.6	1209.6	1208.6	1209.6
127.0	6.0	6.0	22.8	2.0	99.0	IDFYFDENPYFENK				

121.0	9.6	9.6	16.2	2.0	99.0	SGPKPFSAPKQSPKPSPKR	1993.1	1994.1	1993.1	1994.1
121.0	9.6	9.6	16.2	1.5	97.0	LEAVSHSTDMHR	1381.6	1382.7	1381.6	1382.6
56.0	6.0	6.0	14.5	2.0	99.0	ADMQLVLR	1116.5	1117.5	1116.5	1117.5
56.0	6.0	6.0	14.5	2.0	99.0	SGPKPFSAPKQSPKPSPK	1837.0	1838.0	1837.0	1838.0
56.0	6.0	6.0	14.5	2.0	99.0	SSLFAGINQGESITHALK	1927.0	1928.0	1927.0	1928.0
110.0	7.1	7.1	21.1	2.0	98.0	ADMQLVLR	1116.5	1117.5	1116.5	1117.5
110.0	7.1	7.1	21.1	2.0	98.0	LEAVSHSTDMHR	1381.6	1382.7	1381.6	1382.6
110.0	7.1	7.1	21.1	2.0	99.0	SGPKPFSAPKQSPKPSPK	1837.0	1838.0	1837.0	1838.0
110.0	7.1	7.1	21.1	1.0	91.0	THKNPALKAQSGPVR	1602.9	1603.9	1602.9	1603.9
Q01844 EWS_HUMAN	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) - Homo sapiens (Human)									
268.0	4.1	4.1	25.8	2.0	99.0	AAVEWFDGKDFGSK	1683.8	1684.8	1683.8	1684.8
268.0	4.1	4.1	25.8	2.0	99.0	AGDWQPCNPGGQNFAWR	2233.9	2234.9	2233.9	2234.9
268.0	4.1	4.1	25.8	0.1	25.0	GGRGGDRGGFRGGMRGGFGGRR	2582.2	2583.2	2582.2	2583.2
115.0	2.8	2.8	23.6	2.0	99.0	AAVEWFDGKDFGSK	1683.8	1684.8	1683.8	1684.8
115.0	2.8	2.8	23.6	0.8	85.0	GGRGGMGAGER	1177.6	1178.6	1177.5	1178.5
312.0	2.0	2.0	16.8	2.0	99.0	AGDWQPCNPGGQNFAWR	2233.9	2234.9	2233.9	2234.9
Q02818 NUCB1_HUMAN	Nucleobindin-1 precursor (CALNUC) - Homo sapiens (Human)									
271.0	4.1	4.1	18.2	2.0	99.0	DLAQYDAAHHEEFKR	1828.9	1829.9	1828.8	1829.9
271.0	4.1	4.1	18.2	2.0	99.0	KQQQQQQGKAPAAHPEGQLK	2464.3	2465.3	2464.3	2465.3
271.0	4.1	4.1	18.2	0.1	21.0	AQRLSQTEALGR	1460.7	1461.7	1460.7	1461.7
150.0	4.7	4.7	23.4	2.0	99.0	DLAQYDAAHHEEFKR	1828.9	1829.9	1828.8	1829.9
150.0	4.7	4.7	23.4	2.0	99.0	QFEHLDPNGHTEFEAR	1978.9	1979.9	1978.9	1979.9
150.0	4.7	4.7	23.4	0.4	58.0	DLELLIQTATR	1271.7	1272.7	1271.7	1272.7
150.0	4.7	4.7	23.4	0.1	29.0	YEMLKEHER	1233.6	1234.6	1233.6	1234.6
150.0	4.7	4.7	23.4	0.1	26.0	EMEEERLMR	1357.7	1358.7	1357.7	1358.7
150.0	4.7	4.7	23.4	0.0	97.0	DLAQYDAAHHEEFKR	1828.9	1829.9	1828.8	1829.9
Q02878 RL6_HUMAN	60S ribosomal protein L6 (TAX-responsive enhancer element-binding protein 107) (TAXREB107) (Neoplasm-related protein C140) - Homo sapiens									
355.0	3.2	3.2	21.2	2.0	99.0	AIPOLGYLR	1157.7	1158.7	1157.7	1158.7
355.0	3.2	3.2	21.2	1.2	94.0	YYPTEVYR	1138.5	1139.5	1138.5	1139.5
332.0	2.0	2.0	12.8	2.0	99.0	AIPOLGYLR	1157.7	1158.7	1157.7	1158.7
Q06033 TIH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy chain H3) (Inter-alpha-inhibitor heavy chain 3) (Serum-derived hyaluronan-ase									
116.0	9.7	9.7	7.3	2.0	99.0	DYIFGNVTR	1289.6	1290.6	1289.6	1290.6
116.0	9.7	9.7	7.3	2.0	99.0	FAHNVVTR	1043.6	1044.6	1043.6	1044.6
116.0	9.7	9.7	7.3	2.0	99.0	GHVSFKPSLDQQR	1497.7	1498.7	1497.8	1498.8
116.0	9.7	9.7	7.3	2.0	99.0	KGHVSFKPSLDQQR	1625.9	1626.9	1625.9	1626.9
116.0	9.7	9.7	7.3	1.7	98.0	VTFELTYEELLKR	1639.9	1640.9	1639.9	1640.9
100.0	3.5	3.5	8.6	2.0	99.0	FAHNVVTR	1043.6	1044.6	1043.6	1044.6
100.0	3.5	3.5	8.6	1.5	97.0	DYIFGNVTR	1289.6	1290.6	1289.6	1290.6
92.0	8.1	8.1	13.8	2.0	99.0	DYIFGNVTR	1289.6	1290.6	1289.6	1290.6
92.0	8.1	8.1	13.8	2.0	99.0	FAHNVVTR	1043.6	1044.6	1043.6	1044.6
92.0	8.1	8.1	13.8	2.0	99.0	KGHVSFKPSLDQQR	1625.9	1626.9	1625.9	1626.9
92.0	8.1	8.1	13.8	2.0	99.0	VTFELTYEELLKR	1639.9	1640.9	1639.9	1640.9
Q06323 PSME1_HUMAN	Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease subu									
68.0	14.7	14.7	38.2	2.0	99.0	AAKQPHVGDYR	1240.6	1241.6	1240.6	1241.6
68.0	14.7	14.7	38.2	2.0	99.0	LEGFHTQSK	1153.6	1154.6	1153.6	1154.6
68.0	14.7	14.7	38.2	2.0	99.0	NAYAVLYDIILK	1394.8	1395.8	1394.8	1395.8
68.0	14.7	14.7	38.2	2.0	99.0	QLVHELDEAEYRDIR	1884.9	1885.9	1884.9	1885.9
68.0	14.7	14.7	38.2	2.0	99.0	OPHVGDYR	953.4	954.4	953.4	954.4
68.0	14.7	14.7	38.2	2.0	99.0	YFSERGDAVTK	1271.6	1272.6	1271.6	1272.6
68.0	14.7	14.7	38.2	1.7	98.0	LMVMEIR	890.5	891.5	890.5	891.5
68.0	14.7	14.7	38.2	1.0	91.0	IVVLLOR	839.6	840.6	839.6	840.6
50.0	6.3	6.3	26.9	2.0	99.0	IVVLLOR	839.6	840.6	839.6	840.6
50.0	6.3	6.3	26.9	2.0	99.0	NAYAVLYDIILK	1394.8	1395.8	1394.8	1395.8
50.0	6.3	6.3	26.9	2.0	99.0	QLVHELDEAEYR	1500.7	1501.7	1500.7	1501.7
50.0	6.3	6.3	26.9	0.3	49.0	LMVMEIR	890.5	891.5	890.5	891.5
59.0	12.9	12.9	34.1	2.0	98.0	AAKQPHVGDYR	1240.6	1241.6	1240.6	1241.6
59.0	12.9	12.9	34.1	2.0	98.0	IEDGNFQGVAVQEK	1520.7	1521.7	1520.7	1521.7
59.0	12.9	12.9	34.1	2.0	98.0	IVVLLOR	839.6	840.6	839.6	840.6
59.0	12.9	12.9	34.1	2.0	99.0	QLVHELDEAEYR	1483.7	1484.7	1483.7	1484.7
59.0	12.9	12.9	34.1	2.0	99.0	QLVHELDEAEYRDIR	1867.9	1868.9	1867.9	1868.9
59.0	12.9	12.9	34.1	1.4	96.0	NAYAVLYDIILK	1394.8	1395.8	1394.8	1395.8
59.0	12.9	12.9	34.1	0.9	88.0	LMVMEIR	890.5	891.5	890.5	891.5
59.0	12.9	12.9	34.1	0.4	57.0	YFSERGDAVTK	1271.6	1272.6	1271.6	1272.6
59.0	12.9	12.9	34.1	0.2	41.0	QPHVGDYR	953.4	954.4	953.4	954.4
59.0	12.9	12.9	34.1	0.0	97.0	QLVHELDEAEYR	1500.7	1501.7	1500.7	1501.7
59.0	12.9	12.9	34.1	0.0	93.0	QLVHELDEAEYRDIR	1884.9	1885.9	1884.9	1885.9
Q06830 PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Proliferation-associated gene protein)									
48.0	18.3	18.3	55.3	2.0	99.0	ATAVMPDGGFKDISLSDYK	2085.0	2086.0	2085.0	2086.0
48.0	18.3	18.3	55.3	2.0	99.0	ATAVMPDGGFKDISLSDYKGGK	2270.1	2271.1	2270.1	2271.1
48.0	18.3	18.3	55.3	2.0	99.0	GLFIIDDKGILR	1358.8	1359.8	1358.8	1359.8
48.0	18.3	18.3	55.3	2.0	99.0	IGHPAPNFK	979.5	980.5	979.5	980.5
48.0	18.3	18.3	55.3	2.0	99.0	KOGGLGPMNIPLVSDPKR	1906.0	1907.0	1906.0	1907.0
48.0	18.3	18.3	55.3	2.0	99.0	LVOAFQFTDK	1195.6	1196.6	1195.6	1196.6
48.0	18.3	18.3	55.3	2.0	99.0	QITVNDLPVGR	1210.7	1211.7	1210.7	1211.7
48.0	18.3	18.3	55.3	2.0	99.0	TIAQDYGVLKADGEGISFR	1106.6	1107.6	1106.6	1107.6
48.0	18.3	18.3	55.3	2.0	99.0	TIAQDYGVLKADGEGISFR	1982.0	1983.0	1982.0	1983.0
48.0	18.3	18.3	55.3	0.3	52.0	ATAVMPDGGFK	1163.6	1164.6	1163.6	1164.6
25.0	12.3	12.3	52.8	2.0	99.0	ATAVMPDGGFKDISLSDYK	2085.0	2086.0	2085.0	2086.0
25.0	12.3	12.3	52.8	2.0	99.0	ATAVMPDGGFKDISLSDYKGGK	2270.1	2271.1	2270.1	2271.1
25.0	12.3	12.3	52.8	2.0	99.0	IGHPAPNFK	979.5	980.5	979.5	980.5
25.0	12.3	12.3	52.8	2.0	99.0	KOGGLGPMNIPLVSDPKR	1906.0	1907.0	1906.0	1907.0
25.0	12.3	12.3	52.8	2.0	99.0	LVOAFQFTDK	1195.6	1196.6	1195.6	1196.6
25.0	12.3	12.3	52.8	2.0	99.0	QITVNDLPVGR	1210.7	1211.7	1210.7	1211.7
25.0	12.3	12.3	52.8	0.3	49.0	TIAQDYGVLKADGEGISFR	1982.0	1983.0	1982.0	1983.0
25.0	12.3	12.3	52.8	0.0	99.0	ATAVMPDGGFKDISLSDYK	2084.1	2085.1	2084.1	2085.1
41.0	18.0	18.0	49.7	2.0	99.0	ATAVMPDGGFK	1163.6	1164.6	1163.6	1164.6
41.0	18.0	18.0	49.7	2.0	99.0	ATAVMPDGGFKDISLSDYK	2085.0	2086.0	2085.0	2086.0
41.0	18.0	18.0	49.7	2.0	99.0	ATAVMPDGGFKDISLSDYKGGK	2270.1	2271.1	2270.1	2271.1
41.0	18.0	18.0	49.7	2.0	99.0	GLFIIDDKGILR	1358.8	1359.8	1358.8	1359.8
41.0	18.0	18.0	49.7	2.0	99.0	IGHPAPNFK	979.5	980.5	979.5	980.5
41.0	18.0	18.0	49.7	2.0	99.0	KOGGLGPMNIPLVSDPKR	1906.0	1907.0	1906.0	1907.0
41.0	18.0	18.0	49.7	2.0	99.0	LVOAFQFTDK	1195.6	1196.6	1195.6	1196.6
41.0	18.0	18.0	49.7	2.0	99.0	QITVNDLPVGR	1210.7	1211.7	1210.7	1211.7
41.0	18.0	18.0	49.7	2.0	99.0	TIAQDYGVLKADGEGISFR	1982.0	1983.0	1982.0	1983.0
41.0	18.0	18.0	49.7	0.0	98.0	IGHPAPNFK	979.5	980.5	979.5	980.5
41.0	18.0	18.0	49.7	0.0	99.0	QITVNDLPVGR	1210.7	1211.7	1210.7	1211.7
Q08380 LG3BP_HUMAN	Galactin-3-binding protein precursor (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (Mac-2 BP) (MAC2BP) (Tumor									
436.0	2.0	2.0	9.1	2.0	99.0	GOWGTVCNDLWLDTASVCCR	2451.1	2452.1	2451.1	2452.1
161.0	2.0	2.0	6.3	2.0	99.0	AVDTWSWGER	1205.5	1206.6	1205.5	1206.6
276.0	2.1	2.1	7.5	2.0	99.0	YSSDYFQAPSDYR	1597.7	1598.7	1597.7	1598.7
Q12906 ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Double-stranded RNA-binding protein 76) (DRBP76									
60.0	16.5	16.5	21.9	2.0	99.0	AEPPOAMNLMR	1327.6	1328.6	1327.6	1328.6
60.0	16.5	16.5	21.9	2.0	99.0	CLAALASLR	956.5	957.5	956.5	957.5
60.0	16.5	16.5	21.9	2.0	99.0	HSSVYPTGEELEAVQNMVSHTER	2670.2	2671.2	2670.2	2671.2
60.0	16.5	16.5	21.9	2.0	99.0	LAAFGLHK	983.6	984.6	983.6	984.6
60.0	16.5	16.5	21.9	2.0	99.0	SGGYSYSGGASVNPSSGGYGGSSGSSYQG	3011.2	3012.2	3011.2	3012.2
60.0	16.5	16.5	21.9	2.0	99.0	SIGTANRPMGAGEALRR	1755.9	1756.9	1755.9	1756.9
60.0	16.5	16.5	21.9	2.0	99.0	VLODMGLPTGAEGR	1442.7	1443.7	1442.7	1443.7
60.0	16.5	16.5	21.9	1.7	98.0	NADHSNMVQYR	1397.6	1398.6	1397.6	1398.6
60.0	16.5	16.5	21.9	0.6	73.0	IFVNDDRHVMMAK	1443.7	1444.7	1443.7	1444.7
60.0	16.5	16.5	21.9	0.2	30.0	WFOAR	706.4	707.4	706.4	707.4
249.0	2.2	2.2	8.2	1.5	97.0	LAAFGLHK	983.6	984.6	983.6	984.6
249.0	2.2	2.								

126.0	9.3	9.3	50.7	0.3	51.0	FTTGDMAMSKR	1112.5	1113.5	1112.5	1113.5
212.0	3.2	3.2	37.3	2.0	99.0	LFAFVR	751.4	752.4	751.4	752.4
212.0	3.2	3.2	37.3	0.9	86.0	ATKIDKEACR	1232.6	1233.6	1232.6	1233.6
212.0	3.2	3.2	37.3	0.4	57.0	YDGSSTVPEQGEAQYHQHFIQQCTDDVR	3112.4	3113.4	3112.4	3113.4
Q14103 HNRPD_HUMAN Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human)										
85.0	12.2	12.2	35.2	2.0	99.0	GFVHDCFLKLDPIGTR	1920.0	1919.0	1920.0	1920.0
85.0	12.2	12.2	35.2	2.0	99.0	GFCFITFK	1018.5	1019.5	1018.5	1019.5
85.0	12.2	12.2	35.2	2.0	99.0	GFCFITKEEPEVKK	1857.9	1858.9	1857.9	1858.9
85.0	12.2	12.2	35.2	2.0	99.0	GFGVLFK	913.5	914.5	913.5	914.5
85.0	12.2	12.2	35.2	2.0	99.0	IFVGLSPDTPPEEK	1487.7	1488.8	1487.8	1488.8
85.0	12.2	12.2	35.2	2.0	99.0	SRGFGVLFK	1156.6	1157.6	1156.6	1157.6
85.0	12.2	12.2	35.2	0.1	21.0	IFVGLSPDTPPEEKIR	1756.9	1757.9	1756.9	1757.9
157.0	2.0	4.0	11.0	2.0	99.0	GFCFITKEEPEVKK	1857.9	1858.9	1857.9	1858.9
157.0	2.0	4.0	11.0	0.0	99.0	GFGVLFK	913.5	914.5	913.5	914.5
Q14152 IF3A_HUMAN Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (eIF3 p167) (eIF3 p180) (eIF3 p185) (eIF3a) - Homo sapiens (Human)										
137.0	8.2	8.2	16.1	2.0	99.0	RGADDDRPSWR	1329.6	1330.6	1329.6	1330.6
137.0	8.2	8.2	16.1	2.0	99.0	WGDRDSEGTWR	1363.6	1364.6	1363.6	1364.6
137.0	8.2	8.2	16.1	1.7	98.0	RGLDDDRGPPWR	1341.7	1342.7	1341.7	1342.7
137.0	8.2	8.2	16.1	1.5	97.0	RGMDDDRGRPR	1203.5	1204.5	1203.5	1204.5
137.0	8.2	8.2	16.1	0.8	83.0	EELDREAELOKVR	1769.9	1770.9	1769.9	1770.9
137.0	8.2	8.2	16.1	0.1	25.0	DLRDDRRRGGPPLR	1761.9	1762.9	1761.9	1762.9
137.0	8.2	8.2	16.1	0.0	96.0	WGDRDSEGTWR	1363.6	1364.6	1363.6	1364.6
404.0	1.3	1.3	16.4	1.2	94.0	WGDRDSEGTWR	1363.6	1364.6	1363.6	1364.6
Q14764 MVP_HUMAN Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human)										
122.0	9.5	9.5	13.9	2.0	99.0	ALOPLEGEDEEKVSHOAGDHWLIR	2886.4	2887.4	2886.3	2887.3
122.0	9.5	9.5	13.9	2.0	99.0	VPNAAVOVVDYR	1530.8	1531.8	1530.8	1531.8
122.0	9.5	9.5	13.9	1.3	95.0	ATEEFIR	1019.5	1020.5	1019.5	1020.5
122.0	9.5	9.5	13.9	1.3	95.0	NFRDFR	853.4	854.4	853.4	854.4
122.0	9.5	9.5	13.9	1.3	95.0	RNRDFR	1009.5	1010.5	1009.5	1010.5
122.0	9.5	9.5	13.9	0.7	78.0	SLQPLRR	880.5	880.5	880.5	881.5
122.0	9.5	9.5	13.9	0.6	77.0	DAQGLVLFVDVGTQVGR	1617.9	1618.9	1617.9	1619.9
122.0	9.5	9.5	13.9	0.2	37.0	LFSVPDFVGDACK	1453.7	1454.7	1453.7	1454.7
145.0	5.1	5.1	15.8	2.0	99.0	DAQGLVLFVDVGTQVGR	1617.9	1619.9	1617.9	1619.9
145.0	5.1	5.1	15.8	2.0	99.0	VPNAAVOVVDYR	1530.8	1531.8	1530.8	1531.8
145.0	5.1	5.1	15.8	1.0	90.0	ATEEFIR	1019.5	1020.5	1019.5	1020.5
Q14847 LASP1_HUMAN LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human)										
72.0	14.1	14.1	37.9	2.0	99.0	GFSVADTPELOR	1417.7	1418.7	1417.7	1418.7
72.0	14.1	14.1	37.9	2.0	99.0	GVEKPKPCNAHYPK	1753.8	1754.8	1753.8	1754.8
72.0	14.1	14.1	37.9	2.0	99.0	KPYCNAHYPK	1276.6	1277.6	1276.6	1277.6
72.0	14.1	14.1	37.9	2.0	99.0	LKQSELOSQVR	1442.8	1443.8	1442.8	1443.8
72.0	14.1	14.1	37.9	2.0	99.0	NYGGEKKKPCNAHYPK	2159.0	2160.0	2159.0	2160.0
72.0	14.1	14.1	37.9	2.0	99.0	OSFTVMADTFENLR	1597.8	1598.8	1597.8	1599.8
72.0	14.1	14.1	37.9	2.0	99.0	TQDQISNIKYHEEFEK	2009.0	2009.0	2009.0	2009.0
124.0	6.0	6.0	33.7	2.0	99.0	GKGSFVADTPELOR	1602.8	1603.8	1602.8	1603.8
124.0	6.0	6.0	33.7	2.0	99.0	NYGGEKKKPCNAHYPK	2159.0	2160.0	2159.0	2160.0
124.0	6.0	6.0	33.7	2.0	99.0	TQDQISNIKYHEEFEK	2008.0	2009.0	2008.0	2009.0
Q15233 NONO_HUMAN Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kD)										
78.0	13.4	15.9	33.3	2.0	99.0	FACHASLTVR	1247.6	1248.6	1247.6	1248.6
78.0	13.4	15.9	33.3	2.0	99.0	FAQPGSEFEYAMR	1694.7	1695.7	1694.7	1695.7
78.0	13.4	15.9	33.3	2.0	99.0	HEHQVLMR	1179.6	1180.6	1179.6	1180.6
78.0	13.4	15.9	33.3	2.0	99.0	ROEQEGKGTFFDPAAR	1635.8	1636.8	1635.8	1636.8
78.0	13.4	15.9	33.3	1.3	95.0	FGQAAATMEGIGAIIGTTPAFNR	2162.0	2163.0	2162.0	2163.0
78.0	13.4	15.9	33.3	1.2	99.0	GIVEFSGKPAAR	1230.7	1231.7	1230.7	1231.7
78.0	13.4	15.9	33.3	1.2	99.0	MEELHNOEQVKR	1540.8	1541.8	1540.8	1541.8
78.0	13.4	15.9	33.3	1.1	99.0	RMEELHNOEQVKR	1695.9	1696.9	1695.8	1696.9
78.0	13.4	15.9	33.3	0.5	67.0	EQPPRFAGPGSEFEYAMR	2302.0	2303.0	2302.0	2303.0
78.0	13.4	15.9	33.3	0.1	21.0	ALIEMEKQQDQVDR	1829.9	1830.9	1829.9	1830.9
232.0	2.6	2.6	21.4	1.4	96.0	MEELHNOEQVKR	1539.7	1540.8	1539.7	1540.8
232.0	2.6	2.6	21.4	1.2	93.0	HEHQVLMR	1179.6	1180.6	1179.6	1180.6
Q16181 SEPT7_HUMAN Septin-7 (CDC10 protein homolog) - Homo sapiens (Human)										
406.0	2.3	2.3	9.8	1.3	95.0	RRFDEKANWEAQOR	2090.0	2091.0	2090.0	2091.0
406.0	2.3	2.3	9.8	0.6	74.0	QFDEKANWEAQOR	1777.8	1778.8	1777.8	1778.8
406.0	2.3	2.3	9.8	0.3	48.0	FEDYLNAEAR	1242.6	1243.6	1242.6	1243.6
406.0	2.3	2.3	9.8	0.1	20.0	NLEGVYGFANLPNQVYR	1953.0	1954.0	1953.0	1954.0
206.0	3.5	3.5	10.3	2.0	99.0	QFDEKANWEAQOR	1777.8	1778.8	1777.8	1778.8
206.0	3.5	3.5	10.3	1.5	97.0	NLEGVYGFANLPNQVYR	1953.0	1954.0	1953.0	1954.0
Q16595 DPYL2_HUMAN Dihydropyrimidinase-related protein 2 (DHRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N26A3) - Homo sapiens (Human)										
286.0	2.0	2.0	9.8	2.0	99.0	THNSLSYVIFEGMECR	2085.9	2086.9	2085.9	2086.9
336.0	3.5	3.5	5.9	2.0	99.0	THNSLSYVIFEGMECR	2085.9	2086.9	2085.9	2086.9
336.0	3.5	3.5	5.9	1.5	97.0	VFNLYPR	907.5	908.5	907.5	908.5
Q16658 FSCN1_HUMAN Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human)										
383.0	2.5	2.5	11.2	2.0	99.0	YLAADKGNVTCEER	1610.7	1611.7	1610.7	1611.7
383.0	2.5	2.5	11.2	0.5	66.0	QIWTLEPPDEAGSAAVCLER	2240.1	2241.1	2240.1	2241.1
344.0	2.0	2.0	4.7	2.0	99.0	NASCYFDIEWR	1459.6	1460.6	1459.6	1460.6
Q16881 TRXR1_HUMAN Thioredoxin reductase 1, cytoplasmic precursor (EC 1.8.1.9) (TR) (TR1) - Homo sapiens (Human)										
392.0	2.4	2.4	9.2	2.0	99.0	WGLGGTCVNVGCIPIK	1616.8	1617.8	1616.8	1617.8
392.0	2.4	2.4	9.2	0.4	58.0	VMVLDVFTPTPLGTR	1644.9	1645.9	1644.9	1645.9
343.0	2.0	2.0	4.6	2.0	99.0	VEETVKHDWDR	1412.7	1413.7	1412.7	1413.7
P62633 CNBP_HUMAN Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9) - Homo sapiens (Human)										
353.0	3.2	3.2	43.5	2.0	99.0	EOCCYVCKGPKHLAR	1849.8	1848.8	1849.8	1848.8
353.0	3.2	3.2	43.5	1.2	94.0	CGESGHLAKDCDLDEDACYNCGR	2697.0	2698.0	2697.0	2698.0
179.0	2.0	2.0	16.5	2.0	99.0	EOCCYVCKGPKHLAR	1848.8	1849.8	1848.8	1849.8
P19105 MLRM_HUMAN Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC) - Homo sapiens (Human)										
151.0	8.0	8.0	29.1	2.0	99.0	ELLTMDGRFTDEEVDELYR	2431.1	2432.1	2431.1	2432.1
151.0	8.0	8.0	29.1	2.0	99.0	FTDEEVDELYR	1414.6	1415.6	1414.6	1415.6
151.0	8.0	8.0	29.1	2.0	99.0	GNFNIEFTR	1259.6	1260.6	1259.6	1260.6
151.0	8.0	8.0	29.1	2.0	99.0	NAFACFDEEATGTIQEDYLR	2349.0	2350.0	2349.0	2350.0
146.0	2.1	2.1	17.4	2.0	99.0	GNFNIEFTR	1259.6	1260.6	1259.6	1260.6
128.0	6.0	6.0	33.9	2.0	99.0	ELLTMDGRFTDEEVDELYR	2432.1	2433.1	2432.1	2433.1
128.0	6.0	6.0	33.9	2.0	99.0	GNFNIEFTR	1259.6	1260.6	1259.6	1260.6
128.0	6.0	6.0	33.9	2.0	99.0	NAFACFDEEATGTIQEDYLR	2349.0	2350.0	2349.0	2350.0
Q6F113 H2A2A_HUMAN Histone H2A type 2-A (H2A.2) - Homo sapiens (Human)										
111.0	3.1	3.1	52.3	2.0	99.0	AGLQFVGR	943.5	944.5	943.5	944.5
111.0	3.1	3.1	52.3	1.1	92.0	HQLQAIR	849.5	850.5	849.5	850.5
129.0	6.0	6.0	39.2	2.0	99.0	AGLQFVGR	943.5	944.6	943.5	944.5
129.0	6.0	6.0	39.2	2.0	99.0	HQLQAIR	849.5	850.5	849.5	850.5
129.0	6.0	6.0	39.2	2.0	99.0	NDEELNKLGR	1299.7	1300.7	1299.7	1300.7
Q71D13 H32_HUMAN Histone H3.2 (H3/m) (H3/o) - Homo sapiens (Human)										
154.0	7.9	7.9	41.2	2.0	99.0	EIAQDFKTDLR	1334.6	1335.6	1334.7	1335.7
154.0	7.9	7.9	41.2	2.0	99.0	KSAPATGGVKKPHR	1488.9	1489.9	1488.9	1489.9
154.0	7.9	7.9	41.2	2.0	99.0	STELLIR	830.5	831.5	830.5	831.5
154.0	7.9	7.9	41.2	1.5	97.0	YRPGTVALR	1031.6	1032.6	1031.6	1032.6
154.0	7.9	7.9	41.2	0.3	54.0	KQLATKAAR	1027.6	1028.6	1027.7	1028.7
154.0	7.9	7.9	41.2	0.0	99.0	EIAQDFKTDLR	1348.7	1349.7	1348.7	1349.7
154.0	7.9	7.9	41.2	0.0	99.0	KSAPATGGVKKPHR	1474.9	1475.9	1474.8	1475.8
112.0	6.9	6.9	37.5	2.0	99.0	EIAQDFKTDLR	1334.7	1335.7	1334.7	1335.7
112.0	6.9	6.9	37.5	2.0	99.0	KSAPATGGVKKPHR	1488.9	1489.9	1488.9	1489.9
112.0	6.9	6.9	37.5	2.0	99.0	YRPGTVALR	1031.6	1032.6	1031.6	1032.6
112.0	6.9	6.9	37.5	0.7	80.0	KLPFQR	787.5	788.5	787.5	788.5
112.0	6.9	6.9	37.5	0.1	23.0	STELLIR	830.5	831.5	830.5	831.5
112.0	6.9	6.9	37.5	0.0	99.0	EIAQDFKTDLR	1348.7	1349.7	1348.7	1349.7
112.0	6.9	6.9	37.5	0.0	53.0	EIAQDFKTDLR	1362.7	1363.7	1362.7	1363.7
112.0	6.9	6.9	37.5	0.0	41.0	KLPFQR	787.5	788.5	787.5	788.5
139.0	2.1	2.1	19.1	2.0	99.0	EIAQDFKTDLR	1334.6	1335.6	1334.7	1335.7
139.0	2.1	2.1	19.1	0.1	24.0	STELLIR	830.5	831.5	830.5	831.5
Q864K7 URP2_HUMAN Unc-112-related protein 2 (Kiflin-3) (MIR2-like) - Homo sapiens (Human)										
409.0	2.2									

260.0	2.2	2.2	16.7	0.3	46.0	SPMDTFLLIK	1163.6	1164.6	1163.6	1164.6
Q92598 HS105_HUMAN Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY-CO-25) - Homo sapiens (Human)										
290.0	4.0	4.0	6.9	2.0	99.0	GCALQCALSPAFK	1534.8	1535.8	1534.8	1535.8
290.0	4.0	4.0	6.9	2.0	99.0	NAVEEYVVEFR	1401.6	1402.6	1401.6	1402.6
290.0	4.0	4.0	6.9	0.0	99.0	NAVEEYVVEFR	1417.7	1418.7	1417.7	1418.7
194.0	1.7	1.7	10.7	1.7	99.0	NAVEEYVVEFR	1417.7	1418.7	1417.7	1418.7
194.0	1.7	1.7	10.7	0.0	97.0	NAVEEYVVEFR	1401.6	1402.6	1401.6	1402.6
315.0	2.0	2.0	9.6	2.0	99.0	NAVEEYVVEFR	1417.7	1418.7	1417.7	1418.7
Q96C23 GALM_HUMAN Aldose 1-epimerase (EC 5.1.3.3) (Galactose mutarotase) - Homo sapiens (Human)										
148.0	8.0	8.0	19.3	2.0	99.0	FQLOSDLLR	1118.6	1119.6	1118.6	1119.6
148.0	8.0	8.0	19.3	2.0	99.0	GFDKVLWTPR	1217.7	1218.7	1217.7	1218.7
148.0	8.0	8.0	19.3	2.0	99.0	HSGFCLQTNWPDVAVNQR	2255.0	2256.0	2255.0	2256.0
148.0	8.0	8.0	19.3	2.0	99.0	OPYFGAVIGR	1106.6	1107.6	1106.6	1107.6
274.0	2.1	2.1	14.0	2.0	99.0	HSGFCLQTNWPDVAVNQR	2255.0	2256.0	2255.0	2256.0
Q96CX2 KCDT12_HUMAN BTB/POZ domain-containing protein KCDT12 (Pretin) (Predominantly fetal expressed T1 domain) - Homo sapiens (Human)										
474.0	2.0	2.0	7.4	2.0	99.0	EAEYFELPELVR	1493.7	1494.8	1493.7	1494.7
139.0	5.7	5.7	25.5	2.0	99.0	DLQLVLPDYFPER	1603.8	1604.8	1603.8	1604.8
139.0	5.7	5.7	25.5	2.0	99.0	MFTQQOQQLAR	1475.7	1476.7	1475.7	1476.7
139.0	5.7	5.7	25.5	1.7	99.0	EAEYFELPELVR	1493.7	1494.7	1493.7	1494.7
Q96EP5 DAZP1_HUMAN DAZ-associated protein 1 (Deleted in azoospermia-associated protein 1) - Homo sapiens (Human)										
283.0	4.0	4.0	11.3	2.0	99.0	LFVGLDWSITTOELR	1821.9	1822.9	1821.9	1822.9
283.0	4.0	4.0	11.3	2.0	99.0	SQAPGPGASQWGSR	1512.7	1513.7	1512.7	1513.7
395.0	1.5	1.5	7.6	1.4	96.0	SQAPGPGASQWGSR	1512.7	1513.7	1512.7	1513.7
Q96IU4 ABHEB_HUMAN Abhydrolase domain-containing protein 14B (EC 3.-.-.-) (CCG1-interacting factor B) - Homo sapiens (Human)										
308.0	4.0	4.0	11.4	2.0	99.0	FSSETWQNLGTLHR	1674.8	1675.8	1674.8	1675.8
308.0	4.0	4.0	11.4	2.0	99.0	FSVLLHIGIR	1153.7	1154.7	1153.7	1154.7
236.0	2.5	2.5	11.4	2.0	99.0	FSSETWQNLGTLHR	1674.8	1675.8	1674.8	1675.8
236.0	2.5	2.5	11.4	0.5	66.0	FSVLLHIGIR	1153.7	1154.7	1153.7	1154.7
Q96KP4 CNPD2_HUMAN Cytosolic nonspecific dipeptidase (CNPD dipeptidase 2) (Glutamate carboxypeptidase-like protein 1) - Homo sapiens (Human)										
347.0	3.3	3.3	8.4	2.0	99.0	WVAIQSYVAWPEKR	1655.9	1656.9	1655.9	1656.9
347.0	3.3	3.3	8.4	1.3	95.0	TGQEIPVNVV	1111.6	1112.6	1111.6	1112.6
253.0	2.2	2.2	7.4	2.0	99.0	TVFGVEPDLTR	1232.6	1233.7	1232.6	1233.6
253.0	2.2	2.2	7.4	0.1	26.0	TGQEIPVNVV	1111.6	1112.6	1111.6	1112.6
Q99497 PARK7_HUMAN Protein DJ-1 (Oncogene DJ1) (Parkinson disease protein 7) - Homo sapiens (Human)										
120.0	9.6	9.6	28.6	2.0	99.0	DKMNGGHYYTSENREVK	2159.0	2160.0	2159.0	2159.9
120.0	9.6	9.6	28.6	2.0	99.0	GAEEMETVIVDVMVR	1674.8	1675.8	1674.8	1675.8
120.0	9.6	9.6	28.6	2.0	99.0	GAEEMETVIVDVMVR	1830.9	1831.9	1830.9	1831.9
120.0	9.6	9.6	28.6	2.0	99.0	MMNGGHYYTSENREVK	1559.6	1560.6	1559.6	1560.6
120.0	9.6	9.6	28.6	1.5	97.0	VTVAGLAGKDPVQCSR	1656.9	1657.9	1656.9	1657.9
266.0	2.1	2.1	20.1	1.4	96.0	AGIKVTVAGLAGKDPVQCSR	2027.1	2028.1	2027.1	2027.1
266.0	2.1	2.1	20.1	0.7	80.0	MMNGGHYYTSENREVK	1915.8	1916.8	1915.8	1916.8
177.0	2.0	2.0	14.8	2.0	99.0	GAEEMETVIVDVMVR	1674.8	1675.8	1674.8	1675.8
Q9BRA2 TXNL5_HUMAN Thioxodioxin-like protein 5 (14 kDa thioxodioxin-related protein) (TRP14) (Protein 42-9) - Homo sapiens (Human)										
307.0	4.0	4.0	19.5	2.0	99.0	TIFAVFTGSK	1133.6	1134.6	1133.6	1134.6
307.0	4.0	4.0	19.5	2.0	99.0	YIEVSVSGFEFFHR	1713.8	1714.8	1713.8	1714.8
358.0	2.0	2.0	11.4	2.0	99.0	YIEVSVSGFEFFHR	1713.8	1714.8	1713.8	1714.8
Q9H299 SH3L3_HUMAN SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1) - Homo sapiens (Human)										
213.0	6.0	6.0	31.2	2.0	99.0	IOYQLVDISODNALR	1774.9	1775.9	1774.9	1775.9
213.0	6.0	6.0	31.2	2.0	99.0	IOYQLVDISODNALRDEMR	2306.1	2307.1	2306.1	2307.1
213.0	6.0	6.0	31.2	2.0	99.0	VYSTSVTGSR	1055.5	1056.5	1055.5	1056.5
176.0	2.0	2.0	20.4	2.0	99.0	IOYQLVDISODNALRDEMR	2306.1	2307.1	2306.1	2307.1
340.0	2.0	2.0	49.5	2.0	99.0	IOYQLVDISODNALRDEMR	2306.1	2307.1	2306.1	2307.1
Q9NUV9 G1MA4_HUMAN GTPase I MAP family member 4 (Immunity-associated protein 4) (Immunity-associated nucleotide 1 protein) (hIAN1) - Homo sapiens (Human)										
105.0	10.4	10.4	24.9	2.0	99.0	AAQYDQVLESTPGASYGPR	2244.0	2245.0	2244.0	2245.0
105.0	10.4	10.4	24.9	2.0	99.0	AEEIIOKQTQAMQELHR	2068.0	2069.0	2068.0	2069.0
105.0	10.4	10.4	24.9	2.0	99.0	AQLLGLLIOR	1010.6	1011.6	1010.6	1011.6
105.0	10.4	10.4	24.9	2.0	99.0	KLAEQEAHYAVR	1413.7	1414.7	1413.7	1414.7
105.0	10.4	10.4	24.9	2.0	99.0	LAEQEAHYAVR	1285.6	1286.6	1285.6	1286.6
105.0	10.4	10.4	24.9	0.4	57.0	SFMILIFTR	1126.6	1127.6	1126.6	1127.6
213.0	1.3	1.3	23.1	1.3	95.0	LAEQEAHYAVR	1285.6	1286.6	1285.6	1286.6
118.0	6.4	6.4	26.1	2.0	99.0	IREEYEEKIR	1363.7	1364.7	1363.7	1364.7
118.0	6.4	6.4	26.1	2.0	99.0	LAEQEAHYAVR	1285.6	1286.6	1285.6	1286.6
118.0	6.4	6.4	26.1	1.3	95.0	IREEYEEKIRKLEDKVEQEKR	2771.5	2772.5	2771.5	2772.5
118.0	6.4	6.4	26.1	0.6	73.0	KLAEQEAHYAVR	1413.7	1414.7	1413.7	1414.7
118.0	6.4	6.4	26.1	0.5	71.0	SFMILIFTR	1126.6	1127.6	1126.6	1127.6
Q9NY33 DPP3_HUMAN Dipeptidyl-peptidase 3 (EC 3.4.14.4) (Dipeptidyl-peptidase III) (DPP III) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) - Homo sapiens (Human)										
185.0	6.2	6.2	15.7	2.0	99.0	LEGSVDLLEYSAAAGLIR	2133.0	2134.0	2133.0	2134.0
185.0	6.2	6.2	15.7	2.0	99.0	LFKEVDGEGKPYEVR	1929.0	1930.0	1929.0	1930.0
185.0	6.2	6.2	15.7	2.0	99.0	VILGSEAAQQHPPEVR	1761.9	1762.9	1761.9	1762.9
170.0	2.0	2.0	6.1	2.0	99.0	LAODFLDSQNLQSAVNT	1954.9	1955.9	1954.9	1955.9
171.0	4.0	4.0	11.9	2.0	99.0	LFKEVDGEGKPYEVR	1928.0	1929.0	1928.0	1929.0
171.0	4.0	4.0	11.9	2.0	99.0	LYAYHLNR	1021.5	1022.5	1021.5	1022.5
Q9NLY9 TMOD3_HUMAN Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod) - Homo sapiens (Human)										
305.0	4.0	4.0	7.1	2.0	99.0	FGYQFTQGGPR	1327.6	1328.6	1327.6	1328.6
305.0	4.0	4.0	7.1	2.0	99.0	SNDPVTAFAMMLK	1492.7	1493.7	1492.7	1493.7
330.0	2.0	2.0	11.6	2.0	99.0	FGYQFTQGGPR	1327.6	1328.6	1327.6	1328.6
Q9P258 RCC2_HUMAN Protein RCC2 (Telophase disk protein of 60 kDa) (RCC1-like protein TD-60) - Homo sapiens (Human)										
273.0	4.1	4.1	8.2	2.0	99.0	NLGNLWGPFR	1290.7	1291.7	1290.7	1291.7
273.0	4.1	4.1	8.2	2.0	99.0	VFSWVGGYGR	1232.6	1233.6	1232.6	1233.6
211.0	3.2	3.2	10.5	2.0	99.0	NLGNLWGPFR	1290.7	1291.7	1290.7	1291.7
211.0	3.2	3.2	10.5	1.2	94.0	YGLAGVVR	894.4	895.4	894.4	895.4
Q9UBR2 CATZ_HUMAN Cathepsin Z precursor (EC 3.4.22.-) (Cathepsin X) (Cathepsin P) - Homo sapiens (Human)										
145.0	8.0	8.0	24.8	2.0	99.0	NQHIPOYCGSCWAHASTSAMADR	2647.1	2648.1	2647.1	2648.1
145.0	8.0	8.0	24.8	2.0	99.0	NSWGEPWGER	1216.5	1217.5	1216.5	1217.5
145.0	8.0	8.0	24.8	2.0	99.0	NVDGVNYSITR	1307.7	1308.7	1307.7	1308.7
145.0	8.0	8.0	24.8	2.0	99.0	YNLAIEEHCFTGDPV	1876.9	1877.9	1876.9	1877.9
99.0	3.7	3.7	11.6	2.0	99.0	YNLAIEEHCFTGDPV	1876.9	1877.9	1876.9	1877.9
99.0	3.7	3.7	11.6	1.7	99.0	NSWGEPWGER	1216.5	1217.5	1216.5	1217.5
113.0	6.8	6.8	38.9	2.0	99.0	NSWGEPWGER	1217.5	1218.5	1217.5	1218.5
113.0	6.8	6.8	38.9	2.0	99.0	NVDGVNYSITR	1307.7	1308.7	1307.7	1308.7
113.0	6.8	6.8	38.9	2.0	99.0	YNLAIEEHCFTGDPV	1876.9	1877.9	1876.9	1877.9
113.0	6.8	6.8	38.9	0.4	58.0	DLPKSVDWVR	1201.6	1202.6	1201.6	1202.6
113.0	6.8	6.8	38.9	0.2	35.0	NQHIPOYCGSCWAHASTSAMADR	2647.1	2648.1	2647.1	2648.1
113.0	6.8	6.8	38.9	0.2	32.0	NSWGEPWGERGWL	1728.8	1729.8	1728.8	1729.8
113.0	6.8	6.8	38.9	0.0	98.0	NSWGEPWGER	1216.5	1217.5	1216.5	1217.5
Q9UJ06 DBNL_HUMAN Drebrin-like protein (SH3 domain-containing protein 7) (Drebrin-F) (Cervical SH3P7) (HPK1-interacting protein of 55 kDa) (HIP-55) (Cervical mucin) - Homo sapiens (Human)										
248.0	4.7	4.7	22.6	2.0	99.0	SPTDWALFYTGNSNDIR	2084.9	2086.0	2084.9	2086.0
248.0	4.7	4.7	22.6	2.0	99.0	TWEQQQEVVSR	1388.7	1389.7	1388.7	1389.7
248.0	4.7	4.7	22.6	0.6	72.0	FVLINWVTGEGVNDVR	1846.0	1847.0	1846.0	1847.0
248.0	4.7	4.7	22.6	0.1	25.0	FVLINWVTGEGVNDVR	1717.9	1718.9	1717.9	1718.9
223.0	3.0	3.0	17.0	2.0	99.0	SPTDWALFYTGNSNDIR	2085.0	2086.0	2084.9	2086.0
223.0	3.0	3.0	17.0	0.9	87.0	TWEQQQEVVSR	1388.7	1389.7	1388.7	1389.7
Q9UL46 PSME2_HUMAN Proteasome activator complex subunit 2 (Proteasome activator 28-subunit beta) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) - Homo sapiens (Human)										
182.0	6.2	6.2	26.4	2.0	99.0	ALVHERDEAAYGELR	1727.9	1728.9	1727.9	1728.9
182.0	6.2	6.2	26.4	2.0	99.0	ASKETHVMIDYR	1335.6	1336.6	1335.6	1336.6
182.0	6.2	6.2	26.4	2.0	99.0	QNLFOEAEEFLYR	1685.8	1686.8	1685.8	1686.8
182.0	6.2	6.2	26.4	0.2	32.0	IVNPKGEEKPSMY	1490.7	1491.7	1490.7	1491.8
182.0	6.2	6.2	26.4	0.0	99.0	QNLFOEAEEFLYR	1668.8	1669.8	1668.8	1669.8
163.0	2.0	2.0	16.3	2.0	99.0	ALVHERDEAAYGELR	1727.9	1728.9	1727.9	1728.9
95.0	8.1	8.1	26.4	2.0	99.0	ALVHERDEAAYGELR	1727.9	1728.9	1727.9	1728.9
95.0	8.1	8.1	26.4	2.0	99.0	ASKETHVMIDYR	1335.6	1336.6	1335.6	1336.6
95.0	8.1	8.1	26.4	2.0	99.0	IVNPKGEEKPSMY	1490.7	1491.7	1490.7	1491.8
95.0	8.1	8.1	26.4	2.0	99.0	QNLFOEAEEFLYR	1685.8	1686.8	1685.8	1686.8
95.0	8.1	8.1	26.4	0.0	99.0	QNLFOEAEEFLYR	1668.8	1669.8	1668.8	1669.8

174.0	6.5	6.5	18.8	2.0	99.0	FDAMPFTLR	1096.5	1097.5	1096.5	1097.5
174.0	6.5	6.5	18.8	2.0	99.0	HELLOPFNVLYEK	1628.9	1629.9	1628.9	1629.9
174.0	6.5	6.5	18.8	2.0	99.0	LVKPGNQNTQVTEAWNK	1926.0	1927.0	1926.0	1927.0
174.0	6.5	6.5	18.8	0.4	61.0	AFFSEVER	983.5	984.5	983.5	984.5
174.0	6.5	6.5	18.8	0.1	23.0	TTIYKRDPKQYGLK	1797.0	1798.0	1797.0	1798.0
288.0	2.0	2.0	6.3	2.0	98.0	AFFSEVER	983.5	984.5	983.5	984.5
Q9Y490 TLN1_HUMAN Talin-1 - Homo sapiens (Human)										
67.0	14.8	14.8	8.8	2.0	99.0	ACKEAAVHPEVAPDVR	1811.9	1812.9	1811.9	1812.9
67.0	14.8	14.8	8.8	2.0	99.0	EAYHPEVAPDVR	1452.7	1453.7	1452.7	1453.7
67.0	14.8	14.8	8.8	2.0	99.0	IGITNHDEYSLVR	1515.8	1516.8	1515.8	1516.8
67.0	14.8	14.8	8.8	2.0	99.0	LHTDDELNLWLDHGR	1719.8	1720.8	1719.8	1720.8
67.0	14.8	14.8	8.8	2.0	99.0	TMQFEPSTMVYDAGR	1834.8	1835.8	1834.8	1835.8
67.0	14.8	14.8	8.8	2.0	99.0	VGAIPANALDDGOWSQGLISAAR	2309.2	2310.2	2309.2	2310.2
67.0	14.8	14.8	8.8	2.0	99.0	VVAPTISSPVCEQLVEAGR	2139.1	2140.1	2139.1	2140.1
67.0	14.8	14.8	8.8	0.7	80.0	AVAEQIPLLQGVGR	1491.9	1492.9	1491.9	1492.9
75.0	9.8	9.8	7.6	2.0	98.0	IGITNHDEYSLVR	1515.8	1516.8	1515.8	1516.8
75.0	9.8	9.8	7.6	2.0	98.0	TMQFEPSTMVYDAGR	1834.8	1835.8	1834.8	1835.8
75.0	9.8	9.8	7.6	2.0	98.0	VVAPTISSPVCEQLVEAGR	2139.1	2140.1	2139.1	2140.1
75.0	9.8	9.8	7.6	1.7	98.0	AVAEQIPLLQGVGR	1491.9	1492.9	1491.9	1492.9
75.0	9.8	9.8	7.6	0.9	87.0	ASAGPQPLLQVQCK	1454.7	1455.7	1454.8	1455.8
75.0	9.8	9.8	7.6	0.5	65.0	KSTVLQQQYNR	1363.7	1364.7	1363.7	1364.7
75.0	9.8	9.8	7.6	0.4	64.0	EAYHPEVAPDVR	1452.7	1453.7	1452.7	1453.7
75.0	9.8	9.8	7.6	0.2	32.0	ACKEAAVHPEVAPDVR	1811.9	1812.9	1811.9	1812.9
75.0	9.8	9.8	7.6	0.1	24.0	HKAGFLDLKDFLPK	1702.9	1703.9	1702.9	1703.9
Q9Y5S9 RBM8A_HUMAN RNA-binding protein 8A (RNA-binding motif protein 8A) (Ribonucleoprotein RBM8A) (RNA-binding protein Y14) (Binder of OVCA1-1) (BOV-1) - Ho										
485.0	2.0	2.0	18.4	2.0	99.0	MREDYDSVEQDGPQQR	2221.9	2222.9	2221.9	2222.9
328.0	2.0	2.0	27.0	2.0	98.0	MREDYDSVEQDGPQQR	2221.9	2222.9	2221.9	2222.9

Online Table III. Differentially expressed proteins in CFUs compared to EPC cultures

No.	Protein identity	Swissprot Number	Theoretical MW	XC Score	Prob	Coverage (%)	Ratio*
Membrane proteins							
1	HLA class II histocompatibility antigen, DR alpha chain	P01903	28588.7	60.22	8.2E-09	15.7	-3.15
Lysosomal enzymes							
2	Cathepsin B	P07858	37796.8	50.25	5.0E-10	12.7	-5.18
3	Cathepsin H	P09668	37353.1	30.24	1.2E-06	9.0	2.49
4	Cathepsin Z	Q9UBR2	33846.2	50.19	1.8E-06	16.2	-1.62
Secreted proteins							
5	Alpha-2-macroglobulin	P01023	163174.3	40.14	1.4E-06	1.3	-11.26
6	Thymidine phosphorylase	P19971	49924.3	220.40	1.6E-14	36.7	2.62
ER proteins							
7	78 kDa glucose-regulated protein	P11021	72288.5	228.27	1.4E-09	34.3	-1.70
8	78 kDa glucose-regulated protein	P11021	72288.5	248.37	1.2E-12	28.7	-3.01
9	Endoplasmic reticulum protein ERp29	P30040	28975.2	40.18	1.2E-07	14.2	-7.49
10	Endoplasmic reticulum resident protein ERp44	Q9BS26	46941.5	40.18	3.1E-10	10.6	3.08
11	Endoplasmin	P14625	92411.2	190.26	2.0E-08	22.9	-2.60
12	Protein disulfide-isomerase A3	P30101	56746.8	408.33	2.4E-11	58.2	-1.55
13	Protein disulfide-isomerase A3	P30101	56746.8	660.38	7.1E-12	67.9	-1.46
14	Protein disulfide-isomerase A3	P30101	56746.8	428.36	2.8E-09	53.9	-1.53
Aminoacid metabolism							
15	Cytosol aminopeptidase	P28838	56130.9	220.26	2.0E-09	46.6	2.13
16	Cytosol aminopeptidase	P28838	56130.9	320.25	3.2E-10	48.7	2.95
17	Tryptophanyl-tRNA synthetase, cytoplasmic	P23381	53131.7	240.33	1.4E-11	37.6	5.19
18	Tryptophanyl-tRNA synthetase, cytoplasmic	P23381	53131.7	260.30	5.4E-11	43.3	11.15
19	Tryptophanyl-tRNA synthetase, cytoplasmic	P23381	53131.7	180.29	1.6E-11	37.8	2.34

Glucose metabolism							
20	Alpha-enolase	P06733	47139.4	158.27	8.5E-13	34.8	2.13
21	Alpha-enolase	P06733	47139.4	146.26	4.1E-14	31.1	2.26
22	Phosphoglycerate mutase 1	P18669	28785.9	90.31	5.1E-12	42.5	1.94
23	Pyruvate kinase isozymes M1/M2	P14618	57900.2	136.21	6.7E-07	17.3	2.74
24	Pyruvate kinase isozymes M1/M2	P14618	57900.2	400.32	5.2E-13	51.0	3.85
25	Triosephosphate isomerase	P60174	26652.7	218.33	8.9E-15	76.7	2.23
Lipid metabolism							
26	Aldehyde dehydrogenase	P05091	56345.7	360.28	1.3E-11	44.5	-1.63
Respiratory chain							
27	ATP synthase D chain	O75947	18479.5	140.25	1.0E-06	40.4	-1.61
28	NADH-ubiquinone oxidoreductase, 75 kDa subunit	P28331	79416.7	138.24	9.8E-10	16.8	-1.93
29	Ubiquinol-cytochrome-c reductase complex core protein 1	P31930	52612.5	260.38	1.6E-11	51.7	-2.18
Cytoskeletal proteins							
30	Gelsolin	P06396	85644.3	30.23	3.6E-05	5.1	-6.15
31	Gelsolin	P06396	85644.3	40.29	7.5E-04	6.5	-6.24
32	Gelsolin	P06396	85644.3	40.27	9.0E-07	5.1	-4.78
33	Gelsolin	P06396	85644.3	50.21	3.2E-06	5.1	-2.16
34	Macrophage-capping protein	P40121	38493.6	90.22	3.1E-08	16.1	6.94
35	Major vault protein	Q14764	99266.1	210.29	1.2E-14	28.9	1.65
36	Major vault protein	Q14764	99266.1	306.26	1.3E-13	33.7	1.91
37	Major vault protein	Q14764	99266.1	190.25	3.6E-08	19.6	1.65
38	Moesin	P26038	67777.9	150.37	1.7E-09	16.8	-1.49
Annexins							
39	Annexin A1	P04083	38690.0	210.30	1.3E-09	46.8	-1.27
Myofilament & Intermediate filament							
40	Vimentin	P08670	53619.2	410.36	3.6E-11	51.9	1.79

Antioxidans							
41	Glutathione S-transferase P	P09211	23341.0	130.34	5.1E-13	53.8	1.66
Proteasome							
42	Proteasome subunit alpha type 3	P25788	28415.1	140.22	1.1E-06	32.5	1.89
Chaperones							
43	Prohibitin	P35232	29785.9	80.19	2.2E-07	22.4	-2.66
44	T-complex protein 1 subunit beta	P78371	57452.3	270.29	3.1E-10	37.4	1.48
45	Translationally-controlled tumor protein (TCTP)	P13693	19582.6	70.22	5.5E-09	30.2	1.93
Signalling							
46	cAMP-dependent protein kinase type I-alpha regulatory subunit	P10644	42955.0	272.26	1.1E-12	44.1	-4.45
47	Elongation factor 1-delta	P29692	31102.8	120.28	1.5E-07	39.5	-2.10
48	Elongation factor 1-delta	P29692	31102.8	130.23	6.8E-10	39.5	-2.24
49	Growth factor receptor-bound protein 2	P62993	25190.4	108.22	6.2E-07	40.6	2.11
50	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	P62873	37353.0	60.18	2.2E-05	16.8	-1.45
	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2	P62879	37307.1	50.18	8.1E-07	13.8	
Protein mixtures							
51	Aldose reductase	P15121	35830.5	98.25	1.4E-07	22.5	1.99
	Annexin A2	P07355	38579.8	90.25	5.0E-06	24.5	
52	Superoxide dismutase [Mn]	P04179	24706.6	60.25	1.7E-06	21.2	-2.94
	Ferritin heavy chain	P02794	21212.3	50.16	4.7E-06	37.2	
	Adenine phosphoribosyltransferase	P07741	19595.4	48.17	5.1E-08	28.3	
53	Vimentin	P08670	53619.2	140.29	5.2E-07	33.9	-4.69
	ATP synthase subunit beta	P06576	56524.7	118.29	6.5E-08	32.5	

* A negative or positive ratio indicates a decrease or an increase CFUs compared cultured EPCs, respectively. Values are average ratios comparing CFUs vs cultured EPCs, "XC" denotes X-correlation score as calculated by the Sequest algorithm, "Prob" denotes protein probability

Online Table IV. Cytokine profiles from CFUs and cultured EPCs

Cytokine (pg/ml)	CFUs (n=15)	EPCs (n=13)	p-value
IL1beta	3.1 ± 1.1	0.1 ± 0.0	0.017
IL2Ra	159.9 ± 45.1	7.4 ± 1.4	0.004
IL2	0.3 ± 0.1	0.0 ± 0.0	0.013
IL4	2.2 ± 0.7	1.0 ± 0.2	0.113
IL5	2.5 ± 1.1	0.0 ± 0.0	0.046
IL6	616.8 ± 224.3	6.3 ± 4.5	0.017
IL7	0.4 ± 0.1	0.9 ± 0.2	0.022
IL8	76,109.3 ± 6452.1	1,415.8 ± 425.1	0.001
IL9	8.4 ± 1.1	27.3 ± 9.3	0.066
IL10	11.5 ± 6.2	9.4 ± 2.0	0.749
IL12	0.5 ± 0.3	1.3 ± 0.4	0.082
IL13	1.3 ± 0.4	0.3 ± 0.1	0.029
IL15	0.0 ± 0.0	0.0 ± 0.0	0.650
IL17	7.5 ± 4.5	0.0 ± 0.0	0.120
Eotaxin	6.3 ± 2.0	2.6 ± 0.3	0.077
FGF basic	1.9 ± 0.7	2.5 ± 0.4	0.442
GCSF	10.8 ± 3.6	0.5 ± 0.2	0.014
GMCSF	0.4 ± 0.2	0.0 ± 0.0	0.056
INFgamma	29.2 ± 9.4	4.4 ± 0.7	0.020
IP10	21,900.8 ± 7,615.8	1,339.4 ± 793.9	0.018
MCP1	4,564.0 ± 1,222.6	516.8 ± 169.3	0.065
MIP1alpha	110.1 ± 52.9	0.1 ± 0.0	0.056
MIP1beta	469.4 ± 107.5	34.2 ± 7.3	0.001
PDGFbb	1.7 ± 1.1	1161.7 ± 403.4	0.014
RANTES	215.8 ± 51.4	40.5 ± 16.0	0.005
TNF	14.5 ± 6.2	0.3 ± 0.2	0.040
VEGF	152.4 ± 85.9	607.8 ± 91.4	0.001

P-values were derived from unpaired Student's t-test. The conditioned media from 13 EPC cultures and 15 CFUs were analyzed according to the manufacturers' instructions. Depending on the cytokine, the intraplate variability of the assay measured as %CV (percent coefficient of variation) is between 2 and 13%, while the interplate %CV is between 4.3 and 21.5%. The limit of detection (LOD) ranges from 0.2 to 19.3 pg/ml.