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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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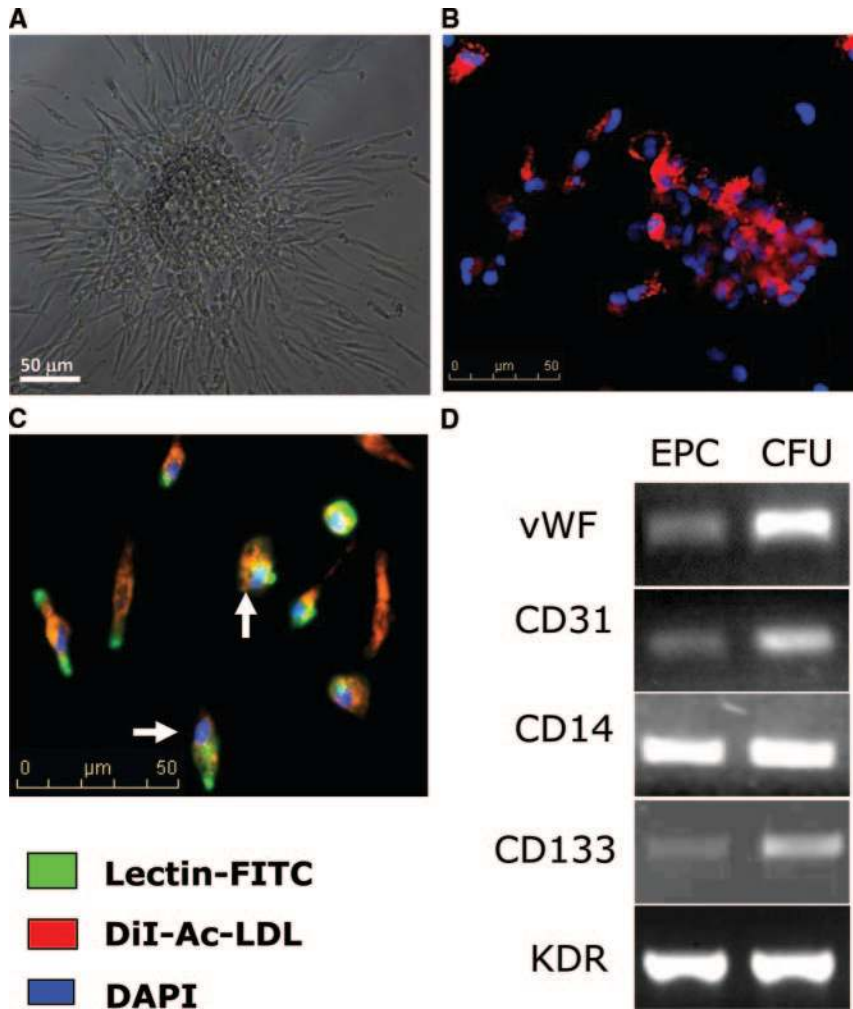


Figure 1. EPC cultures and CFUs. A and B, Morphology of CFUs (A) and endocytosis of acLDL (red fluorescence) (B). C, EPC cultures endocytose acLDL (red fluorescence) and bind to the lectin *Ulex europaeus* agglutinin (green fluorescence). Arrows indicate double positive cells. Blue labeling represents 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

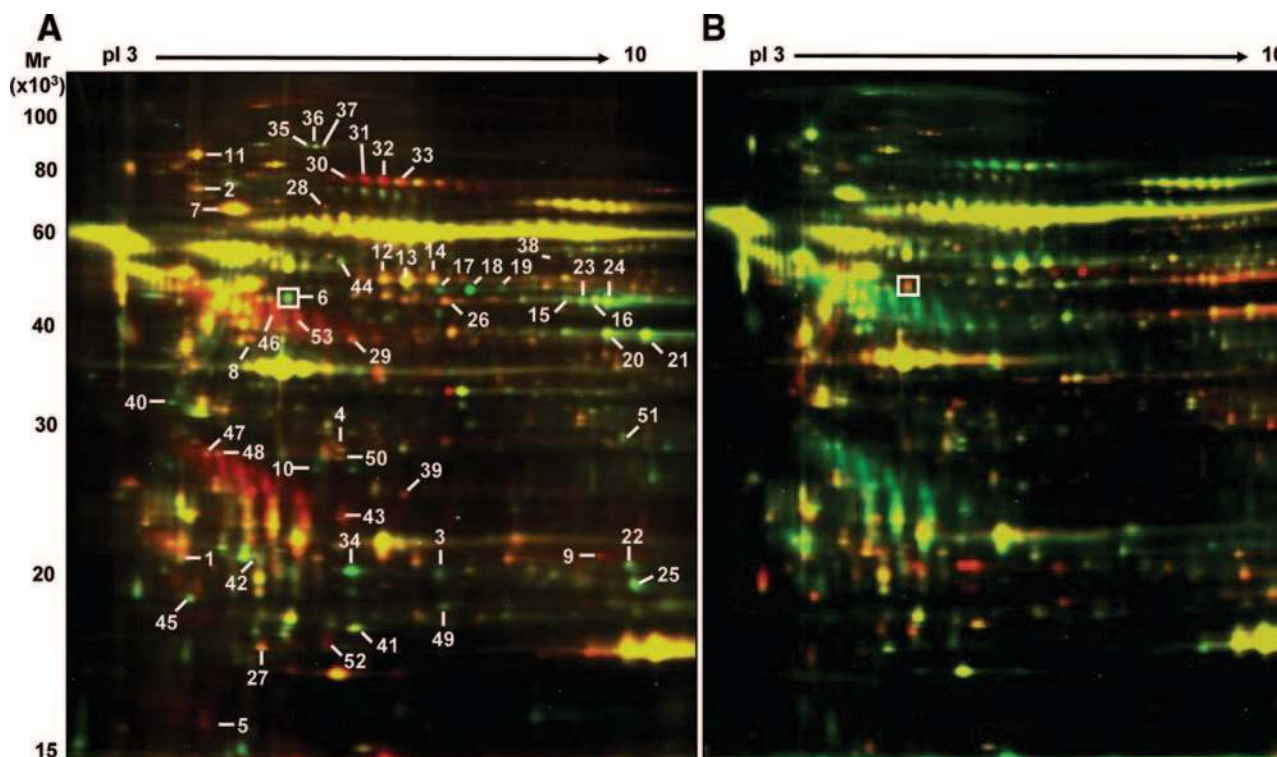


Figure 2. Difference in-gel electrophoresis. A, The proteins from CFUs are stained in green, whereas the proteins from EPC cultures are stained in red. B, Results are reproduced with different biological replicates using reverse-labeling (red for CFUs and green for EPCs). The protein corresponding to 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

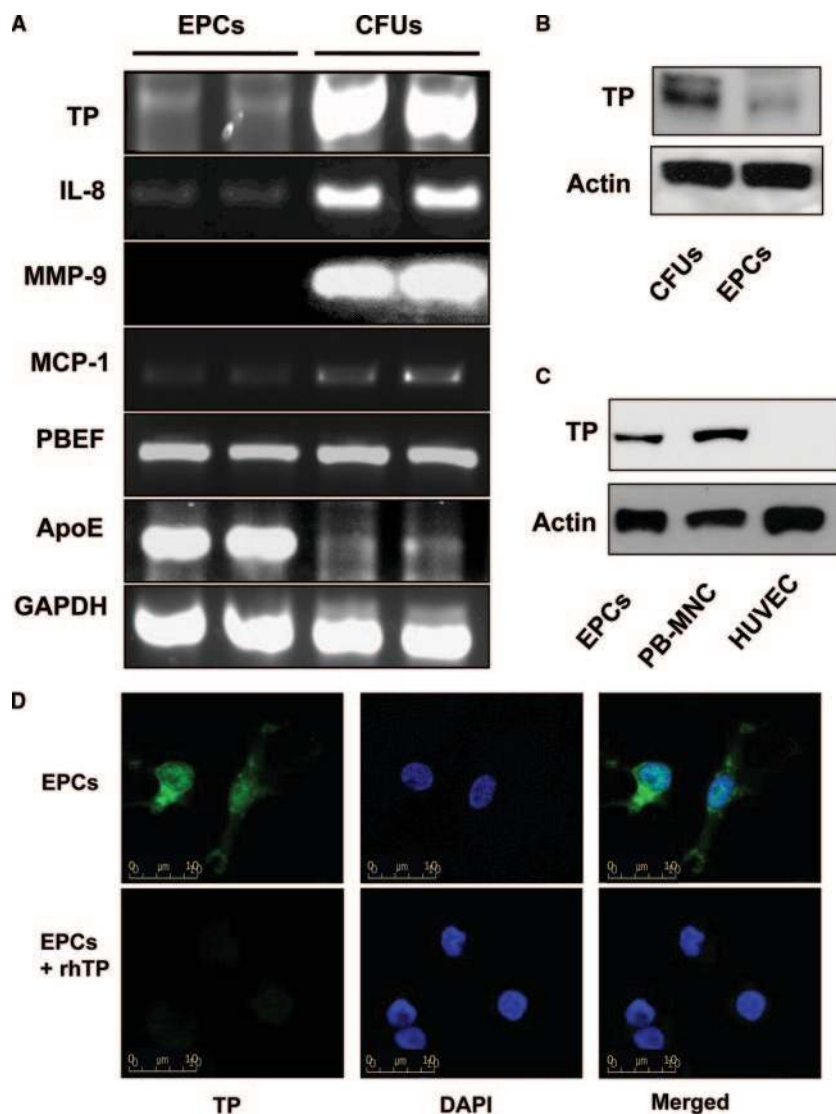


Figure 3. Expression of TP among other angiogenic factors. A, mRNA expression of TP, IL-8, MMP-9, MCP-1, pre-B cell-enhancing factor 4 (PBEF), and apolipoprotein E (ApoE) in EPC cultures and CFUs as assessed by RT-PCR. GAPDH was used as loading control. B, Protein expression of TP in EPC cultures and 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 $\alpha v\beta 3$

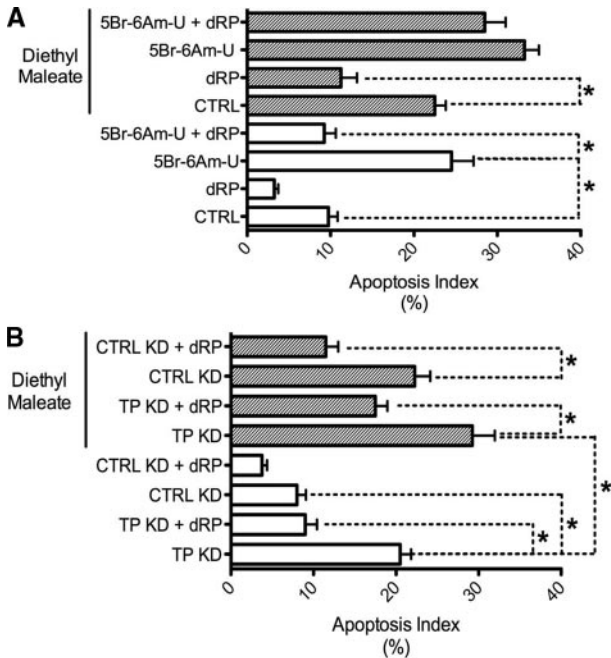


Figure 4. TP protects against apoptosis. A, Apoptosis in EPC cultures following treatment with 5Br-6Am-U (100 μ mol/L) was assessed by ELISA. Where indicated, apoptosis was induced by diethyl maleate (5 mmol/L, 12 hours). B, Apoptosis following knockdown of TP in EPC cultures by siRNA (TP KD) in the 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

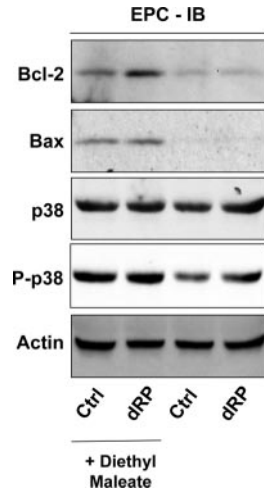


Figure 5. dRP enhances Bcl-2 expression under oxidative stress. EPC cultures with and without supplementation of dRP (50 μ mol/L) were subjected to treatment with diethyl maleate (5 mmol/L) and probed for Bcl-2, Bax, p38 MAPK, and phospho-p38 MAPK by immunoblotting. Actin served as loading control. Protein 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.

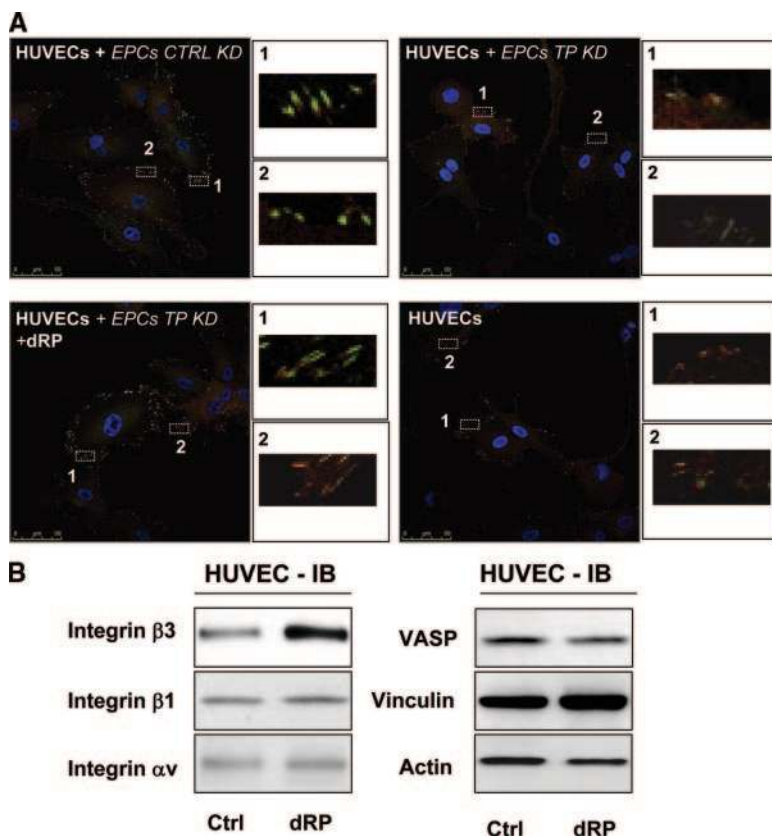


Figure 6. TP expression and release of dRP by EPCs stimulates focal adhesion formation and integrin $\beta 3$ expression in HUVECs. A, HUVECs were cultured for 24 hours in the presence of conditioned medium from EPC cultures (ratio 1:2) treated with either siRNA directed toward TP (TP KD) (top right) 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-

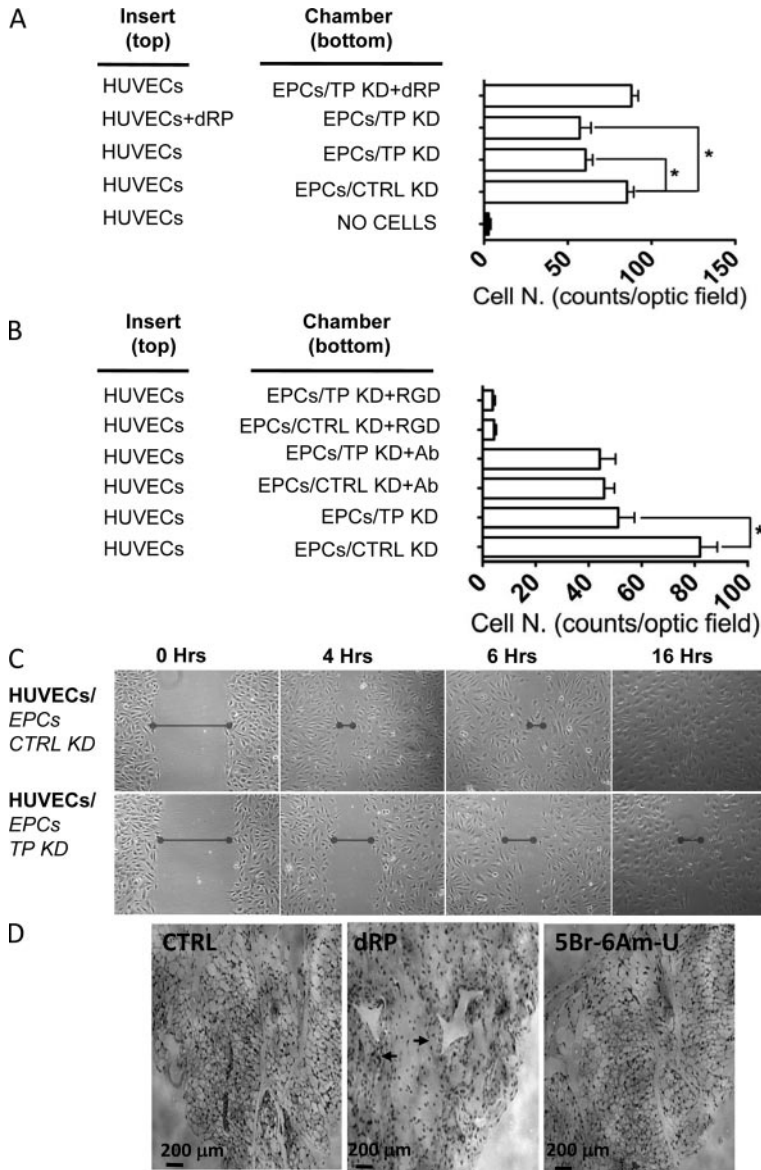


Figure 7. TP stimulates endothelial cell migration. The motility of HUVECs in response to paracrine factors released by EPCs was investigated in a modified Boyden chamber. The bottom chamber was either empty or seeded with EPCs treated with TP siRNA (TP KD) or scrambled control siRNA (CTRL KD). A and 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 kVh 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).

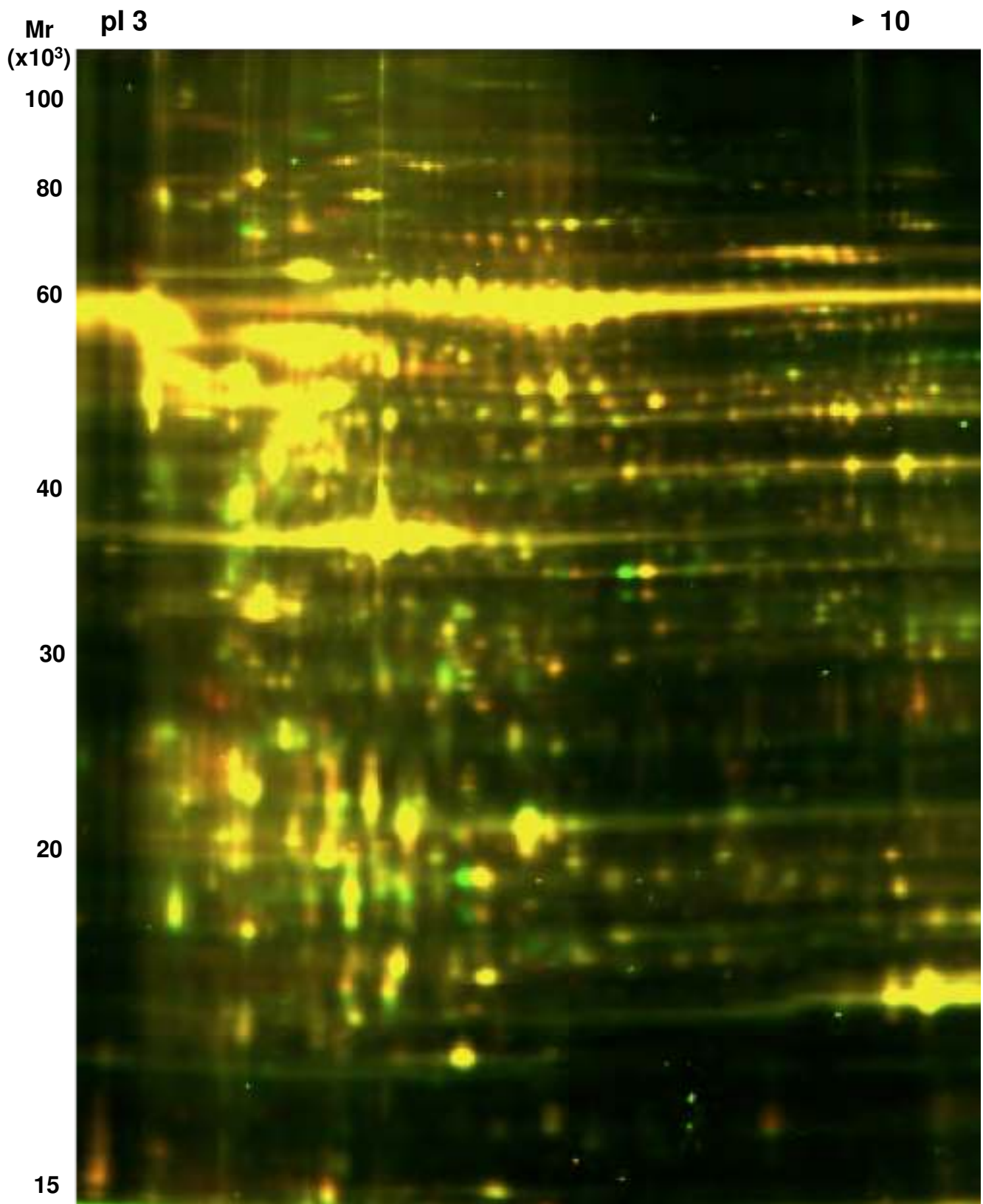
Online Table III. Differentially expressed proteins in CFUs compared to EPC

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.

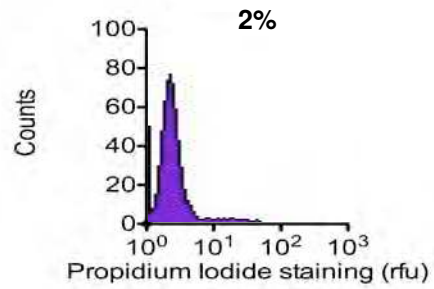
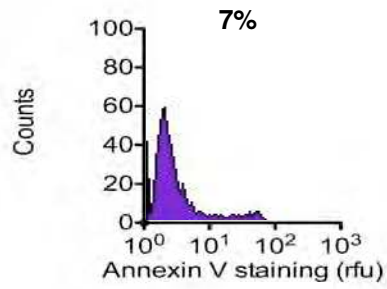
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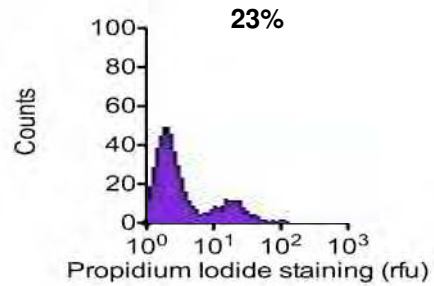
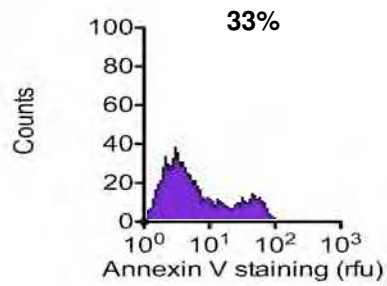


A

CTRL

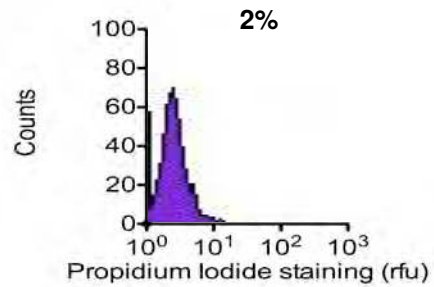
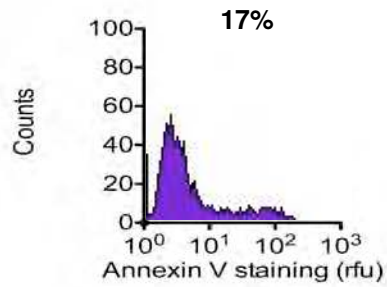


5Br-6Am-U

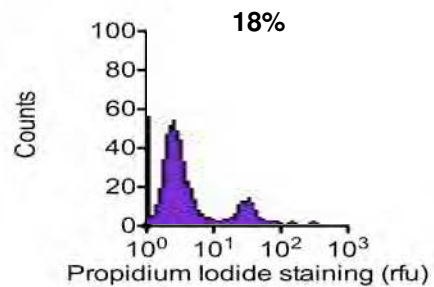
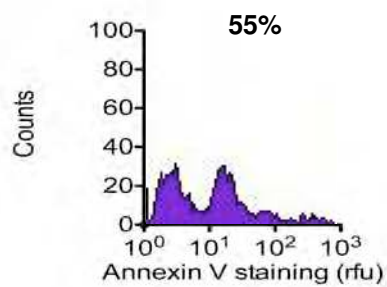


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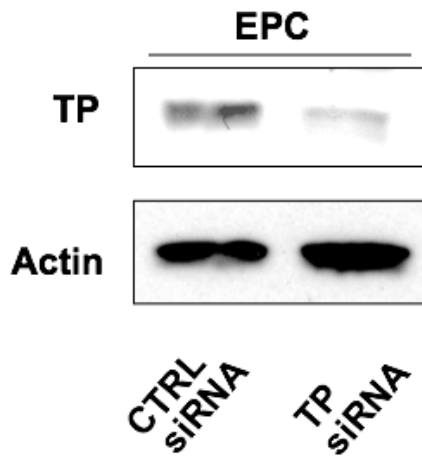
CTRL KD



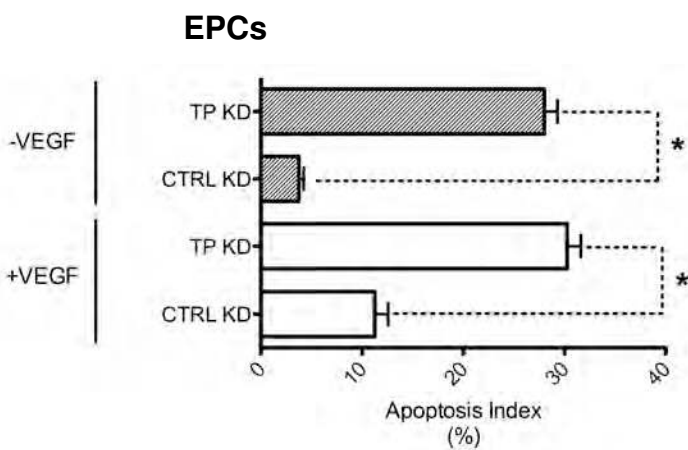
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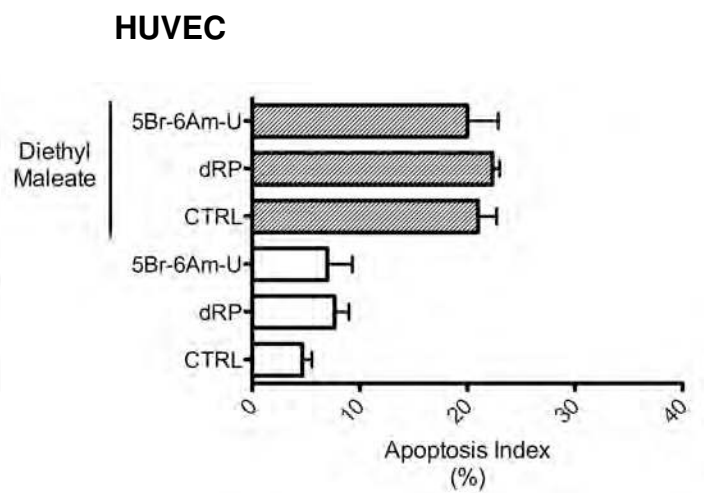
A



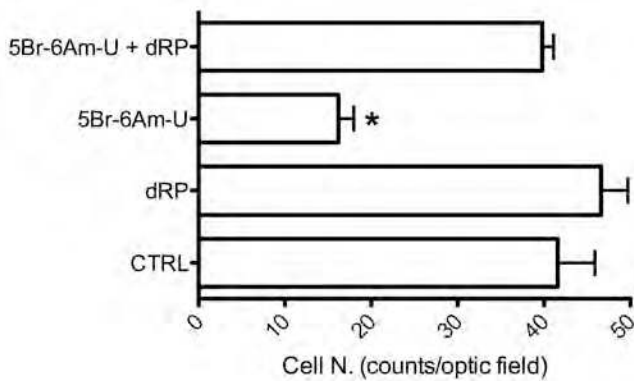
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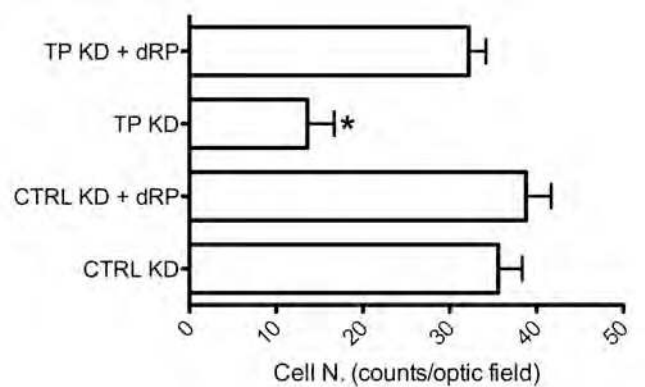
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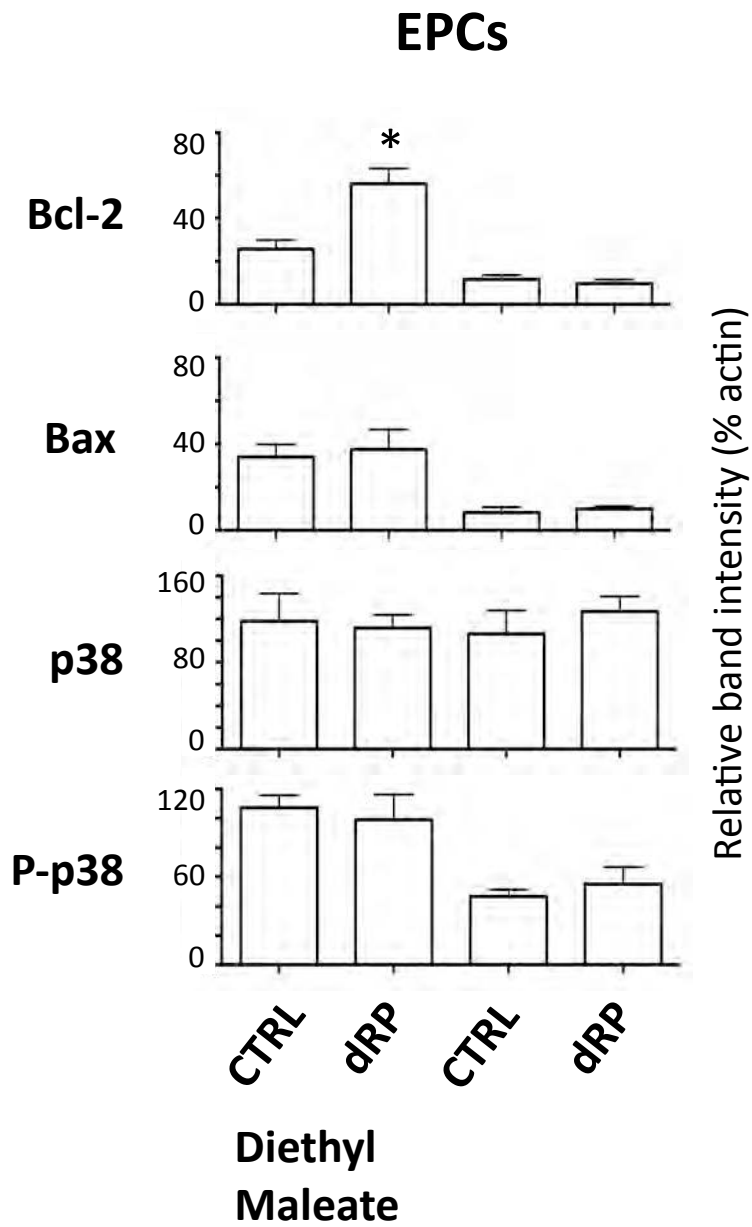


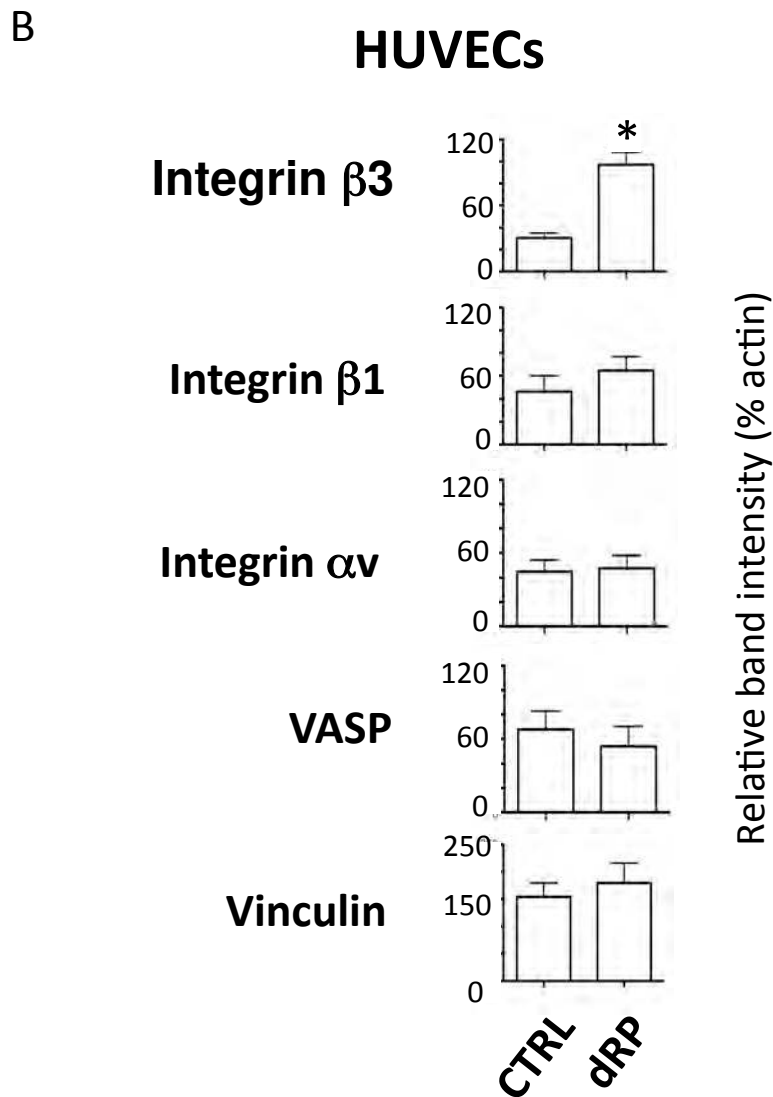
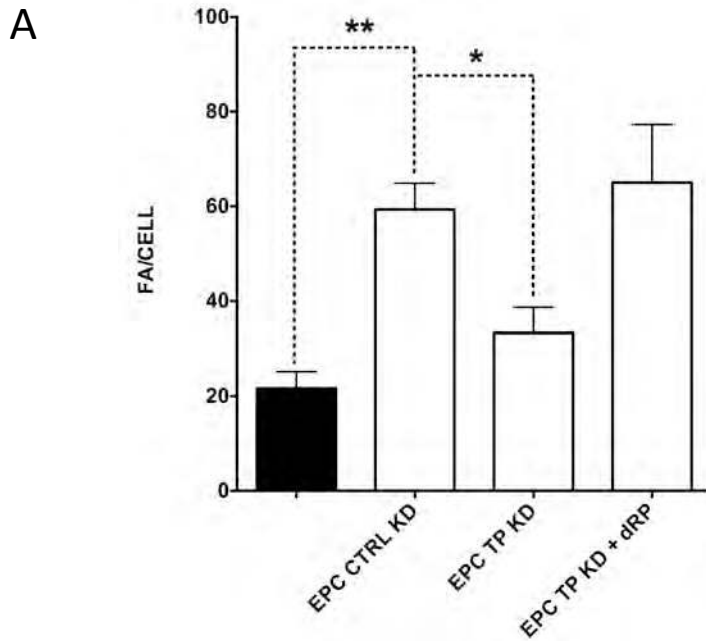
D

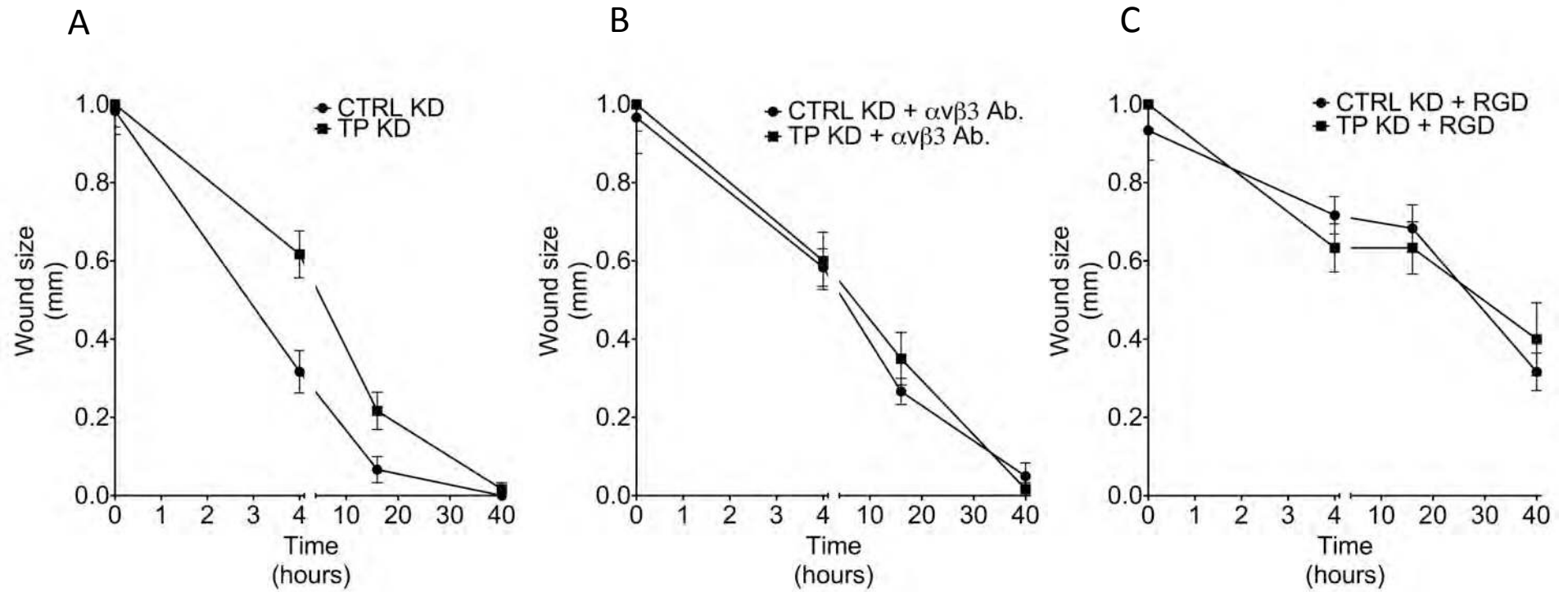


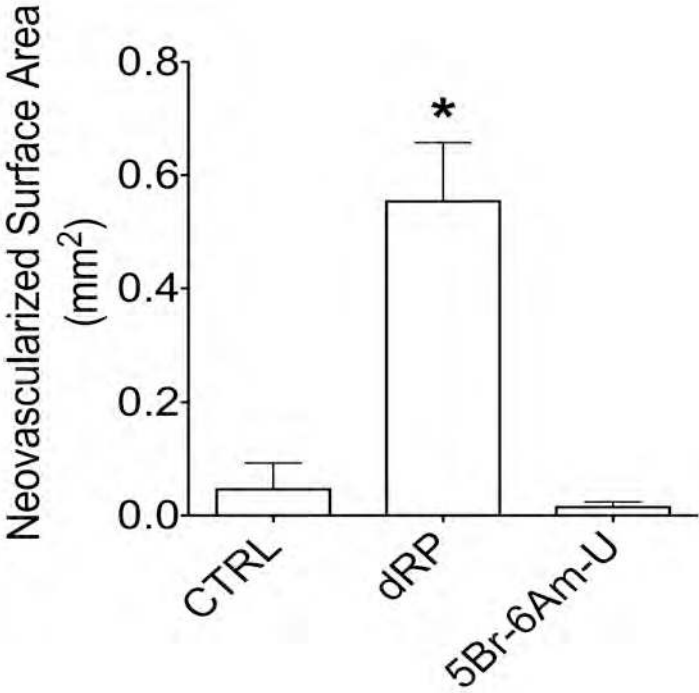
E











ONLINE TABLE I

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

Rank N.	Total Score	% Coverage	Accession	Protein name
108	6.2	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 QSCN6_HUMAN	Sulphydryl oxidase 1 precursor (EC 1.8.3.2) (Quiescin Q6) (hOSOX) - Homo sapiens (Human)
201	6.0	12.2	O00391 QSCN6_HUMAN	Sulphydryl oxidase 1 precursor (EC 1.8.3.2) (Quiescin Q6) (hOSOX) - Homo sapiens (Human)
338	2.0	51.1	O04079 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	O04079 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) (LPI) (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) (LPI) (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) (LPI) (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 HNRNP_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R) - Homo sapiens (Human)
287	4.2	20.7	O43390 HNRNP_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) (AIPI) (NORI-1) - Homo sapiens (Human)
125	2.3	14.9	O75083 WDR1_HUMAN	WD repeat protein 1 (Actin-interacting protein 1) (AIPI) (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) (GRB) (P98) (Hematopoietic cell-associated adapter protein GrpL) (Adapter protein GRD) (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) (GRB) (P98) (Hematopoietic cell-associated adapter protein GrpL) (Adapter protein GRD) (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 A2MG_HUMAN	Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Human)
16	16.5	18.1	P01023 A2MG_HUMAN	Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Human)
65	15.3	11.9	P01023 A2MG_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 FNC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (ClG) - Homo sapiens (Human)
22	13.3	13.7	P02751 FNC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (ClG) - Homo sapiens (Human)
584	1.4	1.1	P02751 FNC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (ClG) - Homo sapiens (Human)
370	2.0	8.6	P02792 FRL_HUMAN	Ferritin light chain (Ferritin L subunit) - Homo sapiens (Human)
550	2.0	8.6	P02792 FRL_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 G6PI_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)
192	11.9	18.6	P06744 G6PI_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 PDI1_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 PDI1_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 TB55_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) - Homo sapiens (Human)
26	11.9	22.5	P07437 TB55_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) - Homo sapiens (Human)
21	28.5	47.3	P07437 TB55_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 HS90A_HUMAN	Heat shock protein HSP 90-alpha (HSP 86) (Renal carcinoma antigen NY-REN-38) - Homo sapiens (Human)
75	4.7	23.5	P07900 HS90A_HUMAN	Heat shock protein HSP 90-alpha (HSP 86) (Renal carcinoma antigen NY-REN-38) - Homo sapiens (Human)
20	29.4	29.9	P07900 HS90A_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 HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 84) (HSP 90) - Homo sapiens (Human)
197	3.6	24.4	P08238 HS90B_HUMAN	Heat shock protein HSP 90-beta (HSP 84) (HSP 90) - Homo sapiens (Human)
57	27.8	30.9	P08238 HS90B_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 LEGI_HUMAN	Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-1) (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 LEGI_HUMAN	Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-1) (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 LEGI_HUMAN	Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-1) (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) (PPG) (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) (PPG) (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) (PPG) (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 (GRP78) (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 (GRP78) (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 (GRP78) (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	7.7	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) (MPR300) (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) (MPR300) (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 G3 botulinum toxin substrate 2 precursor (p21-Rac2) (Small G protein) (GX) - Homo sapiens (Human)
304	4.0	9.4	P15153 RAC2_HUMAN	Ras-related G3 botulinum toxin substrate 2 precursor (p21-Rac2) (Small G protein) (GX) - Homo sapiens (Human)
67	23.1	38.4	P15311 EZRI_HUMAN	Ezrin (p81) (Cytoovillin) (Villin-2) - Homo sapiens (Human)
127	10.3	24.9	P15311 EZRI_HUMAN	Ezrin (p81) (Cytoovillin) (Villin-2) - Homo sapiens (Human)
46	27.2	41.1	P15311 EZRI_HUMAN	Ezrin (p81) (Cytoovillin) (Villin-2) - Homo sapiens (Human)
156	4.6	7.5	P16070 CD44_HUMAN	CD44 antigen precursor (Phagocytic glycoprotein 1) (PGP-1) (HUTCH-1) (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 1) (PGP-1) (HUTCH-1) (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 1) (PGP-1) (HUTCH-1) (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 [NADPH]) (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 [NADPH]) (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 Pz22) - 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 Pz22) - 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 Pz22) - 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	P18451 B57_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	P18451 B57_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) (Glostatin) - 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) (Glostatin) - 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 CSRPI_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP1) (CRP) - Homo sapiens (Human)
527	2.0	7.8	P21291 CSRPI_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)
284	8.2	39.7	P26583 HMGB2_HUMAN	High mobility group protein B2 (High mobility group protein 2) (HMG-2) - Homo sapiens (Human)
288	16.0	50.7	P26583 HMGB2_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 peroxiredoxin) (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 peroxiredoxin) (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)
542	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 RLI2_HUMAN	60S ribosomal protein L12 - Homo sapiens (Human)
411	2.2	19.4	P30050 RLI2_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) (HCNPPp) (Neuropeptide h3) (Raf kinase inhibitor protein) (RKIP) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNPp)] - Homo sapiens (Human)
102	10.6	55.1	P30086 PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (HCNPPp) (Neuropeptide h3) (Raf kinase inhibitor protein) (RKIP) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNPp)] - Homo sapiens (Human)
97	6.0	16.4	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 glucose-regulated protein) - Homo sapiens (Human)
61	5.8	17.8	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 glucose-regulated protein) - Homo sapiens (Human)
63	15.7	23.6	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 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)
59	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 IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (p195) - Homo sapiens (Human)
180	6.4	6.8	P46940 IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 (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 GDI_R_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) - Homo sapiens (Human)
82	4.1	26.0	P52565 GDI_R_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) - Homo sapiens (Human)
28	24.6	49.0	P52565 GDI_R_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) - Homo sapiens (Human)
269	2.1	49.3	P52566 GDI_S_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI) - Homo sapiens (Human)
101	12.0	49.8	P52566 GDI_S_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI) - Homo sapiens (Human)
230	2.7	12.3	P52597 HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo sapiens (Human)
334	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 I) (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 I) (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 (ARPC2/3 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 (ARPC2/3 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 (ARPC2/3 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 1433E_HUMAN	14-3-3 protein epsilon (14-3-3E) - Homo sapiens (Human)
109	12.0	37.3	P62258 1433E_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 1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIIP-1) - Homo sapiens (Human)
67	5.1	35.1	P63104 1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIIP-1) - Homo sapiens (Human)
34	22.8	65.7	P63104 1433Z_HUMAN	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIIP-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 H31_HUMAN	Histone H3.1 (H3/a) (H3/b) (H3/c) (H3/d) (H3/e) (H3/f) (H3/g) (H3/h) (H3/i) (H3/j) (H3/k) (H3/l) - Homo sapiens (Human)
139	2.1	19.1	P68431 H31_HUMAN	Histone H3.1 (H3/a) (H3/b) (H3/c) (H3/d) (H3/e) (H3/f) (H3/g) (H3/h) (H3/i) (H3/j) (H3/k) (H3/l) - Homo sapiens (Human)
154	7.9	41.2	P68431 H31_HUMAN	Histone H3.1 (H3/a) (H3/b) (H3/c) (H3/d) (H3/e) (H3/f) (H3/g) (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	Q00610 CLH1_HUMAN	Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)
408	2.3	3.6	Q00610 CLH1_HUMAN	Clathrin heavy chain 1 (CLH-17) - Homo sapiens (Human)
140	5.7	20.6	Q00839 HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (pp120) - Homo sapiens (Human)
93	11.9	23.1	Q00839 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) (IGAAD) - 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) (IGAAD) - 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 ITH3_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 ITH3_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 ITH3_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-acylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA2) (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-acylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA2) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase) - Homo sapiens (Human)
346	2.0	8.2	Q13151 ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0) - Homo sapiens (Human)
591	1.4	24.3	Q13151 ROA0_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 (eIF3 theta) (eIF3 p167) (eIF3 p185) (eIF3a) - Homo sapiens (Human)
137	8.2	16.1	Q14152 IF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit 10 (eIF3 theta) (eIF3 p167) (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(nr)) (p54nr) (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(nr)) (p54nr) (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 DPY2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human)
336	3.5	5.9	Q16555 DPY2_HUMAN	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human)
344	2.0	4.7	Q16658 FSCN1_HUMAN	Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human)
383	2.5	11.2	Q16658 FSCN1_HUMAN	Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human)
343	2.0	4.6	Q16881 TRX1_HUMAN	Thioredoxin reductase 1, cytoplasmic precursor (EC 1.8.1.9) (TR) (TR1) - Homo sapiens (Human)
392	2.4	9.2	Q16881 TRX1_HUMAN	Thioredoxin reductase 1, cytoplasmic precursor (EC 1.8.1.9) (TR) (TR1) - Homo sapiens (Human)
129	4.0	39.2	Q6FI13 H2A2_HUMAN	Histone H2A type 2-A (H2A.2) - Homo sapiens (Human)
111	3.1	52.3	Q6FI13 H2A2_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 HS105_HUMAN	Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY-CO-25) - Homo sapiens (Human)
194	1.7	10.7	Q92598 HS105_HUMAN	Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY-CO-25) - Homo sapiens (Human)
290	4.0	6.9	Q92598 HS105_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 (Pletin) (Predominantly fetal expressed T1 domain) - Homo sapiens (Human)
474	2.0	7.4	Q96CX2 KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12 (Pletin) (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	Q96IUA ABHEB_HUMAN	Abhydrolase domain-containing protein 14B (EC 3.-.-.-) (CCG1-interacting factor B) - Homo sapiens (Human)
308	4.0	11.4	Q96IUA 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	Q9H299 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	Q9H299 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	Q9H299 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	Q9NUV9 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	Q9NUV9 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	Q9NUV9 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	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)
170	2.0	6.1	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	6.2	15.7	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)
330	2.0	11.6	Q9NYL9 TMOD3_HUMAN	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod) - Homo sapiens (Human)
305	4.0	7.1	Q9NYL9 TMOD3_HUMAN	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod) - Homo sapiens (Human)
211	3.2	10.5	Q9P258 RCC2_HUMAN	Protein RCC2 (Telophase disk protein of 60 kDa) (RCC1-like protein TD-60) - Homo sapiens (Human)
273	4.1	8.2	Q9P258 RCC2_HUMAN	Protein RCC2 (Telophase disk protein of 60 kDa) (RCC1-like protein TD-60) - Homo sapiens (Human)
113	6.8	38.9	Q9UBR2 CATZ_HUMAN	Cathepsin Z precursor (EC 3.4.22.-) (Cathepsin X) (Cathepsin P) - Homo sapiens (Human)
99	3.7	11.6	Q9UBR2 CATZ_HUMAN	Cathepsin Z precursor (EC 3.4.22.-) (Cathepsin X) (Cathepsin P) - Homo sapiens (Human)
145	8.0	24.8	Q9UBR2 CATZ_HUMAN	Cathepsin Z precursor (EC 3.4.22.-) (Cathepsin X) (Cathepsin P) - Homo sapiens (Human)
223	3.0	17.0	Q9UJU6 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	Q9UJU6 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	Q9UL46 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	Q9UL46 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	Q9UL46 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	Q9ULV4 COR1C_HUMAN	Coronin-1C (Coronin-3) (hCRNN4) - Homo sapiens (Human)
200	1.8	17.3	Q9ULV4 COR1C_HUMAN	Coronin-1C (Coronin-3) (hCRNN4) - Homo sapiens (Human)
223	6.0	18.1	Q9ULV4 COR1C_HUMAN	Coronin-1C (Coronin-3) (hCRNN4) - Homo sapiens (Human)
288	2.0	6.3	Q9UC80 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	Q9UC80 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	Q9Y490 TLN1_HUMAN	Talin-1 - Homo sapiens (Human)
67	14.8	8.8	Q9Y490 TLN1_HUMAN	Talin-1 - Homo sapiens (Human)
328	2	27.0	Q9Y5S9 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	Q9Y5S9 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	AEEPOVELFVK	1457.7	1458.8	1457.7	1458.7
123.0	9.5	9.5	31.1	2.0	99.0	EFASTCPDDEEELAYEVQAK	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	YRGFTIPEAFR	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	YRGFTIPEAFR	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	EEQPQVELFVK	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	YRGFTIPEAFR	1355.7	1356.7	1355.7	1356.7
108.0	7.3	8.2	20.7	1.2	93.0	IGNCFPSOR	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) (hQSOX) - Homo sapiens (Human)										
201.0	6.0	6.0	12.2	2.0	99.0	LAGAPSEDPOFPK	1355.7	1356.7	1355.7	1356.7
201.0	6.0	6.0	12.2	2.0	99.0	NNEEYLALFEK	1481.8	1482.8	1481.7	1482.7
201.0	6.0	6.0	12.2	2.0	99.0	SFYTAYLOR	1147.6	1148.6	1147.6	1148.6
160.0	2.0	2.0	11.1	2.0	99.0	NNEEYLALFEK	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	99.0	LSAKPAPPKPEPRPK	1611.9	1613.0	1611.9	1613.0
014773 TPP1_HUMAN										
Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase I) (TPP-1) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatin insen										
490.0	2.0	2.0	4.6	2.0	99.0	LYQOHGAGLFDVTR	1603.8	1604.8	1603.8	1604.8
138.0	2.1	2.1	14.9	2.0	99.0	LFGGNFAHQSVAR	1473.7	1474.7	1473.7	1474.8
138.0	2.1	2.1	14.9	0.1	26.0	LYQOHGAGLFDVTR	1603.8	1604.8	1603.8	1604.8
189.0	4.0	4.0	5.0	2.0	99.0	LFGGNFAHQSVAR	1473.7	1474.8	1473.7	1474.8
189.0	4.0	4.0	5.0	2.0	99.0	LYQOHGAGLFDVTR	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	KICALDDNVCMFAGLTADAR	2311.1	2312.1	2311.1	2312.1
177.0	6.5	6.5	17.3	2.0	99.0	LYQDPSGTYHAWK	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	KICALDDNVCMFAGLTADAR	2183.0	2184.0	2183.0	2184.0
202.0	3.7	3.7	11.7	2.0	99.0	KICALDDNVCMFAGLTADAR	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) (hnHNR-DL) (JKT41-binding protein) (AU-rich element RNA-binding factor)										
452.0	2.0	6.0	9.8	2.0	99.0	RGFCFTYTDDEPVK	1989.0	1990.0	1989.0	1990.0
452.0	2.0	6.0	9.8	0.0	99.0	GFQFVLVK	913.5	914.5	913.5	914.5
452.0	2.0	6.0	9.8	0.0	99.0	SRGFGVLVK	1156.6	1157.6	1156.6	1157.6
87.0	4.0	4.0	18.8	2.0	99.0	GFQFVLVK	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	GFQFVLVK	913.5	914.5	913.5	914.5
015143 ARCB_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	CSQFCTTGMDDGMSIWDVK	2164.9	2165.9	2164.9	2165.9
152.0	8.0	8.0	17.7	2.0	99.0	TWKPTLVILR	1225.8	1226.8	1225.8	1226.8
152.0	8.0	8.0	17.7	2.0	99.0	VHEIKHINMGVGTGIDWAPESNR	2517.2	2518.2	2517.2	2518.2
152.0	8.0	8.0	17.7	2.0	99.0	WAPNEKFAVGGSGSR	1618.8	1619.8	1618.8	1619.8
152.0	8.0	8.0	17.7	0.0	99.0	CSQFCTTGMDDGMSIWDVK	2178.9	2179.9	2178.9	2179.9
152.0	8.0	8.0	17.7	0.0	99.0	CSQFCTTGMDDGMSIWDVK	2163.9	2164.9	2163.9	2164.9
128.0	2.3	2.3	24.7	2.0	99.0	CSQFCTTGMDDGMSIWDVK	2162.9	2163.9	2162.9	2163.9
128.0	2.3	2.3	24.7	0.3	48.0	TWKPTLVILR	1225.8	1226.8	1225.8	1226.8
128.0	2.3	2.3	24.7	0.0	99.0	CSQFCTTGMDDGMSIWDVK	2178.9	2179.9	2178.9	2179.9
85.0	8.9	8.9	22.3	2.0	99.0	AYHSFLVEPISSHAWNKR	2371.1	2372.1	2371.1	2372.1
85.0	8.9	8.9	22.3	2.0	99.0	CSQFCTTGMDDGMSIWDVK	2161.9	2162.9	2161.9	2162.9
85.0	8.9	8.9	22.3	2.0	99.0	EVEERPAFTPWGSK	1581.8	1582.8	1581.8	1582.8
85.0	8.9	8.9	22.3	2.0	99.0	WAPNEKFAVGGSGSR	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	DNTINLHTFR	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	YFQFQEEKGEENR	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	DNTINLHTFR	1342.7	1343.7	1342.7	1343.7
196.0	1.7	1.7	21.0	0.5	71.0	YFQFQEEKGEENR	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	SOFGKAPR	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	ECTNLCEALTKC	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	YLLSQPK	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	DLYEDELVLFVK	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	DLYEDELVLFVK	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	ASFNHFDKDHGGALGPEEFK	2199.0	2200.0	2202.0	2203.0
10.0	41.3	41.3	35.2	2.0	99.0	COLEINLTLOTK	1590.8	1591.8	1590.8	1591.8
10.0	41.3	41.3	35.2	2.0	99.0	DGLARNAIILR	1225.6	1226.6	1225.7	1226.7
10.0	41.3	41.3	35.2	2.0	99.0	EGLLWCOER	1173.6	1174.6	1173.6	1174.6
10.0	41.3	41.3	35.2	2.0	99.0	GISOEQMOEPR	1351.6	1352.6	1351.6	1352.6
10.0	41.3	41.3	35.2	2.0	99.0	ICDQWDALGSLTHSR	1757.8	1758.8	1757.8	1758.8
10.0	41.3	41.3								

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	DAKGISQEQMOEFR	1665.8	1666.8	1665.8	1666.8
10.0	41.3	41.3	35.2	0.0	99.0	LEDFRDYR	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	VGWQLLTTIAR	1385.7	1386.8	1385.8	1386.8
44.0	6.9	6.9	13.9	1.7	99.0	LEDFRDYR	1432.7	1433.7	1432.5	1433.5
44.0	6.9	6.9	13.9	0.9	88.0	LSNRPAMFMSSEK	1432.7	1433.7	1432.7	1433.7
44.0	6.9	6.9	13.9	0.3	44.0	LEDFRDYR	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	LEDFRDYR	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	EGLLLWGOR	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	GISQEQMOEFR	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	KTFTAWCNSHLR	1519.7	1520.7	1519.7	1520.7
22.0	22.9	22.9	32.3	2.0	99.0	LEDFRDYR	1112.5	1113.5	1112.5	1113.5
22.0	22.9	22.9	32.3	2.0	99.0	LSNRPAMFMSSEK	1432.7	1433.7	1432.7	1433.7
22.0	22.9	22.9	32.3	2.0	99.0	TINEVENOLTR	1429.8	1429.8	1429.8	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	LEDFRDYR	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	EALAIKAEAR	1377.8	1378.8	1377.8	1378.8
22.0	22.9	22.9	32.3	0.0	99.0	ASFNFHFKDHGGALGPEEFK	2202.0	2203.0	2202.0	2203.0
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	LEDFRDYR	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	EGIDPTPYWYTDQR	1902.8	1903.9	1902.8	1903.8
212.0	6.0	6.0	9.3	2.0	99.0	IFDSEELAGYKR	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
295.0	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	IKDIAWTEDSKR	1460.8	1461.8	1460.8	1461.8
108.0	10.0	10.0	16.5	2.0	99.0	MTVDESGLQSCSMDTIVR	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	IKDIAWTEDSKR	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	LATGSDDNCAAFFEGPPFKFK	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	ENNAVYAFGLTAPGSK	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	YLQHHHFHOER	1530.7	1531.7	1530.7	1531.7
384.0	1.7	1.7	11.2	1.7	98.0	YLQHHHFHOER	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	GEMM1LQHGSLFLR	1632.8	1633.8	1632.8	1633.8
129.0	9.1	11.3	30.4	2.0	99.0	KSADTLWGIQKELQF	1762.9	1763.9	1762.9	1763.9
129.0	9.1	11.3	30.4	2.0	99.0	SADTLWGIQKELQF	1634.8	1635.8	1634.8	1635.8
129.0	9.1	11.3	30.4	1.5	99.0	SADTLWGIQK	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	1167.7	1167.7	1167.7	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	VIGSGNLSAR	1247.6	1248.6	1247.6	1248.6
156.0	2.0	4.0	11.1	2.0	99.0	SADTLWGIQKELQF	1634.8	1635.9	1634.8	1635.8
156.0	2.0	4.0	11.1	0.0	99.0	SADTLWGIQK	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	1469.7	1470.7	1469.7	1470.7
166.0	7.0	7.0	32.9	2.0	99.0	LGADAVYGMSTPEVIVAR	1784.0	1785.0	1784.0	1785.0
166.0	7.0	7.0	32.9	1.0	99.0	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	1469.7	1470.7	1469.7	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	AEPKIEAFR	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	LDVYVNDAFGTADR	1634.8	1635.8	1634.8	1635.8
22.0	28.0	28.0	53.0	2.0	99.0	TGOATVASGIPAGWMGLDCGPESK	2476.1	2477.1	2476.1	2477.1
22.0	28.0	28.0	53.0	2.0	99.0	TGOATVASGIPAGWMGLDCGPESK	2604.2	2605.2	2604.2	2605.2
22.0	28.0	28.0	53.0	2.0	99.0	VDFNVPKNNQITNNQR	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	VLNMEIGTSLFDEEGAK	1965.9	1966.9	1965.9	1966.9
22.0	28.0	28.0	53.0	2.0	99.0	WNTEDKSHVSTGGGASLELEK	2513.2	2514.2	2513.2	2514.2
22.0	28.0	28.0	53.0	0.0	99.0	AEPKIEAFR	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	LDVYVNDAFGTADR	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	LDVYVNDAFGTADR	1634.8	1635.8	1634.8	1635.8
76.0	4.6	4.6	30.5	0.3	53.0	VDFNVPKNNQITNNQR	2031.0	2032.0	2031.0	2032.0
76.0	4.6	4.6	30.5	0.2	39.0	VLNMEIGTSLFDEEGAK	1965.9	1967.0	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	AEPKIEAFR	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	LDVYVNDAFGTADR	1634.8	1635.8	1634.8	1635.8
30.0	20.8	20.8	45.6	2.0	99.0	SLLGKDFLFLKDCVGPVEEK	2245.2	2246.2	2245.2	2246.2
30.0	20.8	20.8	45.6	2.0	99.0	VDFNVPKNNQITNNQR	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	1761.9	1762.9	1761.9	1762.9
30.0	20.8	20.8	45.6	0.0	99.0	LDVYVNDAFGTADR	1634.8	1635.8	1634.8	1635.8
30.0	20.8	20.8	45.6	0.0	99.0	VDFNVPKNNQITNNQR	2031.0	2032.0	2031.0	2032.0
P01023 A2MG_HUMAN Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (Human)										
65.0	15.3	15.3	11.9	2.0	99.0	AI GYLNTGYOR	1310.7	1311.7	1310.7	1311.7
65.0	15.3	15.3	11.9	2.0	99.0	MVSGFLPKPTVK	1415.8	1416.8	1415.8	1416.8
65.0	15.3	15.3	11.9	2.0	99.0	NALFCLESAWK	1323.6	1324.6	1323.6	1324.6
65.0	15.3	15.3	11.9	2.0	99.0	SGGRTEHPFTVEEVLPK	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	

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	1607.9	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	AIQYLNTGYQR	1310.7	1311.7	1310.7	1311.7
18.0	26.1	26.1	17.1	2.0	99.0	DMYSFLEDMGLK	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	SKAIGYLNTGYQR	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	1609.9	1608.9	1609.9
18.0	26.1	26.1	17.1	0.5	70.0	KSGRTEHPFTVEEFVLPK	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	EPLGLTQWSLR	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	EPLGLTQWSLR	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	ALDFAVGEYK	1225.6	1226.6	1225.6	1226.6
302.0	4.0	4.0	25.3	2.0	99.0	LVGSPMDASVEEGRVRR	1607.9	1608.9	1607.9	1608.9
104.0	3.4	3.4	26.0	2.0	99.0	ALDFAVGEYK	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	ALDFAVGEYK	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	ADYEKHVYACEVTHQGLSSPVTK	2746.3	2747.3	2746.3	2747.3
260.0	4.5	4.5	37.7	2.0	99.0	VYACEVTHQGLSSPVTK	1874.9	1875.9	1874.9	1875.9
260.0	4.5	4.5	37.7	0.4	64.0	SGTASVCLLNNFYPR	1797.9	1798.9	1797.9	1798.9
188.0	4.0	4.0	31.1	2.0	99.0	SGTASVCLLNNFYPR	1797.9	1798.9	1797.9	1798.9
188.0	4.0	4.0	31.1	2.0	99.0	VYACEVTHQGLSSPVTK	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	SYSCQVTHEGSTVEK	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	QSNNKYAASSYLSLTPEQWK	2314.1	2315.1	2314.1	2315.1
203.0	3.7	3.7	28.6	2.0	99.0	SYSCQVTHEGSTVEK	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
106.0	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	GQPLSPEKYVTSAPMPEPQAPGR	2436.2	2437.2	2436.2	2437.2
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	FDHVTNMINNVEPR	1862.8	1863.8	1862.8	1863.8
95.0	4.0	4.0	13.5	2.0	99.0	VPGLYFTYHASSR	1659.8	1660.8	1659.8	1660.8
337.0	2.0	2.0	14.3	2.0	99.0	VPGLYFTYHASSR	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
954.0	2.0	2.0	10.2	2.0	99.0	QTHOPPAPNSLIR	1457.8	1458.8	1457.8	1458.8
P02751 FNC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (ClG) - Homo sapiens (Human)									
584.0	1.4	1.4	1.1	1.4	95.0	YQCYCYGR	1168.4	1169.5	1168.4	1169.5
22.0	13.3	13.3	13.7	2.0	99.0	GEWTCIAVSQLR	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	LLCQCLGFSSGHFR	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	ODGHLWCSTTSNVEQDK	2195.9	2196.9	2195.9	2196.9
22.0	13.3	13.3	13.7	1.4	96.0	EYLGAI CSCTCFGGQR	1877.8	1878.8	1877.8	1878.8
22.0	13.3	13.3	13.7	0.6	72.0	GATYNI IVEALKDQOR	1817.9	1818.9	1817.9	1818.9
22.0	13.3	13.3	13.7	0.1	11.0	IFYSCTIEGR	1220.5	1221.5	1220.5	1221.5
27.0	21.3	21.3	16.4	2.0	99.0	GATYNIIVEALKDQOR	1818.0	1819.0	1818.0	1819.0
27.0	21.3	21.3	16.4	2.0	99.0	GEWTCIAVSQLR	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	HYQIQOWER	1400.7	1401.7	1400.7	1401.7
27.0	21.3	21.3	16.4	2.0	99.0	LLCQCLGFSSGHFR	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	IGDOWDKQHDGMHMMR	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	LGDFEALGCELYFER	1606.8	1607.8	1606.8	1607.8
370.0	2.0	2.0	8.6	2.0	99.0	LGDFEALGCELYFER	1606.8	1607.8	1606.8	1607.8
P02795 MT2_HUMAN	Metallothionein-2 (MT-2) (Metallothionein-II) (MT-II) (Metallothionein-2A) - Homo sapiens (Human)									
216.0	6.0	6.0	82.0	2.0	99.0	CAQGCICKAGSDKSCCA	2074.7	2075.7	2074.8	2075.8
216.0	6.0	6.0	82.0	2.0	99.0	MDPNCSCAAGDSTCAGSCK	2249.8	2250.8	2249.8	2250.8
216.0	6.0	6.0	82.0	2.0	99.0	SCCSOCPVGCAGK	1444.5	1445.5	1444.5	1445.5
216.0	6.0	6.0	82.0	0.0	99.0	MDPNCSCAAGDSTCAGSCK	2252.8	2253.8	2252.8	2253.8
216.0	6.0	6.0	82.0	0.0	99.0	MDPNCSCAAGDSTCAGSCK	2192.7	2193.7	2192.7	2193.7
216.0	6.0	6.0	82.0	0.0	99.0	MDPNCSCAAGDSTCAGSCK	2253.8	2254.8	2253.7	2254.7
216.0	6.0	6.0	82.0	0.0	47.0	MDPNCSCAAGDSTCAGSCK	2207.7	2208.7	2207.7	2208.7
216.0	6.0	6.0	82.0	0.0	99.0	SCCSOCPVGCAGK	1447.5	1448.5	1447.5	1448.5
216.0	6.0	6.0	82.0	0.0	99.0	SCCSOCPVGCAGK	1447.5	1448.5	1447.5	1448.5
114.0	6.7	6.7	62.3	2.0	99.0	KSCSCOPVGCAGK	1573.6	1574.6	1573.6	1574.6
114.0	6.7	6.7	62.3	2.0	99.0	MDPNCSCAAGDSTCAGSCK	2249.8	2250.8	2249.8	2250.8
114.0	6.7	6.7	62.3	2.0	99.0	SCCSOCPVGCAGK	1444.5	1445.5	1444.5	1445.5
114.0	6.7	6.7	62.3	0.7	81.0	MDPNCSCAAGDSTCAGSCKCKECK	2955.0	2956.0	2955.0	2956.0
114.0	6.7	6.7	62.3	0.0	99.0	MDPNCSCAAGDSTCAGSCK	2250.7	2251.7	2250.7	2251.7
114.0	6.7	6.7	62.3	0.0	99.0	MDPNCSCAAGDSTCAGSCK	2253.8	2254.8	2253.7	2254.7
114.0	6.7	6.7	62.3	0.0	97.0	MDPNCSCAAGDSTCAGSCK	2265.8	2266.8	2265.8	2266.8
114.0	6.7	6.7	62.3	0.0	99.0	SCCSOCPVGCAGK	1446.5	1447.5	1446.5	1447.5
114.0	6.7	6.7	62.3	0.0	99.0	SCCSOCPVGCAGK	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	DVWGI EGPIDAAFTR	1645.8	1646.8	1645.8	1646.8
119.0										

16.0	37.1	37.1	57.7	2.0	99.0	DGADFAKWR	1064.5	1065.5	1064.5	1065.5
16.0	37.1	37.1	57.7	2.0	99.0	IGEHTPSALAIMENANVLAR	2106.1	2107.1	2106.1	2107.1
16.0	37.1	37.1	57.7	2.0	99.0	IVAPGKGLAADESTGSIAGR	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	PYQYPALTPQEK	1433.7	1433.7	1433.7	1434.7
16.0	37.1	37.1	57.7	2.0	99.0	PYQYPALTPQEK	1561.8	1562.8	1561.8	1562.8
16.0	37.1	37.1	57.7	2.0	99.0	PYQYPALTPQEKKELSDIAHR	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	YTPSGOAGAAASESLFVSNHAY	2227.0	2228.0	2227.0	2228.0
16.0	37.1	37.1	57.7	1.7	98.0	YOYPALTPQEKKELSDIAHR	2479.2	2480.2	2479.2	2480.2
16.0	37.1	37.1	57.7	1.4	96.0	KENLKAQEEYVYKR	1704.9	1705.9	1704.9	1705.9
16.0	37.1	37.1	57.7	0.7	82.0	ENLKAQEEYVYKR	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	MPYOYPALTPQEKKELSDIAHR	2495.3	2496.3	2495.3	2496.3
16.0	37.1	37.1	57.7	0.0	58.0	LOSIGTENTENRR	1648.8	1648.8	1648.8	1648.8
52.0	6.2	6.2	29.4	2.0	99.0	IGEHTPSALAIMENANVLAR	2106.1	2107.1	2106.1	2107.1
52.0	6.2	6.2	29.4	2.0	99.0	PYQYPALTPQEK	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	YTPSGOAGAAASESLFVSNHAY	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	ADDGRPFPOVIK	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	AWGGKENLKAQEEYVYKR	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	IGEHTPSALAIMENANVLAR	2106.1	2107.1	2106.1	2107.1
23.0	22.8	22.8	50.5	2.0	99.0	KENLKAQEEYVYKR	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	PYQYPALTPQEK	1433.7	1433.7	1433.7	1434.7
23.0	22.8	22.8	50.5	2.0	99.0	PYQYPALTPQEK	1561.8	1562.8	1561.8	1562.8
23.0	22.8	22.8	50.5	2.0	99.0	PYQYPALTPQEKKELSDIAHR	2483.3	2484.3	2483.3	2484.3
23.0	22.8	22.8	50.5	2.0	99.0	YTPSGOAGAAASESLFVSNHAY	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	IGEHTPSALAIMENANVLAR	2107.1	2108.1	2107.1	2108.1
23.0	22.8	22.8	50.5	0.0	99.0	PYQYPALTPQEK	1564.8	1565.9	1564.8	1565.8
23.0	22.8	22.8	50.5	0.0	98.0	PYQYPALTPQEKKELSDIAHR	2484.3	2485.3	2484.3	2485.3
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	MMCGAPSATOPATAEQHIADQVR	2612.2	2613.2	2612.2	2613.2
318.0	4.0	4.0	36.7	2.0	99.0	VHVGDIEDFVHLR	1421.7	1422.7	1421.7	1422.7
277.0	2.1	2.1	30.6	2.0	99.0	VHVGDIEDFVHLR	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	1738.9	1739.9	1738.9	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	IISNASCTTNCLAPLAK	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	VIIISAPSADAPMFVGMVNHKEYDNLK	2932.4	2933.5	2932.4	2933.5
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	WGDAGAEYVVESTGVFTTMEK	2277.1	2278.1	2277.0	2278.0
30.0	24.2	24.2	49.6	1.3	95.0	VIFELNGLTGMAFR	1645.9	1646.9	1645.9	1646.9
30.0	24.2	24.2	49.6	0.5	67.0	LTGMAFR	794.4	795.4	794.4	795.4
30.0	24.2	24.2	49.6	0.4	60.0	LTGMAFRVPNTANVSVVDLTCR	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	PELNGKLTGMAFR	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	1754.8	1755.8
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	IISNASCTTNCLAPLAK	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	WGDAGAEYVVESTGVFTTMEK	2277.0	2278.0	2277.0	2278.0
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	LTGMAFR	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	98.0	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	GNFHAYRRDLKK	1561.8	1562.8	1561.8	1562.8
317.0	4.0	4.0	25.8	2.0	99.0	LLETECPOYI	1420.7	1421.7	1420.7	1421.7
161.0	4.4	4.4	25.8	2.0	99.0	GNFHAYRRDLKK	1561.8	1562.8	1561.8	1562.8
161.0	4.4	4.4	25.8	2.0	99.0	LLETECPOYI	1420.7	1421.7	1420.7	1421.7
161.0	4.4	4.4	25.8	0.4	63.0	GNFHAYVR	962.5	963.5	962.5	963.5
161.0	4.4	4.4	25.8	0.0	33.0	GNFHAYRRDLKK	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) - Homo sapiens (Human)								
114.0	10.0	10.0	13.5	2.0	99.0	ITNGLFFGR	1239.6	1240.7	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	TPVQMMYL	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	AIILOQAADKIHSSFR	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	TPVQMMYL	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	AIILOQAADKIHSSFR	1754.9	1755.9	1754.9	1756.0
17.0	26.4	26.4	37.3	2.0	99.0	GKIPNLLPEGSDVDGTR	1766.9	1767.9	1766.9	1767.9
17.0	26.4	26.4	37.3	2.0	99.0	GSYPDAILDQAQADKIHSSFR	2274.1	2275.1	2274.1	2275.1
17.0	26.4	26.4	37.3	2.0	99.0	ITNGLFFGR	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	26.4	37.3	2.0	99.0	MVLNVAVYFK	1182.6	1183.7		

P06576] ATPB_HUMAN		ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (Human)							
251.0	2.2	2.2	15.7	2.0	99.0	AHGYSVFAVGGER	1405.7	1405.7	1406.7
251.0	2.2	2.2	15.7	0.2	38.0	IMDPNIVGSEHYDVAR	1814.9	1815.9	1815.9
316.0	4.0	4.0	6.6	2.0	99.0	AI AELGIYPAVDPLDSTSR	1987.0	1988.0	1987.0
316.0	4.0	4.0	6.6	2.0	99.0	IMDPNIVGSEHYDVAR	1814.9	1815.9	1815.9
P06739] ENOA_HUMAN		Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc)							
15.0	38.3	38.3	62.9	2.0	99.0	AAVPSGASTGIYEALERL	1803.9	1804.9	1804.9
15.0	38.3	38.3	62.9	2.0	99.0	AGAVEKGVPLYR	1258.7	1259.7	1259.7
15.0	38.3	38.3	62.9	2.0	99.0	EI FDSRGNPTVEVDLFTSK	2153.1	2154.1	2154.1
15.0	38.3	38.3	62.9	2.0	99.0	FTASAGIQVVGDDLTVTNPKR	2188.1	2189.1	2189.2
15.0	38.3	38.3	62.9	2.0	99.0	IGAEVYHNKL	1142.6	1143.6	1143.6
15.0	38.3	38.3	62.9	2.0	99.0	LAKYNQLLR	1117.6	1118.6	1118.7
15.0	38.3	38.3	62.9	2.0	99.0	LAMQEFMILPVGAANFR	1907.0	1908.0	1908.0
15.0	38.3	38.3	62.9	2.0	99.0	LAQANGWGMVMSHR	1525.7	1526.7	1526.8
15.0	38.3	38.3	62.9	2.0	99.0	NFRNPLAK	958.5	959.5	959.5
15.0	38.3	38.3	62.9	2.0	99.0	SCNCLLKL	1006.5	1007.5	1007.5
15.0	38.3	38.3	62.9	2.0	99.0	SGKYDLDFKSPDDPSR	1825.8	1826.8	1826.9
15.0	38.3	38.3	62.9	2.0	99.0	VNOIGSVTESLQACK	1632.8	1633.8	1633.8
15.0	38.3	38.3	62.9	2.0	99.0	VNOIGSVTESLQACKL	1784.8	1785.8	1785.8
15.0	38.3	38.3	62.9	2.0	99.0	VVIGMDVAASEFFR	1539.8	1540.8	1540.8
15.0	38.3	38.3	62.9	2.0	99.0	YGKDATNVGDEGGFAPNILENK	2308.1	2309.1	2309.1
15.0	38.3	38.3	62.9	2.0	99.0	YGKDATNVGDEGGFAPNILENKEGLELLK	3090.6	3091.6	3091.6
15.0	38.3	38.3	62.9	2.0	99.0	YISPDQADLYK	1424.7	1425.7	1425.7
15.0	38.3	38.3	62.9	1.3	95.0	AGYTKVVGMDVAASEFFR	2176.1	2177.1	2176.1
15.0	38.3	38.3	62.9	1.3	95.0	EI FDSR	765.4	766.4	766.4
15.0	38.3	38.3	62.9	1.1	92.0	AAVPSGASTGIYEALERLNDKTR	2533.2	2534.2	2534.2
15.0	38.3	38.3	62.9	0.6	75.0	GVPLYR	703.4	704.4	704.4
15.0	38.3	38.3	62.9	0.0	45.0	AGAVEKGVPLYR	1260.7	1261.7	1259.7
15.0	38.3	38.3	62.9	0.0	99.0	LAKYNQLLR	1117.7	1118.7	1118.7
15.0	38.3	38.3	62.9	0.0	99.0	LAMQEFMILPVGAANFR	1910.0	1911.0	1908.0
15.0	38.3	38.3	62.9	0.0	53.0	LAQANGWGMVMSHR	1541.7	1542.7	1542.7
15.0	38.3	38.3	62.9	0.0	23.0	LAQANGWGMVMSHR	1522.7	1523.8	1523.8
15.0	38.3	38.3	62.9	0.0	99.0	NFRNPLAK	958.5	959.5	959.5
15.0	38.3	38.3	62.9	0.0	99.0	YISPDQADLYK	1420.7	1421.7	1425.7
15.0	38.3	38.3	62.9	0.0	57.0	YISPDQADLYK	1423.7	1424.7	1425.7
19.0	14.1	14.1	35.3	2.0	99.0	GNPTVEVDLFTSK	1405.7	1406.7	1406.7
19.0	14.1	14.1	35.3	2.0	99.0	IGAEVYHNKL	1142.6	1143.6	1143.6
19.0	14.1	14.1	35.3	2.0	99.0	LAMQEFMILPVGAANFR	1907.0	1908.0	1908.0
19.0	14.1	14.1	35.3	2.0	99.0	LAQANGWGMVMSHR	1525.7	1526.8	1526.8
19.0	14.1	14.1	35.3	2.0	99.0	YISPDQADLYK	1422.7	1423.7	1425.7
19.0	14.1	14.1	35.3	1.4	96.0	AAVPSGASTGIYEALERL	1803.9	1804.9	1804.9
19.0	14.1	14.1	35.3	0.8	83.0	VNOIGSVTESLQACK	1632.8	1633.8	1633.8
19.0	14.1	14.1	35.3	0.7	91.0	LAKYNQLLR	1117.6	1118.7	1118.7
19.0	14.1	14.1	35.3	0.5	70.0	SGKYDLDFKSPDDPSR	1825.8	1826.9	1826.9
19.0	14.1	14.1	35.3	0.4	57.0	NFRNPLAK	958.5	959.5	959.5
19.0	14.1	14.1	35.3	0.3	50.0	YNQLLR	805.5	806.5	806.5
19.0	14.1	14.1	35.3	0.0	99.0	YISPDQADLYK	1423.7	1424.7	1425.7
12.0	31.0	31.0	55.8	2.0	99.0	AAVPSGASTGIYEALERL	1803.9	1804.9	1804.9
12.0	31.0	31.0	55.8	2.0	99.0	AGYTKVVGMDVAASEFFR	2176.0	2177.1	2176.1
12.0	31.0	31.0	55.8	2.0	99.0	DATNVGDEGGFAPNILENKEGLELLK	2742.3	2743.3	2743.3
12.0	31.0	31.0	55.8	2.0	99.0	EI FDSRGNPTVEVDLFTSK	2153.1	2154.1	2154.1
12.0	31.0	31.0	55.8	2.0	99.0	GNPTVEVDLFTSK	1405.7	1406.7	1406.7
12.0	31.0	31.0	55.8	2.0	99.0	IGAEVYHNKL	1142.6	1143.6	1143.6
12.0	31.0	31.0	55.8	2.0	99.0	LAQANGWGMVMSHR	1525.7	1526.8	1526.8
12.0	31.0	31.0	55.8	2.0	99.0	NFRNPLAK	958.5	959.5	959.5
12.0	31.0	31.0	55.8	2.0	99.0	SGKYDLDFKSPDDPSR	1825.8	1826.8	1826.9
12.0	31.0	31.0	55.8	2.0	99.0	VNOIGSVTESLQACK	1632.8	1633.8	1633.8
12.0	31.0	31.0	55.8	2.0	99.0	VVIGMDVAASEFFR	1539.8	1540.8	1540.8
12.0	31.0	31.0	55.8	2.0	99.0	YISPDQADLYK	1424.7	1425.7	1425.7
12.0	31.0	31.0	55.8	1.5	97.0	VNOIGSVTESLQACKL	1784.8	1785.8	1785.8
12.0	31.0	31.0	55.8	1.5	97.0	YNQLLR	805.5	806.5	806.5
12.0	31.0	31.0	55.8	1.3	95.0	SGETEDTFIADLVVGLCTGQIK	2352.2	2353.2	2353.1
12.0	31.0	31.0	55.8	1.0	91.0	AAVPSGASTGIYEALERLNDKTR	2533.2	2534.2	2534.1
12.0	31.0	31.0	55.8	0.7	82.0	SCNCLLKL	1006.5	1007.5	1007.5
12.0	31.0	31.0	55.8	0.3	49.0	GVPLYR	703.4	704.4	704.4
12.0	31.0	31.0	55.8	0.2	42.0	LAMQEFMILPVGAANFR	1907.0	1908.0	1908.0
12.0	31.0	31.0	55.8	0.2	52.0	LAKYNQLLR	1117.6	1118.7	1118.7
12.0	31.0	31.0	55.8	0.1	25.0	AVNEKSONCLLKL	1562.8	1563.8	1563.8
12.0	31.0	31.0	55.8	0.0	48.0	GVPLYR	703.4	704.4	704.4
12.0	31.0	31.0	55.8	0.0	95.0	IGAEVYHNKL	1142.6	1143.6	1143.6
12.0	31.0	31.0	55.8	0.0	99.0	NFRNPLAK	958.5	959.5	959.5
12.0	31.0	31.0	55.8	0.0	94.0	NFRNPLAK	956.5	957.5	958.5
12.0	31.0	31.0	55.8	0.0	29.0	NFRNPLAK	959.5	960.5	960.5
12.0	31.0	31.0	55.8	0.0	42.0	YISPDQADLYK	1420.7	1421.7	1425.7
P06744] G6PI_HUMAN		Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin) (NLK) (S)							
92.0	11.9	11.9	18.6	2.0	99.0	AALTRDPOFOK	1315.7	1316.7	1316.7
92.0	11.9	11.9	18.6	2.0	99.0	MFNGEKINYTEGR	1558.7	1559.7	1559.7
92.0	11.9	11.9	18.6	2.0	99.0	MIPCDPLIPVQTHPIRK	2194.2	2195.2	2193.2
92.0	11.9	11.9	18.6	2.0	99.0	SGDQYGVYK	1098.5	1099.5	1098.5
92.0	11.9	11.9	18.6	2.0	99.0	VWVYSNIDGTHIAK	1601.8	1602.8	1602.8
92.0	11.9	11.9	18.6	1.2	94.0	LOQWYR	892.5	893.5	893.5
92.0	11.9	11.9	18.6	0.6	75.0	TLAQLNPRESSLFIASK	1831.0	1832.0	1832.0
92.0	11.9	11.9	18.6	0.0	93.0	LOQWYR	892.5	893.5	893.5
103.0	7.7	7.7	15.2	2.0	99.0	AALTRDPOFOK	1315.7	1316.7	1316.7
103.0	7.7	7.7	15.2	2.0	99.0	LOQWYR	892.5	893.5	893.5
103.0	7.7	7.7	15.2	2.0	99.0	MIPCDPLIPVQTHPIRK	2192.2	2193.2	2193.2
103.0	7.7	7.7	15.2	1.7	98.0	FAAYFOQGDMEISNGKYTK	2198.0	2199.0	2199.0
103.0	7.7	7.7	15.2	0.0	98.0	LOQWYR	892.5	893.5	893.5
P06753] TPM3_HUMAN		Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5) - Homo sapiens (Human)							
255.0	4.6	16.4	40.8	2.0	99.0	ALKDEEKMEIQELQKKAQ	2273.1	2274.1	2272.2
255.0	4.6	16.4	40.8	1.4	96.0	KLVIIEGDLERTFEER	1799.0	1800.0	1800.0
255.0	4.6	16.4	40.8	2.0	99.0	KLVIIEGDLER	1283.7	1284.7	1284.8
255.0	4.6	16.4	40.8	0.0	99.0	HI AEEADRKYEEVAR	1828.9	1829.9	1827.9
255.0	4.6	16.4	40.8	0.0	99.0	HI AEEADRKYEEVAR	1814.9	1815.9	1815.9
255.0	4.6	16.4	40.8	0.0	74.0	HI AEEADRKYEEVAR	1814.9	1815.9	1815.9
255.0	4.6	16.4	40.8	0.0	99.0	IQLVEEELDR	1242.6	1243.6	1243.7
255.0	4.6	16.4	40.8	0.0	99.0	IQLVEEELDR	1242.6	1243.6	1243.7
255.0	4.6	16.4	40.8	0.0	99.0	IQLVEEELDR	1242.6	1243.6	1243.7
255.0	4.6	16.4	40.8	0.0	99.0	LATALOKLEEAKAEDESER	1726.9	1727.9	1727.9
255.0	4.6	16.4	40.8	0.0	99.0	LATALOKLEEAKAEDESER	2201.1	2202.1	2202.1
255.0	4.6	16.4	40.8	0.0	89.0	LEEAEKAADESER	1475.7	1476.7	1476.7
255.0	4.6	16.4	40.8	0.0	99.0	RIQLVEEELDR	1883.0	1884.0	1884.0
391.0	1.5	9.7	21.5	1.5	97.0	KLVIIEGDLER	1279.7	1280.8	1284.8
391.0	1.5	9.7	21.5	0.0	50.0	HI AEEADRKYEEVAR	1814.9	1815.9	1815.9
391.0	1.5	9.7	21.5	0.0	99.0	IQLVEEELDR	1242.6	1243.6	1243.7
391.0	1.5	9.7	21.5	0.0	99.0	LATALOKLEEAKAEDESER	1726.9	1727.9	1727.9
391.0	1.5	9.7	21.5	0.0	99.0	LATALOKLEEAKAEDESER	2201.1	2202.1	2202.1
391.0	1.5	9.7	21.5	0.0	83.0	LEEAEKAADESER	1475.7	1476.7	1476.7
391.0	1.5	9.7	21.5	0.0	92.0	RIQLVEEELDR	1398.7		

P07339] CATD_HUMAN		Cathepsin D precursor (EC 3.4.23.5)		[Contains: Cathepsin D light chain; Cathepsin D heavy chain] - Homo sapiens (Human)					
199.0	6.0	6.0	18.2	2.0	99.0	FDGILGMAYPR	1238.6	1239.6	1239.6
199.0	6.0	6.0	18.2	2.0	99.0	QVFGKATKQPGITFIAAK	1905.0	1906.0	1906.0
199.0	6.0	6.0	18.2	2.0	99.0	RI SVNNVLPFDNLMOQK	2211.1	2212.1	2212.1
70.0	4.9	4.9	20.9	2.0	99.0	AI GAVPLI OGEYMI PCEK	1989.0	1989.0	1989.0
70.0	4.9	4.9	20.9	2.0	99.0	FDGILGMAYPR	1238.6	1239.6	1239.6
70.0	4.9	4.9	20.9	0.9	86.0	YYTVFDRDNNR	1462.7	1463.7	1463.7
70.0	4.9	4.9	20.9	0.0	81.0	YYTVFDRDNNR	1461.7	1462.7	1462.7
149.0	4.9	4.9	16.0	2.0	99.0	AIGAVPLIOGEYMIPCEK	1989.0	1989.0	1989.0
149.0	4.9	4.9	16.0	2.0	99.0	FDGILGMAYPR	1238.6	1239.6	1239.6
149.0	4.9	4.9	16.0	0.7	82.0	YYTVFDRDNNR	1461.7	1462.7	1462.7
149.0	4.9	4.9	16.0	0.1	20.0	QVFGKATKQPGITFIAAK	1905.0	1906.0	1906.0
P07437] TBB5_HUMAN		Tubulin beta chain (Tubulin beta-5 chain) - Homo sapiens (Human)							
21.0	28.5	28.5	47.3	2.0	99.0	ALVPELTQQVFDK	1658.9	1659.9	1659.9
21.0	28.5	28.5	47.3	2.0	99.0	EI VHIQAGQGNQIGAK	1821.9	1822.9	1822.9
21.0	28.5	28.5	47.3	2.0	99.0	FWEIVSDEHGIDPTGTGTHGSDSLQLDR	3101.4	3102.4	3102.4
21.0	28.5	28.5	47.3	2.0	99.0	GHYTEGAELVDSVLDVVR	1957.9	1958.9	1959.0
21.0	28.5	28.5	47.3	2.0	99.0	ISEQFTAMFR	1228.6	1229.6	1229.6
21.0	28.5	28.5	47.3	2.0	99.0	ISVYNEATGGK	1300.6	1301.6	1301.6
21.0	28.5	28.5	47.3	2.0	99.0	ISVYNEATGGKYVPR	1815.9	1816.9	1816.9
21.0	28.5	28.5	47.3	2.0	99.0	LAVNMFVPPR	1142.6	1143.6	1143.6
21.0	28.5	28.5	47.3	2.0	99.0	MSMKEVDQMLNVQNK	1922.9	1923.9	1923.9
21.0	28.5	28.5	47.3	2.0	99.0	NSSYFVEWIPNNVK	1695.8	1696.8	1696.8
21.0	28.5	28.5	47.3	2.0	99.0	YLTVAAVFR	1038.6	1039.6	1039.6
21.0	28.5	28.5	47.3	1.7	98.0	IMNTFSVPSPK	1318.7	1319.7	1319.7
21.0	28.5	28.5	47.3	1.5	97.0	LHFFMPGFAPLTSR	1619.8	1620.8	1620.8
21.0	28.5	28.5	47.3	1.3	95.0	IREEYPRIMNTFSVPSPK	2377.2	2378.2	2378.2
21.0	28.5	28.5	47.3	0.9	87.0	RI SEQFTAMFR	1384.7	1385.7	1385.7
21.0	28.5	28.5	47.3	0.5	69.0	IREEYPR	1076.5	1077.5	1077.5
21.0	28.5	28.5	47.3	0.5	66.0	ALVLEPSTGTMDSVR	1614.8	1615.8	1615.8
21.0	28.5	28.5	47.3	0.1	24.9	GQLNADLR	887.4	888.4	888.4
26.0	11.9	11.9	22.5	2.0	99.0	ISVYNEATGGKYVPR	1815.9	1816.9	1816.9
26.0	11.9	11.9	22.5	2.0	99.0	KLAVNMFVPPR	1270.7	1271.7	1271.7
26.0	11.9	11.9	22.5	2.0	99.0	LAVNMFVPPR	1142.6	1143.6	1143.6
26.0	11.9	11.9	22.5	2.0	99.0	NSSYFVEWIPNNVK	1695.8	1696.8	1696.8
26.0	11.9	11.9	22.5	2.0	99.0	YLTVAAVFR	1038.6	1039.6	1039.6
26.0	11.9	11.9	22.5	1.7	98.0	ISEQFTAMFR	1228.6	1229.6	1229.6
26.0	11.9	11.9	22.5	0.1	26.0	ALVPELTQQVFDK	1658.9	1659.9	1659.9
47.0	15.8	15.8	30.0	2.0	99.0	ALVPELTQQVFDK	1658.9	1659.9	1659.9
47.0	15.8	15.8	30.0	2.0	99.0	ISEQFTAMFR	1228.6	1229.6	1229.6
47.0	15.8	15.8	30.0	2.0	99.0	ISVYNEATGGK	1300.6	1301.6	1301.6
47.0	15.8	15.8	30.0	2.0	99.0	ISVYNEATGGKYVPR	1815.9	1816.9	1816.9
47.0	15.8	15.8	30.0	2.0	99.0	KLAVNMFVPPR	1270.7	1271.7	1271.7
47.0	15.8	15.8	30.0	2.0	99.0	LAVNMFVPPR	1142.6	1143.6	1143.6
47.0	15.8	15.8	30.0	2.0	99.0	YLTVAAVFR	1038.6	1039.6	1039.6
47.0	15.8	15.8	30.0	1.4	96.0	NSSYFVEWIPNNVK	1696.8	1697.8	1697.8
47.0	15.8	15.8	30.0	0.3	45.0	RI SEQFTAMFR	1384.7	1385.7	1385.7
47.0	15.8	15.8	30.0	0.0	99.0	ISVYNEATGGKYVPR	1815.9	1816.9	1816.9
47.0	15.8	15.8	30.0	0.0	99.0	YLTVAAVFR	1038.6	1039.6	1039.6
P07602] SAP_HUMAN		Proactivator polypeptide precursor [Contains: Saposin A (Protein A); Saposin B-Va; Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebro							
204.0	6.0	6.0	9.7	2.0	99.0	DNGDVQDCIQMVTDIQTAVR	2420.1	2421.1	2420.0
204.0	6.0	6.0	9.7	2.0	99.0	GDVQDCIQMVTDIQTAVR	2208.0	2209.0	2209.0
204.0	6.0	6.0	9.7	2.0	99.0	SDVYCEVCEFLVK	1646.7	1647.7	1646.7
92.0	4.0	4.0	5.7	2.0	99.0	DVYCEVCEFLVK	1559.7	1560.7	1560.7
92.0	4.0	4.0	5.7	2.0	99.0	SDVYCEVCEFLVK	1646.7	1647.7	1646.7
89.0	8.3	8.3	11.8	2.0	99.0	DNGDVQDCIQMVTDIQTAVR	2438.1	2439.1	2439.1
89.0	8.3	8.3	11.8	2.0	99.0	GDVQDCIQMVTDIQTAVR	2208.0	2209.0	2209.0
89.0	8.3	8.3	11.8	2.0	99.0	NGDVQDCIQMVTDIQTAVR	2323.0	2324.0	2324.0
89.0	8.3	8.3	11.8	2.0	99.0	SDVYCEVCEFLVK	1646.7	1647.7	1647.7
89.0	8.3	8.3	11.8	0.1	27.0	LGPMDADICK	1060.5	1061.5	1061.5
89.0	8.3	8.3	11.8	0.1	24.0	SDVYCEVCEFLVKEVTK	2103.9	2104.9	2105.0
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							
438.0	2.0	2.0	7.8	2.0	99.0	NSWGEWGMGGYVK	1598.7	1599.7	1599.7
438.0	2.0	2.0	7.8	0.0	99.0	NSWGEWGMGGYVK	1614.7	1615.7	1614.7
210.0	1.4	1.4	5.1	1.4	96.0	NSWGEWGMGGYVK	1598.7	1599.7	1599.7
210.0	1.4	1.4	5.1	0.0	94.0	NSWGEWGMGGYVK	1614.7	1615.7	1614.7
225.0	2.9	2.9	22.2	2.0	99.0	NSWGEWGMGGYVK	1598.7	1599.7	1599.7
225.0	2.9	2.9	22.2	0.9	85.0	VFGPEVLEAPR	1494.7	1495.7	1495.8
225.0	2.9	2.9	22.2	0.0	99.0	NSWGEWGMGGYVK	1614.7	1615.7	1614.7
P07737] PROF1_HUMAN		Profilin-1 (Profilin I) - Homo sapiens (Human)							
36.0	22.5	22.5	82.1	2.0	99.0	CSVIRDSLLDGEFSMDLR	2223.0	2224.0	2223.0
36.0	22.5	22.5	82.1	2.0	99.0	CYEMASHLR	1148.5	1149.5	1148.5
36.0	22.5	22.5	82.1	2.0	99.0	DSLLDGEFSMDLR	1624.7	1625.7	1624.7
36.0	22.5	22.5	82.1	2.0	99.0	EGVHGGLNKK	1150.6	1151.6	1151.7
36.0	22.5	22.5	82.1	2.0	99.0	KCYEMASHLR	1293.6	1294.6	1294.6
36.0	22.5	22.5	82.1	2.0	99.0	SSFVYNGTLGGQK	1470.7	1471.7	1471.7
36.0	22.5	22.5	82.1	2.0	99.0	STGGAPTFNVTVK	1378.7	1379.7	1379.7
36.0	22.5	22.5	82.1	2.0	99.0	STGGAPTFNVTVKTDK	1722.9	1723.9	1723.9
36.0	22.5	22.5	82.1	2.0	99.0	TFVNITPAEVLGVGKDR	1642.9	1643.9	1643.9
36.0	22.5	22.5	82.1	2.0	99.0	TFVNITPAEVLGVGKDR	1914.1	1915.1	1915.1
36.0	22.5	22.5	82.1	2.0	99.0	TKSTGGAPTFNVTVK	1607.9	1608.9	1608.9
36.0	22.5	22.5	82.1	0.3	55.0	CYEMASHLR	1304.6	1305.6	1305.6
36.0	22.5	22.5	82.1	0.2	31.0	KCYEMASHLR	1449.7	1450.7	1449.7
36.0	22.5	22.5	82.1	0.0	99.0	CSVIRDSLLDGEFSMDLR	2240.0	2241.0	2241.1
36.0	22.5	22.5	82.1	0.0	99.0	CYEMASHLR	1165.5	1166.5	1165.5
36.0	22.5	22.5	82.1	0.0	41.0	CYEMASHLR	1321.6	1322.6	1322.6
36.0	22.5	22.5	82.1	0.0	99.0	SSFVYNGTLGGQK	1470.7	1471.7	1471.7
36.0	22.5	22.5	82.1	0.0	99.0	STGGAPTFNVTVK	1378.7	1379.7	1379.7
36.0	22.5	22.5	82.1	0.0	99.0	TKSTGGAPTFNVTVK	1607.9	1608.9	1608.9
21.0	13.4	13.4	61.4	2.0	99.0	CYEMASHLR	1165.5	1166.5	1165.5
21.0	13.4	13.4	61.4	2.0	99.0	CYEMASHLR	1321.6	1322.6	1322.6
21.0	13.4	13.4	61.4	2.0	99.0	DSLLDGEFSMDLR	1624.7	1625.7	1624.7
21.0	13.4	13.4	61.4	2.0	99.0	SSFVYNGTLGGQK	1469.8	1470.8	1469.8
21.0	13.4	13.4	61.4	2.0	99.0	TFVNITPAEVLGVGKDR	1914.0	1915.0	1914.1
21.0	13.4	13.4	61.4	2.0	99.0	TKSTGGAPTFNVTVK	1607.9	1608.9	1608.9
21.0	13.4	13.4	61.4	1.0	89.0	KCYEMASHLR	1293.6	1294.6	1294.6
21.0	13.4	13.4	61.4	0.5	67.0	CSVIRDSLLDGEFSMDLR	2240.1	2241.1	2241.1
21.0	13.4	13.4	61.4	0.0	46.0	CSVIRDSLLDGEFSMDLR	2223.0	2224.0	2224.0
21.0	13.4	13.4	61.4	0.0	96.0	CYEMASHLR	1148.5	1149.5	1148.5
21.0	13.4	13.4	61.4	0.0	39.0	CYEMASHLR	1304.6	1305.6	1305.6
21.0	13.4	13.4	61.4	0.0	99.0	SSFVYNGTLGGQK	1470.7	1471.7	1471.7
21.0	13.4	13.4	61.4	0.0	99.0	SSFVYNGTLGGQK	1470.7	1471.7	1471.7
29.0	20.9	20.9	61.4	2.0	99.0	CYEMASHLR	1148.5	1149.5	1149.5
29.0	20.9	20.9	61.4	2.0	99.0	CYEMASHLR	1305.6	1306.6	1305.6
29.0	20.9	20.9	61.4	2.0	99.0	DSLLDGEFSMDLR	1624.7	1625.7	1624.7
29.0	20.9	20.9	61.4	2.0	99.0	EGVHGGLNKK	1150.6	1151.6	1151.7
29.0	20.9	20.9	61.4	2.0	99.0	SSFVYNGTLGGQK	1470.7	1471.7	1471.7
29.0	20.9	20.9	61.4	2.0	99.0	STGGAPTFNVTVK	1378.7	1379.7	1379.7
29.0	20.9	20.9	61.4	2.0	99.0	STGGAPTFNVTVKTDK	1722.9	1723.9	1723.9
29.0	20.9	20.9	61.4	2.0	99.0	TFVNITPAEVLGVGKDR	1642.9	1643.9	1643.9
29.0	20.9	20.9	61.4	2.0	99.0	TFVNITPAEVLGVGKDR	1914.1	1915.1	1915.1
29.0	20.9	20.9	61.4	2.0	99.0	TKSTGGAPTFNVTVK	1607.9	1608.9	1608.9
29.0	20.9	20.9	61.4	0.5	69.0	KCYEMASHLR	1449.7	1450.7	1449.7
29.0	20.9	20.9	61.4	0.3	48.0	KCYEMASHLR	1293.6	1294.6	1294.6
29.0	20.9	20.9	61.4	0.1	29.0	DRSSFVYNGTLGGQK	1741.8	1742.8	1741.9
29.0	20.9	20.9	61.4	0.0	95.0	CYEMASHLR	1148.5	1149.5	1148.5
29.0	20.9	20.9	61.4	0.0	74.0	CYEMASHLR	1165.5	1166.5	1165.5
29.0	20.9	20.9	61.4	0.0	68.0	CYEMASHLR	1164.5	1165.5	1165.5
29.0	20.9	20.9	61.4	0.0	25.0	CYEMASHLR	1165.5	1166.5	1165.5
29.0	20.9	20.9	61.4	0.0	21.0	CYEMASHLR	1473.6	1474.6	1473.5
29.0	20.9	20.9	61.4	0.0	96.0	DSLLDGEFSMDLR	1640.7	1641.7	1641.7

51.0	17.4	17.4	38.3	2.0	99.0	LOGTFLGGPKPPQR	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	SGVYQHVTGEMMGHHAIR	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	EGWPOCPPTIK	1285.6	1286.6	1285.6	1286.6
51.0	17.4	17.4	38.3	1.2	94.0	ILRGDQHOGIESEVAGIPR	2205.1	2206.1	2205.1	2206.1
51.0	17.4	17.4	38.3	0.5	67.0	DQSGSCGSWAFGAVEAISDR	2171.9	2172.9	2171.9	2172.9
51.0	17.4	17.4	38.3	0.1	26.0	RLCGTFLGGPKPPQR	1682.9	1683.9	1682.9	1683.9
71.0	4.9	4.9	28.0	2.0	99.0	EGWPOCPPTIK	1683.8	1684.8	1683.8	1684.8
71.0	4.9	4.9	28.0	2.0	99.0	SGVYQHVTGEMMGHHAIR	1928.9	1929.9	1928.9	1929.9
71.0	4.9	4.9	28.0	0.9	86.0	EGWPOCPPTIK	1285.6	1286.6	1285.6	1286.6
48.0	15.7	15.7	34.2	2.0	99.0	DQSGSCGSWAFGAVEAISDR	2171.9	2172.9	2171.9	2172.9
48.0	15.7	15.7	34.2	2.0	99.0	EGWPOCPPTIK	1683.8	1684.8	1683.8	1684.8
48.0	15.7	15.7	34.2	2.0	99.0	ICEPGSPTYKQDK	1684.8	1685.8	1684.8	1685.8
48.0	15.7	15.7	34.2	2.0	99.0	ILRGDQHOGIESEVAGIPR	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	SGVYQHVTGEMMGHHAIR	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	98.0	EGWPOCPPTIK	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	KhLEINPDHSIIETLR	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	HIYYITGETKDOVANSFAVFR	2442.2	2443.2	2442.2	2443.2
20.0	29.4	29.4	29.9	2.0	99.0	KhLEINPDHSIIETLR	1915.0	1916.0	1915.0	1916.0
20.0	29.4	29.4	29.9	2.0	99.0	LVTSPCCIVTSTYGVWTANMER	2445.1	2446.1	2445.1	2446.1
20.0	29.4	29.4	29.9	2.0	99.0	NPPDITNEEYGFYK	1832.8	1833.8	1832.8	1833.8
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	VIHLKEDQTEYLEER	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	YYTSAGDEMVLKDYCTR	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	GFAFVQYNER	1328.7	1329.7	1328.7	1329.7
241.0	5.0	5.0	8.8	2.0	99.0	SVPARVPPPIAR	1516.8	1517.8	1516.8	1517.8
241.0	5.0	5.0	8.8	0.6	72.0	MYSVPARVPPPIAR	1811.0	1812.0	1811.0	1812.0
241.0	5.0	5.0	8.8	0.4	63.0	VPPPPPIAR	942.6	943.6	942.6	943.6
213.0	3.2	3.2	27.5	2.0	99.0	GFAFVQYNER	1328.6	1329.6	1328.7	1329.7
213.0	3.2	3.2	27.5	1.2	93.0	VPPPPPIAR	942.6	943.6	942.6	943.6
P08170 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	LLQDFFRGRDLNK	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	ATAGDTHLGGEDFDR	1674.7	1675.7	1674.7	1675.7
127.0	9.2	14.3	29.2	0.3	46.0	DAGYIAGLNVLK	1196.7	1197.7	1196.7	1197.7
127.0	9.2	14.3	29.2	0.0	45.0	LDKAIQIIDLVLGGSTR	1837.0	1838.0	1837.0	1838.0
127.0	9.2	14.3	29.2	0.0	99.0	TPSYVAFTDTER	1486.7	1487.7	1486.7	1487.7
127.0	9.2	14.3	29.2	0.0	99.0	VEIANDQGNR	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	ATAGDTHLGGEDFDR	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	TPSYVAFTDTER	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	VLSIAQAHSFASFCQVR	1999.0	2000.0	1999.0	2000.0
145.0	2.1	2.1	16.3	2.0	99.0	VLSIAQAHSFASFCQVR	1999.0	2000.0	1999.0	2000.0
182.0	4.0	4.0	18.1	2.0	99.0	AFPALTSLDSDNPNGLGR	1972.0	1973.0	1972.0	1973.0
182.0	4.0	4.0	18.1	2.0	99.0	VLSIAQAHSFASFCQVR	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	FOLHDCQVQEK	1403.7	1404.7	1403.7	1404.7
250.0	4.7	4.7	3.7	2.0	99.0	LFLAEFOSIPR	1319.7	1320.7	1319.7	1320.7
250.0	4.7	4.7	3.7	0.7	80.0	TDFGSPGEPQII FCR	1722.8	1723.8	1722.8	1723.8
323.0	2.0	2.0	6.7	2.0	99.0	LFLAEFOSIPR	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	EKLOEEMLQREAEENTLQFR	2607.2	2608.2	2607.3	2608.3
3.0	63.4	63.4	70.0	2.0	99.0	EMEEFVAVEAANYQDTIGR	2187.0	2188.0	2187.0	2188.0
3.0	63.4	63.4	70.0	2.0	99.0	FADLSEANRNNDALR	1775.9	1776.9	1775.9	1776.9
3.0	63.4	63.4	70.0	2.0	99.0	FANVYDKVR	1124.6	1125.6	1124.6	1125.6
3.0	63.4	63.4	70.0	2.0	99.0	FSLADAINTEFK	1354.7	1355.7	1354.7	1355.7
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	HLREYDNLNVK	1526.8	1527.8	1526.8	1527.8
3.0	63.4	63.4	70.0	2.0	99.0	KLHEEELQELQAIQEQHVQID	2684.3	2685.3	2684.3	2685.3
3.0	63.4	63.4	70.0	2.0	99.0	KVESLQEEI AFLK	1532.8	1533.8	1532.8	1533.8
3.0	63.4	63.4	70.0	2.0	99.0	KVESLQEEI AFLKK	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	LGDLYEEMRELRL	1651.8	1652.8	1651.8	1652.8
3.0	63.4	63.4	70.0	2.0	99.0	LGDLYEEMRELRLR	1807.9	1808.9	1807.9	1808.9
3.0	63.4	63.4	70.0	2.0	99.0	LHEEELQELQAIQEQHVQID	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	LOEEMLQREAEENTLQFR	2350.1	2351.1	2350.1	2351.1
3.0	63.4	63.4	70.0	2.0	99.0	MFGGPTASRPSSSR	1493.7	1494.7	1493.7	1494.7
3.0	63.4	63.4	70.0	2.0	99.0	NLQEAEEWYK	1308.6	1309.6	1308.6	1309.6
3.0	63.4	63.4	70.0	2.0	99.0	NLQEAEEWYKSK	1523.7	1524.7	1523.7	1524.7
3.0	63.4	63.4	70.0	2.0	99.0	QVDLTDNKAR	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	QVQSLTCEVDALKGTNESLER	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	SRLGDLYEEMRELRLR	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	TVETRDGGVINEQSQHDDLE	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	VESLQEEI AFLK	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	EYVDLNVK	1120.6	1121.6	1120.6	1121.6
3.0	63.4	63.4	70.0	1.2	94.0	FADLSEANR	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	EEAENTLOSFR	1322.6	1323.6	1322.6	1323.6
3.0	63.4	63.4	70.0	0.0	99.0	EMEEFVAVEAANYQDTIGR	2191.0	2192.0	2186.0	2187.0
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				

8.0	22.8	22.8	70.6	0.1	28.0	HLREYODLLNVK	1526.8	1527.8	1526.8	1527.8
8.0	22.8	22.8	70.6	0.1	18.0	FANYIDKVR	1124.6	1124.6	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	TNEKVELOELNDR	1586.8	1587.8	1587.8	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	EEAEFLQSFROVDVNASLAR	2392.1	2392.1	2392.1	2392.1
8.0	44.3	44.3	62.2	2.0	99.0	EKLOEMLQR	1302.7	1302.7	1302.7	1302.7
8.0	44.3	44.3	62.2	2.0	99.0	EKLOEEMLOREAEANTLOSFR	2607.3	2608.3	2608.3	2608.3
8.0	44.3	44.3	62.2	2.0	99.0	EMENFAVEAANYODTIGR	2185.9	2186.9	2186.9	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	HLREYODLLNVK	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	LODEIQNKEMMAR	1733.8	1734.8	1733.8	1734.8
8.0	44.3	44.3	62.2	2.0	99.0	LOEBMLQR	1045.5	1045.5	1045.5	1045.5
8.0	44.3	44.3	62.2	2.0	99.0	NLQEAEEYWK	1308.6	1308.6	1308.6	1308.6
8.0	44.3	44.3	62.2	2.0	99.0	QVQSLTCEVDALKGTNESLER	2359.1	2360.2	2359.1	2360.1
8.0	44.3	44.3	62.2	2.0	99.0	RQVDLQTNDKAR	1442.8	1443.8	1442.8	1443.8
8.0	44.3	44.3	62.2	2.0	99.0	TNEKVELOELNDR	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	EYQDILLNVK	1120.6	1121.6	1120.6	1121.6
8.0	44.3	44.3	62.2	1.2	93.0	VELOELNDR	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	EEAENTLOSFR	1322.6	1323.6	1322.6	1323.6
8.0	44.3	44.3	62.2	0.2	42.0	QVDLQTNDKAR	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	QVDLQTNDKAR	1270.6	1271.6	1270.6	1271.6
8.0	44.3	44.3	62.2	0.0	99.0	QVQSLTCEVDALKGTNESLER	2376.2	2377.2	2376.2	2377.2
8.0	44.3	44.3	62.2	0.0	94.0	TNEKVELOELNDR	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	AFLASPEYVNLPI NGNGKQ	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	FODGDLTYQSNTILR	1882.9	1883.9	1882.9	1883.9
96.0	11.7	11.7	37.6	2.0	99.0	MLLADQGGQSWK	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	PPYTVVYFVPRGR	1549.8	1550.8	1549.8	1550.8
96.0	11.7	11.7	37.6	0.0	99.0	PPYTVVYFVPRGR	1552.8	1553.8	1552.8	1553.8
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	PPYTVVYFVPRGR	1549.8	1550.8	1549.8	1550.8
47.0	6.6	6.6	23.3	0.6	72.0	FODGDLTYQSNTILR	1882.9	1883.9	1882.9	1883.9
99.0	8.0	8.0	18.6	2.0	99.0	ASCLYGQLPK	1136.6	1136.6	1136.6	1136.6
99.0	8.0	8.0	18.6	2.0	99.0	FODGDLTYQSNTILR	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	PPYTVVYFVPRGR	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) (Galactin) (14)										
99.0	11.2	11.2	61.5	2.0	99.0	ACGLVASNLNLPKGECLR	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	FNAHGDANTI VCN SK	1646.8	1647.8	1646.7	1647.7
99.0	11.2	11.2	61.5	2.0	99.0	LNLEAINMAADGDKP	1783.8	1784.8	1783.8	1784.9
99.0	11.2	11.2	61.5	2.0	99.0	LPGDYEFKFPNR	1481.7	1482.7	1481.7	1482.7
99.0	11.2	11.2	61.5	1.2	94.0	DGGAWGTEQR	1075.5	1076.5	1075.5	1076.5
99.0	11.2	11.2	61.5	0.0	71.0	LPGDYEFKFPNR	1480.7	1481.7	1480.7	1481.7
68.0	4.9	4.9	61.5	2.0	99.0	ACGLVASNLNLPKGECLR	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	FNAHGDANTI VCN SK	1646.8	1647.8	1646.7	1647.8
68.0	4.9	4.9	61.5	0.2	38.0	LPGDYEFKFPNR	1481.7	1482.7	1481.7	1482.7
142.0	5.7	5.7	29.6	2.0	99.0	ACGLVASNLNLPKGECLR	2013.0	2014.0	2013.0	2014.0
142.0	5.7	5.7	29.6	2.0	99.0	LPGDYEFKFPNR	1481.7	1482.7	1481.7	1482.7
142.0	5.7	5.7	29.6	1.7	98.0	DGGAWGTEQR	1075.5	1076.5	1075.5	1076.5
P09429 HMGB1_HUMAN High mobility group protein B1 (High mobility group protein 1) (HMGB-1) - Homo sapiens (Human)										
42.0	20.0	20.0	45.6	2.0	99.0	GKMSYAFFVOTCR	1680.8	1681.8	1680.8	1681.8
42.0	20.0	20.0	45.6	2.0	99.0	GKMSYAFFVOTCR	2332.1	2333.1	2332.1	2333.1
42.0	20.0	20.0	45.6	2.0	99.0	KHPDASVNFSEFSK	1719.9	1720.9	1719.9	1720.9
42.0	20.0	20.0	45.6	2.0	99.0	KLGMWNNTAADDKQPYEK	2237.0	2238.0	2237.0	2238.0
42.0	20.0	20.0	45.6	2.0	99.0	LGEMWNNTAADDKQPYEK	2109.0	2110.0	2109.0	2110.0
42.0	20.0	20.0	45.6	2.0	99.0	LGEMWNNTAADDKQPYEK	2237.0	2238.0	2237.0	2238.0
42.0	20.0	20.0	45.6	2.0	99.0	LKEKYEDIAAYR	1625.9	1626.9	1625.9	1626.9
42.0	20.0	20.0	45.6	2.0	99.0	MSSYAFFVOTCR	1495.7	1496.7	1495.7	1496.7
42.0	20.0	20.0	45.6	2.0	99.0	MSSYAFFVOTCR	2147.0	2148.0	2147.0	2148.0
42.0	20.0	20.0	45.6	2.0	99.0	YEKDIAAYR	1127.6	1128.6	1127.6	1128.6
42.0	20.0	20.0	45.6	0.0	99.0	MSSYAFFVOTCR	1495.7	1496.7	1495.7	1496.7
40.0	7.5	7.5	33.5	2.0	99.0	LKEKYEDIAAYR	1625.9	1626.9	1625.9	1626.9
40.0	7.5	7.5	33.5	2.0	99.0	MSSYAFFVOTCR	1495.7	1496.7	1495.7	1496.7
40.0	7.5	7.5	33.5	2.0	99.0	MSSYAFFVOTCR	2147.0	2148.0	2147.0	2148.0
40.0	7.5	7.5	33.5	1.3	95.0	KLGMWNNTAADDKQPYEK	2237.0	2238.0	2237.0	2238.0
40.0	7.5	7.5	33.5	0.2	40.0	YEKDIAAYR	1127.6	1128.6	1127.6	1128.6
73.0	10.0	10.0	53.5	2.0	99.0	GKMSYAFFVOTCR	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	LKEKYEDIAAYR	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	YEKDIAAYR	1127.6	1128.6	1127.6	1128.6
73.0	10.0	10.0	53.5	0.0	35.0	LKEKYEDIAAYR	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	AKELEWYAR	2351.0	2352.0	2351.0	2352.0
315.0	4.0	4.0	12.9	2.0	99.0	AKELEWYAR	1406.7	1407.7	1406.7	1407.7
203.0	1.5	1.5	11.3	1.5	97.0	AKELEWYAR	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 sa										
32.0	23.7	28.6	63.4	2.0	99.0	ALSKQEMASASSQRGR	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	GFAFVTFDDHSDVKI VIKQ	2280.1	2281.2	2280.1	2281.1
32.0	23.7	28.6	63.4	2.0	99.0	KALSKQEMASASSQRGR	1949.0	1950.0	1949.0	1950.0
32.0	23.7	28.6	63.4	2.0	99.0	NQGGYGGSSSSSYGSGR	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	SHEFQWGLTDCVVMRDPNTRK	2676.3	2677.3	2676.3	2677.2
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	IEVIEIMTDR	1217.6	1218.6	1217.6	1218.6
32.0	23.7	28.6	63.4	1.2	99.0	LFI GGLSFETTD E S L R	1783.9	1784.9	1783.9	1784.9
32.0	23.7	28.6	63.4	0.4	59.0	KLFI GGLSFETTD E S L R	1912.0	1913.0	1912.0	1913.0
32.0	23.7	28.6	63.4	0.3	44.7	SKSESPEPEQLRK	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	IFVGGIKEDTEEHHLR	1879.0	1880.0	1879.0	1880.0
32.0	23.7	28.6	63.4	0.0	99.0	IFVGGIKEDTEEHHLR	18			

65.0	11.9	13.9	51.1	0.0	99.0	IFVGGIKEDTEEHHLR	1878.9	1880.0	1879.0	1880.0
65.0	11.9	13.9	51.1	0.0	99.0	IFVGGIKEDTEEHHLR	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 sap										
125.0	9.4	9.4	16.2	2.0	99.0	NREELGFRPEYSASLQK	2023.0	2023.0	2023.0	2024.0
125.0	9.4	9.4	16.2	2.0	99.0	SDAYNYCTGDTAWTK	1736.8	1737.8	1736.7	1737.7
125.0	9.4	9.4	16.2	2.0	99.0	VGHSPRFDVVDVDFSELRL	2149.2	2149.2	2149.1	2149.1
125.0	9.4	9.4	16.2	2.0	99.0	WYHRCFCFK	1192.5	1193.5	1192.5	1193.5
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	WYHRCFCFK	1192.5	1193.5	1192.5	1193.5
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	HRNALGGWGLONSVK	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	TLTGTAALTVQSGEDNLR	1917.0	1918.0	1917.0	1918.0
115.0	9.9	9.9	14.1	1.7	98.0	APRLRGLHKRR	1100.7	1101.7	1100.7	1101.7
115.0	9.9	9.9	14.1	0.2	34.0	MKFTFRPLK	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	GFMPFLLPGESNKIPR	1783.9	1784.9	1783.9	1784.9
179.0	6.4	6.4	39.2	2.0	99.0	NLPSSDQDLGQHGLEEDFML	2244.0	2245.0	2244.0	2245.0
179.0	6.4	6.4	39.2	2.0	99.0	YQLVDESDFHNDLR	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	YQLVDESDFHNDLR	1820.8	1821.8	1820.8	1821.8
48.0	6.5	6.5	39.2	2.0	99.0	GFMPFLLPGESNKIPR	1783.9	1784.9	1783.9	1784.9
48.0	6.5	6.5	39.2	2.0	99.0	NLPSSDQDLGQHGLEEDFML	2244.0	2245.0	2244.0	2245.0
48.0	6.5	6.5	39.2	1.5	97.0	YQLVDESDFHNDLR	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	750.4	751.4	750.4	751.4
82.0	9.0	9.0	39.2	2.0	99.0	GFMPFLLPGESNKIPR	1783.9	1784.9	1783.9	1784.9
82.0	9.0	9.0	39.2	2.0	99.0	NLPSSDQDLGQHGLEEDFML	2244.0	2245.0	2244.0	2245.0
82.0	9.0	9.0	39.2	2.0	99.0	SLDRNLPSSDQDLGQHGLEEDFML	2715.3	2716.3	2715.2	2716.3
82.0	9.0	9.0	39.2	2.0	99.0	YQLVDESDFHNDLR	1820.8	1821.8	1820.8	1821.8
82.0	9.0	9.0	39.2	0.5	69.0	YQWVR	750.4	751.4	750.4	751.4
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	YQLVDESDFHNDLR	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	ECLCLDPKENWVQR	1685.8	1686.8	1685.8	1686.8
133.0	8.4	8.4	49.5	2.0	99.0	LSDGRELCLDPKENWVQR	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	2.0	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	LSDGRELCLDPKENWVQR	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	ECLCLDPKENWVQR	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	ECLCLDPKENWVQR	1685.8	1686.8	1685.8	1686.8
105.0	7.7	7.7	56.6	2.0	99.0	LSDGRELCLDPKENWVQR	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 B58_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	AYLEGLCVWEILR	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	YFYTAMSPRGRGEPR	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	DGEDQIQDTELVEVTRPAGDRITFOK	2735.3	2736.3	2735.3	2736.3
160.0	7.4	12.3	40.6	2.0	99.0	YTCVGHGELPKPLT	1779.9	1779.9	1779.9	1779.9
160.0	7.4	12.3	40.6	1.2	99.0	MYGQVVDGDR	1225.5	1226.5	1225.5	1226.5
160.0	7.4	12.3	40.6	0.2	38.0	AYLEGLCVWEILR	1507.8	1508.8	1507.7	1508.8
160.0	7.4	12.3	40.6	0.0	99.0	FIAVGVYDDTQFVLR	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	SETAPAAPAAPAPAEK	1519.8	1520.8	1519.8	1520.8
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAPAEKTPVK	1945.0	1946.0	1945.0	1946.0
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAPAEKTPVKK	2073.1	2074.1	2073.1	2074.1
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAPAEKTPVKKK	2201.2	2202.2	2201.2	2202.2
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAPAEKTPVKKKKAR	2428.4	2429.4	2428.3	2429.4
74.0	14.0	14.0	18.3	0.0	99.0	ALAAAGYDVEKNNSR	1577.8	1578.8	1577.8	1578.8
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	SETAPAAPAAPAPAEKTPVKK	2073.1	2074.1	2073.1	2074.1
160.0	4.4	7.7	24.2	1.2	99.0	SETAPAAPAAPAPAEKTPVK	1945.0	1946.0	1945.0	1946.0
160.0	4.4	7.7	24.2	1.2	99.0	SETAPAAPAAPAPAEKTPVKKK	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	1188.5
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	CMPTFOFFKKGQK	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	VGEFSGANKKLELATINELV	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	1188.5
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	1188.5
81.0	9.1	9.1	42.9	2.0	99.0	CMPTFOFFKKGQK	1628.8	1629.8	1628.8	1629.8
81.0	9.1	9.1	42.9	2.0	99.0	MIKPFHLSSEK	1473.8	1474.8	1473.8	1474.8
81.0	9.1	9.1	42.9	2.0	99.0	VGEFSGANKKLELATINELV	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	1190.5
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	10.4	13.3	22.3	2.0	99.0	KSDIDELVLVGGSTR	1587.8	1588.8	1587.8	1

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	1252.6	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	ARFEELNADLFR	1479.7	1480.8	1479.7	1480.8
9.0	43.1	43.1	46.0	2.0	99.0	ATVDEKLGQKINDEKQK	2229.1	2230.2	2229.1	2230.2
9.0	43.1	43.1	46.0	2.0	99.0	FEELNADLFR	1252.6	1252.6	1252.6	1253.6
9.0	43.1	43.1	46.0	2.0	99.0	HWFPMVNDAGRPK	1652.8	1653.8	1652.8	1653.8
9.0	43.1	43.1	46.0	2.0	99.0	LDKSIQIHDIIVLGGSTR	1837.0	1838.0	1837.0	1838.0
9.0	43.1	43.1	46.0	2.0	99.0	LLODFGKELNK	1565.8	1566.8	1565.8	1566.8
9.0	43.1	43.1	46.0	2.0	99.0	MVNHFAEFK	1234.6	1235.6	1234.6	1235.6
9.0	43.1	43.1	46.0	2.0	99.0	MVNHFAEFKR	1390.7	1391.7	1390.7	1391.7
9.0	43.1	43.1	46.0	2.0	99.0	MVQEAQYKADEKQK	1980.0	1981.0	1980.0	1982.0
9.0	43.1	43.1	46.0	2.0	99.0	MVQEAQYKADEKQKRVSSK	2625.3	2626.3	2625.3	2626.3
9.0	43.1	43.1	46.0	2.0	99.0	NQVAMPNTVFDAR	1648.8	1649.8	1648.8	1649.8
9.0	43.1	43.1	46.0	2.0	99.0	NQVAMPNTVFDADR	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	SPYPEVSSMLVTK	1615.8	1616.8	1615.8	1616.8
9.0	43.1	43.1	46.0	2.0	99.0	SOIHDIIVLGGSTR	1480.8	1481.8	1480.8	1481.8
9.0	43.1	43.1	46.0	2.0	99.0	STAGDTHLGGEDFNR	1690.7	1691.7	1690.7	1691.7
9.0	43.1	43.1	46.0	2.0	99.0	TTPSYVAFDTER	1486.7	1487.7	1486.7	1487.7
9.0	43.1	43.1	46.0	2.0	99.0	TVTNAVTVPAYFNDQSR	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	RFDADVQSDMK	1409.7	1410.7	1409.7	1410.7
9.0	43.1	43.1	46.0	1.3	95.0	MVQEAQYKADEKQK	2224.1	2225.1	2224.1	2225.1
9.0	43.1	43.1	46.0	0.0	79.0	MVQEAQYKADEKQK	1981.0	1982.0	1981.0	1982.0
9.0	43.1	43.1	46.0	0.0	99.0	STAGDTHLGGEDFNR	1693.8	1694.8	1693.8	1694.8
15.0	16.6	16.6	32.5	2.0	99.0	IINEPTAAAIAYGLDKK	1787.0	1788.0	1787.0	1788.0
15.0	16.6	16.6	32.5	2.0	99.0	MVNHFAEFK	1234.6	1235.6	1234.6	1235.6
15.0	16.6	16.6	32.5	2.0	99.0	MVNHFAEFKR	1390.7	1391.7	1390.7	1391.7
15.0	16.6	16.6	32.5	2.0	99.0	SPYPEVSSMLVTK	1615.7	1616.7	1615.8	1616.8
15.0	16.6	16.6	32.5	2.0	99.0	STAGDTHLGGEDFNR	1690.7	1691.7	1690.7	1691.7
15.0	16.6	16.6	32.5	2.0	99.0	TTPSYVAFDTER	1486.7	1487.7	1486.7	1487.7
15.0	16.6	16.6	32.5	1.4	96.0	TVTNAVTVPAYFNDQSR	1981.0	1982.0	1981.0	1982.0
15.0	16.6	16.6	32.5	1.2	93.0	NQVAMPNTVFDADR	1804.9	1805.9	1804.9	1805.9
15.0	16.6	16.6	32.5	1.0	91.0	MVQEAQYKADEKQK	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	DAGTIAGLNLVR	1198.7	1199.7	1198.7	1199.7
26.0	21.5	21.5	28.8	2.0	99.0	DAGTIAGLNLVR	1198.7	1199.7	1198.7	1199.7
26.0	21.5	21.5	28.8	2.0	99.0	LDKSIQIHDIIVLGGSTR	1837.0	1838.0	1837.0	1838.0
26.0	21.5	21.5	28.8	2.0	99.0	MVNHFAEFK	1234.6	1235.6	1234.6	1235.6
26.0	21.5	21.5	28.8	2.0	99.0	NQVAMPNTVFDADR	1804.9	1805.9	1804.9	1805.9
26.0	21.5	21.5	28.8	2.0	99.0	QATKDAGTIAGLNLVR	1609.9	1610.9	1609.9	1610.9
26.0	21.5	21.5	28.8	2.0	99.0	SPYPEVSSMLVTK	1615.8	1616.8	1615.8	1616.8
26.0	21.5	21.5	28.8	2.0	99.0	STAGDTHLGGEDFNR	1690.7	1691.7	1690.7	1691.7
26.0	21.5	21.5	28.8	2.0	99.0	TTPSYVAFDTER	1486.7	1487.7	1486.7	1487.7
26.0	21.5	21.5	28.8	2.0	99.0	TVTNAVTVPAYFNDQSR	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	MVNHFAEFKR	1390.7	1391.7	1390.7	1391.7
26.0	21.5	21.5	28.8	0.0	99.0	STAGDTHLGGEDFNR	1694.8	1695.8	1694.8	1695.8
26.0	21.5	21.5	28.8	0.0	99.0	STAGDTHLGGEDFNR	1693.8	1694.8	1693.8	1694.8
26.0	21.5	21.5	28.8	0.0	99.0	STAGDTHLGGEDFNR	1689.7	1690.7	1689.7	1690.7
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	DGLLEPTFIIVGVAR	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	NIHESCMSIQIWNRR	1730.8	1731.8	1730.8	1731.8
100.0	11.1	11.1	20.8	2.0	99.0	NSYVAGQYDDAASYOR	1806.8	1807.8	1806.8	1807.8
100.0	11.1	11.1	20.8	0.6	74.0	WDGVPFILR	1101.6	1102.6	1101.6	1102.6
100.0	11.1	11.1	20.8	0.5	69.0	LOFHDVAGDIFHQQCKR	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	LOFHDVAGDIFHQQCKR	2098.0	2099.0	2098.0	2099.0
101.0	7.7	7.7	22.9	2.0	99.0	LKLEDFAR	1137.6	1138.6	1137.6	1138.6
101.0	7.7	7.7	22.9	2.0	99.0	LOFHDVAGDIFHQQCKR	1941.9	1942.9	1941.9	1942.9
101.0	7.7	7.7	22.9	2.0	99.0	NSYVAGQYDDAASYOR	1806.8	1807.8	1806.8	1807.8
101.0	7.7	7.7	22.9	1.7	98.0	DGLLEPTFIIVGVAR	1663.9	1664.9	1663.9	1664.9
101.0	7.7	7.7	22.9	0.0	99.0	NSYVAGQYDDAASYOR	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) (In-										
201.0	1.5	1.5	6.2	1.5	97.0	GHOAFDVGQPR	1210.6	1211.6	1210.6	1211.6
322.0	2.0	2.0	2.5	2.0	99.0	GHOAFDVGQPR	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	GFGVFSFER	1044.5	1045.5	1044.5	1045.5
194.0	6.0	6.0	21.2	2.0	99.0	QAHLTNQVMQR	1371.6	1372.6	1371.6	1372.6
194.0	6.0	6.0	21.2	2.0	99.0	SLGYAYVNFQPADAEAR	1927.9	1928.9	1927.9	1928.9
194.0	6.0	6.0	21.2	0.0	99.0	QAHLTNQVMQR	1388.7	1389.7	1388.7	1389.7
117.0	2.6	2.6	18.4	1.4	96.0	SLGYAYVNFQPADAEAR	1927.9	1928.9	1927.9	1928.9
117.0	2.6	2.6	18.4	1.2	94.0	GFGVFSFER	1044.5	1045.5	1044.5	1045.5
199.0	3.7	3.7	11.9	2.0	99.0	GFGVFSFER	1044.5	1045.5	1044.5	1045.5
199.0	3.7	3.7	11.9	1.7	98.0	GYGFMVHETQEAER	1739.8	1740.8	1739.8	1740.8
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	AFTPSPGK	950.5	951.5	950.5	951.5
367.0	2.0	2.0	2.0	2.0	99.0	VPLALFALNR	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 su										
49.0	18.0	18.0	20.2	2.0	99.0	DTGIFLDLMLK	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	IILEDQFKGQGGQKR	1787.0	1788.0	1787.0	1788.0
49.0	18.0	18.0	20.2	2.0	99.0	IMATPEQVQK	1073.6	1074.6	1073.6	1074.6
49.0	18.0	18.0	20.2	2.0	99.0	IMLFNEDNPHGNDQSAK	1901.9	1902.9	1901.9	1902.9
49.0	18.0	18.0	20.2	2.0	99.0	NWVQLGELNPAKAR	1729.9	1730.9	1729.9	1730.9
49.0	18.0	18.0	20.2	2.0	99.0	SDSFENPVLQGHFR	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	VHFESKLELLR	1700.9	1701.9	1700.9	1701.9
49.0	18.0	18.0	20.2	0.0	99.0	SDSFENPVLQGHFR	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	KPGGFDISLFYR	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	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
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	1256.6	1257.6	1256.6	1257.6
366.0	2.0	2.0	4.2	2.0	99.0	GMQLMHANAQR	1256.6	1257.6	1256.6	1257.6
366.0	2.0	2.0	4.2	0.0	99.0	GMQLMHANAQR	1256.6	1257.6	1256.6	1257.6
366.0	2.0	2.0	4.2	0.0	99.0	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 (Hur										
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	TLWIWECGITAK	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	SCSFATAACCSHFSSVLAQNR	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	ARPPDGLAEDI DKGEVSAR	2142.1	2143.1	2142.1	2143.1
35.0	22.8	22.8	20.3	2.0	99.0	AYLPVNES				

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	GHVFEESVAGTPMFVVK	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	YEWVDVAER	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	37.0	CELLYEGPDPDEAAMGK	1939.9	1939.9	1939.9	1939.9
51.0	15.4	15.4	27.2	2.0	99.0	CLYASVLTQAPR	1367.0	1367.7	1367.0	1367.7
51.0	15.4	15.4	27.2	2.0	99.0	GHVFEESVAGTPMFVVK	1961.0	1962.0	1961.0	1962.0
51.0	15.4	15.4	27.2	2.0	99.0	IMGPNYTPGKEDLYLKPQIR	2460.3	2461.3	2460.3	2461.3
51.0	15.4	15.4	27.2	2.0	99.0	VNFTVDQIR	1090.6	1091.6	1090.6	1091.6
51.0	15.4	15.4	27.2	2.0	99.0	YEWVDVAER	1137.5	1138.5	1137.5	1138.5
51.0	15.4	15.4	27.2	2.0	99.0	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	GGGQIPTARR	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	MDPNCSCAAAGVSCTCASSCK	2334.8	2335.8	2334.8	2335.9
460.0	2.0	4.0	53.2	0.0	99.0	SCSCSCPVGCAK	1444.5	1445.5	1444.5	1445.5
460.0	2.0	4.0	53.2	0.0	99.0	SCSCSCPVGCAK	1447.5	1448.5	1447.5	1448.5
460.0	2.0	4.0	53.2	0.0	99.0	SCSCSCPVGCAK	1447.5	1448.5	1447.5	1448.5
182.0	2.0	2.0	53.2	2.0	99.0	SCSCSCPVGCAK	1444.5	1445.5	1444.5	1445.5
305.0	2.0	6.0	54.8	2.0	99.0	MDPNCSCAAAGVSCTCASSCK	2334.8	2335.9	2334.8	2335.9
305.0	2.0	6.0	54.8	0.0	99.0	KSCSCSCPVGCAK	1573.6	1574.6	1573.6	1573.6
305.0	2.0	6.0	54.8	0.0	99.0	MDPNCSCAAAGVSCTCASSCK	2338.8	2339.9	2338.8	2339.9
305.0	2.0	6.0	54.8	0.0	99.0	SCSCSCPVGCAK	1444.5	1445.5	1444.5	1445.5
305.0	2.0	6.0	54.8	0.0	99.0	SCSCSCPVGCAK	1446.5	1447.5	1446.5	1447.5
305.0	2.0	6.0	54.8	0.0	99.0	SCSCSCPVGCAK	1446.5	1447.5	1446.5	1447.5
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	FOETFDVFSDR	1518.7	1519.7	1518.7	1519.7
247.0	4.9	4.9	12.3	2.0	99.0	FVAVGDWGGVNPAPFHTAR	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	FVAVGDWGGVNPAPFHTAR	1997.0	1998.0	1997.0	1998.0
299.0	2.0	2.0	6.5	2.0	99.0	FOETFDVFSDR	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)				
25.0	26.0	26.0	32.2	2.0	99.0	AECMLQOAEK	1234.5	1235.5	1234.5	1235.5
25.0	26.0	26.0	32.2	2.0	99.0	FSLVGGDGLNEGNR	1674.8	1675.8	1674.8	1675.8
25.0	26.0	26.0	32.2	2.0	99.0	GDEEGVPAVIDMSGLR	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	1859.9	1860.9	1859.9	1860.9
25.0	26.0	26.0	32.2	2.0	99.0	MINLSVPTIDER	1501.7	1502.7	1501.7	1502.7
25.0	26.0	26.0	32.2	2.0	99.0	QFVATDVVR	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	VYALPEDLVEVNP	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	TRFNWMSLGVNPR	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	FSLVGGDGLNEGNR	1674.8	1675.8	1674.8	1675.8
18.0	14.2	14.2	31.4	2.0	99.0	GDEEGVPAVIDMSGLR	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	NWMSLGVNPR	1286.6	1287.6	1286.6	1287.6
18.0	14.2	14.2	31.4	2.0	99.0	VYALPEDLVEVNP	1584.8	1585.8	1584.8	1585.8
18.0	14.2	14.2	31.4	1.0	91.0	QFVATDVVR	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	MINLSVPTIDER	1501.7	1502.7	1501.7	1502.8
18.0	14.2	14.2	31.4	0.1	23.0	QFVATDVVRGNPK	1530.8	1531.8	1530.8	1531.8
18.0	14.2	14.2	31.4	0.1	21.2	DLLKTENLNDEK	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	QFVATDVVR	1130.6	1131.6	1130.6	1135.6
24.0	22.6	22.6	37.5	2.0	99.0	AECMLQOAEK	1234.5	1235.5	1234.5	1235.6
24.0	22.6	22.6	37.5	2.0	99.0	FSLVGGDGLNEGNR	1674.8	1675.8	1674.8	1675.8
24.0	22.6	22.6	37.5	2.0	99.0	GDEEGVPAVIDMSGLR	1742.8	1743.9	1742.9	1743.9
24.0	22.6	22.6	37.5	2.0	99.0	IKVPVDWNR	1125.6	1126.6	1125.6	1126.6
24.0	22.6	22.6	37.5	2.0	99.0	KLENCNYAVELGKNOAK	1978.0	1979.0	1978.0	1979.0
24.0	22.6	22.6	37.5	2.0	99.0	QFVATDVVR	1134.6	1135.6	1134.6	1135.6
24.0	22.6	22.6	37.5	2.0	99.0	TRFNWMSLGVNPR	1690.8	1691.8	1690.8	1691.8
24.0	22.6	22.6	37.5	2.0	99.0	VNDDIIVNWNENLTLR	1798.9	1799.9	1798.9	1799.9
24.0	22.6	22.6	37.5	2.0	99.0	VYALPEDLVEVNP	1584.8	1585.8	1584.8	1585.8
24.0	22.6	22.6	37.5	2.0	99.0	YAFVNWINK	1153.6	1154.6	1153.6	1154.6
24.0	22.6	22.6	37.5	1.7	98.0	EGICAIGGTEQSSVGTQHSYSEEEK	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	99.0	QFVATDVVR	1117.6	1118.6	1117.6	1118.6
P14174	MIF_HUMAN					Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) - Homo sapiens (Human)				
193.0	6.0	6.0	22.6	2.0	99.0	LLCGLLAER	1043.6	1044.6	1043.6	1044.6
193.0	6.0	6.0	22.6	2.0	99.0	PMFIVNTNPR	1286.7	1287.7	1286.7	1287.7
193.0	6.0	6.0	22.6	2.0	99.0	SYSKLLCGLLAER	1508.8	1509.8	1508.8	1509.8
193.0	6.0	6.0	22.6	0.0	99.0	PMFIVNTNPR	1298.7	1299.7	1298.7	1299.7
193.0	6.0	6.0	22.6	0.0	92.0	PMFIVNTNPR	1289.7	1290.7	1286.7	1287.7
193.0	6.0	6.0	22.6	0.0	90.0	PMFIVNTNPR	1314.7	1315.7	1314.7	1315.7
94.0	4.0	4.0	17.4	2.0	99.0	LLCGLLAER	1043.6	1044.6	1043.6	1044.6
94.0	4.0	4.0	17.4	2.0	99.0	PMFIVNTNPR	1286.7	1287.7	1286.7	1287.7
94.0	4.0	4.0	17.4	0.0	99.0	PMFIVNTNPR	1298.7	1299.7	1298.7	1299.7
94.0	4.0	4.0	17.4	0.0	99.0	PMFIVNTNPR	1287.7	1288.7	1287.7	1288.7
94.0	4.0	4.0	17.4	0.0	99.0	PMFIVNTNPR	1287.7	1288.7	1287.7	1288.7
194.0	4.0	4.0	17.4	2.0	99.0	LLCGLLAER	1043.6	1044.6	1043.6	1044.6
194.0	4.0	4.0	17.4	2.0	99.0	PMFIVNTNPR	1286.7	1287.7	1286.7	1287.7
194.0	4.0	4.0	17.4	0.0	99.0	PMFIVNTNPR	1298.7	1299.7	1298.7	1299.7
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	EHPVPLLR	1169.7	1170.7	1169.7	1170.7
130.0	8.7	8.7	13.8	2.0	99.0	GFGGOYGIQK	1053.5	1054.5	1053.5	1054.5
130.0	8.7	8.7	13.8	2.0	99.0	RSPEAPQPIAMEEPAVPAPLPK	2423.3	2424.3	2423.3	2424.3
130.0	8.7	8.7	13.8	2.0	99.0	TEHINIHLR	1259.7	1260.7	1259.7	1260.7
130.0	8.7	8.7	13.8	0.5	71.0	TEGSGRTEHINIHLR	1960.0	1961.0	1960.0	1961.0
130.0	8.7	8.7	13.8	0.2	36.0	GFGGOYGIQKDR	1324.7	1325.7	1324.7	1325.7
130.0	8.7	8.7	13.8	0.0	99.0	TEHINIHLR	1259.7	1260.7	1259.7	1260.7
137.0	2.1	2.1	30.0	2.0	99.0	GFGGOYGIQK	1053.5	1054.5	1053.5	1054.5
153.0	4.6	4.6	17.9	2.0	99.0	EHPVPLLR	1169.7	1170.7	1169.7	1170.7
153.0	4.6	4.6	17.9	2.0	99.0	TEHINIHLR	1259.7	1260.7	1259.7	1260.7
153.0	4.6	4.6	17.9	0.5	68.0	ASHGYGRRFVGR	1391.7	1392.7	1391.7	1392.7
153.0	4.6	4.6	17.9	0.1	29.0	GFGGOYGIQKDRVK	1666.8	1667.8	1666.8	1667.8
P14318	KPYM_HUMAN					Pyruvate kinase isozymes M1/ M2 (EC 2.7.1.40) (Pyruvate kinase muscle isozyme				

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	YRPPAPIAVTR	1411.8	1412.8	1411.8	1412.8
14.0	38.4	38.4	54.6	0.6	72.0	EAEAIIYHLQLFEELRR	2087.1	2088.1	2087.1	2088.1
14.0	38.4	38.4	54.6	0.3	55.0	TATESFASDPILYRPPVAVALDTKGPEIR	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	CDENILWLDYKNIQK	1965.9	1966.9	1965.9	1966.9
14.0	38.4	38.4	54.6	0.0	99.0	LAPITSDPTTEATAVGAVEASF	2174.1	2175.1	2174.1	2175.1
14.0	38.4	38.4	54.6	0.0	58.0	LAPITSDPTTEATAVGAVEASF	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	GDGLGIEIPEAKVFLAQK	1827.0	1828.0	1827.0	1828.0
49.0	6.4	6.4	37.1	1.2	94.0	LAPITSDPTTEATAVGAVEASF	2174.1	2175.1	2174.1	2175.1
49.0	6.4	6.4	37.1	0.2	32.0	IISKIENHEGVR	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	EAEAIIYHLQLFEELR	1931.0	1932.0	1931.0	1932.0
16.0	27.4	27.4	51.2	2.0	99.0	FGVEQDDVMVFASFIR	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	LAPITSDPTTEATAVGAVEASF	2174.1	2175.1	2174.1	2175.1
16.0	27.4	27.4	51.2	2.0	99.0	LDIDSPPIAR	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	NTGIICITGPASR	1358.7	1359.7	1358.7	1359.7
16.0	27.4	27.4	51.2	2.0	99.0	RFDEILEASDGMIVAR	1820.9	1821.9	1820.9	1821.9
16.0	27.4	27.4	51.2	1.1	92.0	GDGLGIEIPEAKVFLAQK	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	FDEILEASDGMIVAR	1664.8	1665.8	1664.8	1665.8
16.0	27.4	27.4	51.2	0.5	68.0	TATESFASDPILYRPPVAVALDTK	2463.3	2464.3	2463.3	2465.3
16.0	27.4	27.4	51.2	0.0	99.0	NTGIICITGPASR	1358.7	1359.7	1358.7	1359.7
16.0	27.4	27.4	51.2	0.0	99.0	RFDEILEASDGMIVAR	1818.9	1819.9	1818.9	1821.9
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	FAFOAEVNR	1080.5	1081.5	1080.5	1081.5
316.0	2.0	2.0	8.8	2.0	99.0	FAFOAEVNR	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	AFALWSAVTPLTFTFR	1679.9	1680.9	1679.9	1680.9
8.0	44.0	44.0	50.2	2.0	99.0	AVIDDFAFAR	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	FGNADGAACHFFPFIEGR	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	GDGLGIEIPEAKVFLAQK	2057.9	2058.9	2057.9	2058.9
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	GSRPQGPFLIADKWVLPALPR	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	LWCATTSNFDSDKK	1671.8	1672.8	1671.8	1672.8
8.0	44.0	44.0	50.2	2.0	99.0	MFPQVPLDTHDVFQYREK	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	QSTLVLPFGDLR	1327.7	1328.7	1327.7	1328.7
8.0	44.0	44.0	50.2	2.0	99.0	QVWVYTGASVGLGPR	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	SLGPALLLQK	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	95.0	QVWVYTGASVGLGPR	1514.8	1515.9	1514.9	1515.9
8.0	44.0	44.0	50.2	1.2	94.0	MULLFSGR	822.4	823.4	822.4	823.4
8.0	44.0	44.0	50.2	1.2	93.0	DGNADGKPCQPFIFOGQSYACTDGR	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	LFFFSGR	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	CGVPLDGR	872.4	873.4	872.4	873.4
8.0	44.0	44.0	50.2	0.1	28.8	QNYSEDLR	1273.5	1274.5	1273.5	1274.5
8.0	44.0	44.0	50.2	0.1	27.0	AYVQDRFYWR	1610.7	1611.7	1610.7	1611.7
8.0	44.0	44.0	50.2	0.1	27.0	GVVVPTR	726.4	727.4	726.4	727.4
8.0	44.0	44.0	50.2	0.0	99.0	FGNADGAACHFFPFIEGR	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	QVWVYTGASVGLGPR	1514.8	1515.8	1514.8	1515.8
6.0	31.5	31.5	42.9	2.0	99.0	AVIDDFAFAR	976.5	977.5	976.5	977.5
6.0	31.5	31.5	42.9	2.0	99.0	FGNADGAACHFFPFIEGR	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	GSRPQGPFLIADKWVLPALPR	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	LWCATTSNFDSDKK	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	QSTLVLPFGDLR	1327.7	1328.7	1327.7	1328.7
6.0	31.5	31.5	42.9	2.0	99.0	QVWVYTGASVGLGPR	1531.8	1532.8	1531.8	1532.8
6.0	31.5	31.5	42.9	2.0	99.0	SDGLPWCSTTANYDTDDR	2068.9	2072.8	2068.9	2073.8
6.0	31.5	31.5	42.9	2.0	99.0	SLGPALLLQK	1151.7	1152.7	1151.7	1152.7
6.0	31.5	31.5	42.9	1.2	93.0	LFFFSGR	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	MULLFSGR	822.5	823.5	822.4	823.4
6.0	31.5	31.5	42.9	0.1	24.0	AFALWSAVTPLTFTFR	1679.9	1680.9	1679.9	1680.9
6.0	31.5	31.5	42.9	0.0	99.0	AVIDDFAFAR	976.5	977.5	976.5	977.5
6.0	31.5	31.5	42.9	0.0	99.0	FGNADGAACHFFPFIEGR	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	QSTLVLPFGDLR	1327.7	1328.7	1327.7	1328.7
6.0	31.5	31.5	42.9	0.0	45.0	QSTLVLPFGDLR	1341.7	1342.7	1341.7	1342.7
6.0	31.5	31.5	42.9	0.0	97.0	QVWVYTGASVGLGPR	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	AVIDDFAFAR	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	FGNADGAACHFFPFIEGR	2013.9	2014.9	2013.9	2014.9
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	GSRPQGPFLIADKWVLPALPR	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	1439.8	1440.8	1439.8	1440.8
6.0	46.9	46.9	48.9	2.0	99.0	LWCATTSNFDSDKK	1671.8	1672.8	1671.8	1672.8
6.0	46.9	46.9								

6.0	46.9	46.9	48.9	0.0	99.0	FGNADGAACHFFPFIEGR	2011.9	2012.9	2011.9	2012.9
6.0	46.9	46.9	48.9	0.0	89.0	FGNADGAACHFFPFIEGR	2013.9	2014.9	2013.9	2014.9
6.0	46.9	46.9	48.9	0.0	99.0	QLAEELYR	1166.6	1167.6	1166.6	1167.6
6.0	46.9	46.9	48.9	0.0	70.0	QLSLPETGLSDSATLK	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
5.0	46.9	46.9	48.9	0.0	99.0	QVWVYFVAVLQSPR	1531.8	1532.8	1531.8	1532.8
P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit VIb 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	TAPFDSRFNNQTR	1777.8	1778.8	1777.8	1778.8
155.0	4.6	4.6	65.1	2.0	99.0	GGDISVCEVYQR	1468.6	1469.6	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	FPNNQTR	1052.4	1053.4	1052.5	1053.5
155.0	4.6	4.6	65.1	0.3	44.0	TAPFDSRFNNQTR	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	AKWPF2VR	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	EWVYFLGHHVDNK	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	1946.0	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	QLLTLSELSQAR	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	VMDQHLTR	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	RITFAEKNERVQR	1670.9	1671.9	1670.9	1671.9
46.0	19.0	27.2	41.1	0.0	99.0	APDFVYAPR	1182.6	1183.6	1182.6	1183.6
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	LFLOVK	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	1182.6	1183.6	1182.6	1183.6
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	1309.7	1310.7	1309.7	1310.7
127.0	2.3	10.3	24.9	0.0	99.0	LFLOVK	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	AKFYPEDVAEELIQDITOK	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	LFLOVK	893.5	894.5	893.5	894.5
67.0	11.1	23.1	38.4	0.0	99.0	RKPDIEVQOMK	1471.8	1472.8	1471.8	1472.8
67.0	11.1	23.1	38.4	0.0	99.0	RRKPDIEVQOMK	1627.9	1628.9	1627.9	1628.9
67.0	11.1	23.1	38.4	0.0	78.0	RRKPDIEVQOMK	1627.9	1628.9	1627.9	1628.9
P16070	CD44_HUMAN	CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-1) (Extracellular matrix receptor-11) (ECMR-11) (GP90 lymphocyte homing/								
346.0	3.3	3.3	4.0	2.0	99.0	YGFIEGHVVI PR	1385.7	1386.7	1385.7	1386.8
346.0	3.3	3.3	4.0	1.3	95.0	ALSI GFETCR	1152.6	1153.6	1152.6	1153.6
109.0	3.2	3.2	6.9	2.0	99.0	YGFIEGHVVI PR	1385.7	1386.7	1385.7	1386.8
109.0	3.2	3.2	6.9	1.2	93.0	ALSI GFETCR	1152.6	1153.6	1152.6	1153.6
156.0	4.6	4.6	7.5	2.0	99.0	YGFIEGHVVI PR	1385.7	1386.7	1385.7	1386.8
156.0	4.6	4.6	7.5	1.3	95.0	ALSI GFETCR	1152.6	1153.6	1152.6	1153.6
156.0	4.6	4.6	7.5	1.3	95.0	FAGV FIVEK	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	KEYGGLDLV LNNAGIAFKVAD	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	KEYGGLDLV LNNAGIAFKVAD	2210.1	2211.1	2210.1	2211.1
193.0	4.0	4.0	13.4	0.0	93.0	KEYGGLDLV LNNAGIAFKVAD	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	SETAPAEATAPAPVEKSPAK	2023.0	2024.0	2023.0	2024.0
235.0	5.2	6.0	23.5	2.0	99.0	SETAPAEATAPAPVEKSPAKK	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	SETAPAEATAPAPVEKSPAK	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	SETAPLAPITPAPA EKTVPVKKK	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	SETAPLAPITPAPA EKTVPVKKK	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	SETAPAPAAAAPPAEKAPVKK	2043.1	2044.1	2043.1	2044.1
227.0	5.4	11.4	22.1	2.0	99.0	SETAPAPAAAAPPAEKAPVKKK	2171.2	2172.2	2171.2	2172.2
227.0	5.4	11.4	22.1	1.4	96.0	SETAPAPAAAAPPAEKAPVK	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	SETAPAPAAAAPPAEKAPVK	1519.8	1520.8	1519.8	1520.8
102.0	7.7	7.7	23.5	2.0	99.0	SETAPAPAAAAPPAEKAPVK	1915.0	1916.0	1915.0	1916.0
102.0	7.7	7.7	23.5	2.0	99.0	SETAPAPAAAAPPAEKAPVKK	2043.1	2044.1	2043.1	2044.1
102.0	7.7	7.7	23.5	2.0	99.0	SETAPAPAAAAPPAEKAPVKKK	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	ASGQAFELLSPR	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	RASGOAFELLSPR	1543.9	1544.9	1543.8	1544.9
149.0	2.0	2.0	12.8	2.0	99.0	ASGQAFELLSPR	1387.7	1388.8	1387.7	1388.8
297.0	2.0	2.0	21.5	2.0	99.0	ASGQAFELLSPR	1387.7	1388.8	1387.7	1388.8
P17931	LEG3_HUMAN	Galectin-3 (Galactose-specific lectin 3) (

160.0	7.4	12.3	40.6	0.0	99.0	WAAVVVPSGEEQR	1426.7	1427.7	1426.7	1427.7
40.0	20.6	20.6	61.0	2.0	99.0	AAAYKLVLIIR	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	HYGGLTGLNKKAETAAK	1629.8	1630.8	1629.8	1630.9
40.0	20.6	20.6	61.0	2.0	99.0	SYDVPPMPDPHPFYNSISK	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	2425.1
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	TWRNLNER	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	HYGGLTGLNKKAETAAK	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	2424.1	2425.1
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	HYGGLTGLNKKAETAAK	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	2425.1
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	AAAYKLVLIIR	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	HYGGLTGLNKKAETAAK	1629.8	1630.8	1629.8	1630.9
40.0	20.6	20.6	61.0	2.0	99.0	SYDVPPMPDPHPFYNSISK	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	2425.1
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	TWRNLNER	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	HYGGLTGLNKKAETAAK	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	2424.1	2425.1
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	HYGGLTGLNKKAETAAK	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	2425.1
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	ELLTTMGDRFTDEEVDLYR	2431.2	2432.2	2431.1	2432.1
128.0	6.0	6.0	33.9	2.0	99.0	GNFNIEFFR	1259.6	1260.6	1259.6	1260.6
128.0	6.0	6.0	33.9	2.0	99.0	NAFACFDEEATGTIQEDVLYR	2349.0	2350.0	2349.0	2350.0
151.0	8.0	8.0	29.1	2.0	99.0	ELLTTMGDRFTDEEVDLYR	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	GNFNIEFFR	1259.6	1260.6	1259.6	1260.6
151.0	8.0	8.0	29.1	2.0	99.0	NAFACFDEEATGTIQEDVLYR	2349.0	2350.0	2349.0	2350.0
146.0	2.1	2.1	17.4	2.0	99.0	GNFNIEFFR	1259.6	1260.6	1259.6	1260.6
P19823 ITI2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin inhibitor chain 2)										
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	1337.7	1338.7	1337.7	1338.7
55.0	16.9	16.9	13.4	2.0	99.0	IQPSGGTNIINEALLR	1581.8	1582.8	1581.8	1582.8
55.0	16.9	16.9	13.4	2.0	99.0	IYGNQDTSSQLK	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	VOFELHYOEVK	1418.7	1419.7	1418.7	1419.7
55.0	16.9	16.9	13.4	2.0	99.0	VOFELHYOEVKWR	1761.9	1762.9	1761.9	1762.9
55.0	16.9	16.9	13.4	2.0	99.0	VVNNSPQPNVDFVQIQPK	2144.1	2145.1	2144.1	2145.1
55.0	16.9	16.9	13.4	0.9	88.0	VIPEQGLR	924.5	925.5	924.5	925.5
55.0	16.9	16.9	13.4	0.0	33.0	FYNOVSTPLLR	1337.7	1338.7	1337.7	1338.7
31.0	10.0	10.0	12.4	2.0	99.0	FYNOVSTPLLR	1337.7	1338.7	1337.7	1338.7
31.0	10.0	10.0	12.4	2.0	99.0	IQPSGGTNIINEALLR	1581.8	1582.8	1581.8	1582.8
31.0	10.0	10.0	12.4	2.0	99.0	VOFELHYOEVK	1418.7	1419.7	1418.7	1419.7
31.0	10.0	10.0	12.4	2.0	99.0	VVNNSPQPNVDFVQIQPK	2144.1	2145.1	2144.1	2145.1
31.0	10.0	10.0	12.4	1.5	97.0	VOFELHYOEVKWR	1760.9	1761.9	1760.9	1761.9
31.0	10.0	10.0	12.4	0.3	47.0	AEDHFSVIDFNQINIR	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	VOFELHYOEVK	1418.7	1419.7	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	1337.7	1338.7	1337.7	1338.7
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	IQPSGGTNIINEALLR	1581.8	1582.8	1581.8	1582.8
20.0	23.9	23.9	20.3	2.0	99.0	IYGNQDTSSQLK	1364.7	1365.7	1364.7	1365.7
20.0	23.9	23.9	20.3	2.0	99.0	IYGNQDTSSQLK	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	TWRNDLISATK	1289.7	1290.7	1289.7	1290.7
20.0	23.9	23.9	20.3	2.0	99.0	VOFELHYOEVK	1418.7	1419.7	1418.7	1419.7
20.0	23.9	23.9	20.3	2.0	99.0	VOFELHYOEVKWR	1760.9	1761.9	1760.9	1761.9
20.0	23.9	23.9	20.3	2.0	99.0	VVNNSPQPNVDFVQIQPK	2144.1	2145.1	2144.1	2145.1
20.0	23.9	23.9	20.3	1.7	98.0	AEDHFSVIDFNQINIR	1814.8	1815.8	1814.8	1815.8
20.0	23.9	23.9	20.3	0.1	28.4	VIPEQGLR	924.5	925.5	924.5	925.5
20.0	23.9	23.9	20.3	0.0	99.0	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	1337.7	1338.7	1337.7	1338.7
P19971 TYPH_HUMAN Thymidine phosphorylase precursor (EC 2.4.2.4) (TdRpase) (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	1490.			

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	1507.8	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	LYKEELOTYHAK	1650.8	1651.8	1650.8	1651.8
100.0	7.8	7.8	27.6	0.8	84.0	LREYEAALNSK	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	QONAQGGFSSTQDTVVALHALSR	2503.2	2504.2	2503.2	2504.2
358.0	3.1	7.7	8.4	0.0	99.0	MVSGFLPKPTVK	1415.8	1416.8	1415.8	1416.8
358.0	3.1	7.7	8.4	0.0	97.0	NGQNTWLTAFLVK	1635.7	1636.7	1635.7	1636.7
358.0	3.1	7.7	8.4	0.0	24.0	YGAATFTR	1013.5	1013.5	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	GRNQGNTWLTAFLVK	1635.8	1636.8	1635.8	1636.8
P121291 CSR1P_HUMAN	Cysteine and glycine-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
960.0	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	ATCAPHGAPGPGPADASK	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	EATTEFVSVDAR	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	VHGPQIQSGTTNKNPKFTVETR	2367.2	2368.2	2367.2	2368.2
24.0	27.7	27.7	14.3	2.0	99.0	VHSPSGALEECYVTEI DODKYAVR	2765.3	2766.3	2765.3	2766.3
24.0	27.7	27.7	14.3	2.0	99.0	WGDEHPGSPYR	1412.6	1413.7	1412.6	1413.7
24.0	27.7	27.7	14.3	2.0	99.0	YGGQVPVNFPSK	1289.6	1290.6	1289.6	1290.6
24.0	27.7	27.7	14.3	2.0	99.0	YNEGVPQSSHFTAR	1602.8	1603.8	1602.8	1603.8
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	IQQNTFTR	1006.5	1007.5	1006.5	1007.5
24.0	27.7	27.7	14.3	0.7	81.0	GAPLRPKLNPKKAR	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	AGNMLLVGVHGPGR	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	WGDEHPGSPYR	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	LOVEPAVDTSVGVQCYGPIEGQGVFR	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	ATCAPHGAPGPGPADASK	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	1226.6
36.0	18.9	18.9	13.4	2.0	99.0	WGDEHPGSPYR	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	YGGQVPVNFPSK	1289.6	1290.7	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	LOVEPAVDTSVGVQCYGPIEGQGVFR	2763.3	2764.3	2762.3	2763.3
36.0	18.9	18.9	13.4	0.7	80.0	TGVAVNKPAEFTVDAK	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	QLVYLQHEAMIKR	1426.7	1427.7	1426.7	1427.7
226.0	5.4	5.4	5.3	1.2	94.0	VGFQCHNR	1017.5	1018.5	1017.4	1018.5
226.0	5.4	5.4	5.3	0.2	30.0	QFLFRWDVTK	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	ALPAVQONNLDELIR	1806.8	1807.8	1806.9	1807.9
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									
140.0	8.0	8.0	48.7	2.0	99.0	GDFCQIVGR	1050.5	1051.5	1050.5	1051.5
140.0	8.0	8.0	48.7	2.0	99.0	SAEKELSLWFKPEELVDYK	2310.2	2311.2	2310.2	2311.2
140.0	8.0	8.0	48.7	2.0	99.0	TFIAIKPDGVQR	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	GDFCQIVGR	1050.5	1051.5	1050.5	1051.5
131.0	6.0	6.0	44.7	2.0	99.0	TFIAIKPDGVQR	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 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	GLDWVKEAPDILCLQETK	2243.1	2244.1	2243.1	2244.1
158.0	7.6	7.6	24.8	2.0	99.0	ICSWNVVDGLR	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	QGFELLOAVPLADSF	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	ICSWNVVDGLR	1218.6	1219.6	1218.6	1219.6
P23246 SFPO_HUMAN	Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing factor) (PSF									
52.0	17.2	17.2	23.6	2.0	99.0	FAQHGTFFEYVSQR	1761.8	1762.8	1761.8	1762.8
52.0	17.2	17.2	23.6	2.0	99.0	FQGGAGPVGGQGR	1340.7	1341.7	1340.7	1341.7
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	LFVGNLPADITDEFK	1963.0	1964.0	1963.0	1964.0
52.0	17.2	17.2	23.6	2.0	99.0	QHPPYHQHHQGGPPGPGGR	2385.1	2386.1	2385.1	2386.1
52.0	17.2	17.2	23.6	2.0	99.0	RMEELHNQEMOKR	1727.8	1728.8	1727.8	1728.8
52.0	17.2	17.2	23.6	2.0	99.0	TERFGGGAGPVGGQGR	1726.9	1727.9	1726.9	1727.9
52.0	17.2	17.2	23.6	1.2	94.0	GGROHPPYHQHHQGGPPGPGGR	2672.2	2673.3	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	FAQHGTFFEYVSQR	1761.8	1762.8	1761.8	1762.8
134.0	6.0	6.0	25.2	2.0	99.0	FAQHGTFFEYVSQR	1761.8	1762.8	1761.8	1762.8
134.0	6.0	6.0	25.2	2.0	99.0	YGERCVRNKIK	1436.7	1437.7	1436.7	1437.7
134.0	6.0	6.0	25.2	1.0	91.0	FQGGAGPVGGQGR	1340.7	1341.7	1340.7	1341.7
134.0	6.0	6.0	25.2	0.4	61.0	RPGEKTYTORCR	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	RMEELHNQEMOKR	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	VI FGLFKG	879.5	880.5	879.5	880.5
248.0	2.3	2.3	10.1	2.0	99.0	SIYGERFPDENFKLK	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) (HRS) - 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	ATGQRPHFLRLR	1478.8	1479.8	1478.8	1479.8
43.0	19.9	19.9	32.9	2.0	99.0	EVTDIEVKEFMTPR	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	HAFSGGRDTEEHR	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	RKEVTDEIVKEFMTPR	1977.0	1978.0	1977.0	1978.0
43.0	19.9	19.9	32.9	2.0	99.0	TDIQCLPCAIQDQPYFR	2224.0	2225.0	2224.0	2225.0
43.0	19.9	19.9	32.9	2.0	99.0	VNKHAFSGGRDTEEHR	1952.0	1953.0	1952.0	1953.0
43.0	19.9	19.9	32.9	1.4						

38.0	18.5	18.5	32.7	0.9	86.0	ATGORPHHFLRR	1474.8	1475.8	1474.8	1475.8
38.0	18.5	18.5	32.7	0.7	80.0	ATGORPHHFLR	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	ATGORPHHFLRR	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	ASGVAVSDGVIKVFNDMK	1879.9	1879.9	1879.0	1879.0
42.0	7.2	7.2	29.5	2.0	99.0	KLTKIKHELOANCYEEVKDR	2430.2	2430.2	2430.2	2431.2
42.0	7.2	7.2	29.5	2.0	99.0	LTGIKHELOANCYEEVKDR	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	ASGVAVSDGVIK	1143.6	1144.6	1143.6	1144.6
37.0	22.3	22.3	51.8	2.0	99.0	ASGVAVSDGVIKVFNDMK	1877.9	1879.0	1879.0	1879.0
37.0	22.3	22.3	51.8	2.0	99.0	ASGVAVSDGVIKVFNDMKVVR	2133.1	2134.1	2133.1	2134.1
37.0	22.3	22.3	51.8	2.0	99.0	ESKKEDLVFIWAPESAPLK	2333.2	2334.2	2333.2	2334.2
37.0	22.3	22.3	51.8	2.0	99.0	ESKKEDLVFIWAPESAPLKSK	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	KEDLVFIWAPESAPLK	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	LTGIKHELOANCYEEVKDR	2302.1	2303.1	2302.1	2303.1
37.0	22.3	22.3	51.8	2.0	99.0	VFNDMKVVR	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	MLPKDKCR	1033.5	1034.5	1033.5	1034.5
54.0	13.7	13.7	60.2	2.0	99.0	ESKKEDLVFIWAPESAPLK	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	2432.2	2432.2	2432.2	2432.2
54.0	13.7	13.7	60.2	2.0	99.0	LTGIKHELOANCYEEVKDR	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	ASGVAVSDGVIKVFNDMKVVR	2133.1	2134.1	2133.1	2134.1
54.0	13.7	13.7	60.2	0.0	99.0	LTGIKHELOANCYEEVKDR	2303.1	2304.1	2303.1	2304.1
P25774 CATS_HUMAN Cathepsin S precursor (EC 3.4.22.27) - Homo sapiens (Human)										
139.0	8.1	8.1	20.5	2.0	99.0	HPSFLVYR	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	YTELPGREDVLK	1581.8	1582.8	1581.8	1582.8
139.0	8.1	8.1	20.5	0.1	22.0	YTELPGYR	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	HPSFLVYR	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	YTELPGREDVLK	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	HPSFLVYR	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	1244.6	1245.6	1244.6	1245.6
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	YTELPGREDVLK	1581.8	1582.8	1581.8	1582.8
58.0	13.0	13.0	23.3	0.9	87.0	GIDSDASYPYKAMDQK	1803.8	1804.8	1803.8	1804.8
58.0	13.0	13.0	23.3	0.1	25.0	YTELPGYR	997.5	998.5	997.5	998.5
58.0	13.0	13.0	23.3	0.0	98.0	HPSFLVYR	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	1678.8
P25786 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	34.0	FVFDRLPLVSR	1331.7	1332.7	1331.7	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	HMSSEFMECNLNLVK	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
P25787 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	1564.7	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
275.0	2.1	2.1	17.9	2.0	99.0	HIGLVYSGMGPDYR	1564.8	1565.8	1564.8	1565.8
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	1225.6	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	AKFYPEDVSEELIQDITQR	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	ESEAVEWQQK	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	EVWFFGLQYQDTK	1659.8	1660.8	1659.8	1660.8
5.0	53.4	53.4	55.3	2.0	99.0	FYPEDVSEELIQDITQR	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	KAQOELEQTRR	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	QKKESEAVEWQQK	1616.8	1617.8	1616.8	1617.8
5.0	53.4	53.4	55.3	2.0	99.0	QRIDEFESM	1136.5	1137.5	1136.5	1137.5
5.0	53.4	53.4	55.3	2.0	99.0	SGYLAGDKLLPQR	1416.8	1417.8	1416.8	1417.8
5.0	53.4	53.4	55.3	2.0	99.0	TAMSTPVAEPAENEQDEQDGEAFASADLR	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	TOEQALEMAELTAR	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	LFQVQK	893.5	894.5	893.5	894.5
5.0	53.4	53.4	55.3	1.4	96.0	DESKKTANDMIHAENMR	1988.9	1989.9	1988.9	1989.9
5.0	53.4	53.4	55.3	1.0	89.0	AQOELEQTRR	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	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	VLEQHKLNKQDWEER	1951.0	1952.0	1951.0	1952.0
5.0	53.4	53.4	55.3	0.0	99.0	YGFNKEVHK	1234.6	1235.6	1234.6	1235.6
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	EVWFFGLQYQDTK	1659.8	1660.8	1659.8	1660.8
11.0	20.7	20.7	37.1	2.0	99.0	IAQDLEMVGVNYSIK	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	1310.7	1309.7	1310.7
11.0	20.7	20.7	37.1	2.0	99.0	LFQVQK	893.5	894.5	893.5	894.5
11.0	20.7	20.7	37.1	2.0						

7.0	44.9	44.9	56.7	2.0	99.0	KAPDFVYFAPR	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	1529.7	1530.7	
7.0	44.9	44.9	56.7	2.0	99.0	RKPDTEVQOMK	1471.8	1472.8	1471.8	1472.8	
7.0	44.9	44.9	56.7	2.0	99.0	RRKPTDTEVQOMK	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	1401.6	1402.6	1401.6	1402.6	
7.0	44.9	44.9	56.7	2.0	99.0	TOEQALALEMELTAR	1702.8	1703.8	1702.8	1703.8	
7.0	44.9	44.9	56.7	2.0	99.0	VLEQHKLNKDKQWEER	1951.0	1952.0	1951.0	1952.0	
7.0	44.9	44.9	56.7	2.0	99.0	YGFNFKVHKH	1235.6	1236.6	1235.6	1236.6	
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	FYPEDVSEELIQQDITQR	2081.0	2082.0	2081.0	2082.0	
7.0	44.9	44.9	56.7	1.2	94.0	ESPLLFKFR	1136.6	1136.6	1136.6	1136.6	
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	1989.9	1989.9	1989.9	1989.9	
7.0	44.9	44.9	56.7	0.5	70.0	ALTSELANAR	1044.6	1045.6	1044.6	1045.6	
7.0	44.9	44.9	56.7	0.4	60.0	PALELEQER	1142.6	1143.6	1142.6	1143.6	
7.0	44.9	44.9	56.7	0.2	30.0	KAQOQLEECOTTRR	1514.8	1515.8	1514.8	1515.8	
7.0	44.9	44.9	56.7	0.1	27.0	EWVFFGLQYQDTR	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	RRKPDTEVQOMK	1627.9	1628.9	1627.9	1628.9	
7.0	44.9	44.9	56.7	0.0	99.0	VLEQHKLNKDKQWEER	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) (Calvasulin) - 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	HMBG2_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	IKSEHPGLSIGDTAK	1551.8	1552.8	1551.8	1552.8	
288.0	4.0	16.0	50.7	2.0	99.0	LGMWVSEQSAKDKOPYEQK	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	GKMSSYAFFVOTCR	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	MSSYAFFVOTCR	2147.0	2148.0	2147.0	2148.0	
288.0	4.0	16.0	50.7	0.0	99.0	YEDIAAYR	1127.6	1128.6	1127.6	1128.6	
264.0	2.1	8.2	39.7	2.0	99.0	KLGMWVSEQSAKDKOPYEQK	2409.1	2410.1	2409.1	2410.1	
264.0	2.1	8.2	39.7	0.1	25.0	IKSEHPGLSIGDTAK	1551.8	1552.8	1551.8	1552.8	
264.0	2.1	8.2	39.7	0.0	99.0	GKMSSYAFFVOTCR	1680.8	1681.8	1680.8	1681.8	
264.0	2.1	8.2	39.7	0.0	99.0	LKEKYEDIAAYR	1625.9	1626.9	1625.9	1626.9	
264.0	2.1	8.2	39.7	0.0	35.0	LKEKYEDIAAYR	1622.8	1623.8	1622.8	1623.8	
264.0	2.1	8.2	39.7	0.0	99.0	YEDIAAYR	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	VSYGIGDEEHDQEGR	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	QGFGLLOAVPLADSR	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	
158.0	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	EPAVYRKEQFLDGGWTSR	2244.0	2244.0	2244.0	2244.0	
86.0	12.2	12.2	25.4	2.0	99.0	EQFLDGGWTSR	1409.6	1410.6	1409.6	1410.6	
86.0	12.2	12.2	25.4	2.0	99.0	FVLSGKPYGDEEKDKGLQTSQDAR	2804.3	2805.4	2804.4	2805.4	
86.0	12.2	12.2	25.4	2.0	99.0	FYGDDEKDKGLQTSQDAR	2086.0	2087.0	2086.0	2087.0	
86.0	12.2	12.2	25.4	2.0	99.0	HEQNI DCGGGYVK	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	AVYFKEQFLDGGWTSR	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	FYGDDEKDKGLQTSQDAR	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	EQFLDGGWTSR	1409.6	1410.6	1409.6	1410.6	
123.0	6.0	6.0	13.9	0.3	60.0	HEQNI DCGGGYVK	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	PSB8_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	GMGLSMCGWVK	1628.7	1629.7	1628.7	1629.7	
149.0	8.0	8.0	21.7	2.0	99.0	KGPLYVDEHGTR	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	2.0	99.0	KGPLYVDEHGTR	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	GMGLSMCGWVK	1628.7	1629.7	1628.7	1629.7	
120.0	6.2	6.2	21.4	2.0	99.0	LLSNMCCOYR	1314.6	1315.6	1314.6	1315.6	
120.0	6.2	6.2	21.4	0.1	26.0	KGPLYVDEHGTR	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	PSA5_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	AIGSASEAGSLSQEVYHK	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	LFQVEYAIK	1422.8	1423.8	1422.8	1423.8	
169.0	6.7	6.7	26.6	0.0	99.0	AIGSASEAGSLSQEVYHK	1958.9	1959.9	1958.9	1960.0	
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	AIGSASEAGSLSQEVYHK	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	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 kin									
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	GOVFDVGR	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	Granulin precursor (Proepithelin) (PEP) [Contains: Acrogranin; Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3 (Gran									
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	QGWACPPYR	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	QGWACPPYR	1179.5	1180.5	1179.5	1180.5	
229.0	2.8	2.8	13.2	0.3	51.0	DVEGEGHFCHDNQTCR	2279.8	2280.8	2279.8	2280.8	
229.0	2.8	2.8	13.2	0.0	21.0	QGWACPPYR	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											

32.0	20.0	20.0	37.2	2.0	99.0	LYGSGDQEAQWOK	1380.6	1381.6	1380.6	1381.6
32.0	20.0	20.0	37.2	2.0	99.0	LYGSGDQEAQWOKGVLFASQGNLAR	2594.3	2594.3	2594.3	2594.3
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	QVVDCLADVNNIGKYR	1991.0	1992.0	1991.0	1992.0
32.0	20.0	20.0	37.2	2.0	99.0	SWIEEQAMGSLVSQAK	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	848.5
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	2095.0	2095.0	2095.0
32.0	20.0	20.0	37.2	0.0	99.0	KAAGIDEQENWHEGKENIR	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 phosphatase)				
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	1953.9
128.0	9.2	9.2	25.0	2.0	99.0	YKNI LPPDFHSR	1388.7	1389.7	1388.7	1389.7
128.0	9.2	9.2	25.0	1.3	95.0	AYGPPSYVNGEHDTEYKLR	2461.1	2461.1	2461.1	2461.1
128.0	9.2	9.2	25.0	1.0	89.0	DLGSLDAETLLK	1303.7	1303.7	1303.7	1303.7
128.0	9.2	9.2	25.0	0.7	82.0	VGDQVTHIR	1023.5	1024.6	1023.5	1024.6
128.0	9.2	9.2	25.0	0.1	26.0	NKCVYWPVEVGMQR	1762.8	1763.9	1762.8	1763.9
287.0	2.0	2.0	7.4	2.0	99.0	YKNI LPPDFHSR	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	LGQSDPAPLQHQMDIYOK	2068.0	2069.0	2068.0	2069.0
53.0	17.1	17.1	30.0	2.0	99.0	MESYHKPQQK	1432.7	1432.7	1432.7	1432.7
53.0	17.1	17.1	30.0	2.0	99.0	MFGIDRDAIAQAVR	1561.8	1562.8	1561.8	1562.8
53.0	17.1	17.1	30.0	2.0	99.0	SVPTSTVYPSDGVATEK	1883.9	1884.9	1883.9	1884.9
53.0	17.1	17.1	30.0	2.0	99.0	TSRPNENIYNNNEDFQVGOAK	2507.2	2508.2	2507.2	2508.2
53.0	17.1	17.1	30.0	2.0	99.0	VLDPFTIKPLDR	1412.8	1413.8	1412.8	1413.8
53.0	17.1	17.1	30.0	0.4	64.0	YFDKASYR	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	VLDPFTIKPLDRK	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	VLDPFTIKPLDR	1412.8	1413.8	1412.8	1413.8
62.0	5.6	5.6	23.4	1.2	94.0	TSRPNENIYNNNEDFQVGOAK	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	MFGIDRDAIAQAVR	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	2276.2	2275.2	2276.2
66.0	11.8	11.8	22.8	2.0	99.0	TSRPNENIYNNNEDFQVGOAK	2507.2	2508.2	2507.2	2508.2
66.0	11.8	11.8	22.8	2.0	99.0	VLDPFTIKPLDR	1412.8	1413.8	1412.8	1413.8
66.0	11.8	11.8	22.8	1.7	98.0	MFGIDRDAIAQAVR	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 3.1.1.35)				
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	PGGLLLGDVAFNFAANTTVGR	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	FFPLESQQWIGK	1350.7	1351.7	1350.7	1351.7
365.0	2.0	2.0	9.3	2.0	99.0	FFPLESQQWIGK	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	HSGNI TFDEIVNIAR	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	HSGNI TFDEIVNIAR	1684.9	1685.9	1684.9	1685.9
P30086	PEBP1_HUMAN					Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (HCNPP) (Neuropeptide h3) (Raf kinase inhibitor protein)				
102.0	10.6	10.6	55.1	2.0	99.0	APVAGTCVQAEWDDYVPK	2069.9	2069.9	2069.9	2069.9
102.0	10.6	10.6	55.1	2.0	99.0	GNDISSGTVLSDYVGGSPKGTGLHR	2570.2	2571.2	2570.2	2571.2
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	YWLVLYEODRPLK	1707.9	1708.9	1707.9	1708.9
102.0	10.6	10.6	55.1	1.4	96.0	NRPTSIWVDGLDSGK	1632.8	1632.8	1632.8	1632.8
102.0	10.6	10.6	55.1	1.2	94.0	YWLVLYEODRPLKCEPILSNR	2792.4	2793.4	2792.4	2793.4
184.0	4.0	4.0	31.0	2.0	99.0	APVAGTCVQAEWDDYVPK	2069.9	2069.9	2069.9	2069.9
184.0	4.0	4.0	31.0	2.0	99.0	GNDISSGTVLSDYVGGSPKGTGLHR	2571.3	2572.3	2571.3	2572.3
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 d)				
63.0	15.7	15.7	23.6	2.0	99.0	AASNLNRDNYR	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	GFPTIYVSPANK	1341.7	1342.7	1341.7	1342.7
63.0	15.7	15.7	23.6	2.0	99.0	IFRDGEEAGAYDGPR	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	1663.8	1664.8	1663.8	1664.8
63.0	15.7	15.7	23.6	1.7	98.0	FVMQEEFSRDGK	1471.7	1472.7	1471.7	1472.7
63.0	15.7	15.7	23.6	0.0	78.0	IFRDGEEAGAYDGPR	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	1663.8	1664.8	1663.8	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	1172.5	1173.5	1172.5	1173.5
97.0	8.0	8.0	16.4	2.0	99.0	IFRDGEEAGAYDGPR	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	APWVEQEPYWDRETOK	2247.0	2248.0	2247.0	2248.0
59.0	16.6	16.6	48.9	2.0	99.0	AYLEGTQVWVLR	1495.7	1496.7	1495.7	1496.7
59.0	16.6	16.6	48.9	2.0	99.0	DGEDQTDDELVETRPAGDGTFOK	2636.2	2637.2	2636.2	2637.2
59.0	16.6	16.6	48.9	2.0	99.0	FIAVGYDDTQFVR	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	YFYTAVSRPGRGEP	1754.9	1755.9	1754.9	1755.9
59.0	16.6	16.6	48.9	0.3	46.0	MYGCDLPGDGR	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	APWVEQEPYWDRETOK	1760.8	1761.8	1760.8	1761.8
270.0	2.1	7.4	30.9	2.0	99.0	APWVEQEPYWDRETOK	2247.0	2248.0	2247.0	2248.0
270.0	2.1	7.4	30.9	0.0	99.0	FIAVGYDDTQFVR	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	YLENGKETLOR	1350.7	1351.7	1350.7	1351.7
P30740	ILEU_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	KLEESYTLNSDLAR	1784.9	1785.9	1784.9	1785.9
155.0	7.7	7.7	14.0	2.0	99.0	TFHNTVEEVHSR	1601.8	1602.8	1601.8	1602.8
155.0	7.7	7.7	14.0	2.0	99.0	TYNFLPEFLVSTOK	1685.9	1686.9	1685.9	1686.9
155.0	7.7	7.7	14.0	1.7	98.0	FOSLNADIINKR	1304.7	1305.7	1304.7	1305.7
272.0	2.1	2.1	11.3	2.0	99.0	TFHNTVEEVHSR	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	CERAMTVPR	1155.5	1156.5	1155.5	1156.5
26.0	25.9	25.9	41.2	2.0	99.0	FRHVFQPAK	1186.6	1187.6	1186.6	1187.6
26.0	25.9	25.9	41.2	2.0	99.0	FRHVFQPAKADQCYEDVR	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	HVFQPAKADQCYEDVR	2018.9	2019.		

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	GTIVAEKDRPHEGTRPVR	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	99.0	FRHVFQPAK	1185.6	1186.6	1185.6	1186.6
25.0	21.5	21.5	32.8	2.0	99.0	FYKLNHER	991.5	992.5	991.5	992.5
25.0	21.5	21.5	32.8	2.0	99.0	HVFQPAKADQCCYEDVR	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	RGLVNMKCEIAR	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	VSQTTWDSGFCFAVNP	1795.8	1796.8	1795.8	1796.8
25.0	21.5	21.5	32.8	0.6	73.0	RDLRLEETVOAK	1456.8	1457.8	1456.8	1457.8
25.0	21.5	21.5	32.8	0.1	20.0	FYKLNHER	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	FYKLNHER	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	DLDDKKPIYQR	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	TOVTVQYMQDR	1367.7	1368.7	1367.7	1368.7
239.0	5.0	5.0	18.7	0.1	25.0	FVIGGPGQDAGLTGR	1443.7	1444.7	1443.7	1444.8
177.0	4.0	4.0	12.2	2.0	99.0	FVIGGPGQDAGLTGR	1443.7	1444.8	1443.7	1444.8
177.0	4.0	4.0	12.2	2.0	99.0	TOVTVQYMQDR	1367.7	1368.7	1367.7	1368.7
P31949 S10AB_HUMAN	Protein S100-A11 (S100 calcium-binding protein A11) (Protein S100C) (Calgizzarin) (BIM 70) - Homo sapiens (Human)									
210.0	6.0	6.0	46.7	2.0	99.0	CIESLI AVFOK	1306.7	1307.7	1306.7	1307.7
210.0	6.0	6.0	46.7	2.0	99.0	TEFLSFMMNTELAFTK	1848.9	1849.9	1848.9	1849.9
210.0	6.0	6.0	46.7	2.0	99.0	YAGKDGYNITLSK	1478.7	1479.7	1478.7	1479.7
189.0	2.0	2.0	10.5	2.0	99.0	CIESLI AVFOK	1306.7	1307.7	1306.7	1307.7
310.0	2.0	2.4	37.1	2.0	99.0	YAGKDGYNITLSK	1478.7	1479.7	1478.7	1479.7
310.0	2.0	2.4	37.1	0.0	59.0	TEFLSFMMNTELAFTK	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	AI AHYEQQMGQK	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	GIQAEEILQTYLK	1504.8	1505.8	1504.8	1505.8
54.0	17.0	17.0	27.2	2.0	99.0	IMKNEIDLOTK	1459.8	1460.8	1459.8	1460.8
54.0	17.0	17.0	27.2	2.0	99.0	KGIQAEEILQTYLK	1533.9	1534.9	1533.9	1534.9
54.0	17.0	17.0	27.2	2.0	99.0	SKESMTDAI LQDQTLTEKEKEI EVER	3151.5	3152.5	3151.5	3152.5
54.0	17.0	17.0	27.2	2.0	99.0	TLGGI QVNGPR	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	CFVFDPRVHR	1331.7	1332.7	1331.7	1332.7
54.0	17.0	17.0	27.2	0.4	62.0	MLQEMQR	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	AI AHYEQQMGQK	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	EAI EIVFR	975.5	976.5	975.5	976.5
42.0	17.7	17.7	37.7	2.0	99.0	GTSOKDETFNLRP	1491.7	1492.7	1491.7	1492.7
42.0	17.7	17.7	37.7	2.0	99.0	KGIQAEEILQTYLK	1533.9	1534.9	1533.9	1534.9
42.0	17.7	17.7	37.7	2.0	99.0	KGTSOKDETFNLRP	1520.8	1521.8	1520.8	1521.8
42.0	17.7	17.7	37.7	2.0	99.0	MENDRVQLLKEQER	1786.9	1787.9	1786.9	1787.9
42.0	17.7	17.7	37.7	1.7	98.0	SVOEHLKOLTEK	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	NSFKVDQDMFOR	1513.7	1514.7	1513.7	1514.7
234.0	5.3	7.3	9.6	1.2	94.0	CFVFDWPAPK	1248.6	1249.6	1248.6	1249.6
234.0	5.3	7.3	9.6	0.0	99.0	AI AHYEQQMGQK	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	AI AHYEQQMGQK	1402.7	1403.7	1402.7	1403.7
P33241 LSP1_HUMAN	Lymphocyte-specific protein 1 (Protein pp25) (52 kDa phosphoprotein) (Lymphocyte-specific antigen WP34) (47 kDa actin-binding protein) - Hom									
84.0	12.3	12.3	35.7	2.0	99.0	IDVILEGDTQIETAGR	2021.0	2022.0	2021.0	2022.0
84.0	12.3	12.3	35.7	2.0	99.0	QOHEGAGALDSEPPQCR	2064.9	2065.9	2064.9	2065.9
84.0	12.3	12.3	35.7	2.0	99.0	WETGEVQAQSAAK	1403.7	1404.7	1403.7	1404.7
84.0	12.3	12.3	35.7	2.0	99.0	YK FVATGHGK	1106.6	1107.6	1106.6	1107.6
84.0	12.3	12.3	35.7	1.7	98.0	LI DRTESLNR	1215.7	1216.7	1215.7	1216.7
84.0	12.3	12.3	35.7	1.4	96.0	QLQAQDEEGGHVPERPK	1974.0	1975.0	1974.0	1975.0
84.0	12.3	12.3	35.7	1.2	94.0	LKPSEAPELDEDEFGDWSORPEQR	2914.4	2915.4	2914.3	2915.3
168.0	4.2	4.2	21.5	2.0	99.0	WETGEVQAQSAAK	1403.7	1404.7	1403.7	1404.7
168.0	4.2	4.2	21.5	2.0	99.0	YK FVATGHGKYEK	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 IIa) (Nonmuscle myosin heavy chain IIa) (NMHC II-a) (NMHC-IIa) (Cellular									
17.0	36.9	36.9	25.6	2.0	99.0	ALEEAMEQKALEER	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	DFSALESQLODTEQLQEEENR	2492.2	2493.2	2492.2	2493.2
17.0	36.9	36.9	25.6	2.0	99.0	IAEFTTNLT EEEKSK	1867.9	1868.9	1867.9	1868.9
17.0	36.9	36.9	25.6	2.0	99.0	IAQLEEELEEEQNTLINDR	2471.1	2472.1	2471.2	2472.2
17.0	36.9	36.9	25.6	2.0	99.0	IAQLEEDLNKTER	1814.9	1815.9	1814.9	1815.9
17.0	36.9	36.9	25.6	2.0	99.0	IMGIP EEEQMLLR	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	LQOELDLLVDLHQR	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	1751.8
17.0	36.9	36.9	25.6	2.0	99.0	MQQNI QLEELQEEEEESAR	2332.0	2333.0	2332.0	2333.0
17.0	36.9	36.9	25.6	2.0	99.0	NAEQYKDAADKASTR	1724.8	1725.8	1724.8	1725.8
17.0	36.9	36.9	25.6	2.0	99.0	QLQANPILEAFGNK	1708.9	1709.9	1708.9	1709.9
17.0	36.9	36.9	25.6	2.0	99.0	OTLENERGELANEVK	1728.9	1729.9	1728.9	1729.9
17.0	36.9	36.9	25.6	2.0	99.0	RGDLPPVPR	1154.7	1155.7	1154.7	1155.7
17.0	36.9	36.9	25.6	2.0	99.0	SMEAMIQLEELAAAER	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	1571.8
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	ASREEI LAQAKENEK	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	VEEEEEERHQLOAEK	1912.8	1913.8	1912.9	1913.9
17.0	36.9	36.9	25.6	0.0	99.0	IAQLEEELEEEQNTLINDR	2472.1	2473.1	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	ELSESQIQLQELLESER	2034.0	2035.0	2034.0	2035.0
35.0	18.9	18.9	31.7	2.0	99.0	IMGIP EEEQMLLR	1614.8	1615.8	1614.8	1615.8
35.0	18.9	18.9	31.7	2.0	99.0	NAEQYKDAADKASTR	1723.8	1724.8	1723.8	1724.8
35.0	18.9	18.9	31.7	2.0	99.0	QLQANPILEAFGNK	1708.9	1709.9	1708.9	1709.9
35.0	18.9	18.9	31.7	1.7	98.0	SMEAMIQLEELAAAER	2045.9	2046.9	2045.0	2046.0
35.0	18.9	18.9	31.7	1.5	97.0	KLOAQMKDCMR	1407.7	1408.7	1407.7	1408.7
35.0	18.9	18.9	31.7	1.4	96.0	AKOTLENERGELANEVK	1928.0	1929.0	1928.0	1929.0

38.0	22.0	22.0	43.9	1.5	97.0	ILGQVPPYATKGNQWVGYDDQESVK	2822.4	2823.4	2822.4	2823.4
38.0	22.0	22.0	43.9	0.4	63.0	GOEDASPRFSNTDYAVGYMLR	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	GTGGHSPFLR	1208.6	1209.6	1208.6	1209.6
38.0	22.0	22.0	43.9	0.0	99.0	ILGQVPPYATK	1216.7	1217.7	1216.7	1217.7
38.0	22.0	22.0	43.9	0.0	99.0	LVMGIFPTFR	1091.6	1092.6	1091.6	1092.6
168.0	2.0	2.0	15.7	2.0	99.0	LVMGIFPTFR	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	GTGGHSPFLR	1208.6	1209.6	1208.6	1209.6
104.0	7.7	7.7	18.3	2.0	99.0	TLLSVGGWVNFQSOR	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	GTGGHSPFLR	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	NFSDNQLQCEKQVIGLQMGNTNR	2462.2	2463.2	2462.2	2463.2
66.0	14.8	14.8	61.3	2.0	99.0	QMEQISQFLQAAER	1660.8	1661.8	1660.8	1661.8
66.0	14.8	14.8	61.3	2.0	99.0	TLMNLGLLAVAR	1214.7	1215.7	1214.7	1215.7
66.0	14.8	14.8	61.3	2.0	99.0	YGINTTDIFOTVDLWEGK	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	QMEQISQFLQAAER	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	QMEQISQFLQAAER	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	QMEQISQFLQAAER	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	QMEQISQFLQAAER	1677.8	1678.8	1677.8	1678.8
P37837 TALDO_HUMAN Transaldolase (EC 2.2.1.2) - Homo sapiens (Human)										
219.0	5.9	5.9	11.9	2.0	99.0	LSDFKDAMVAR	1251.6	1252.6	1251.6	1252.6
219.0	5.9	5.9	11.9	2.0	99.0	WLHNEDQMAVEK	1498.7	1499.7	1498.7	1499.7
219.0	5.9	5.9	11.9	1.3	95.0	IYNYKK	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	WLHNEDQMAVEK	1498.7	1499.7	1498.7	1499.7
220.0	3.1	3.1	18.4	2.0	99.0	WLHNEDQMAVEK	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	DSYGGPPRRPLPSRR	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-I) (eIF-4A-I) - Homo sapiens (Human)										
428.0	2.1	2.1	10.8	2.0	99.0	GIYAYGFKPSAIQQR	1826.9	1827.9	1826.9	1827.9
231.0	2.7	2.7	12.3	2.0	99.0	GIYAYGFKPSAIQQR	1826.9	1827.9	1826.9	1827.9
231.0	2.7	2.7	12.3	0.7	81.0	DFTVSAMHGDMDOKER	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	QAAALQVAEGFISR	1371.7	1372.7	1371.7	1372.7
181.0	6.4	6.4	19.3	2.0	99.0	QAAALQVAEGFISR	1371.7	1372.7	1371.7	1372.7
181.0	6.4	6.4	19.3	0.0	98.0	QAAALQVAEGFISR	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	QAAALQVAEGFISR	1371.7	1372.7	1371.7	1372.7
30.0	10.0	10.0	23.0	2.0	99.0	QAAALQVAEGFISR	1371.7	1372.7	1371.7	1372.7
30.0	10.0	10.0	23.0	2.0	99.0	QFFKDWK	997.5	998.5	997.5	998.5
30.0	10.0	10.0	23.0	2.0	99.0	YQEGGVESAFHK	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	QAAALQVAEGFISR	1388.7	1389.7	1388.7	1389.7
30.0	10.0	10.0	23.0	0.0	55.0	QFFKDWK	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	QAAALQVAEGFISR	1371.7	1372.7	1371.7	1372.7
72.0	10.1	10.1	30.2	2.0	99.0	YQEGGVESAFHK	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	QAAALQVAEGFISR	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	NVIIWGNHSSTQYDPVNHAK	2279.1	2280.1	2279.1	2280.1
90.0	12.0	12.0	31.4	2.0	99.0	SAPSIKPKNFSLCTR	1705.8	1706.8	1705.8	1706.9
90.0	12.0	12.0	31.4	2.0	99.0	VI VVGNFRANTNGLTASK	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	SAPSIKPKNFSLCTR	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	NVIIWGNHSSTQYDPVNHAK	2279.1	2280.1	2279.1	2280.1
63.0	12.0	12.0	26.3	2.0	99.0	SAPSIKPKNFSLCTR	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	AGAGSATSLSMAYAGAR	1453.7	1454.7	1453.7	1454.7
71.0	14.1	14.1	42.6	2.0	99.0	CYLQFQLPDLCK	1489.7	1490.7	1489.7	1490.7
71.0	14.1	14.1	42.6	2.0	99.0	IFGVTTLDIR	1232.7	1233.7	1232.7	1233.7
71.0	14.1	14.1	42.6	2.0	99.0	LTLVDIAHTPTGVAADLSHETK	2364.2	2365.2	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	TIIPLISQCTPK	1369.8	1370.8	1369.8	1370.8
71.0	14.1	14.1	42.6	2.0	99.0	VDFPDQLTALTGR	1559.8	1560.8	1559.8	1560.8
280.0	2.1	2.1	17.2	2.0	99.0	HGVYVNPKNKIFGVTTLDIR	2142.2	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	ELGAIPTTWER	1307.7	1308.7	1307.7	1308.7
58.0	16.7	16.7	19.1	2.0	99.0	ELSAVTFPDIIR	1359.7	1360.7	1359.7	1360.7
58.0	16.7	16.7	19.1	2.0	99.0	FHDLLSQDLDQYSR	1735.8	1736.8	1735.8	1736.8
58.0	16.7	16.7	19.1	2.0	99.0	QDWEHAANDVSFATIR	1841.8	1842.8	1841.8	1842.8
58.0	16.7	16.7	19.1	2.0	99.0	OYLAQWLEK	1160.6	1161.6	1160.6	1161.6
58.0	16.7	16.7	19.1	2.0	99.0	SLEDLQDEYDFK	1500.7	1501.7	1500.7	1501.7
58.0	16.7	16.7	19.1	2.0	99.0	SQWYELQLQDLSK	1565.7	1566.7	1565.7	1566.7
58.0	16.7	16.7	19.1	2.0	99.0	YLYPNIKDHFAGFK	1679.8	1680.8	1679.8	1680.8
58.0	16.7	16.7	19.1	0.7	80.0	GLNVDQLNMLGEK	1429.7	1430.7	1429.7	1430.7
58.0	16.7	16.7	19.1	0.0	99.0	QDWEHAANDVSFATIR	1858.9	1859.9	1858.9	1859.9
83.0	4.1	4.1	11.2	2.0	99.0	FHDLLSQDLDQYSR	1735.8	1736.8	1735.8	1736.8
83.0	4.1	4.1	11.2	2.0	99.0	SQWYELQLQDLSK	1565.7	1566.7	1565.7	1566.7
83.0	4.1	4.1	11.2	0.1	21.0	QDWEHAANDVSFATIR	1858.9			

55.0	13.4	13.4	20.2	2.0	99.0	LLPYLR	870.5	871.5	870.5	871.5
55.0	13.4	13.4	20.2	2.0	99.0	MNPAAEAENILLATDSYK	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	IWGEDLR	887.5	888.5	887.5	888.5
55.0	13.4	13.4	20.2	0.0	97.0	LHDFGFR	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	KAHAAIARENPVYKPK	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	RFGPDYSEKFEKNAEVHVK	2295.1	2296.1	2295.1	2296.1
79.0	13.3	13.3	35.0	1.7	98.0	YLMEEDEDAYKKQFQSOYIK	2427.1	2428.1	2427.1	2428.1
79.0	13.3	13.3	35.0	1.5	97.0	AHAAIARENPVYK	1496.8	1497.8	1496.8	1497.8
79.0	13.3	13.3	35.0	0.1	20.0	AHAAIARENPVYKPK	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	AHAAIARENPVYK	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	RLGQVFR	1018.6	1019.6	1018.6	1019.6
220.0	5.8	5.8	28.4	1.7	98.0	QVWNPISFIVR	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	KNAKKGGGAGAGDDEE	1613.8	1614.8	1613.7	1614.7
220.0	5.8	5.8	28.4	0.0	98.0	QVWNPISFIVR	1270.7	1271.7	1270.7	1271.7
210.0	3.3	3.3	47.9	1.2	93.0	KQVWNPISFIVR	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	QVWNPISFIVR	1270.7	1271.7	1270.7	1271.7
210.0	3.3	3.3	47.9	0.2	35.0	ELLTLDKOPRR	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	IFYPETDIDYRK	1659.8	1660.8	1659.8	1660.8
180.0	6.4	6.4	6.8	2.0	99.0	QNVAYEYLCHLEAKR	2022.0	2023.0	2022.0	2023.0
180.0	6.4	6.4	6.8	0.4	59.0	MREVEITLDR	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	IFYPETDIDYRK	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	QLLSDKQKR	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	AMTGVQWVPR	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	KIGDEYFTITDCKDPK	2076.0	2077.0	2076.0	2077.0
87.0	12.2	12.2	23.9	2.0	99.0	NLQDAMQVCR	1233.6	1234.6	1233.6	1234.6
87.0	12.2	12.2	23.9	0.9	86.0	MLLDPMGIVMTNDGNAILR	2130.0	2131.0	2130.1	2131.1
87.0	12.2	12.2	23.9	0.8	84.0	TLIQNGASTIR	1332.7	1333.7	1332.7	1333.7
87.0	12.2	12.2	23.9	0.5	69.0	TAVETAVALLR	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 GDIB_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	DLGTESIQIFIR	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	NPYYGSESASITPLEDLYKR	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	TYDATTFHETTCDDIKNI YKR	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	1402.7	1403.7	1402.7	1403.7
54.0	6.1	6.1	16.0	2.0	99.0	DLGTESIQIFIR	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	DLGTESIQIFIR	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	TYDATTFHETTCDDIK	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	GKWNEPFDYTR	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
P50552 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	SGGGGLMEEMNAMLAR	1622.7	1623.7	1622.7	1623.7
83.0	12.7	12.7	31.8	2.0	99.0	SSSSVITSETQPTPSSSDYDLQR	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	WLPKQTPQAFSR	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	MKSSSVITSETQPTPSSSDYDLQR	2965.3	2966.3	2965.3	2966.3
83.0	12.7	12.7	31.8	0.2	41.0	QQPGSEHER	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	FAEAFEAI PR	1149.6	1150.6	1149.6	1150.6
208.0	6.0	6.0	6.4	2.0	99.0	HFGLEAAVYR	1306.6	1307.6	1306.6	1307.6
208.0	6.0	6.0	6.4	2.0	99.0	KFAEAFEAI PR	1277.7	1278.7	1277.7	1278.7
208.0	6.0	6.0	6.4	0.0	0.0	FAEAFEAI PR	1149.6	1149.6	1149.6	1149.6
113.0	2.9	2.9	7.3	2.0	99.0	FAEAFEAI PR	1149.6	1150.6	1149.6	1150.6
113.0	2.9	2.9	7.3	0.9	88.0	HFGLEAAVYR	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	EAINVEAQFOTIAR	1588.8	1589.8	1588.8	1589.8
362.0	3.0	3.0	20.3	1.0	99.0	FOSLGVAFYR	1186.6	1187.6	1186.6	1187.6
209.0	3.4	3.4	11.6	2.0	99.0	FOSLGVAFYR	1186.6	1187.6	1186.6	1187.6
209.0	3.4	3.4	11.6	1.4	96.0	EAINVEAQFOTIAR	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	YGKIEIEMEDR	1581.8	1582.8	1581.8	1582.8
162.0	7.3	7.4	39.7	2.0	99.0	YHTINGHNCVKK	1599.7	1600.7	1599.7	1600.8
162.0	7.3	7.4	39.7	1.3	95.0	SSGSPYGGYGGGGGGYGSR	1909.8	1910.8	1909.8	1910.8
162.0	7.3	7.4	39.7	0.0	94.0	YHTINGHNCVKK	1537.8	1538.8	1537.8	1538.8
208.0	3.4	3.7	29.6	2.0	99.0	YGKIEIEMEDR	1581.8	1582.8	1581.8	1582.8
208.0	3.4	3.7	29.6	0.9	88.0	SSGSPYGGYGGGGGGYGSR	1909.8	1910.8	1909.8	1910.8
208.0	3.4	3.7	29.6	0.5	67.0	YHTINGHNCVKK	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	GILFVGGVSGGEGAR	1590.8	1591.8	1590.8	1591.8
121.0	2.4	2.4	10.8	2.0	99.0	GILFVGGVSGGEGAR	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	FQDITDGKHLIPK	1397.7	1398.7	1397.7	1398.7
50.0	15.5	15.5	26.3	2.0	99.0	GILFVGGVSGGEGAR	1590.8	1591.8	1590.8	1591.8
50.0	15.5	15.5	26.							

28.0	24.6	24.6	49.0	2.0	99.0	KYKALLGR	1076.6	1077.6	1076.6	1077.6
28.0	24.6	24.6	49.0	2.0	99.0	QSFVLKGEVEYR	1453.8	1454.8	1453.8	1454.8
28.0	24.6	24.6	49.0	2.0	99.0	SIQEIQLDKDDESLR	1914.9	1915.9	1916.9	1917.9
28.0	24.6	24.6	49.0	2.0	99.0	SIQEIQLDKDDESLRK	2045.0	2046.0	2045.0	2046.0
28.0	24.6	24.6	49.0	2.0	99.0	YIQTHTYR	979.5	980.5	979.5	980.5
28.0	24.6	24.6	49.0	2.0	99.0	YIQTHTYR	1107.6	1107.6	1107.6	1107.6
28.0	24.6	24.6	49.0	2.0	99.0	YKAEALLGR	948.5	949.5	948.5	949.5
28.0	24.6	24.6	49.0	1.7	98.0	AEEVEFLTPVEEAPKGMALAR	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	AEEVEFLTPVEEAPKGMALAR	2279.1	2280.1	2279.1	2280.1
28.0	24.6	24.6	49.0	0.0	99.0	SIQEIQLDKDDESLR	1916.9	1917.9	1916.9	1917.9
82.0	4.1	4.1	26.0	2.0	99.0	AEEVEFLTPVEEAPKGMALAR	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	AEEVEFLTPVEEAPKGMALAR	2279.1	2280.1	2279.1	2280.1
86.0	8.8	8.8	51.0	2.0	99.0	IKDIDYVMVGSYGPR	1600.8	1601.8	1600.8	1601.8
86.0	8.8	8.8	51.0	2.0	99.0	SIQEIQLDKDDESLR	1916.9	1917.9	1916.9	1917.9
86.0	8.8	8.8	51.0	2.0	99.0	YKAEALLGR	948.5	949.5	948.5	949.5
86.0	8.8	8.8	51.0	0.5	69.0	KYKALLGR	1076.6	1077.6	1076.6	1077.6
86.0	8.8	8.8	51.0	0.2	94.0	KOSFVLKGEVEYR	1630.8	1631.8	1630.8	1631.8
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	ATFMVGSYGPRPEEVEFLTPVEEAPK	2943.4	2944.4	2943.4	2944.4
101.0	11.1	12.0	49.8	2.0	99.0	ETIVLKGESYR	1422.7	1423.8	1422.7	1423.8
101.0	11.1	12.0	49.8	2.0	99.0	IHFKNVR	912.5	913.5	912.5	913.5
101.0	11.1	12.0	49.8	2.0	99.0	SKLEQEMDKDDESLIK	2020.0	2021.0	2020.0	2021.0
101.0	11.1	12.0	49.8	1.5	97.0	APNVVVTTR	854.5	855.5	854.5	855.5
101.0	11.1	12.0	49.8	1.0	99.0	YQOHTYR	965.5	966.5	965.5	966.5
101.0	11.1	12.0	49.8	0.5	66.0	TLLGDGVPVTDPAKPNVVVTR	2147.2	2148.2	2147.2	2148.2
269.0	2.1	2.1	49.3	2.0	99.0	IHFKNVR	912.5	913.5	912.5	913.5
269.0	2.1	2.1	49.3	0.0	98.0	IHFKNVR	912.5	913.5	912.5	913.5
P52997 HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F (hRNP F) (Nucleolin-like protein mcs94-1F) - Homo sapiens (Human)										
334.0	3.6	6.0	20.7	2.0	99.0	HSGPNASDANDGFVR	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	ATENDIYNFFSPLNPVR	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	HSGPNASDANDGFVR	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	FI THAPPGERNEFNDVR	2088.0	2089.0	2088.0	2089.0
233.0	5.3	5.3	19.9	2.0	99.0	TIDGQOQTIACIESHOFQPK	2313.2	2314.2	2313.1	2314.1
233.0	5.3	5.3	19.9	1.3	95.0	LLLLNNDNLR	1196.7	1197.7	1196.7	1197.7
166.0	2.0	2.0	19.2	2.0	99.0	FI THAPPGERNEFNDVR	2088.0	2089.0	2088.0	2089.0
282.0	2.1	2.1	15.4	2.0	99.0	TIDGQOQTIACIESHOFQPK	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 O) (Cathepsin J) (Dipeptidyl transferase) [Con]										
101.0	3.5	3.5	11.9	1.4	96.0	NVHGINFVSPVR	1337.7	1338.7	1337.7	1338.7
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	NVHGINFVSPVR	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	LOAYHTQTPLIEYR	1996.0	1997.0	1996.0	1997.0
189.0	6.1	6.1	34.7	2.0	99.0	NGFLLDGFPR	1136.6	1136.6	1136.6	1136.6
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	LOAYHTQTPLIEYR	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	LOAYHTQTPLIEYR	1996.0	1997.0	1996.0	1997.0
126.0	6.0	6.0	28.9	2.0	99.0	NGFLLDGFPR	1136.6	1136.6	1136.6	1136.6
126.0	6.0	6.0	28.9	0.0	99.0	LOAYHTQTPLIEYR	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	ELQELVQVPVEHPDKFLK	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	GPPELLMWFGESEANVR	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	98.0	WALSQSNPSALR	1329.7	1329.7	1329.7	1329.7
45.0	19.1	19.1	25.3	1.2	94.0	RDFHEEAMR	1189.5	1189.5	1189.5	1189.5
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	1189.5	1189.5	1189.5
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	1329.7	1329.7	1329.7
61.0	12.8	12.8	18.7	0.0	80.0	RDFHEEAMR	1189.5	1189.5	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	KYAVLYQRLFDKDR	1639.9	1640.9	1639.9	1640.9
198.0	6.0	6.0	10.5	2.0	99.0	NVDLLSDMVOEHDEPLK	2094.0	2095.1	2094.0	2095.0
98.0	3.8	3.8	10.2	2.0	99.0	KYAVLYQRLFDKDR	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	YAVLYQRLFDKDR	1511.8	1512.8	1511.8	1512.8
187.0	4.0	4.0	10.0	2.0	99.0	FYEEVHDLER	1336.6	1336.6	1336.6	1336.6
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	AFESHAPSAER	1444.7	1445.7	1444.7	1445.7
407.0	2.3	2.3	3.8	0.2	36.0	YAAVTFQETDAR	1441.7	1442.7	1441.7	1442.7
152.0	2.0	2.0	7.5	2.0	99.0	DAESHQVLLOR	1471.7	1472.7	1471.7	1472.7
181.0	4.0	4.0	6.7	2.0	99.0	AFESHAPSAER	1444.7	1445.7	1444.7	1445.7
181.0	4.0	4.0	6.7	2.0	99.0	DAESHQVLLOR	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	IVAEFLK	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	DCGATWVVLGHSER	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	HVFGSEDELIQOK	1457.7	1458.7	1457.7	1458.7
23.0	28.0	28.0	61.0	2.0	99.0	IIVAQCNCKY	1136.6	1137.6	1136.6	1137.6
23.0	28.0	28.0	61.0	2.0	99.0	IYGGSVTGATCK	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	QSLGELJGTLNAAK	1396.8	1397.8	1396.8	1397.8
23.0	28.0	28.0	61.0	2.0	99.0	RHVFGSEDELIQOK	1613.8	1614.8	1613.8	1614.8
23.0	28.0	28.0	61.0	2.0	99.0	TATPQQAQEVHEK	1465.7	1466.7	1465.7	1466.7
23.0	28.0	28.0	61.0	2.0	99.0	TATPQQAQEVHEKLR	1734.9	1735.9	1734.9	1735.9
23.0	28.0	28.0	61.0	2.0	99.0	VPADTEVVCAPPTAIFYDFAR	2191.1	2192.1	2191.1	2192.1
23.0	28.0	28.0	61.0	2.0	99.0	VTNGAFTEIISPGMIK	1621.8	1622.8	1621.8	1622.8
23.0	28.0	28.0	61.0	2.0	99.0	VVLAPEPVWAGTGK	1601.9	1602.9	1601.9	1602.9
23.0	28.0	28.0	61.0	1.2	94.0	VVFEQTK	849.5	850.5	849.5	850.5
23.0	28									

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	VVLALEYVWAIQTGK	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	2192.1	2193.1	2191.1	2192.1
40.0	18.1	18.1	57.0	2.0	99.0	DCGATVWVLGHSEIR	1585.7	1586.7	1585.7	1586.7
40.0	18.1	18.1	57.0	2.0	99.0	FFVGGNWK	953.5	954.5	953.5	954.5
40.0	18.1	18.1	57.0	2.0	99.0	IYVGSVGTGATCK	1325.7	1326.7	1325.7	1326.7
40.0	18.1	18.1	57.0	2.0	99.0	KFFVGGNWK	1081.6	1082.6	1081.6	1082.6
40.0	18.1	18.1	57.0	2.0	99.0	TATPQQAQEVHEK	1465.7	1466.7	1465.7	1466.7
40.0	18.1	18.1	57.0	2.0	99.0	VAHALAEGLVGVIACIGEK	1807.0	1808.0	1807.0	1808.0
40.0	18.1	18.1	57.0	2.0	99.0	VPADTEVVCAPPTAYIDFAR	2191.1	2192.1	2191.1	2192.1
40.0	18.1	18.1	57.0	2.0	99.0	VVLALEYVWAIQTGK	1601.9	1602.9	1601.9	1602.9
40.0	18.1	18.1	57.0	1.5	97.0	DCGATVWVLGHSEIR	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] MYLB_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	ALGNPTNAEVLK	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	MCDFTEDQTAEFKEAFQLFDR	2538.1	2539.1	2538.1	2539.1
112.0	10.0	10.0	50.3	2.0	99.0	NKDQGTIEDYVEGLR	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	NKDQGTIEDYVEGLR	1785.8	1786.8	1785.8	1786.8
65.0	5.2	5.2	31.1	0.3	48.0	ALGNPTNAEVLK	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	NKDQGTIEDYVEGLR	1785.8	1786.8	1785.8	1786.8
122.0	6.1	6.1	50.3	2	99.00	FKDKEGNGTVMGSAEIR	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	DDI1AALVVDNGSGMCK	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	975.5	976.5	975.5	976.4
449.0	2.0	54.1	69.9	0.0	99.0	AVFPSI VGRPR	1041.6	1042.6	1041.6	1042.6
449.0	2.0	54.1	69.9	0.0	99.0	AVFPSI VGRPR	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	DDI1AALVVDNGSGMCK	1973.8	1974.8	1973.8	1974.8
449.0	2.0	54.1	69.9	0.0	99.0	DDI1AALVVDNGSGMCK	1821.8	1822.8	1821.8	1822.8
449.0	2.0	54.1	69.9	0.0	99.0	DDI1AALVVDNGSGMCK	1821.8	1822.8	1821.8	1822.8
449.0	2.0	54.1	69.9	0.0	99.0	DDI1AALVVDNGSGMCK	1973.8	1974.8	1973.8	1974.8
449.0	2.0	54.1	69.9	0.0	99.0	DLYANTVLSGGTTMYPGIADR	2214.0	2215.0	2214.0	2215.1
449.0	2.0	54.1	69.9	0.0	99.0	E1TALAPSTMK	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	GYSFTTAEIRV	1628.8	1629.8	1628.8	1629.8
449.0	2.0	54.1	69.9	0.0	99.0	GYSFTTAEIRVVDIK	1985.1	1986.1	1985.0	1986.0
449.0	2.0	54.1	69.9	0.0	95.0	GYSFTTAEIRVVDIKKEK	2242.2	2243.2	2242.2	2243.2
449.0	2.0	54.1	69.9	0.0	86.0	GYSFTTAEIRVVDIKKEK	2243.2	2244.2	2243.2	2243.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQK	1170.6	1171.6	1170.6	1171.6
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	HQGMVGMGQKDSYVGEAQS	2366.1	2367.1	2366.1	2367.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAQS	2351.1	2352.1	2351.1	2351.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAQS	2394.1	2395.1	2394.1	2395.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAQS	2366.1	2367.1	2366.1	2367.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAQS	2378.1	2379.1	2378.1	2379.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAQS	2522.2	2523.2	2522.2	2523.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAQS	2522.2	2523.2	2522.2	2523.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAQS	2506.2	2507.2	2506.2	2507.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAQS	2534.2	2535.2	2534.2	2535.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGMVGMGQKDSYVGEAQS	2518.2	2519.2	2518.2	2519.2
449.0	2.0	54.1	69.9	0.0	95.0	HQGMVGMGQKDSYVGEAQS	2538.2	2539.2	2538.2	2539.2
449.0	2.0	54.1	69.9	0.0	23.0	I1APPER	794.5	795.5	794.5	795.5
449.0	2.0	54.1	69.9	0.0	83.0	I1APPERK	922.6	923.6	922.6	923.6
449.0	2.0	54.1	69.9	0.0	99.0	I1I1APPER	1035.6	1036.6	1035.6	1036.7
449.0	2.0	54.1	69.9	0.0	99.0	I1I1APPER	1036.7	1037.7	1036.7	1037.7
449.0	2.0	54.1	69.9	0.0	86.0	I1I1APPERK	1163.7	1164.7	1163.7	1164.7
449.0	2.0	54.1	69.9	0.0	41.4	ISKQEVDESGPSVHR	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	1246.6
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	1500.7	1499.7	1500.7
449.0	2.0	54.1	69.9	0.0	44.0	IWHHTFYNELR	1471.7	1472.7	1471.7	1472.7
449.0	2.0	54.1	69.9	0.0	99.0	KDLYANTVLSGGTTMYPGIADR	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	MQKEIT1ALAPSTMK	1547.8	1548.8	1547.8	1548.8
449.0	2.0	54.1	69.9	0.0	99.0	QEVDESGPSVHR	1515.7	1516.7	1515.7	1516.7
449.0	2.0	54.1	69.9	0.0	99.0	QEVDESGPSVHR	1498.7	1499.7	1498.7	1499.7
449.0	2.0	54.1	69.9	0.0	99.0	QEVDESGPSVHRK	1643.8	1644.8	1643.8	1644.8
449.0	2.0	54.1	69.9	0.0	99.0	QEVDESGPSVHRK	1626.8	1627.8	1626.8	1627.8
449.0	2.0	54.1	69.9	0.0	92.0	RGL1TLK	799.5	800.5	799.5	800.5
449.0	2.0	54.1	69.9	0.0	28.4	SLSTFOQMW1SK	1454.7	1455.7	1454.7	1455.7
449.0	2.0	54.1	69.9	0.0	99.0	SYELPDGOVITIGNER	1789.9	1790.9	1789.9	1790.9
449.0	2.0	54.1	69.9	0.0	99.0	SYELPDGOVITIGNER	1789.9	1790.9	1789.9	1790.9
449.0	2.0	54.1	69.9	0.0	99.0	SYELPDGOVITIGNER	1791.9	1792.9	1791.9	1792.9
449.0	2.0	54.1	69.9	0.0	95.0	SYELPDGOVITIGNER	1786.0	1787.0	1785.9	1786.9
449.0	2.0	54.1	69.9	0.0	96.0	SYELPDGOVITIGNERFR	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	1954.1
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	YPIEHG1VTNWDDMEK	1959.9	1960.9	1959.9	1960.9
449.0	2.0	54.1	69.9	0.0	99.0	YPIEHG1VTNWDDMEK	1945.9	1946.9	1945.9	1946.9
5.0	31.5	31.5	66.4	2.0	99.0	AVFPSI VGRPR	1197.7	1198.7	1197.7	1198.7
5.0	31.5	31.5	66.4	2.0	99.0	DDI1AALVVDNGSGMCK	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	DLYANTVLSGGTTMYPGIADR	2214.0	2215.0	2214.0	2215.1
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	HQGMVGMGQKDSYVGEAQS	2350.1	2351.1	2350.1	2351.1
5.0	31.5	31.5	66.4	2.0	99.0	HQGMVGMGQKDSYVGEAQS	2506.2	2507.2	2506.2	2507.1
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	2550.1
5.0	31.5	31.5	66.4	2.0	99.0	QEVDESGPSVHRK	1643.8	1644.8	1643.8	1644.8
5.0	31.5	31.5	66.4	2.0	99.0	SYELPD				

5.0	31.5	31.5	66.4	0.0	74.0	QEYDESGPSIVHRK	1626.8	1627.8	1626.8	1627.8
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	1031.55481	1032.562	1031.55525	1032.562527
304.0	4.0	4.0	9.4	2.0	99.0	YLECSALTQR	1239.592773	1240.6	1239.591772	1240.599048
356.0	2.0	2.0	5.2	2.0	99.0	YLECSALTQR	1239.595703	1240.603	1239.591772	1240.599048
P60842 IF4A1_HUMAN										
Eukaryotic initiation factor 4A-1 (EC 3.6.1.1) (ATP-dependent RNA helicase eIF4A-1) (eIF4A-1) (eIF4A-1) - Bos taurus (Bovine) ; Eukaryotic Initiat										
231.0	2.7	2.7	12.3	2.0	99.0	GIYAGFEKPSAIQQR	1826.9	1827.9	1826.9	1827.9
231.0	2.7	2.7	12.3	0.7	81.0	DFTVSAAMHGDMQKER	1865.8	1866.8	1865.8	1866.8
428.0	2.1	2.1	10.8	2.0	99.0	GIYAGFEKPSAIQQR	1826.9	1827.9	1826.9	1827.9
P60866 RS20_HUMAN										
40S ribosomal protein S20 - Homo sapiens (Human)										
354.0	3.2	3.2	29.4	2.0	99.0	AFKDTGKTPVEVAIHR	2036.1	2037.1	2036.1	2037.1
354.0	3.2	3.2	29.4	1.2	93.0	TWDRFQMR	1138.5	1139.5	1138.5	1139.5
165.0	4.4	4.4	21.8	2.0	99.0	AFKDTGKTPVEVAIHR	2036.1	2037.1	2036.1	2037.1
165.0	4.4	4.4	21.8	1.4	96.0	TWDRFQMR	1138.5	1139.5	1138.5	1139.5
165.0	4.4	4.4	21.8	1.0	89.0	DTGKTPVEVAIHR	1647.9	1648.9	1647.9	1648.9
P60900 PSA6_HUMAN										
Proteasome subunit alpha type 6 (EC 3.4.25.1) (Proteasome iota chain) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain)										
69.0	14.4	14.4	40.2	2.0	99.0	AINOGGLTSVAVR	1284.7	1285.7	1284.7	1285.7
69.0	14.4	14.4	40.2	2.0	99.0	CDPRLPGYVCGFK	1319.5	1320.5	1319.5	1320.5
69.0	14.4	14.4	40.2	2.0	99.0	HITIFSPGGR	1155.6	1156.6	1155.6	1156.6
69.0	14.4	14.4	40.2	2.0	99.0	ILTEAEIDAHVALAERD	1978.0	1979.0	1978.0	1979.0
69.0	14.4	14.4	40.2	2.0	99.0	ITENIGCVMTGMTADSR	1854.8	1855.8	1854.8	1855.8
69.0	14.4	14.4	40.2	2.0	99.0	LYQVYAFK	1159.6	1160.6	1159.6	1160.6
69.0	14.4	14.4	40.2	2.0	99.0	YGYEIPVDMCKCR	1642.8	1643.8	1642.8	1643.8
69.0	14.4	14.4	40.2	0.4	64.0	GSSAGDFRHITIFSPGGR	1932.9	1934.0	1932.9	1934.0
180.0	2.0	2.0	8.5	2.0	99.0	HITIFSPGGR	1155.6	1156.6	1155.6	1156.6
94.0	8.1	8.1	24.8	2	99.0	AINOGGLTSVAVR	1284.7	1285.7	1284.7	1285.7
94.0	8.1	8.1	24.8	2	99.0	HITIFSPGGR	1155.6	1156.6	1155.6	1156.6
94.0	8.1	8.1	24.8	2	99.0	ILTEAEIDAHVALAERD	1978.0	1979.0	1978.0	1979.0
94.0	8.1	8.1	24.8	2	99.0	LYQVYAFK	1159.6	1160.6	1159.6	1160.6
P61150 ARP3_HUMAN										
Actin-like protein 3 (Actin-related protein 3) - Homo sapiens (Human)										
111.0	10.0	10.0	14.4	2.0	99.0	AGRLPACVDCGTGYTK	1865.9	1866.9	1865.9	1866.9
111.0	10.0	10.0	14.4	2.0	99.0	EFSDIVGYER	1213.6	1214.6	1213.6	1214.6
111.0	10.0	10.0	14.4	2.0	99.0	KDYEEIGPISCR	1465.7	1466.7	1465.7	1466.7
111.0	10.0	10.0	14.4	2.0	99.0	KEFSDIVGYER	1341.7	1342.7	1341.7	1342.7
111.0	10.0	10.0	14.4	2.0	99.0	NIVLSGGSTMFR	1280.7	1281.7	1280.7	1281.7
111.0	10.0	10.0	14.4	0.0	99.0	KDYEEIGPISCR	1465.7	1466.7	1465.7	1466.7
79.0	9.5	9.5	18.2	2.0	99.0	AGRLPACVDCGTGYTK	1865.9	1866.9	1865.9	1866.9
79.0	9.5	9.5	18.2	2.0	99.0	EFSDIVGYER	1213.6	1214.6	1213.6	1214.6
79.0	9.5	9.5	18.2	2.0	99.0	KDYEEIGPISCR	1465.7	1466.7	1465.7	1466.7
79.0	9.5	9.5	18.2	2.0	99.0	LKPKPIDVQVITHMQR	2039.1	2040.1	2039.1	2040.2
79.0	9.5	9.5	18.2	1.4	96.0	DYEEIGPISCR	1337.6	1338.6	1337.6	1338.6
P61160 ARP2_HUMAN										
Actin-like protein 2 (Actin-related protein 2) - Homo sapiens (Human)										
141.0	8.0	8.0	24.6	2.0	99.0	GVAFNHSADFEYR	1612.7	1613.7	1612.7	1613.7
141.0	8.0	8.0	24.6	2.0	99.0	HIVLSGGSTMYPGLPSR	1770.9	1771.9	1770.9	1771.9
141.0	8.0	8.0	24.6	2.0	99.0	HLWDYTFGPEK	1391.7	1392.7	1391.7	1392.7
141.0	8.0	8.0	24.6	2.0	99.0	SMLEVNYPMENGIVR	1751.8	1752.8	1751.8	1752.8
141.0	8.0	8.0	24.6	0.0	99.0	SMLEVNYPMENGIVR	1751.8	1752.8	1751.8	1752.8
112.0	2.9	2.9	15.5	1.4	96.0	VGNIIEIKDLVGVDEASELR	2087.1	2088.1	2087.1	2088.1
112.0	2.9	2.9	15.5	1.0	89.0	HLWDYTFGPEK	1391.7	1392.7	1391.7	1392.7
112.0	2.9	2.9	15.5	0.6	74.0	SMLEVNYPMENGIVR	1750.8	1751.8	1750.8	1751.8
364.0	2.0	2.0	4.8	2.0	99.0	VGNIIEIKDLVGVDEASELR	2088.0	2089.0	2088.0	2089.0
P61247 RS3A_HUMAN										
40S ribosomal protein S3a - Homo sapiens (Human)										
73.0	14.0	14.0	30.7	2.0	99.0	ACQSIYPLHDVFR	1703.8	1704.9	1703.8	1704.9
73.0	14.0	14.0	30.7	2.0	99.0	APAMFNIR	918.5	919.5	918.5	919.5
73.0	14.0	14.0	30.7	2.0	99.0	KTSYAQHQVVR	1344.7	1345.7	1344.7	1345.7
73.0	14.0	14.0	30.7	2.0	99.0	LFCVGFTEK	970.5	971.5	970.5	971.5
73.0	14.0	14.0	30.7	2.0	99.0	NCLTNFHGMDLTR	1577.7	1578.7	1577.7	1578.7
73.0	14.0	14.0	30.7	2.0	99.0	TSYAQHQVVR	1216.6	1217.6	1216.6	1217.6
73.0	14.0	14.0	30.7	2.0	99.0	VVDFPFSKDWYDVK	1724.9	1725.9	1724.9	1725.9
63.0	5.5	5.5	16.3	2.0	99.0	APAMFNIR	918.5	919.5	918.5	919.5
63.0	5.5	5.5	16.3	2.0	99.0	NCLTNFHGMDLTR	1577.7	1578.7	1577.7	1578.7
63.0	5.5	5.5	16.3	1.5	97.0	ACQSIYPLHDVFR	1703.8	1704.9	1703.8	1704.9
136.0	5.8	5.8	18.2	2.0	99.0	ACQSIYPLHDVFR	1703.8	1704.8	1703.8	1704.9
136.0	5.8	5.8	18.2	2.0	99.0	APAMFNIR	918.5	919.5	918.5	919.5
136.0	5.8	5.8	18.2	1.7	98.0	NCLTNFHGMDLTR	1577.7	1578.7	1577.7	1578.7
136.0	5.8	5.8	18.2	0.1	20.0	KTSYAQHQVVR	1361.7	1362.7	1361.7	1362.7
P61254 RL26_HUMAN										
60S ribosomal protein L26 - Homo sapiens (Human)										
445.0	2.0	2.0	15.2	2.0	99.0	MKFNFTSDR	1340.7	1341.7	1340.7	1341.7
271.0	2.1	2.1	29.7	2.0	99.0	MKFNFTSDR	1340.7	1341.7	1340.7	1341.7
P61604 CH10_HUMAN										
10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (CPN10) (Early-pregnancy factor) (EPF) - Homo sapiens (Human)										
221.0	5.7	5.7	26.5	2.0	99.0	KFLPLFDR	1034.6	1035.6	1034.6	1035.6
221.0	5.7	5.7	26.5	2.0	99.0	VVLDKDYVLFRR	1528.8	1529.8	1528.8	1529.8
221.0	5.7	5.7	26.5	1.7	98.0	FLPLFDR	906.5	907.5	906.5	907.5
374.0	1.9	1.9	26.5	1.7	98.0	FLPLFDR	906.5	907.5	906.5	907.5
374.0	1.9	1.9	26.5	0.2	34.0	VVLDKDYVLFRR	1528.8	1529.8	1528.8	1529.8
P61626 LYSC_HUMAN										
Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) - Homo sapiens (Human)										
41.0	20.4	20.4	81.8	2.0	99.0	ATNYYAGDRSTDYGIQINSR	2362.1	2363.1	2362.1	2363.1
41.0	20.4	20.4	81.8	2.0	99.0	GISLANWMCCLAK	1378.7	1379.7	1378.7	1379.7
41.0	20.4	20.4	81.8	2.0	99.0	QYVQCGV	909.4	910.4	909.4	910.4
41.0	20.4	20.4	81.8	2.0	99.0	RVVRDPQIGR	1194.7	1195.7	1194.7	1195.7
41.0	20.4	20.4	81.8	2.0	99.0	STDYGIQINSR	1400.7	1401.7	1400.7	1401.7
41.0	20.4	20.4	81.8	2.0	99.0	STDYGIQINSRY	1503.7	1504.7	1503.7	1504.7
41.0	20.4	20.4	81.8	2.0	99.0	WESGYNTR	1011.4	1012.4	1011.4	1012.4
41.0	20.4	20.4	81.8	1.7	98.0	YWCNDGK	941.4	942.4	941.4	942.4
41.0	20.4	20.4	81.8	1.2	94.0	LGMMDGYR	810.4	811.4	810.4	811.4
41.0	20.4	20.4	81.8	1.0	91.0	DVRQYVQCGV	1279.6	1280.6	1279.6	1280.6
41.0	20.4	20.4	81.8	1.0	90.0	AWVAWR	787.4	788.4	787.4	788.4
41.0	20.4	20.4	81.8	0.8	83.0	RAWVAWR	959.4	960.4	959.5	960.5
41.0	20.4	20.4	81.8	0.4	56.0	RLGMDGYR	966.5	967.5	966.5	967.5
41.0	20.4	20.4	81.8	0.3	45.0	VVRDPQIGR	1038.6	1039.6	1038.6	1039.6
41.0	20.4	20.4	81.8	0.0	99.0	GISLANWMCCLAK	1362.7	1363.7	1362.7	1363.7
41.0	20.4	20.4	81.8	0.0	99.0	GISLANWMCCLAK	1362.7	1363.7	1362.7	1363.7
41.0	20.4	20.4	81.8	0.0	99.0	GISLANWMCCLAK	1362.7	1363.7	1362.7	1363.7
41.0	20.4	20.4	81.8	0.0	99.0	GISLANWMCCLAK	1362.7	1363.7	1362.7	1363.7
41.0	20.4	20.4	81.8	0.0	99.0	QYVQCGV	911.4	912.4	911.4	912.4
41.0	20.4	20.4	81.8	0.0	99.0	QYVQCGV	910.4	911.4	909.4	910.4
41.0	20.4	20.4	81.8	0.0	99.0	STDYGIQINSR	1399.7	1400.7	1399.7	1400.7
41.0	20.4	20.4	81.8	0.0	99.0	STDYGIQINSR	1382.7	1383.7	1382.7	1383.7
41.0	20.4	20.4	81.8	0.0	97.0	WESGYNTR	1023.4	1024.4	1023.4	1024.4
41.0	20.4	20.4	81.8	0.0	93.0	WESGYNTR	1012.4	1013.4	1012.4	1013.4
41.0	20.4	20.4	81.8	0.0	44.0	WESGYNTR	1015.5	1016.5	1011.4	1012.4
23.0	12.6	12.6	81.1	2.0	99.0	ATNYYAGDRSTDYGIQINSR	2362.1	23		

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 Beta-2-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	IEKVEHSDLSFSK	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	VNHVLSOPK	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	VNHVLSOPK	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	VNHVLSOPK	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	IEKVEHSDLSFSK	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	VNHVLSOPK	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	VNHVLSOPK	1122.6	1123.6	1122.6	1123.6
69.0	10.4	10.4	37.8	0.0	99.0	VNHVLSOPK	1104.6	1105.6	1104.6	1105.6
P61916 NPC2_HUMAN Epidermal secretory protein E1 precursor (Niemann-Pick disease type C2 protein) (hE1) - Homo sapiens (Human)										
536	2.0	2.0	10.6	2.0	99.0	EVNVPCTQPQLSK	1842.9	1843.9	1842.9	1843.9
386.0	1.7	1.7	10.6	1.7	98.0	EVNVPCTQPQLSK	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	EADIDGQGVNVEEFVQMATAK	2489.1	2490.1	2489.1	2490.1
237.0	5.2	5.2	36.9	1.2	94.0	HVMNTLGEKLTDEEVDEMI R	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	VFDKDNQYISAAELR	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	969.5	968.5	969.5
106.0	10.1	10.1	52.4	2.0	99.0	IIDVYRNSNDELVR	1717.9	1718.9	1717.9	1718.9
106.0	10.1	10.1	52.4	2.0	99.0	ISSLSLEQFOQK	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	LLACIASRPGQCGR	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	HGYGFEFIDDDR	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	HGYGFEFIDDDR	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	GGGHVAAQIYAIR	1240.7	1241.7	1240.7	1241.7
159.0	7.4	7.4	47.3	2.0	99.0	LLEPVLLGK	1093.7	1094.7	1093.7	1094.7
159.0	7.4	7.4	47.3	2.0	99.0	PSKGPLQSVQVFGFR	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	VKGGGHVAAQIYAIR	1467.8	1468.8	1467.8	1468.8
106.0	3.3	3.3	35.6	2.0	99.0	PSKGPLQSVQVFGFR	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	GGGHVAAQIYAIR	1240.7	1241.7	1240.7	1241.7
68.0	10.9	10.9	52.1	2.0	99.0	PSKGPLQSVQVFGFR	1498.8	1499.8	1498.8	1499.8
68.0	10.9	10.9	52.1	2.0	99.0	VKGGGHVAAQIYAIR	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	ALVAYYQK	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	10.0	37.3	2.0	99.0	IISSEIOKEENKGGEDKLLK	2144.1	2145.1	2144.1	2145.1
109.0	10.0	10.0	37.3	2.0	99.0	LAEQAEYDEMVEVMGK	2056.0	2057.0	2056.0	2057.0
109.0	10.0	10.0	37.3	2.0	99.0	MDDREDLYQAK	1523.7	1524.7	1523.7	1524.7
109.0	10.0	10.0	37.3	2.0	99.0	YLAEFATGDRK	1383.7	1384.7	1383.7	1384.7
109.0	10.0	10.0	37.3	2.0	99.0	YLAEFATGDRKAAENSLVAYK	2559.2	2560.2	2559.3	2560.3
109.0	10.0	10.0	37.3	0.0	99.0	DSTLIQLLR	1188.7	1189.7	1188.7	1189.7
256.0	2.2	3.5	18.8	2.0	99.0	MDDREDLYQAK	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	DSTLIQLLR	1188.7	1189.7	1188.7	1189.7
P62269 RS18_HUMAN 40S ribosomal protein S18 (K6-9) (K63) - Homo sapiens (Human)										
164.0	7.2	7.2	34.9	2.0	99.0	IPDWFNLR	1059.5	1060.5	1059.6	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	VITIMQNPR	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	HRWGLR	814.4	815.4	814.4	815.4
164.0	7.2	7.2	34.9	0.0	70.0	VITIMQNPR	1070.6	1071.6	1070.6	1071.6
164.0	7.2	7.2	34.9	0.0	45.0	VITIMQNPR	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	1059.6	1060.6
135.0	5.9	5.9	37.5	2.0	99.0	VITIMQNPR	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	HRWGLR	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	YGLNMC R	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	YGLNMC R	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	AYQKQPTIFONKRR	1749.0	1750.0	1749.0	1750.0
82.0	12.8	12.8	39.2	2.0	99.0	DYLHYIR	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	VLLGETGKELPR	1438.9	1439.9	1438.9	1439.9
82.0	12.8	12.8	39.2	1.1	92.0	RDYLHYIR	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	DYLHYIR	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	DYLHYIR	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

29.0	24.5	24.5	97.7	2.0	99.0	KTETQEKNLPSKETIEQEKOAGES	2828.4	2829.4	2828.4	2829.4
29.0	24.5	24.5	97.7	2.0	99.0	LKKTETQEKNLPSKETIEQEKE	2597.4	2598.4	2597.4	2598.4
29.0	24.5	24.5	97.7	2.0	99.0	LKKTETQEKNLPSKETIEQEKOAGES	3069.6	3070.6	3069.6	3070.6
29.0	24.5	24.5	97.7	2.0	99.0	NPLPSKETIEQEKE	1511.8	1512.8	1511.8	1512.8
29.0	24.5	24.5	97.7	2.0	99.0	NPLPSKETIEQEKOAGES	1984.0	1985.0	1984.0	1985.0
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAIEIEKFDKSK	1693.8	1694.8	1693.8	1694.8
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	SDKPDMAIEIEKFDKSK	2150.1	2151.1	2150.1	2151.1
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAIEIEKFDKSK	2278.2	2279.2	2278.2	2279.2
29.0	24.5	24.5	97.7	2.0	99.0	TETQEKNLPSKETIEQEKE	2228.1	2229.1	2228.1	2229.1
29.0	24.5	24.5	97.7	2.0	99.0	TETQEKNLPSKETIEQEKOAGES	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	LKKTETQEKNLPSKETIEQEKOAGES	3069.6	3070.6	3069.6	3070.6
28.0	21.1	21.1	97.7	2.0	99.0	KTETQEKNLPSKETIEQEKE	2356.3	2357.3	2356.2	2357.2
28.0	21.1	21.1	97.7	2.0	99.0	KTETQEKNLPSKETIEQEKOAGES	2828.4	2829.4	2828.4	2829.4
28.0	21.1	21.1	97.7	2.0	99.0	LKKTETQEKNLPSKETIEQEKE	2597.4	2598.4	2597.4	2598.4
28.0	21.1	21.1	97.7	2.0	99.0	NPLPSKETIEQEKOAGES	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	SDKPDMAIEIEKFDKSK	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	SDKPDMAIEIEKFDKSK	2150.1	2151.1	2150.1	2151.1
28.0	21.1	21.1	97.7	2.0	99.0	TETQEKNLPSKETIEQEKE	2228.1	2229.1	2228.1	2229.1
28.0	21.1	21.1	97.7	2.0	99.0	TETQEKNLPSKETIEQEKOAGES	2700.3	2701.3	2700.3	2701.3
28.0	21.1	21.1	97.7	1.1	92.0	LKKTETQEKNLPSKETIEQEKOAGES	3070.6	3071.6	3070.6	3071.6
28.0	21.1	21.1	97.7	0.0	40.0	TETQEKNLPSKETIEQEKE	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 protein 9) - Bos taurus (Bovine)									
353.0	3.2	3.2	43.5	2.0	99.0	EOCCYCNCKPGHLAR	1848.8	1849.8	1848.8	1849.8
353.0	3.2	3.2	43.5	1.2	94.0	CGESGHLAKCDLQEDACYNCGR	2697.0	2698.0	2697.0	2698.0
179.0	2.0	2.0	16.5	2.0	99.0	EOCCYCNCKPGHLAR	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	ECLPLIIFLR	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	GNKPWISLPR	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	ECLPLIIFLR	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	GNKPWISLPR	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	MATEVAADALGEEWKGVYVVR	2194.1	2195.1	2194.1	2195.1
192.0	6.0	6.0	27.3	2.0	99.0	MKLNISFPATGGCK	1593.8	1594.8	1593.8	1594.8
140.0	2.1	2.1	37.8	2.0	99.0	MATEVAADALGEEWKGVYVVR	2194.1	2195.1	2194.1	2195.1
140.0	2.1	2.1	37.8	0.1	25.0	MKLNISFPATGGCK	1593.8	1594.8	1593.8	1594.8
291.0	2.0	2.0	24.9	2.0	99.0	MATEVAADALGEEWKGVYVVR	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	ISGLIYEETRGVLK	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	1466.8	1467.8	1466.8	1467.8
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	DAVITYTEHAKR	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	1480.8	1481.9	1480.8	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	1466.8	1467.8	1466.8	1467.8
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	1324.8	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	1466.8	1467.8	1466.8	1467.8
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	DAVITYTEHAK	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	VGENIPIVLGKGVVDIKDRK	2369.3	2370.3	2369.3	2370.3
397.0	2.3	2.3	28.7	0.7	78.0	AAQGEPOVQFK	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	GPKFNWDTAGQEK	1688.8	1689.8	1688.8	1689.8
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	1469.8	1470.8	1469.8	1470.8
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	AAQGEPOVQFK	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	LHYVVSCHAIHSK	1473.7	1474.7	1473.7	1474.7
222.0	5.7	5.7	51.3	1.7	98.0	NIVEAAVIR	941.5	942.5	941.5	942.5
292.0	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	ALSTGEKGFYK	1256.6	1257.6	1256.6	1257.6
24.9	24.9	24.9	81.8	2.0	99.0	ALSTGEKGFYKGSFHR	2000.9	2002.0	2000.9	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	FGYKGSFHR	1314.6	1315.6	1314.6	1315.6
27.0	24.9	24.9	81.8	2.0	99.0	HTGPGILSMANAGPNTNGSOFFCTAK	2791.3	2792.3	2791.3	2792.3
27.0	24.9	24.9	81.8	2.0	99.0	IIPGFMCGGDFTR	1597.7	1598.7	1597.7	1598.7
27.0	24.9	24.9	81.8	2.0	99.0	IIPGFMCGGDFTRRHNGTGGK	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	VNPTVFDIIVDGEPLGR	1945.0	1946.0	1945.0	1946.0
27.0	24.9	24.9	81.8	2.0	99.0	VSELFADKVPK	1378.7	1379.8	1378.7	1379.8
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	FGYKGSFHR	1314.6	1315.6	1314.6	1315.6
27.0	24.9	24.9	81.8	0.0	83.0	FGYKGSFHR	1466.6	1467.6	1466.6	1467.6
27.0	24.9	24.9	81.8	0.0	99.0	SIYGEKFEDENFILK				

87.0	8.7	8.7	45.5	0.7	79.0	VNPTVFDDIADGPELGR	1987.0	1988.0	1987.0	1988.0
87.0	8.7	8.7	45.5	0.0	99.0	GFGYKGSFCFHR	1314.6	1315.6	1314.6	1315.6
87.0	8.7	8.7	45.5	0.0	91.0	GFGYKGSFCFHR	1315.6	1316.7	1314.6	1315.6
87.0	8.7	8.7	45.5	0.0	99.0	SYGKGFEDENFILK	1834.9	1835.9	1834.9	1831.9
87.0	8.7	8.7	45.5	0.0	99.0	VKGGMNVVEMER	1504.7	1505.7	1504.7	1505.7
P62942 FKB1A_HUMAN	2.0	2.0	29.6	2.0	99.0	GWEEGVAQMSVGQR	1532.7	1533.7	1532.7	1533.7
174.0	2.0	2.0	29.6	2.0	99.0	GVQVETISPGDGR	1313.7	1314.7	1313.7	1314.7
215.0	6.0	6.0	29.6	2.0	99.0	GWEEGVAQMSVGQR	1532.7	1533.7	1532.7	1533.7
215.0	6.0	6.0	29.6	2.0	99.0	QEVIRGWEEGVAQMSVGQR	2158.1	2159.1	2158.1	2159.1
191.0	4.0	4.0	25.0	2.0	99.0	GVQVETISPGDGR	1313.7	1314.7	1313.7	1314.7
191.0	4.0	4.0	25.0	2.0	99.0	GWEEGVAQMSVGQR	1532.7	1533.7	1532.7	1533.7
P62979 RS27A_HUMAN	2.8	2.8	55.0	1.7	98.0	CCLTYCFNKPEDK	1716.7	1717.7	1716.7	1717.7
372.0	2.8	2.8	55.0	0.6	77.0	YKVDENKISR	1471.8	1472.8	1471.8	1472.7
372.0	2.8	2.8	55.0	0.5	67.0	ECPDSECGAGVFMASHFDR	2170.9	2171.9	2170.9	2171.9
157.0	4.6	4.6	55.0	2.0	99.0	CCLTYCFNKPEDK	1716.7	1717.7	1716.7	1717.8
157.0	4.6	4.6	55.0	2.0	99.0	ECPDSECGAGVFMASHFDR	2170.9	2171.9	2170.9	2171.9
157.0	4.6	4.6	55.0	0.6	74.0	YKVDENKISR	1471.7	1472.7	1471.7	1472.7
P63104 1433Z_HUMAN	22.8	22.8	65.7	2.0	99.0	AKLAEOAERYDDMAACMK	2099.9	2100.9	2099.9	2101.0
34.0	22.8	22.8	65.7	2.0	99.0	DICNDVLSLLEK	1417.7	1418.7	1417.7	1418.7
34.0	22.8	22.8	65.7	2.0	99.0	DSTLJMLQLR	1188.7	1189.7	1188.7	1189.7
34.0	22.8	22.8	65.7	2.0	99.0	FLIPNASQAESKVPYLK	1954.1	1955.1	1954.1	1955.1
34.0	22.8	22.8	65.7	2.0	99.0	GIVDQSQAYQEAFAEISKK	2168.1	2169.1	2168.1	2169.1
34.0	22.8	22.8	65.7	2.0	99.0	KEMOPTHPIR	1235.6	1236.6	1235.6	1236.6
34.0	22.8	22.8	65.7	2.0	99.0	MDKNELVOK	1145.6	1146.6	1145.6	1146.6
34.0	22.8	22.8	65.7	2.0	99.0	NLLSVAYKNVVGAR	1502.9	1503.9	1502.9	1503.9
34.0	22.8	22.8	65.7	2.0	99.0	SVTEQGAELSNEER	1547.7	1548.7	1547.7	1548.7
34.0	22.8	22.8	65.7	2.0	99.0	YDIAACMK	1103.4	1104.4	1103.4	1104.4
34.0	22.8	22.8	65.7	2.0	99.0	YLAEVAAGDDKK	1278.6	1279.6	1278.6	1279.7
34.0	22.8	22.8	65.7	0.6	72.0	VVSSIEQKTEGAEKQOQMAR	2246.2	2247.2	2246.2	2247.2
34.0	22.8	22.8	65.7	0.1	25.0	MKGQDYYR	931.4	932.4	931.4	932.4
67.0	5.1	5.1	35.1	2.0	99.0	GIVDQSQAYQEAFAEISKK	2168.1	2169.1	2168.1	2169.1
67.0	5.1	5.1	35.1	2.0	99.0	NLLSVAYKNVVGAR	1502.9	1503.9	1502.9	1503.9
67.0	5.1	5.1	35.1	1.0	91.0	DSTLJMLQLR	1188.7	1189.7	1188.7	1189.7
56.0	13.3	13.3	51.4	2.0	99.0	GIVDQSQAYQEAFAEISKK	2168.1	2169.1	2168.1	2169.1
56.0	13.3	13.3	51.4	2.0	99.0	NLLSVAYKNVVGAR	1502.8	1503.9	1502.9	1503.9
56.0	13.3	13.3	51.4	2.0	99.0	VVSSIEQKTEGAEKQOQMAR	2246.2	2247.2	2246.2	2247.2
56.0	13.3	13.3	51.4	1.7	98.0	VVSSIEQKTEGAEK	1503.8	1504.8	1503.8	1504.8
56.0	13.3	13.3	51.4	1.5	97.0	EMOPTHPIR	1107.6	1108.6	1107.5	1108.6
56.0	13.3	13.3	51.4	1.5	97.0	KEMOPTHPIR	1235.6	1236.7	1235.6	1236.7
56.0	13.3	13.3	51.4	1.2	94.0	DSTLJMLQLR	1188.7	1189.7	1188.7	1189.7
56.0	13.3	13.3	51.4	0.7	81.0	MDKNELVOK	1145.6	1146.6	1145.6	1146.6
56.0	13.3	13.3	51.4	0.5	68.0	TAFDEAIELDITLSEESYK	2131.0	2132.0	2131.0	2132.0
56.0	13.3	13.3	51.4	0.1	21.0	DICNDVLSLLEK	1417.7	1418.7	1417.7	1418.7
P63244 GBLP_HUMAN	2.0	2.0	4.1	2.0	99.0	LTRDETNYGIPOR	1561.8	1562.8	1561.8	1562.8
533.0	2.0	2.0	4.1	2.0	99.0	LTRDETNYGIPOR	1561.8	1562.8	1561.8	1562.8
382.0	1.7	1.7	8.5	1.7	98.0	LTRDETNYGIPOR	1561.8	1562.8	1561.8	1562.8
P63261 ACTG_HUMAN	54.2	54.2	69.9	2.0	99.0	AGFAGDDAPR	975.4	976.4	975.4	976.4
4.0	54.2	54.2	69.9	2.0	99.0	AVFPSI VGRPR	1041.6	1042.6	1041.6	1042.6
4.0	54.2	54.2	69.9	2.0	99.0	AVFPSI VGRPR	1197.7	1198.7	1197.7	1198.7
4.0	54.2	54.2	69.9	2.0	99.0	CYVAIFQEQEMATAASSSSLEK	2549.0	2550.0	2549.0	2550.0
4.0	54.2	54.2	69.9	2.0	99.0	DLYANTVLSGGTTMYPGIADR	2214.1	2215.1	2214.1	2215.1
4.0	54.2	54.2	69.9	2.0	99.0	EEEEAALVIDNGSGMCK	1878.9	1879.9	1878.9	1879.9
4.0	54.2	54.2	69.9	2.0	99.0	EITALAPSTMK	1161.6	1162.6	1161.6	1162.6
4.0	54.2	54.2	69.9	2.0	99.0	GYSFTTAEER	1131.5	1132.5	1131.5	1132.5
4.0	54.2	54.2	69.9	2.0	99.0	GYSFTTAEERIVRDIK	1985.1	1986.1	1985.0	1986.0
4.0	54.2	54.2	69.9	2.0	99.0	HQGVMMGMGQK	1170.6	1171.6	1170.6	1171.6
4.0	54.2	54.2	69.9	2.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2351.1	2352.1	2351.1	2352.1
4.0	54.2	54.2	69.9	2.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2506.2	2507.2	2506.2	2507.2
4.0	54.2	54.2	69.9	2.0	99.0	KIIAPPER	1035.6	1036.6	1035.6	1036.7
4.0	54.2	54.2	69.9	2.0	99.0	IWHHTFYNELR	1514.7	1515.7	1514.7	1515.7
4.0	54.2	54.2	69.9	2.0	99.0	KDLYANTVLSGGTTMYPGIADR	2342.2	2343.2	2342.1	2343.1
4.0	54.2	54.2	69.9	2.0	99.0	MCKEITALAPSTMK	1547.8	1548.8	1547.8	1548.8
4.0	54.2	54.2	69.9	2.0	99.0	QEYDESGPSIVHR	1515.7	1516.7	1515.7	1516.7
4.0	54.2	54.2	69.9	2.0	99.0	QEYDESGPSIVHRK	1843.8	1844.8	1843.8	1844.8
4.0	54.2	54.2	69.9	2.0	99.0	SVLPDGGQVITIGNER	1789.9	1790.9	1789.9	1790.9
4.0	54.2	54.2	69.9	2.0	99.0	VAPEEHPVLLTEAPLNPK	1953.0	1954.0	1953.0	1954.1
4.0	54.2	54.2	69.9	2.0	99.0	VAPEEHPVLLTEAPLNPKANR	2294.2	2295.2	2294.2	2295.2
4.0	54.2	54.2	69.9	2.0	99.0	YPIEHGVTNWDDMEK	1959.9	1960.9	1959.9	1960.9
4.0	54.2	54.2	69.9	1.7	98.0	GYSFTTAEERIVR	1628.8	1629.8	1628.8	1629.8
4.0	54.2	54.2	69.9	1.4	96.0	SVLPDGGQVITIGNERFR	2093.1	2094.1	2093.1	2094.1
4.0	54.2	54.2	69.9	1.3	95.0	GYSFTTAEERIVRDIKEK	2242.2	2243.2	2242.2	2243.2
4.0	54.2	54.2	69.9	1.2	94.0	VAPEEHPVLLTEAPLNPKANREK	2551.4	2552.4	2551.4	2552.4
4.0	54.2	54.2	69.9	1.1	92.0	RGIITLTK	799.5	800.5	799.5	800.5
4.0	54.2	54.2	69.9	1.0	89.0	IWHHTFYNE	1245.5	1246.5	1245.5	1246.5
4.0	54.2	54.2	69.9	0.9	86.0	KIIAPPERK	1163.7	1164.7	1163.7	1164.7
4.0	54.2	54.2	69.9	0.8	83.0	IIAPPERK	923.6	924.6	923.6	923.6
4.0	54.2	54.2	69.9	0.2	41.4	ISKQEYDESGPSIVHR	1843.9	1844.9	1843.9	1844.9
4.0	54.2	54.2	69.9	0.1	28.4	SLSTFOQMWISK	1454.7	1455.7	1454.7	1455.7
4.0	54.2	54.2	69.9	0.1	28.1	EEEEAALVIDNGSGMCKA	2028.9	2029.9	2028.8	2029.8
4.0	54.2	54.2	69.9	0.1	26.8	IWHHTFYNEL	1359.7	1360.7	1358.6	1359.6
4.0	54.2	54.2	69.9	0.1	23.0	IIAPPER	794.5	795.5	794.5	795.5
4.0	54.2	54.2	69.9	0.1	21.0	LDLAGRDLDYLMK	1622.8	1623.8	1622.8	1623.8
4.0	54.2	54.2	69.9	0.0	99.0	AGFAGDDAPR	978.5	979.5	978.5	979.5
4.0	54.2	54.2	69.9	0.0	99.0	EEEEAALVIDNGSGMCK	1877.8	1878.8	1877.8	1878.8
4.0	54.2	54.2	69.9	0.0	99.0	EEEEAALVIDNGSGMCK	2029.9	2030.9	2029.9	2030.8
4.0	54.2	54.2	69.9	0.0	99.0	EEEEAALVIDNGSGMCK	2029.8	2030.8	2029.8	2030.8
4.0	54.2	54.2	69.9	0.0	99.0	GYSFTTAEERIVRDIKEK	2242.2	2243.2	2242.2	2243.2
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQK	1186.6	1187.6	1186.6	1187.6
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQK	1182.6	1183.6	1182.6	1183.6
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQK	1172.6	1173.6	1172.6	1173.6
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQK	1186.6	1187.6	1186.6	1187.6
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2366.1	2367.1	2366.1	2367.1
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2394.1	2395.1	2394.1	2395.1
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2366.1	2367.1	2366.1	2367.1
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2378.1	2379.1	2378.1	2379.1
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2522.2	2523.2	2522.2	2523.2
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2522.2	2523.2	2522.2	2523.2
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2534.2	2535.2	2534.2	2535.2
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMMGMGQKDSYVGDEAQS	2518.2	2519.2	2518.2	2519.2
4.0	54.2	54.2	69.9	0.0	95.0	HQGVMMGMGQKDSYVGDEAQS	2538.2	2539.2	2538.2	2539.2
4.0	54.2	54.2	69.9	0.0	99.0	KIIAPPER	1035.6	1036.6	1035.6	1036.7
4.0	54.2	54.2	69.9	0.0	99.0	IWHHTFYNELR	1515.7	1516.7	1515.7	1516.7
4.0	54.2	54.2	69.9	0.0	99.0	IWHHTFYNELR	1516.7	1517.7	1516.7	1517.7
4.0	54.2	54.2	69.9	0.0	99.0	IWHHTFYNELR	1530.7	1531.7	1530.7	1531.7
4.0	54.2	54.2	69.9	0.0	99.0	IWHHTFYNELR	1546.7	1547.7	1546.7	1547.7
4.0	54.2	54.2	69.9	0.0	99.0	IWHHTFYNELR	1515.7	1516.7	1515.7	1516.7
4.0	54.2	54.2	69.9							

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	HQGMVGMGQK	1170.6	1170.6	1170.6	1171.6
154.0	2.0	31.4	66.4	0.0	94.0	HQGMVGMGQK	1171.6	1172.6	1170.6	1171.6
154.0	2.0	31.4	66.4	0.0	22.0	HQGMVGMGQK	1186.6	1187.6	1186.6	1187.6
154.0	2.0	31.4	66.4	0.0	99.0	HQGMVGMGQKDSYVGDEAOSK	2350.1	2351.1	2350.1	2351.1
154.0	2.0	31.4	66.4	0.0	99.0	HQGMVGMGQKDSYVGDEAOSKR	2506.2	2507.2	2506.2	2507.2
154.0	2.0	31.4	66.4	0.0	96.0	HQGMVGMGQKDSYVGDEAOSKR	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	SYELPDGQVITIGNER	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	YPIEHGVTINWDDMEK	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	GILTLKYPIEHGVTINWDDMEK	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	HQGMVGMGQK	1170.6	1171.6	1170.6	1171.6
5.0	50.7	50.7	69.1	2.0	99.0	HQGMVGMGQKDSYVGDEAOSK	2350.1	2351.1	2350.1	2351.1
5.0	50.7	50.7	69.1	2.0	99.0	HQGMVGMGQKDSYVGDEAOSKR	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	1514.7	1515.7	1514.7	1515.7
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	MOKEITALAPSTMK	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	SYELPDGQVITIGNER	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	YPIEHGVTINWDDMEK	1975.9	1976.9	1975.9	1976.9
5.0	50.7	50.7	69.1	1.5	97.0	LDLAGRDLTDYLMK	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	1351.6	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	HQGMVGMGQK	1173.6	1174.6	1173.6	1174.6
5.0	50.7	50.7	69.1	0.0	99.0	HQGMVGMGQK	1186.6	1187.6	1186.6	1187.6
5.0	50.7	50.7	69.1	0.0	99.0	HQGMVGMGQK	1182.6	1183.6	1182.6	1183.6
5.0	50.7	50.7	69.1	0.0	99.0	HQGMVGMGQKDSYVGDEAOSKR	2522.2	2523.2	2522.2	2523.2
5.0	50.7	50.7	69.1	0.0	99.0	HQGMVGMGQKDSYVGDEAOSKR	2518.2	2519.2	2518.2	2519.2
5.0	50.7	50.7	69.1	0.0	96.0	HQGMVGMGQKDSYVGDEAOSKR	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	1514.7	1515.7	1514.7	1515.7
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	1496.7	1497.7	1496.7	1497.7
5.0	50.7	50.7	69.1	0.0	97.0	QEYDESGPSIVHR	1496.7	1497.7	1496.7	1497.7
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	SYELPDGQVITIGNER	1789.9	1790.9	1789.9	1790.9
5.0	50.7	50.7	69.1	0.0	99.0	SYELPDGQVITIGNER	1789.9	1790.9	1789.9	1790.9
5.0	50.7	50.7	69.1	0.0	99.0	SYELPDGQVITIGNER	1802.9	1803.9	1802.9	1803.9
5.0	50.7	50.7	69.1	0.0	99.0	SYELPDGQVITIGNER	1791.9	1792.9	1791.9	1792.9
5.0	50.7	50.7	69.1	0.0	99.0	YPIEHGVTINWDDMEK	1959.9	1960.9	1959.9	1960.9
P63279	UBC9_HUMAN	SUMO-conjugating enzyme UBC9 (E6-3,2-)	(SUMO-protein ligase)	(Ubiquitin-conjugating enzyme E2 1)	(Ubiquitin-conjugating enzyme E2 1)	(Ubiquitin-conjugating enzyme E2 1)	1091.5	1091.5	1091.5	1091.6
497.0	2.0	2.0	7.0	2.0	99.0	GTPWEGGLFK	1091.5	1091.5	1091.5	1091.6
173.0	2.0	2.0	15.8	2.0	99.0	GTPWEGGLFK	1090.5	1091.5	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	1980.9	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	IQALQQQADEAEDR	1613.8	1614.8	1613.8	1614.8
39.0	21.0	21.0	45.6	2.0	99.0	IQALQQQADEAEDRAOGLQR	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	1243.7
39.0	21.0	21.0	45.6	2.0	99.0	IQLVEELDR	1242.6	1243.6	1242.6	1243.7
39.0	21.0	21.0	45.6	2.0	99.0	IQLVEELDR	1242.6	1243.6	1242.6	1243.7
39.0	21.0	21.0	45.6	2.0	99.0	IQALQQQADEAEDR	1726.9	1727.9	1726.9	1727.9
39.0	21.0	21.0	45.6	2.0	99.0	IQALQQQADEAEDR	1741.9	1742.9	1741.9	1742.9
39.0	21.0	21.0	45.6	2.0	99.0	KIQALQQQADEAEDRAOGLQR	2395.2	2396.2	2395.2	2396.2
39.0	21.0	21.0	45.6	2.0	99.0	LATALQKLEEAKADESER	2201.1	2202.1	2201.1	2202.1
39.0	21.0	21.0	45.6	2.0	99.0	RIQLVEELDR	1883.0	1884.0	1883.0	1884.0
39.0	21.0	21.0	45.6	1.0	89.0	LEEAKADESER	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	IQALQQQADEAEDR	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	IQLVEELDR	1242.6	1243.6	1242.6	1243.7
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	LATALQKLEEAKADESER	2201.1	2202.1	2201.1	2202.1
57.0	13.2	13.2	49.6	2.0	99.0	IQLVEELDR	1242.6	1243.6	1242.6	1243.7
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	KIQALQQQADEAEDRAOGLQR	2395.2	2396.2	2395.2	2396.2
57.0	13.2	13.2	49.6	2.0	99.0	LATALQKLEEAKADESER	2201.1	2202.1	2201.1	2202.1
57.0	13.2	13.2	49.6	2.0	99.0	RIQLVEELDR	1883			

90.0	8.2	8.2	22.1	2.0	99.0	YYVTIADPAGHRDFIK	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	AVCMLSNTTAAIEAWAR	1863.9	1864.9	1863.9	1864.9
33.0	23.4	23.4	38.6	2.0	99.0	AVFVDEPTVIDEVR	1709.9	1710.9	1709.9	1710.9
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	VGINYQPTVVPVGGDLAK	1824.0	1825.0	1824.0	1825.0
33.0	23.4	23.4	38.6	2.0	99.0	YMACCLLYR	1248.5	1249.5	1248.5	1249.5
33.0	23.4	23.4	38.6	2.0	99.0	YMACCLLYRGGVVPK	1843.9	1844.9	1843.9	1844.9
33.0	23.4	23.4	38.6	1.4	96.0	RSIQFVDWCPTGFK	1739.9	1740.9	1739.9	1740.9
33.0	23.4	23.4	38.6	1.3	95.0	AFVHWVYVGGMEEGFSEAR	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	AFVHWVYVGGMEEGFSEAR	2329.0	2330.0	2329.0	2330.0
49.0	15.5	15.5	29.9	2.0	99.0	AVCMLSNTTAAIEAWAR	1863.9	1864.9	1863.9	1864.9
49.0	15.5	15.5	29.9	2.0	99.0	AVFVDEPTVIDEVR	1709.9	1710.9	1709.9	1710.9
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	YMACCLLYR	1248.5	1249.5	1248.5	1249.5
49.0	15.5	15.5	29.9	1.5	97.0	YMACCLLYRGGVVPK	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/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	1490.9	1489.9	1490.9
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	1489.9	1490.9	1489.9	1490.9
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	KLPFOR	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	KLPFOR	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	VPSLVGFSIR	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	VPSLVGFSIR	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	GIRHEVINLNLIK	1408.8	1409.8	1408.8	1409.8
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	SCCSCCPVGGCAK	1444.5	1445.5	1444.5	1445.5
459.0	2.0	4.0	52.5	0.0	99.0	SCCSCCPVGGCAK	1447.5	1448.5	1447.5	1448.5
459.0	2.0	4.0	52.5	0.0	99.0	SCCSCCPVGGCAK	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	KSCCSCPVGGCAK	1573.6	1574.6	1573.6	1573.6
304.0	2.0	6.0	54.1	0.0	99.0	SCCSCCPVGGCAK	1444.5	1445.5	1444.5	1445.5
304.0	2.0	6.0	54.1	0.0	99.0	SCCSCCPVGGCAK	1446.5	1447.5	1446.5	1447.5
304.0	2.0	6.0	54.1	0.0	99.0	SCCSCCPVGGCAK	1446.5	1447.5	1446.5	1447.5
304.0	2.0	6.0	54.1	0.0	99.0	SCCSCCPVGGCAK	1444.5	1445.5	1444.5	1445.5
182.0	2.0	2.0	53.2	2.0	99.0	SCCSCCPVGGCAK	1444.5	1445.5	1444.5	1445.5
P84103 SFRS3_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	NRPGFVFEFEDPRDAADAVR	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	FLENPYDSR	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	NRPSEGLQTR	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	CHSDQFQWLSR	2395.1	2396.1	2395.1	2396.1
93.0	11.9	11.9	23.1	2.0	99.0	GVEYIEENKYSR	1697.8	1698.8	1697.8	1698.8
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	SSGPTSLFAVTVAPPGAR	1713.9	1714.9	1713.9	1714.9
93.0	11.9	11.9	23.1	1.7	98.0	FIEI AAR	818.5	819.5	818.5	819.5
93.0	11.9	11.9	23.1	0.2	31.0	RGNMPPQRGGGGGGGGI GYPYPR	2303.1	2304.1	2303.1	2304.1
93.0	11.9	11.9	23.1	0.0	98.0	SSGPTSLFAVTVAPPGAR	1713.9	1714.9	1713.9	1714.9
140.0	5.7	5.7	20.6	2.0	99.0	FIEI AAR	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	GVEYIEENKYSR	1698.8	1699.8	1698.8	1699.8
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	DLDQDFQWLSR	1381.6	1382.6	1381.6	1382.6
119.0	9.6	9.6	8.6	2.0	99.0	EVDDEQWIAER	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	DASVAEAWLLGQEPYLSR	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	LOAAAYAGDKADDIQKR	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	DASVAEAWLLGQEPYLSR	2091.0	2092.0	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 12P22A) ((-12P2A) (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	SGYRIDFYFDENPYFENK	2304.1	2305.1	2304.1	2305.1
61.0	16.1	16.1	15.2	2.0	99.0	VEVTEFEDIK	1207.6	1208.6	1207.6	1208.6
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	LRQPFQKR	1218.7	1219.7	1218.7	1219.7
61.0	16.1	16.1	15.2	1.5	97.0	QPFFQKR	949.5	950.5	949.5	950.5
61.0	16.1	16.1	15.2	1.1	92.0	LRQPFQKR	1062.6	1063.6	1062.6	1063.6
61.0	16.1	16.1	15.2	0.0	99.0	VEVTEFEDIK	12			

121.0	9.6	9.6	16.2	2.0	99.0	SGPKPFSAPKQTSPPSPKR	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	ADMQLNLSVER	1116.5	1117.5	1116.5	1117.5
56.0	6.0	6.0	14.5	2.0	99.0	SGPKPFSAPKQTSPPSPK	1837.0	1838.0	1837.0	1838.0
56.0	6.0	6.0	14.5	2.0	99.0	SSLFQAINQGESITHALK	1927.0	1928.0	1927.0	1928.0
110.0	7.1	7.1	21.1	2.0	99.0	ADMQLNLSVER	1116.5	1117.5	1116.5	1117.5
110.0	7.1	7.1	21.1	2.0	99.0	LEAVSHSTDMHR	1381.6	1382.7	1381.6	1382.6
110.0	7.1	7.1	21.1	2.0	99.0	SGPKPFSAPKQTSPPSPK	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	AAVEWFDKGFQGSK	1683.8	1684.8	1683.8	1684.8
268.0	4.1	4.1	25.8	2.0	99.0	AGDWOCPPNPGCGNONFAWR	2233.9	2234.9	2233.9	2234.9
268.0	4.1	4.1	25.8	0.1	25.0	GGRGGDRGGFRGGRGMDRGGFGGGRR	2582.2	2583.2	2582.2	2583.2
115.0	2.8	2.8	23.6	2.0	99.0	AAVEWFDKGFQGSK	1683.8	1684.8	1683.8	1684.8
115.0	2.8	2.8	23.6	0.8	85.0	GGRGGMGSAGER	1177.6	1178.6	1177.5	1178.5
312.0	2.0	2.0	16.8	2.0	99.0	AGDWOCPPNPGCGNONFAWR	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	KQQQQQQGHHKAPAAHPEGQLK	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	QFEHLDPONQHTFEAR	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	EMEEERLMMR	1357.7	1358.7	1357.7	1358.7
150.0	4.7	4.7	23.4	0.0	97.0	DLAQYDAAHHEEFKR	1828.8	1829.8	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	AIPOLQGYLR	1157.7	1158.7	1157.7	1158.7
355.0	3.2	3.2	21.2	1.2	94.0	YYPTEDVPR	1138.5	1139.5	1138.5	1139.5
332.0	2.0	2.0	12.8	2.0	99.0	AIPOLQGYLR	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	DYIFGNYLR	1289.6	1290.6	1289.6	1290.6
116.0	9.7	9.7	7.3	2.0	99.0	FAHNVVIMR	1043.6	1044.6	1043.6	1044.6
116.0	9.7	9.7	7.3	2.0	99.0	GHSVFKPSLDQQR	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	FAHNVVIMR	1043.6	1044.6	1043.6	1044.6
100.0	3.5	3.5	8.6	1.5	97.0	DYIFGNYLR	1289.6	1290.6	1289.6	1290.6
92.0	8.1	8.1	13.8	2.0	99.0	DYIFGNYLR	1289.6	1290.6	1289.6	1290.6
92.0	8.1	8.1	13.8	2.0	99.0	FAHNVVIMR	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	LEGFHTQISK	1043.6	1044.6	1043.6	1044.6
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	QPHVGDYR	953.4	954.4	953.4	954.4
68.0	14.7	14.7	38.2	2.0	99.0	YFSEKDAVTK	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	99.0	AAKQPHVGDYR	1240.6	1241.6	1240.6	1241.6
59.0	12.9	12.9	34.1	2.0	99.0	IEDGNINFGVAQVEK	1519.7	1520.7	1519.7	1520.7
59.0	12.9	12.9	34.1	2.0	99.0	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	YFSEKDAVTK	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 1.1.1.15) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxidase 2) (Proliferation-associated gene protein)									
48.0	18.3	18.3	55.3	2.0	99.0	ATAVMPDGGQFKDISLSDYK	2085.0	2086.0	2085.0	2086.0
48.0	18.3	18.3	55.3	2.0	99.0	ATAVMPDGGQFKDISLSDYKGGK	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	LVOAQFOTDK	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	TIQADYGVLLKDEGIFSR	1106.6	1107.6	1106.6	1107.6
48.0	18.3	18.3	55.3	2.0	99.0	TIQADYGVLLKDEGIFSR	1982.0	1983.0	1982.0	1983.0
48.0	18.3	18.3	55.3	0.3	52.0	ATAVMPDGGQFK	1163.6	1164.6	1163.6	1164.6
25.0	12.3	12.3	52.8	2.0	99.0	ATAVMPDGGQFKDISLSDYK	2085.0	2086.0	2085.0	2086.0
25.0	12.3	12.3	52.8	2.0	99.0	ATAVMPDGGQFKDISLSDYKGGK	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	LVOAQFOTDK	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	TIQADYGVLLKDEGIFSR	1982.0	1983.0	1982.0	1983.0
25.0	12.3	12.3	52.8	0.0	99.0	ATAVMPDGGQFKDISLSDYK	2084.1	2085.1	2084.1	2085.1
41.0	18.0	18.0	49.7	2.0	99.0	ATAVMPDGGQFK	1163.6	1164.6	1163.6	1164.6
41.0	18.0	18.0	49.7	2.0	99.0	ATAVMPDGGQFKDISLSDYK	2085.0	2086.0	2085.0	2086.0
41.0	18.0	18.0	49.7	2.0	99.0	ATAVMPDGGQFKDISLSDYKGGK	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	LVOAQFOTDK	1195.6	1196.6	1195.6	1196.6
41.0	18.0	18.0	49.7	2.0	99.0	QITVNDLPVGR	1193.6	1194.6	1193.6	1194.6
41.0	18.0	18.0	49.7	2.0	99.0	TIQADYGVLLKDEGIFSR	1982.0	1983.0	1982.0	1983.0
41.0	18.0	18.0	49.7	0.0	99.0	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	Galectin-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	GOWGTGVDNLWDLTASVVR	2451.1	2452.1	2451.1	2452.1
161.0	2.0	2.0	6.3	2.0	99.0	AVDTSWVGER	1205.5	1206.6	1205.5	1206.6
276.0	2.1	2.1	7.5	2.0	99.0	YSSDYFQAQPSDYR	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	AEPQAMNLMR	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	HSSVYPTQEELEAVQNMVSHTER	2670.2	2671.2	2670.2	2671.2
60.0	16.5	16.5	21.9	2.0	99.0	LAAFGLQHK	983.6	984.6	983.6	984.6
60.0	16.5	16.5	21.9	2.0	99.0	SGGNSYGGSGGASYNPSSGGYGGGSSGSSYQG	3012.2	3013.2	3012.2	3013.2
60.0	16.5	16.5	21.9	2.0	99.0	SIGTANRPMGAGEALRR	1756.9	1757.9	1756.9	1757.9
60.0	16.5	16.5	21.9	2.0	99.0	VLDQMLPTGAEGR	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.						

126.0	9.3	9.3	50.7	0.3	51.0	FTTGDAMSKR	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	YDGGSTVPEQEGEAQYHQFQQCTDDVR	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	FGFVDTLKLDDPI TGR	1820.0	1821.0	1820.0	1820.0
85.0	12.2	12.2	35.2	2.0	99.0	GFCFITK	1018.0	1019.0	1018.0	1019.0
85.0	12.2	12.2	35.2	2.0	99.0	GFCFITKKEEPPVKK	1857.9	1858.9	1857.9	1858.9
85.0	12.2	12.2	35.2	2.0	99.0	GFGFVLK	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	SRGFGFVLK	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	GFCFITKKEEPPVKK	1857.9	1858.9	1857.9	1858.9
157.0	2.0	4.0	11.0	0.0	99.0	GFGFVLK	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	RGADDHRPSWR	1329.6	1330.6	1329.6	1330.6
137.0	8.2	8.2	16.1	2.0	99.0	WGDRDSEG TWR	1363.6	1364.6	1363.6	1364.6
137.0	8.2	8.2	16.1	1.7	98.0	RLDDDDRRG PWR	1241.7	1242.7	1241.7	1242.7
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	EELEREARELQKVR	1769.9	1770.9	1769.9	1770.9
137.0	8.2	8.2	16.1	0.1	25.0	DLRDDDRRGG PPLR	1761.9	1762.9	1761.9	1762.9
137.0	8.2	8.2	16.1	0.0	96.0	WGDRDSEG TWR	1363.6	1364.6	1363.6	1364.6
404.0	1.3	1.3	16.4	1.2	94.0	WGDRDSEG TWR	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	ALQLEEGEEDKVS HQAGDHWLIR	2886.4	2887.4	2886.3	2887.3
122.0	9.5	9.5	13.9	2.0	99.0	VPNAAVQVYD YR	1530.8	1531.8	1530.8	1531.8
122.0	9.5	9.5	13.9	1.3	95.0	ATEEPIR	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	RNFRDFR	1009.5	1010.5	1009.5	1010.5
122.0	9.5	9.5	13.9	0.7	78.0	SLQPLRR	880.5	881.5	880.5	881.5
122.0	9.5	9.5	13.9	0.6	77.0	DAQGLVDFDVTGQVR	1616.9	1617.9	1616.9	1617.9
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	DAQGLVDFDVTGQVR	1616.9	1617.9	1616.9	1617.9
145.0	5.1	5.1	15.8	2.0	99.0	VPNAAVQVYD YR	1530.8	1531.8	1530.8	1531.8
145.0	5.1	5.1	15.8	1.0	90.0	ATEEPIR	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	GVEKPKPCYNAHYPK	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	LKQSELOSGQVR	1442.8	1443.8	1442.8	1443.8
72.0	14.1	14.1	37.9	2.0	99.0	NYKGYEKKPYCNAHYPK	2159.0	2160.0	2159.0	2160.0
72.0	14.1	14.1	37.9	2.0	99.0	QSFTWVADTPEENLR	1590.7	1591.7	1590.7	1591.7
72.0	14.1	14.1	37.9	2.0	99.0	TQDQISNIKYHEEFK	2009.0	2010.0	2009.0	2010.0
124.0	6.0	6.0	33.7	2.0	99.0	GKGSVADTPELOR	1602.8	1603.8	1602.8	1603.8
124.0	6.0	6.0	33.7	2.0	99.0	NYKGYEKKPYCNAHYPK	2159.0	2160.0	2159.0	2160.0
124.0	6.0	6.0	33.7	2.0	99.0	TQDQISNIKYHEEFK	2009.0	2010.0	2009.0	2010.0
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	FAQPSFEYAYMR	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	ROQEGFKGTFPPDR	1635.8	1636.8	1635.8	1636.8
78.0	13.4	15.9	33.3	1.3	95.0	FGQAATMEGIGAI GTPPAFNR	2162.0	2163.0	2162.0	2163.0
78.0	13.4	15.9	33.3	1.2	99.0	GIVFSPGPAAR	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	1695.9	1696.9
78.0	13.4	15.9	33.3	0.5	67.0	EQPPRFQAQPSFEYAYMR	2302.0	2303.0	2302.0	2303.0
78.0	13.4	15.9	33.3	0.1	21.0	ALIMKQOQDQVDR	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	RRQFEDEKANWEAQOR	2090.0	2091.0	2090.0	2091.0
406.0	2.3	2.3	9.8	0.6	74.0	QFEDEKANWEAQOR	1777.8	1778.8	1777.8	1778.8
406.0	2.3	2.3	9.8	0.3	48.0	FEDYLNAESR	1242.6	1243.6	1242.6	1243.6
406.0	2.3	2.3	9.8	0.1	20.0	NLEQYVGFANLPNQVYR	1953.0	1954.0	1953.0	1954.0
206.0	3.5	3.5	10.3	2.0	99.0	QFEDEKANWEAQOR	1777.8	1778.8	1777.8	1778.8
206.0	3.5	3.5	10.3	1.5	97.0	NLEQYVGFANLPNQVYR	1953.0	1954.0	1953.0	1954.0
Q16555 DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 (DHP-2) (Collapsin response mediator protein 2) (CRMP-2) (M2A3) - Homo sapiens (Human)									
286.0	2.0	2.0	9.9	2.0	99.0	THNSLSLEYVFEQMECR	2085.9	2086.9	2085.9	2086.9
336.0	3.5	3.5	5.9	2.0	99.0	THNSLSLEYVFEQMECR	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	YLAADKGNVTCTER	1611.7	1612.7	1611.7	1612.7
383.0	2.5	2.5	11.2	0.5	66.0	QIWTLEQPPDEAGSAAVCLR	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	WGLGGTCVNGCIPK	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	EQDQYKCGPHLAR	1849.8	1849.8	1849.8	1849.8
353.0	3.2	3.2	43.5	1.2	94.0	CGESGHLAKDDLOEDACYNCGR	2697.0	2698.0	2697.0	2698.0
179.0	2.0	2.0	16.5	2.0	99.0	EQCCYKCGPHLAR	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	ELLTMDGRFTDEEVDEL YR	2431.1	2432.1	2431.1	2432.1
151.0	8.0	8.0	29.1	2.0	99.0	FTDEEVDEL YR	1414.6	1415.6	1414.6	1415.6
151.0	8.0	8.0	29.1	2.0	99.0	GNFN YIEFTR	1259.6	1260.6	1259.6	1260.6
151.0	8.0	8.0	29.1	2.0	99.0	NAFACFDEEATGTIQED YLR	2349.0	2350.0	2349.0	2350.0
146.0	2.1	2.1	17.4	2.0	99.0	GNFN YIEFTR	1259.6	1260.6	1259.6	1260.6
128.0	6.0	6.0	33.9	2.0	99.0	ELLTMDGRFTDEEVDEL YR	2431.1	2432.1	2431.1	2432.1
128.0	6.0	6.0	33.9	2.0	99.0	GNFN YIEFTR	1259.6	1260.6	1259.6	1260.6
128.0	6.0	6.0	33.9	2.0	99.0	NAFACFDEEATGTIQED YLR	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	AGLQFPVGR	943.5	944.5	943.5	944.5
111.0	3.1	3.1	52.3	1.1	92.0	HLOLAIR	849.5	850.5	849.5	850.5
129.0	6.0	6.0	39.2	2.0	99.0	AGLQFPVGR	943.5	944.6	943.5	944.5
129.0	6.0	6.0	39.2	2.0	99.0	HLOLAIR	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
Q71DI3 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	KLPFOR	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	KLPFOR	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	1.0	24.0	STELLIR				

260.0	2.2	2.2	16.7	0.3	46.0	SPMDTFLIK	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	NAVEEYVYFRR	1401.6	1402.6	1401.6	1402.6
290.0	4.0	4.0	6.9	0.0	99.0	NAVEEYVYFRR	1417.7	1418.7	1417.7	1418.7
194.0	1.7	1.7	10.7	1.7	99.0	NAVEEYVYFRR	1417.7	1418.7	1417.7	1418.7
194.0	1.7	1.7	10.7	0.0	97.0	NAVEEYVYFRR	1401.6	1402.6	1401.6	1402.6
315.0	2.0	2.0	9.6	2.0	99.0	NAVEEYVYFRR	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	FOLQSDLLR	1118.6	1119.6	1118.6	1119.6
148.0	8.0	8.0	19.3	2.0	99.0	GFDKLVWTPR	1217.7	1218.7	1217.7	1218.7
148.0	8.0	8.0	19.3	2.0	99.0	HSGFCLTEQNWPDAVNQPR	2255.0	2256.0	2255.0	2256.0
148.0	8.0	8.0	19.3	2.0	99.0	QPYFGAVIGR	1106.6	1107.6	1106.6	1107.6
274.0	2.1	2.1	14.0	2.0	99.0	HSGFCLTEQNWPDAVNQPR	2255.0	2256.0	2255.0	2256.0
Q96CX2	KCD12_HUMAN	BTB/POZ domain-containing protein KCD12 (Pfeitin) (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	MFTQQCQQLAR	1475.7	1476.7	1475.7	1476.7
139.0	5.7	5.7	25.5	1.7	98.0	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	LFVGLDWSITQETLR	1821.9	1822.9	1821.9	1822.9
283.0	4.0	4.0	11.3	2.0	99.0	SOAPGPGASOWGSR	1512.7	1513.7	1512.7	1513.7
395.0	1.5	1.5	7.6	1.4	96.0	SOAPGPGASOWGSR	1512.7	1513.7	1512.7	1513.7
Q961U4	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	FSSETWNLGTLHR	1674.8	1675.8	1674.8	1675.8
308.0	4.0	4.0	11.4	2.0	99.0	FSVLLHLHGR	1153.7	1154.7	1153.7	1154.7
236.0	2.5	2.5	11.4	2.0	99.0	FSSETWNLGTLHR	1674.8	1675.8	1674.8	1675.8
236.0	2.5	2.5	11.4	0.5	66.0	FSVLLHLHGR	1153.7	1154.7	1153.7	1154.7
Q96KP4	CNDP2_HUMAN	Cytosolic nonspecific dipeptidase (CNDP dipeptidase 2) (Glutamate carboxypeptidase-like protein 1) - Homo sapiens (Human)								
347.0	3.3	3.3	8.4	2.0	99.0	WVAIQSVAVWPEKR	1655.9	1656.9	1655.9	1656.9
347.0	3.3	3.3	8.4	1.3	95.0	TGQEIPVNVRR	1111.6	1112.6	1111.6	1112.6
253.0	2.2	2.2	7.4	2.0	99.0	TVFGVEPDLTR	1232.6	1233.6	1232.6	1233.6
253.0	2.2	2.2	7.4	0.1	26.0	TGQEIPVNVRR	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	DKMNGGHYTYSENREVK	2159.0	2160.0	2158.9	2159.9
120.0	9.6	9.6	28.6	2.0	99.0	GAEEMETVIVPDMRR	1674.8	1675.8	1674.8	1675.8
120.0	9.6	9.6	28.6	2.0	99.0	GAEEMETVIVPDMVRR	1830.9	1831.9	1830.9	1831.9
120.0	9.6	9.6	28.6	2.0	99.0	MMNGGHYTYSENRE	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	2028.1
266.0	2.1	2.1	20.1	0.7	80.0	MMNGGHYTYSENREVK	1915.8	1916.8	1915.8	1916.8
177.0	2.0	2.0	14.8	2.0	99.0	GAEEMETVIVPDMVRR	1674.8	1675.8	1674.8	1675.8
Q9BR42	TXNL5_HUMAN	Thioredoxin-like protein 5 (14 kDa thioredoxin-related protein) (TRP14) (Protein 42-9) - Homo sapiens (Human)								
307.0	4.0	4.0	19.5	2.0	99.0	TIFAFTYTSK	1133.6	1134.6	1133.6	1134.6
307.0	4.0	4.0	19.5	2.0	99.0	YEEVSVSGFEEFHR	1713.8	1714.8	1713.8	1714.8
358.0	2.0	2.0	11.4	2.0	99.0	YEEVSVSGFEEFHR	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	IQYQLVDSODNALR	1774.9	1775.9	1774.9	1775.9
213.0	6.0	6.0	31.2	2.0	99.0	IQYQLVDSODNALRDEMRR	2306.1	2307.1	2306.1	2307.1
213.0	6.0	6.0	31.2	2.0	99.0	VYSTSVTGSRR	1055.5	1056.5	1055.5	1056.5
176.0	2.0	2.0	20.4	2.0	99.0	IQYQLVDSODNALRDEMRR	2306.1	2307.1	2306.1	2307.1
340.0	2.0	2.0	49.5	2.0	99.0	IQYQLVDSODNALRDEMRR	2306.1	2307.1	2306.1	2307.1
Q9NUV9	GIMA4_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	AAGSISMFNPSTPGASVYGPGR	2244.0	2245.0	2244.0	2245.0
105.0	10.4	10.4	24.9	2.0	99.0	AEEIQKQYQAMQGLHR	2068.0	2069.0	2068.0	2069.0
105.0	10.4	10.4	24.9	2.0	99.0	AQLLGLIQR	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	SFMIIFTR	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	IREEYEEKIRKLEDKVEQEKRR	2772.5	2773.5	2772.5	2773.5
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	SFMIIFTR	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	LESGDQVYVYSAAGLIR	2134.0	2135.0	2134.0	2135.0
185.0	6.2	6.2	15.7	2.0	99.0	LFKEVDGEGKPYEVR	1928.0	1929.0	1928.0	1929.0
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	LAQDFLDSONLSAYNTR	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	LYAYHLRR	1021.5	1022.5	1021.5	1022.5
Q9NYL9	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	SNDPVATAFAMLKK	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	NLGNLWGPVHR	1290.7	1291.7	1290.7	1291.7
273.0	4.1	4.1	8.2	2.0	99.0	VFSWVGGVYGR	1232.6	1233.6	1232.6	1233.6
211.0	3.2	3.2	10.5	2.0	99.0	NLGNLWGPVHR	1290.7	1291.7	1290.7	1291.7
211.0	3.2	3.2	10.5	1.2	94.0	YGLAGVRR	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	NQHIPOYGGSCWAHASTSAMADR	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	NVDGVNYASITR	1307.7	1308.7	1307.7	1308.7
145.0	8.0	8.0	24.8	2.0	99.0	YNLAI EEHCFTGDPV	1876.9	1877.9	1876.9	1877.9
99.0	3.7	3.7	11.6	2.0	99.0	YNLAI EEHCFTGDPV	1876.9	1877.9	1876.9	1877.9
99.0	3.7	3.7	11.6	1.7	98.0	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	NVDGVNYASITR	1307.7	1308.7	1307.7	1308.7
113.0	6.8	6.8	38.9	2.0	99.0	YNLAI EEHCFTGDPV	1876.9	1877.9	1876.9	1877.9
113.0	6.8	6.8	38.9	0.4	58.0	DLPKSVDWVRR	1202.6	1203.6	1202.6	1203.6
113.0	6.8	6.8	38.9	0.2	35.0	NQHIPOYGGSCWAHASTSAMADR	2647.1	2648.1	2647.1	2648.1
113.0	6.8	6.8	38.9	0.2	32.0	NSWGEPWGERGWLRR	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
Q9UJU6	DBNL_HUMAN	Drebrin-like protein (SH3 domain-containing protein 7) (Drebrin-F) (Cervical SH3P7) (HPK1-interacting protein of 55 kDa) (HIP-55) (Cervical mucin 5) - Homo sapiens (Human)								
248.0	4.7	4.7	22.6	2.0	99.0	SPTDWFALTYEGNSNDIR	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	FVLI NWTGEGVNDVRK	1846.0	1847.0	1846.0	1847.0
248.0	4.7	4.7	22.6	0.1	25.0	FVLI NWTGEGVNDVR	1717.9	1718.9	1717.9	1718.9
223.0	3.0	3.0	17.0	2.0	99.0	SPTDWFALTYEGNSNDIR	2085.0	2086.0	2085.0	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	ASKETHVMYDR	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	1685.8	1686.8	1685.8	1686.8
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	ASKETHVMYDR	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.

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	HELLOPPNVLYEK	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	APFSEVER	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
289.0	2.0	2.0	6.3	2.0	99.0	APFSEVER	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	EAAYHPEVAPDVR	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	LHTDDELNWLHGR	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	VGAI PANALDDGQWSQGLISAAR	2309.2	2310.2	2309.2	2310.2
67.0	14.8	14.8	8.8	2.0	99.0	VVAPTISSPVCQEQLEAGR	2139.1	2140.1	2139.1	2140.1
67.0	14.8	14.8	8.8	0.7	80.0	AVAEQIPLLQGVVR	1491.9	1492.9	1491.9	1492.9
75.0	9.8	9.8	7.6	2.0	99.0	IGITNHDEYSLVR	1515.8	1516.8	1515.8	1516.8
75.0	9.8	9.8	7.6	2.0	99.0	TMQFEPSTMVYDAGR	1834.8	1835.8	1834.8	1835.8
75.0	9.8	9.8	7.6	2.0	99.0	VVAPTISSPVCQEQLEAGR	2139.1	2140.1	2139.1	2140.1
75.0	9.8	9.8	7.6	1.7	98.0	AVAEQIPLLQGVVR	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	KSTVLLQQQYNR	1363.7	1364.7	1363.7	1364.7
75.0	9.8	9.8	7.6	0.4	64.0	EAAYHPEVAPDVR	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	MREDYDSVEQDDEPGPQR	2221.9	2222.9	2221.9	2222.9
328.0	2.0	2.0	27.0	2.0	99.0	MREDYDSVEQDDEPGPQR	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.