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Molecular Medicine

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

uman 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. S. 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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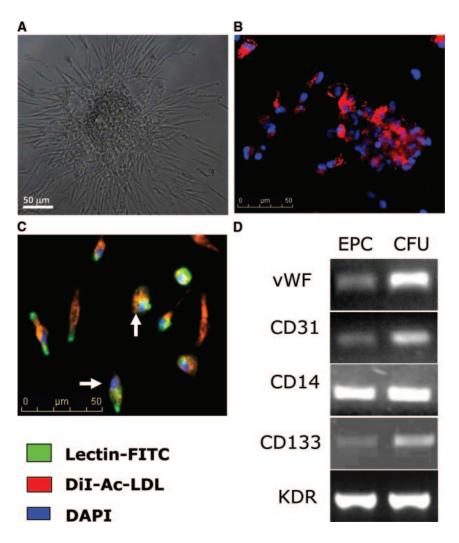


Figure 1. EPC cultures and CFUs. A and B, Morphology of CFUs (A) and endocytosis of acLDL (red fluorescence) (B). C, EPC cultures endocytose acLDL (red fluorescence) and bind to the lectin *Ulex europaeus* agglutinin (green fluorescence). Arrows indicate double positive cells. Blue labeling represents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

		CFU		EPC	
Protein Name	Swiss Protein Accession No.	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- $lpha$ -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
lpha-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 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 spindleshaped 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

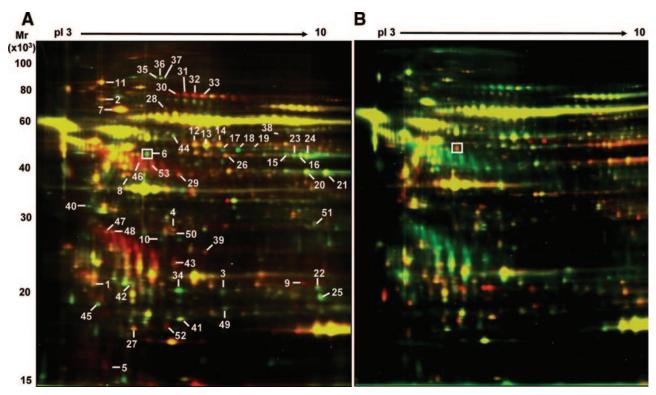


Figure 2. Difference in-gel electrophoresis. A, The proteins from CFUs are stained in green, whereas the proteins from EPC cultures are stained in red. B, Results are reproduced with different biological replicates using reverse-labeling (red for CFUs and green for EPCs). The protein corresponding to 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 B3 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

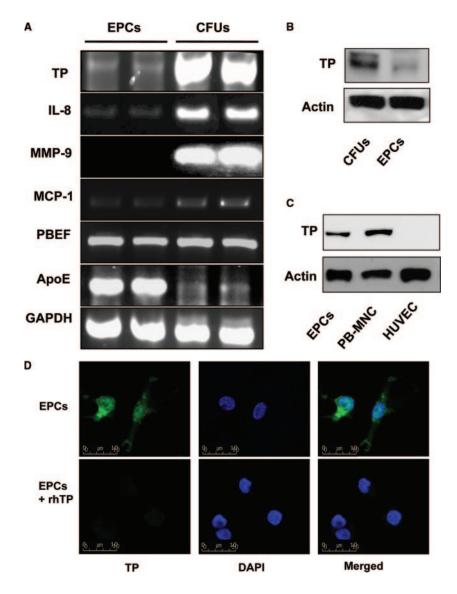


Figure 3. Expression of TP among other angiogenic factors. A, mRNA expression of TP, IL-8, MMP-9, MCP-1, pre-B cellenhancing factor 4 (PBEF), and apolipoprotein E (ApoE) in EPC cultures and CFUs as assessed by RT-PCR. GAPDH was used as loading control. B, Protein expression of TP in EPC cultures and 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 β 3, but not integrin β 1 or α v, 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 μ 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 $\alpha v \beta 3$

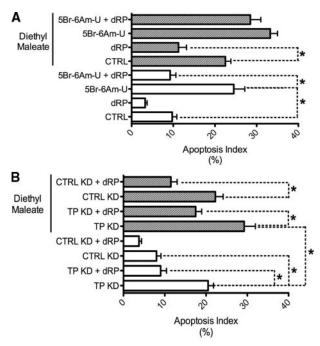


Figure 4. TP protects against apoptosis. A, Apoptosis in EPC cultures following treatment with 5Br-6Am-U (100 $\mu \text{mol/L})$ was assessed by ELISA. Where indicated, apoptosis was induced by diethyl maleate (5 mmol/L, 12 hours). B, Apoptosis following knockdown of TP in EPC cultures by siRNA (TP KD) in the presence or absence of dRP (50 $\mu \text{mol/L})$ 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

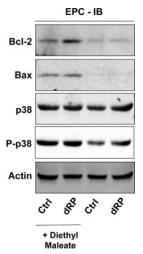


Figure 5. dRP enhances Bcl-2 expression under oxidative stress. EPC cultures with and without supplementation of dRP (50 μ mol/L) were subjected to treatment with diethyl maleate (5 mmol/L) and probed for Bcl-2, Bax, p38 MAPK, and phospho-p38 MAPK by immunoblotting. Actin served as loading control. Protein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

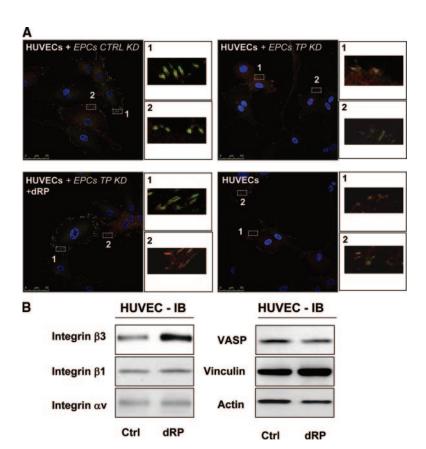


Figure 6. TP expression and release of dRP by EPCs stimulates focal adhesion formation and integrin β 3 expression in HUVECs. A, HUVECs were cultured for 24 hours in the presence of conditioned medium from EPC cultures (ratio 1:2) treated with either siRNA directed toward TP (TP KD) (top right) or scrambled controls (CTRL KD) (top left). dRP (50 μ 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 β 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 μ mol/L dRP for 24 hours and protein extracts were probed for expression of integrin β 3, integrin β 1, integrin αv , vasodilator stimulated phosphoprotein (VASP), and vinculin. Untreated HUVECs served as controls. The densitometric data were normalized to actin (means ± 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 β 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-

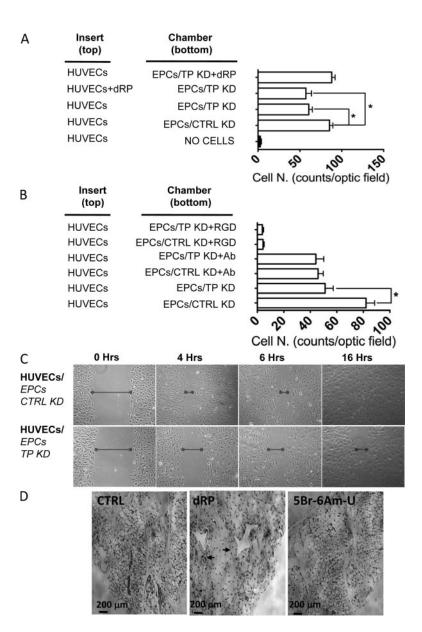


Figure 7. TP stimulates endothelial cell migration. The motility of HUVECs in response to paracrine factors released by EPCs was investigated in a modified Boyden chamber. The bottom chamber was either empty or seeded with EPCs treated with TP siRNA (TP KD) or scrambled control siRNA (CTRL KD). A and B, dRP (50 μ mol/L), anti- α v β 3 inhibitory antibody (Ab) (10 µg/mL), or RGD peptide (10 μ mol/L) was added where indicated. The number of transmigrated cells was counted in 3 independent experiments and presented as means±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 pretreated 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 μ g/mL anti- $\alpha v \beta 3$ inhibitory antibody or 10 μ 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 μ mol/L dRP (n=4), or 500 μ 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 LymphoprepTM 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 previously ¹. 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% CO₂enriched 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-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. detailed methodology A is available website on our 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 TurboSEQUEST 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-003.

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 μg 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: CTGCGCCAACACACAGAAATTA; 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: TATCCACCCAACACACAAGCAA, PBEF

GCTCCTATGCCAGCAGTCTC: reverse: MCP-1 forward: TCTGTGCCTGCTCATAG, MCP-1 reverse: GCAATTTCCCCAAGTCTCTG; CD133 GGTGCATTTCTCCACCACAT: vWF forward: GACCCTTTGTGCAGAAGGAA; VWF reverse: TCCCCAAGA TACACGGAGAG; CD14 forward: CTGCAACTTCTCCGAACCTC; CD14 reverse: TAGGTCCTCGAGCGTCAGTT: KDR forward: GCTTTGGCCCAATAATCAGA: KDR reverse: ACACGACTCCATGTTGGTCA; CD31 forward: TATTTTCCAA CD31 reverse: ATGACCTCAAACTGGGCATC; GAPDH GCCCGAACTG: CGGAGTCAACGGATTTG forward: GTCGTAT; and **GAPDH** reverse: AGCCTTCTCCATGGTGGAAGAC. 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 β1 (Santa Cruz Biotechnology, sc-8978), integrin αν (Santa Cruz Biotechnology, sc-6616), integrin β3 (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 μg ml⁻¹) and cultured for a further 2 days. Alternatively, HUVECs were cultured for 24 hours on collagen I-coated coverslips (20 μg/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 1.5μg/ml anti-human PD-ECGF antibody (R&D Systems, AF1143), 1 μg/ml DAPI (Sigma), and 0.8 μg/ml fluorescein isothiocyanate (FITC)-labeled anti-mouse IgG antibody (Molecular Probes). For HUVECs, the staining was performed with 2 μg/ml anti-integrin β3 antibody (R&D Systems, AF2266), 20 μg/ml FITC-conjugated anti-vinculin antibody (Sigma, F7053), 1 μg/ml DAPI and 0.8 μg/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 administrated 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 centrufugation. 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, 10⁵ cells were added to the top inserts of 24 well-transmigration microplates (pore size 8 μm, Corning), coated with collagen-I (20μg/ml, Sigma). The bottom chamber of the transmigration microplate was seeded with 2x10⁵ EPCs (either TP KD or CTRL KD), following coating with fibronectin (20μg/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

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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. Apopotosis in EPC cultures following treatment with 5Br-6Am-U (100μM) was assessed by flow cytometric analysis of annexin V and propidium iodide staining (A). Apopotosis 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 ± 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 β 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- α v β 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-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).

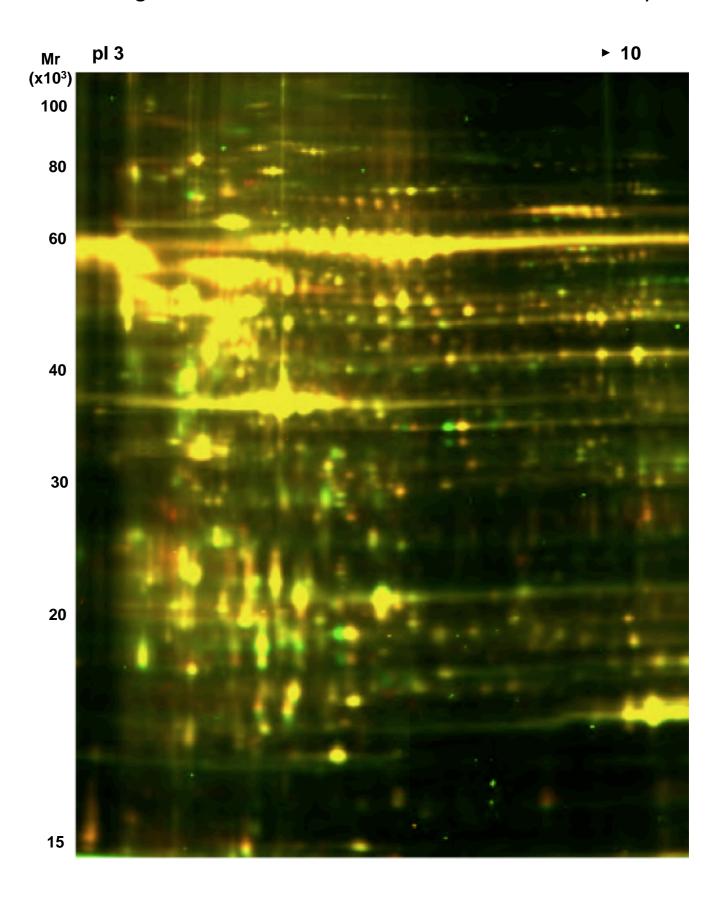
Online Table III. Differentially expressed proteins in CFUs compared to EPC cultures. CFUs and EPC cultures were compared by difference in-gel electrophoresis (DIGE). Results from 4 independent images were analyzed using SameSpot software (Nonlinear Dynamics). Spots exhibiting differential expression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

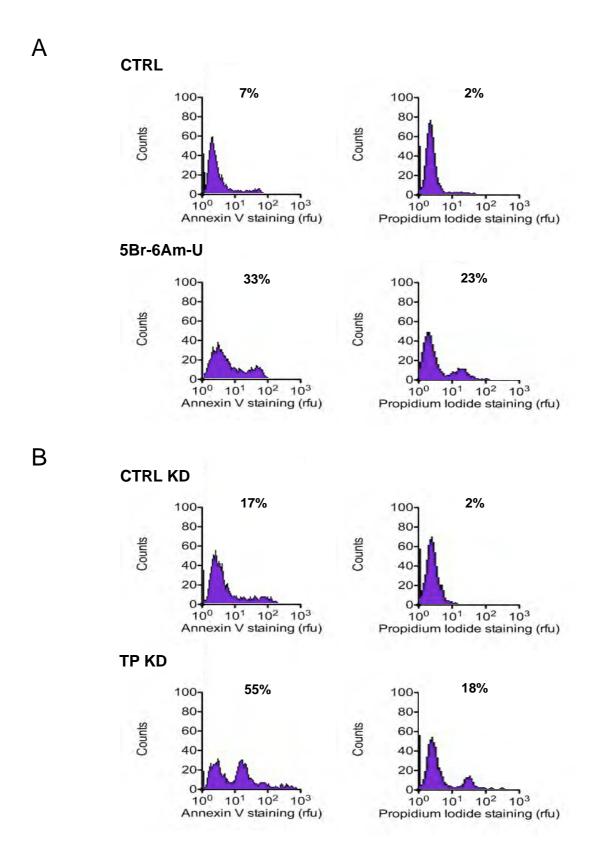
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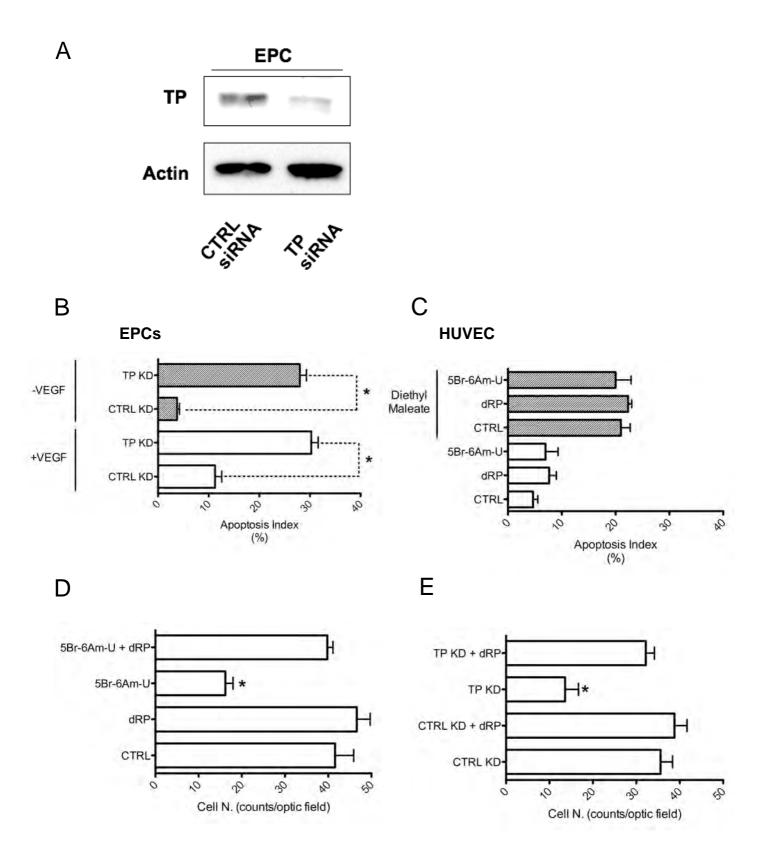
Online Table IV. Cytokine secretion. Cytokine concentrations in the conditioned medium were measured using the 27-plex cytokine assay from Biorad. The conditioned media from the 13 independent EPC cultures and 15 independent CFU preparations were analyzed according to the manufacturers' instructions. 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.

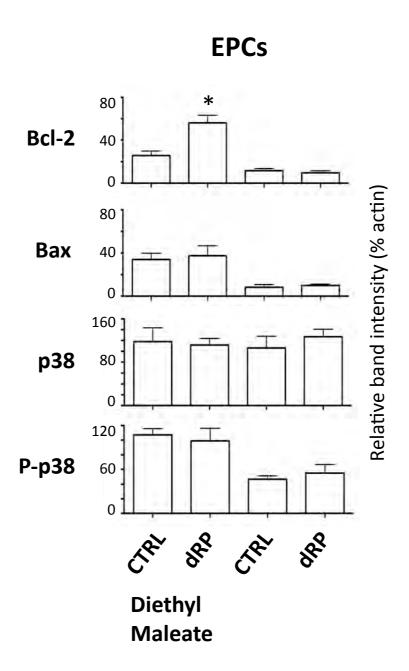
References

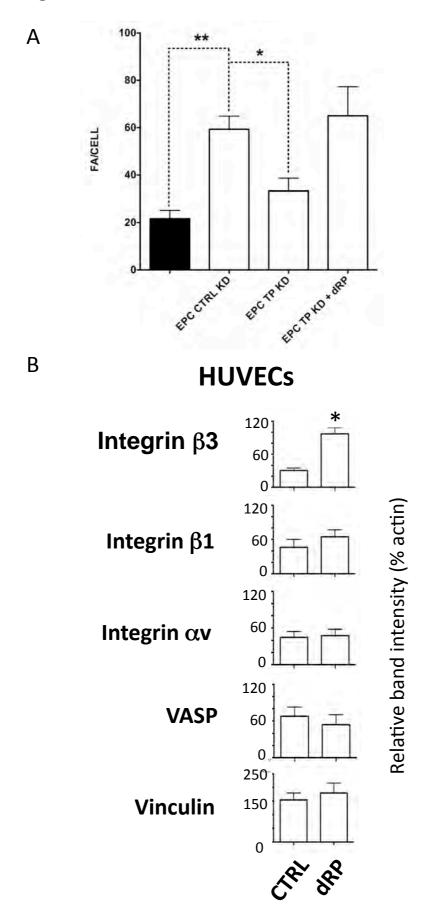
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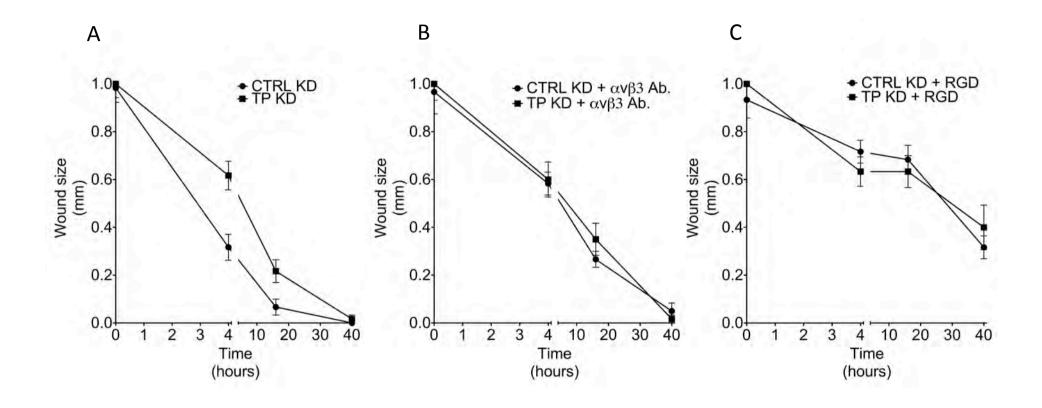


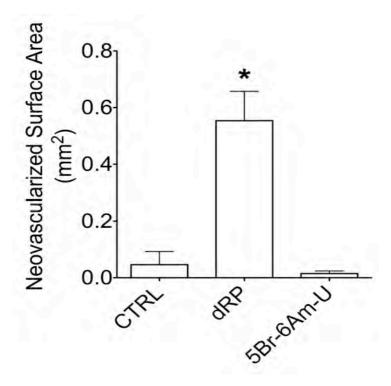












ONLINE TABLE I

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

Rank N.	Total Score	% Coverage	Accession	Protein name
108	8.2	20.7	O00299 CLIC1_HUMAN	Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (Chloride channel ABP) (Regulatory nuclear chloride ion channel protein) (hRNCC) - Homo sapiens (Human)
69	4.9	30.3	O00299 CLIC1_HUMAN	Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (Chloride channel ABP) (Regulatory nuclear chloride ion
123	9.5	31.1	O00299 CLIC1_HUMAN	channel protein) (hRNCC) - Homo sapiens (Human) Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (Chloride channel ABP) (Regulatory nuclear chloride ion
160	2.0	11.1	O00391 QSCN6_HUMAN	channel protein) (hRNCC) - Homo saplens (Human) Sulfhydryl oxidase 1 precursor (EC 1.8.3.2) (Quiescin Q6) (hQSOX) - Homo saplens (Human)
201	6.0	12.2	O00391 QSCN6_HUMAN	Sulfhydryl oxidase 1 precursor (EC 1.8.3.2) (Quiescin Q6) (hQSOX) - Homo sapiens (Human) High-mobility group nucleosome-binding domain-containing protein 4 (Nonhistone chromosomal protein HMG-17-like 3) (Non-histone
338	2.0	51.1	O00479 HMGN4_HUMAN	chromosomal protein) - Homo sapiens (Human) High-mobility group nucleosome-binding domain-containing protein 4 (Nonhistone chromosomal protein HMG-17-like 3) (Non-histone
285	4.0	44.4	O00479 HMGN4_HUMAN	chromosomal protein) - Homo sapiens (Human) Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase I) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal peptatir
189	4.0	5.0	O14773 TPP1_HUMAN	insensitive protease) (LPIC) (Cell growth-inhibiting gene 1 protein) - Homo sapiens (Human)
138	2.1	14.9	O14773 TPP1_HUMAN	Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase I) (TPP-I) (TPP-I) (Tripeptidyl aminopeptidase) (Lysosomal pepstatir insensitive protease) (LPIC) (Cell growth-inhibiting gene 1 protein) - Homo sapiens (Human)
490	2.0	4.6	O14773 TPP1_HUMAN	Tripeptidyl-peptidase 1 precursor (EC 3.4.14.9) (Tripeptidyl-peptidase I) (TPP-1) (Tripeptidyl aminopeptidase) (Lysosomal pepstatir insensitive protease) (LPIC) (Cell growth-inhibiting gene 1 protein) - Homo sapiens (Human)
202 177	3.7 6.5	11.7 17.3	O14818 PSA7_HUMAN O14818 PSA7_HUMAN	Proteasome subunit alpha type 7 (EC 3.4.25.1) (Proteasome subunit RC6-1) (Proteasome subunit XAPC7) - Homo sapiens (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 (hnRPD-like protein) (hnHNRP-DL) (JKT41-binding protein) (AU-rich element RNA-binding factor) (Protein IaAUF1) - Homo sapiens (Human)
87	4.0	18.8	O14979 HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRPD-like protein) (hnHNRP-DL) (JKT41-binding protein) (AU-rich element RNA-binding factor) (Protein laAUF1) - Homo saplens (Human)
452	6.0	9.8	O14979 HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like (hnRPD-like protein) (hnHNRP-DL) (JKT41-binding protein) (AU-rich element RNA-binding factor) (Protein laAUF1) - Homo sapiens (Human)
85	8.9	22.3	O15143 ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC) - Homo sapiens (Human)
128 152	2.3 8.0	24.7 17.7	O15143 ARC1B_HUMAN O15143 ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC) - Homo sapiens (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)
196 172	1.7 6.7	21.0 20.7	O15144 ARPC2_HUMAN O15144 ARPC2_HUMAN	Actin-related protein 2/3 complex subunit 2 (ARP2/3 complex 34 kDa subunit) (p34-ARC) - Homo sapiens (Human) Actin-related protein 2/3 complex subunit 2 (ARP2/3 complex 34 kDa subunit) (p34-ARC) - Homo sapiens (Human)
247 238	2.3 5.1	15.2 21.9	O15145 ARPC3_HUMAN O15145 ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3 (ARP2/3 complex 21 kDa subunit) (p21-ARC) - Homo sapiens (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) -
81	4.2	7.7	O15204 ADEC1_HUMAN	Homo sapiens (Human) ADAM DEC1 precursor (EC 3.4.24) (A disintegrin and metalloproteinase domain-like protein decysin 1) (ADAM-like protein decysin 1) -
264	4.3	10.4	O15204 ADEC1_HUMAN	Homo sapiens (Human) ADAM DEC1 precursor (EC 3.4.24) (A disintegrin and metalloproteinase domain-like protein decysin 1) (ADAM-like protein decysin 1) -
166	4.3	14.5	O43390 HNRPR_HUMAN	Homo saplens (Human) Heterogeneous nuclear ribonucleoprotein R (hnRNP R) - Homo saplens (Human)
267	4.2	20.7 32.3	O43390 HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R (hnRNP R) - Homo sapiens (Human)
22 44	22.9 6.9	13.9	O43707 ACTN4_HUMAN O43707 ACTN4_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross-linking protein) - Homo sapiens (Human) Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross-linking protein) - Homo sapiens (Human)
10 295	41.3 2.0	35.2 6.4	O43707 ACTN4_HUMAN O43776 SYNC_HUMAN	Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross-linking protein) - Homo sapiens (Human) Asparaginyl-tRNA synthetase, cytoplasmic (EC 6.1.1.22) (AsparaginetRNA ligase) (AsnRS) - Homo sapiens (Human)
212	6.0	9.3	O43776 SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic (EC 6.1.1.22) (AsparaginetRNA ligase) (AsnRS) - Homo saplens (Human)
111 125	6.9 2.3	14.4 14.9	O75083 WDR1_HUMAN O75083 WDR1_HUMAN	WD repeat protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1) - Homo sapiens (Human) WD repeat protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1) - Homo sapiens (Human)
373	2.0	8.8	O75368 SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein - Homo sapiens (Human)
320	4.0	24.6	075368 SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein - Homo sapiens (Human) GRB2-related adapter protein 2 (GADS protein) (Growth factor receptor-binding protein) (GRBLG) (Grf40 adapter protein) (Grf-40) (GRB-2
384	1.7	11.2	O75791 GRAP2_HUMAN	like protein) (GRB2L) (GRBX) (P38) (Hematopoletic cell-associated adapter protein GrpL) (Adapter protein GRID) (SH3-SH2-SH3 adapter Mona) - Homo sapiens (Human)
553	2.0	3.3	O75791 GRAP2_HUMAN	GRB2-related adapter protein 2 (GADS protein) (Growth factor receptor-binding protein) (GRBLG) (Grf40 adapter protein) (Grf-40) (GRB-2 like protein) (GRB2L) (GRBX) (P38) (Hematopoletic cell-associated adapter protein GrpL) (Adapter protein GRID) (SH3-SH2-SH3 adapter
88	4.0	11.1	P00338 LDHA_HUMAN	Mona) - Homo sapiens (Human) L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH muscle subunit) (LDH-M) (Proliferation-inducing gene 19 protein) (Renal
129	11.3	30.4	P00338 LDHA_HUMAN	carcinoma antigen NY-REN-59) - Homo sapiens (Human) L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH muscle subunit) (LDH-M) (Proliferation-Inducing gene 19 protein) (Renal
141	5.7	29.1	P00491 PNPH_HUMAN	carcinoma antigen NY-REN-59) - Homo sapiens (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) Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2) (Cell migration-inducing gene 10 protein) - Homo sapiens
30	20.8	45.6	P00558 PGK1_HUMAN	(Human) Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2) (Cell migration-inducing gene 10 protein) - Homo sapiens
76	4.6	30.5	P00558 PGK1_HUMAN	(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 16	26.1 16.5	17.1 18.1	P01023 A2MG_HUMAN P01023 A2MG_HUMAN	Alpha-2-macroglobulin precursor (Alpha-2-M) - Homo sapiens (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) - Homo saplens (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)
355 104	2.0 3.4	13.7 26.0	P01034 CYTC_HUMAN P01034 CYTC_HUMAN	Cystatin-C precursor (Cystatin-3) (Neuroendocrine basic polypeptide) (Gamma-trace) (Post-gamma-globulin) - Homo sapiens (Human) Cystatin-C precursor (Cystatin-3) (Neuroendocrine basic polypeptide) (Gamma-trace) (Post-gamma-globulin) - Homo sapiens (Human)
302	4.0	25.3	PO1034 CYTC_HUMAN	Cystatin-C precursor (Cystatin-3) (Neuroendocrine basic polypeptide) (Gamma-trace) (Post-gamma-globulin) - Homo sapiens (Human)
188 260	4.0 4.5	31.1 37.7	P01834 KAC_HUMAN P01834 KAC_HUMAN	Ig kappa chain C region - Homo sapiens (Human) Ig kappa chain C region - Homo sapiens (Human)
203 64	3.7 5.3	28.6 19.0	P01842 LAC_HUMAN 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) Ig lambda chain C regions - Homo sapiens (Human)
106 195	7.6 1.7	17.2 7.0	P01871 MUC_HUMAN P01871 MUC_HUMAN	Ig mu chain C region - Homo sapiens (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 95	2.0 4.0	14.3 13.5	P02746 C1QB_HUMAN P02746 C1QB_HUMAN	Complement C1q subcomponent subunit B precursor - Homo saplens (Human) Complement C1q subcomponent subunit B precursor - Homo saplens (Human)
354	2.0	10.2	P02747 C1QC_HUMAN	Complement C1q subcomponent subunit C precursor - Homo saplens (Human)
190 386	2.0 2.4	3.7 14.7	P02747 C1QC_HUMAN P02747 C1QC_HUMAN	Complement C1q subcomponent subunit C precursor - Homo saplens (Human) Complement C1q subcomponent subunit C precursor - Homo saplens (Human)
27 22	21.3 13.3	16.4 13.7	P02751 FINC_HUMAN P02751 FINC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo sapiens (Human) Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo sapiens (Human)
584	1.4	1.1	P02751 FINC_HUMAN	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - Homo sapiens (Human)
370 550	2.0 2.0	8.6 8.6	P02792 FRIL_HUMAN P02792 FRIL_HUMAN	Ferritin light chain (Ferritin L subunit) - Homo sapiens (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	Metallothlonein-2 (MT-2) (Metallothlonein-II) (MT-II) (Metallothlonein-2A) - Homo sapiens (Human) Vitronectin precursor (Serum-spreading factor) (S-protein) (V75) [Contains: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomer
159	4.5	13.6	P04004 VTNC_HUMAN	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 16	6.2 37.1	29.4 57.7	P04075 ALDOA_HUMAN P04075 ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Lung cancer antigen NY-LU-1) - Homo sapiens (Human) Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Lung cancer antigen NY-LU-1) - Homo sapiens (Human)
277 318	2.1 4.0	30.6 36.7	P04080 CYTB_HUMAN P04080 CYTB_HUMAN	Cystatin-B (Stefin-B) (Liver thiol proteinase inhibitor) (CPI-B) - Homo sapiens (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 saplens (Human)
74 30	4.7 24.2	25.4 49.6	P04406 G3P_HUMAN P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) - Homo sapiens (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 saplens (Human) Plasminogen activator inhibitor 2 precursor (PAI-2) (Placental plasminogen activator inhibitor) (Monocyte Arg-serpin) (Urokinase inhibitor) -
38	8.1	21.2	P05120 PAI2_HUMAN	Homo sapiens (Human) Plasminogen activator inhibitor 2 precursor (PAI-2) (Placental plasminogen activator inhibitor) (Monocyte Arg-serpin) (Urokinase inhibitor) -
114	10.0	13.5	P05120 PAI2_HUMAN	Homo sapiens (Human) Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein (hUCRP) (Interferon-induced 15 kDa protein)] -
353	2.0	10.9	P05161 UCRP_HUMAN	Homo sapiens (Human) Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein (hUCRP) (Interferon-induced 15 kDa protein)] -
502 369	2.0	12.7 2.1	P05161 UCRP_HUMAN P05362 ICAM1_HUMAN	Homo sapiens (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) - Horno sapiens (Human)
251 316	2.2 4.0	15.7 6.6	P06576 ATPB_HUMAN P06576 ATPB_HUMAN	ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (Human) ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Homo sapiens (Human)
12	31.0	55.8	P06733 ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-
19	14.1	35.3	P06733 ENOA_HUMAN	myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein) - Homo sapiens (Human) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-
15	38.3	62.9	P06733 ENOA_HUMAN	myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein) - Homo sapiens (Human) Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-
103	7.7	15.2	P06744 G6PI_HUMAN	myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein) - Homo sapiens (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) Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin)
92 391	9.7	18.6 21.5	P06744 G6PI_HUMAN P06753 TPM3_HUMAN	(NLK) (Sperm antigen 36) (SA-36) - Homo sapiens (Human) Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5) - Homo sapiens (Human)
255	16.4	40.8	P06753 TPM3_HUMAN	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma) (hTM5) - Homo sapiens (Human)
196	3.8	17.4	P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46) - Homo sapiens (Human)
207	4.0	20.1	P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46) - Homo sapiens (Human)
56	16.9	32.6	P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46) - Homo sapiens (Human)
298	2.0	6.7	P07237 PDIA1_HUMAN	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-hydroxylase subunit beta) (Cellular thyroid hormone-binding protein) (p55) - Homo sapiens (Human)
481	2.0	6.5	P07237 PDIA1_HUMAN	Protein disulfide-Isomerase precursor (EC 5.3.4.1) (PDI) (Prolyl 4-hydroxylase subunit beta) (Cellular thyroid hormone-binding protein) (p55) - Homo sapiens (Human)
149	4.9	16.0	P07339 CATD_HUMAN	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain] - Homo sapiens (Human)
70 199	4.9 6.0	20.9 18.2	P07339 CATD_HUMAN P07339 CATD_HUMAN	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain] - Homo saplens (Human) Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy chain] - Homo saplens (Human)
47 26	15.8 11.9	30.0 22.5	P07437 TBB5_HUMAN	Tubulin beta chain (Tubulin beta-5 chain) - Homo sapiens (Human) Tubulin beta chain (Tubulin beta-5 chain) - Homo sapiens (Human)
26	28.5	47.3	P07437 TBB5_HUMAN P07437 TBB5_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-Vall: Saposin B (Sphignolipidi activator protein 1) (SAP-1) (Cerebroside sulfate activator) (CSAP: (Dispersin) (Sulfatide/GMI activator): Saposin C (Co-beta-glucosidase), (AI activator) (Giucosylceramidase 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 (Sphipingibidi activator protein 1) (SAP-1) (Cerebroside sulfate activator) (CSAP: (Dispersin) (Sulfatide/GM1 activator): Saposin C (O-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) (Glucosylcoramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D (Protein C) (Component C)] - Homo saplens (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 saplens (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 saplens (Human)
29 21	20.9 13.4	61.4 61.4	P07737 PROF1_HUMAN P07737 PROF1_HUMAN	Profilin 1 (Profilin 1) - Homo sapiens (Human)
36	22.5	82.1	P07737 PROF1_HUMAN	Profilin-1 (Profilin I) - Homo sapiens (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 saplens (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 20	4.7 29.4	23.5 29.9	P07900 HS90A_HUMAN P07900 HS90A_HUMAN	Heat shock protein HSP 90-alpha (HSP 86) (Renal carcinoma antigen NY-REN-38) - Homo sapiens (Human) Heat shock protein HSP 90-alpha (HSP 86) (Renal carcinoma antigen NY-REN-38) - Homo sapiens (Human)
213 241	3.2 5.0	27.5 8.8	P07910 HNRPC_HUMAN P07910 HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1 / hnRNP C2) - Homo sapiens (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 37	14.3 18.7	29.2 28.2	P08107 HSP71_HUMAN P08238 HS90B_HUMAN	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2) - Homo sapiens (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)
182	27.8 4.0	30.9	P08238 HS90B_HUMAN P08571 CD14_HUMAN	Heat shock protein HSP 90-beta (HSP 84) (HSP 90) - Homo saplens (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) Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein) [Contains: Monocyte differentiation antigen
145	2.1	16.3	P08571 CD14_HUMAN	CD14, urinary form: Monocyte differentiation antigen CD14, membrane-bound form] - Homo sapiens (Human) Monocyte differentiation antigen CD14 precursor (Myeloid cell-specific leucine-rich glycoprotein) [Contains: Monocyte differentiation antigen
548 323	2.0	6.7	P08571 CD14_HUMAN P08575 CD45_HUMAN	CD14, urinary form: Monocyte differentiation antigen CD14, membrane-bound formi - Homo sapiens (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 22.8	62.2 70.6	P08670 VIME_HUMAN P08670 VIME_HUMAN	Vimentin - Homo sapiens (Human) Vimentin - Homo sapiens (Human)
3	63.4	70.0	P08670 VIME_HUMAN	Vimentin - Homo sapiens (Human)
99 47	8.0 6.6	18.6 23.3	P09211 GSTP1_HUMAN P09211 GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1) - Homo sapiens (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) Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-I) (Lactose-binding lectin 1) (S-Lac lectin 1)
142	5.7	29.6	P09382 LEG1_HUMAN	(Galaptin) (14 kDa lectin) (HPL) (HBL) (Putative MAPK-activating protein MP12) - Homo sapiens (Human)
68	4.9	61.5	P09382 LEG1_HUMAN	Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-I) (Lactose-binding lectin 1) (S-Lac lectin 1) (Galaptin) (14 KDa lectin) (IHPL) (HBL) (Putative MAPK-activating protein MP12) - Homo sapiens (Human)
99	11.2	61.5	P09382 LEG1_HUMAN	Galectin-1 (Lectin galactoside-binding soluble 1) (Beta-galactoside-binding lectin L-14-I) (Lactose-binding lectin 1) (S-Lac lectin 1) (Galaptin) (14 kDa lectin) (HPL) (HBL) (Putative MAPK-activating protein MP12) - Homo sapiens (Human)
73	10.0 7.5	53.5 33.5	P09429 HMGB1_HUMAN P09429 HMGB1_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1) - Homo sapiens (Human) High mobility group protein B1 (High mobility group protein 1) (HMG-1) - Homo sapiens (Human)
40			P09429 HMGB1_HUMAN	High mobility group protein B1 (High mobility group protein 1) (HMG-1) - Homo saplens (Human)
40 42 203	20.0	45.6 11.3	P09429 HMGB1_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 saplens (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 82	9.9	39.2	P10124 PGSG_HUMAN	Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase) (Leukotriene A(4) hydrolase) - Homo saplens (Human) Secretory granule proteoglycan core protein precursor (Platelet proteoglycan core protein) (P.P.G) (Hematopoetic proteoglycan core protein)
48	6.5	39.2	P10124 PGSG_HUMAN	(Serglycin) - Homo saplens (Human) Secretory granule proteoglycan core protein precursor (Platelet proteoglycan core protein) (P.P.G) (Hematopoetic proteoglycan core protein)
179	6.4	39.2	P10124 PGSG_HUMAN	(Serglycin) - Homo sapiens (Human) Secretory granule proteoglycan core protein precursor (Platelet proteoglycan core protein) (P.PG) (Hematopoetic proteoglycan core protein)
			<u> </u>	(Serqlvcin) - Homo sapiens (Human) Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-
105	7.7	56.6	P10145 IL8_HUMAN	activating protein 1) (NAP-1) (Protein 3-10C) (Granulocyte chemotactic protein 1) (GCP-1) (Monocyt-derived neutrophil-activating peptide) (MONAP) (Emoctakin) [Contains: MDNCF-a (ILB/NAP1 form II) (GCP/IL-B protein II) (ILB/NAP1 form III) (GCP/IL-B protein III) (GIA:IL-B)77); IL-8(5-77); IL-8(5-77); IL-8(5-77) (Lymphocyte-derived neutrophil-activating factor) (LYNAP) (Neutrophil-activating factor) (NAF) (MDNCF-c) (ILB/NAP1 form III) (GCP/IL-B protein I) ((Ser-IL-B)72); IL-8(7-77) (ILB/NAP1 form IV) (GCP/IL-B protein III)] - Homo sapiens (Human)
73	4.8	43.4	P10145 IL8_HUMAN	Interleukin-8 precursor (IL-8) (XXCL8) (Moncoyte-derived neutrophil chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-activating protein 1) (XMP-1) (Protein 3-10C) (Granulocyte chemotactic protein 1) (GCP-1) (Moncoyte-derived neutrophil-activating peptide) (MONAP) (Emoctakin) (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 IV): Interleukin-8 (IL-8(1-77)) (MDNCF-c) (IL8/NAP1 form III) (GCP/IL-8 protein I) (GEP-IL-8)72): IL-8(7-77) (IL8/NAP1 form IV) (GCP/IL-8 protein I) (IL8/NAP1 form IV) (GCP/IL-8 protein IV): IL-8(8-77) (IL8/NAP1 form IV) (GCP/IL-8 protein
133	8.4	49.5	P10145 IL8_HUMAN	Interleukin-8 precursor (IL-8) (XXCL8) (Monccyte-derived neutrophil chemotactic factor) (MDNCF) (T-cell chemotactic factor) (NDNCF) (T-cell chemotactic factor) (NDNCF) (T-cell chemotactic patch (NDNCF) (T-cell chemotactic patch) (NDNCF) (MDNCF) (MDNCF) (MDNCF) (MDNCF) (MDNCF) (MDNCF) (MDNCF) (ILB/NAP1 form II) (GCP/IL-8 protein IV): Interleukin-8 (IL-8(1-77)) (MDNCF-b) (ILB/NAP1 form II) (GCP/IL-8 protein II) (All-IL-8)77); IL-8(6-77) (ILP/NAP1 form) (MDNCF-c) (ILB/NAP1 form III) (GCP/IL-8 protein II) (Ser-IL-8)72; IL-8(7-77) (ILB/NAP1 form IV) (GCP/IL-8 protein II) (Ser-IL-8)72; IL-8(7-77) (ILB/NAP1 form IV) (GCP/IL-8 protein II) (Ser-IL-8)72; IL-8(7-77) (ILB/NAP1 form IV) (GCP/IL-8 protein III) IL-8(8-77) (ILB/NAP1 form IV) (GCP/IL-8 protein IV) IL-8(8-77) (ILB/NAP1 form IV) (GCP
107 160	3.2 12.5	41.7 47.8	P10319 1B58_HUMAN P10319 1B58_HUMAN	HLA class I histocompatibility antigen, B-58 alpha chain precursor (MHC class I antigen B*58) (Bw-58) - Homo saplens (Human) HLA class I histocompatibility antigen, B-58 alpha chain precursor (MHC class I antigen B*58) (Bw-58) - Homo saplens (Human)
160	7.7	24.2	P10412 H14_HUMAN	Histone H1.4 (Histone H1b) - Homo sapiens (Human)
74 81	9.1	18.3 42.9	P10412 H14_HUMAN P10599 THIO_HUMAN	Histone H1.4 (Histone H1b) - Homo sapiens (Human) Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphydryl protein) (SASP) - Homo sapiens (Human)
80 113	4.3 10.0	33.3 42.9	P10599 THIO_HUMAN P10599 THIO_HUMAN	Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphydryl protein) (SASP) - Homo sapiens (Human) Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphydryl protein) (SASP) - Homo sapiens (Human)
83	10.6	15.3	P11021 GRP78_HUMAN	78 kba glucose-regulated protein precursor (GRP 78) (Heat shock 70 kba protein 5) (Immunoglobulin heavy chain-binding protein) (BIP) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) - Homo sapiens (Human)
105	3.5	20.6	P11021 GRP78_HUMAN	(Endoplasmic reticulum fulnerial Ca(2+7-billing) protein giz/p3 - normb aspiers (runnan) 78 kDa glucose-regulated protein precursor (GRP 78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) - Homo sapiens (Human)
104	13.3	22.3	P11021 GRP78_HUMAN	(Endoplasmic reticulum lumenal Ca(2+)-binding protein grp79) - Hono sapiens (Human) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) - Hono 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 9	16.6 43.1	32.5 46.0	P11142 HSP7C_HUMAN P11142 HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) - Homo sapiens (Human) Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) - Homo sapiens (Human)
101 205	7.7 1.5	22.9 6.8	P11413 G6PD_HUMAN P11413 G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD) - Homo saplens (Human) Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD) - Homo saplens (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 11 receptor) (Insulin-like growth factor 11 receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (300 kDa mannose 6-phosphate receptor) (MPR 300) (MPR300) (CD222 antigen) - Homo sapiens (Human) Cation-Independent mannose-6-phosphate receptor precursor (CI Man-6-P receptor) (CI-MPR) (M6PR) (Insulin-like growth factor 2
201	1.5	6.2	P11717 MPRI_HUMAN	receptor) (Insulin-like growth factor II receptor) (IGF-II receptor) (M6P/IGF2 receptor) (M6P/IGF2R) (300 kDa mannose 6-phosphate receptor) (MPR 300) (MPR300) (CD222 antigen) - Homo sapiens (Human)
199 117	3.7 2.6	11.9 18.4	P11940 PABP1_HUMAN P11940 PABP1_HUMAN	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) - Homo sapiens (Human) Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) - Homo sapiens (Human)
194	6.0 2.0	21.2	P11940 PABP1_HUMAN	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) - Homo sapiens (Human) Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptidase) (Proline dipeptidase) (Prolinedipeptidase) (Imidodipeptidase) - Homo sapiens (Human)
367 572	1.5	3.4	P12955 PEPD_HUMAN 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) (Ku/70) (70 kDa subunit of Ku antigen) (TIPA) (TCT box-binding factor 75 kDa subunit) (CTCEP) (CTC75) (DNA-repair protein XRCC6) - Homo sapiens (Human) ATP-dependent DNA helicase 2 subunit 1 (ATP-dependent DNA helicase II 70 kDa subunit) (Lupus Ku autoantigen protein p70) (Ku/70) (70
49	18.0	20.2	P12956 KU70_HUMAN	KDa subunit of Ku antigen) (Thyroid-lupus autoantigen) (TLAA) (CTC box-binding factor 75 kDa subunit) (CTCBF) (CTC75) (DNA-repair protein RRC6) - Homo sapiens (Human)
366 183	2.0	4.2 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 P13284 GILT_HUMAN	Gamma-interferon-inducible lysosomal thiol reductase precursor (Gamma-interferon-inducible protein IP-30) - Homo sapiens (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 33	15.4 9.8	27.2 18.4	P13639 EF2_HUMAN P13639 EF2_HUMAN	Elongation factor 2 (EF-2) - Homo sapiens (Human) Elongation factor 2 (EF-2) - Homo sapiens (Human)
35 305	22.8 6.0	20.3 54.8	P13639 EF2_HUMAN P13640 MT1G_HUMAN	Elongation factor 2 (EF-2) - Homo sapiens (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-1G) (MT-IG) (Metallothionein-1K) (MT-1K) - Homo sapiens (Human)
460 299	2.0	53.2 6.5	P13640 MT1G_HUMAN P13686 PPA5_HUMAN	Metallothionein-1G (MT-1G) (Metallothionein-1G) (MT-IG) (Metallothionein-1K) (MT-1K) - Homo sapiens (Human) Tartrate-resistant acid phosphatase type 5 precursor (EC 3.1.3.2) (TR-AP) (Tartrate-resistant acid ATPase) (TrATPase) (Acid phosphatase 5,
144	2.1	15.7	P13686 PPA5_HUMAN	tartrate resistant) - Homo sapiens (Human) Tartrate-resistant acid phosphatase type 5 precursor (EC 3.1.3.2) (TR-AP) (Tartrate-resistant acid ATPase) (TrATPase) (Acid phosphatase 5,
247	4.9	12.3	P13686 PPA5_HUMAN	tartrate resistant) - Homo sapiens (Human) Tartrate-resistant acid phosphatase type 5 precursor (EC 3.1.3.2) (TR-AP) (Tartrate-resistant acid ATPase) (TrATPase) (Acid phosphatase 5,
24	22.6	37.5	P13796 PLSL_HUMAN	tartrate resistant) - Homo sapiens (Human) Plastin-2 (L-plastin) (Lymphocyte cytosolic protein 1) (LCP-1) (LC64P) - Homo sapiens (Human)
18 25	14.2 26.0	31.4 32.2	P13796 PLSL_HUMAN P13796 PLSL_HUMAN	Plastin-2 (L-plastin) (Lymphocyte cytosolic protein 1) (LCP-1) (LC64P) - Homo sapiens (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 saplens (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 saplens (Human)
153 137	4.6 2.1	17.9 30.0	P14317 HCLS1_HUMAN P14317 HCLS1_HUMAN	Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75) - Homo sapiens (Human) Hematopoietic lineage cell-specific protein (Hematopoietic cell-specific LYN substrate 1) (LckBP1) (p75) - Homo sapiens (Human)
137	8.7	13.8	P14317 HCLS1_HUMAN	Hematopoletic lineage cell-specific protein (Hematopoletic 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	Endoplasmin 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	Endoplasmin 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 - 1 - Homo sapiens (Human)
155 344	4.6 3.4	65.1 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	P14854 CX6B1_HUMAN P15153 RAC2_HUMAN	Cytochrome c oxidase subunit VIb Isoform 1 (EC 1.9.3.1) (COX VIb-1) - Homo sapiens (Human) Ras-related C3 botulinum toxin substrate 2 precursor (p21-Rac2) (Small G protein) (GX) - Homo sapiens (Human)
304 67	4.0 23.1	9.4 38.4	P15153 RAC2_HUMAN P15311 EZRI_HUMAN	Ras-related C3 botulinum toxin substrate 2 precursor (p21-Rac2) (Small G protein) (GX) - Homo sapiens (Human) Ezrin (p81) (Cytovillin) (Villin-2) - Homo sapiens (Human)
127	10.3	24.9	P15311 EZRI_HUMAN	Ezrin (p81) (Cytovillin) (Villin-2) - Homo sapiens (Human)
156	4.6	7.5	P15311 EZRI_HUMAN P16070 CD44_HUMAN	Ezrin (ps1) (Cytovillin) (Villin-2) - Homo sapiens (Human) CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (Heperan sulfate proteoglycan) (Epican) (CDw44) - Homo sapiens
109	3.2	6.9	P16070 CD44_HUMAN	(Human) CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (Heparan sulfate proteoglycan) (Epican) (CDw44) - Homo sapiens
346	3.3	4.0	P16070 CD44_HUMAN	(Human) CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I) (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (Heparan sulfate proteoglycan) (Epican) (CDw44) - Homo sapiens
193	4.0	13.4	P16152 CBR1_HUMAN	(Human) Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) (Prostaglandin-E(2) 9-reductase) (EC 1.1.1.189) (Prostaglandin 9-ketoreductase) (15-hydroxyprostaglandin dehydrogenase [NADP+]) (EC 1.1.1.197) - Homo sapiens (Human)
329	3.7	13.4	P16152 CBR1_HUMAN	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) (Prostaglandin-E(2) 9-reductase) (EC 1.1.1.189) (Prostaglandin 9-ketoreductase) (15-hydroxyprostaglandin dehydrogenase [NADP+]) (EC 1.1.1.197) - Homo sapiens (Human)
246 235	2.3 6.0	22.6 23.5	P16401 H15_HUMAN	Histone H1.5 (Histone H1a) - Homo sapiens (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)
451 102	7.7	23.5 23.5	P16402 H13_HUMAN P16403 H12_HUMAN	Histone H1.3 (Histone H1c) - Homo sapiens (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) Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia-associated phosphoprotein p18) (pp17) (Prosolin) (Metablastin)
297	2.0	21.5	P16949 STMN1_HUMAN	(Protein Pr22) - Homo sapiens (Human)
149	2.0	12.8	P16949 STMN1_HUMAN	Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia-associated phosphoprotein p18) (pp17) (Prosolin) (Metablastin) (Protein Pr22) - Homo sapiens (Human)
243	4.9	27.5	P16949 STMN1_HUMAN	Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia-associated phosphoprotein p18) (pp17) (Prosolin) (Metablastin) (Protein Pr22) - Homo saplens (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 saplens (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 saplens (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 saplens (Human)
107 160	3.2 12.3	36.7 40.6	P18465 1B57_HUMAN P18465 1B57_HUMAN	HLA class I histocompatibility antigen, B-57 alpha chain precursor (MHC class I antigen B*57) (Bw-57) - Homo sapiens (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
36	8.6	38.6	P18669IPGAM1 HUMAN	1) - Homo sapiens (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
40	20.6	61.0	P18669 PGAM1_HUMAN	1) - Homo sapiens (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
128	6.0	33.9	P19105 MLRM_HUMAN	1) - Homo saplens (Human) Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC) - Homo saplens (Human)
146	2.1	17.5	P19105 MLRM_HUMAN	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC) - Homo sapiens (Human)
151	23.9	29.2	P19105 MLRM_HUMAN P19823 ITIH2_HUMAN	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC) - Homo sapiens (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) Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin
31	10.0	12.4	P19823 ITIH2_HUMAN	Inhibitor complex component II) (Serum-derived hyaluronan-associated protein) (SHAP) - Homo sapiens (Human) Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin
55	16.9	13.4	P19823 ITIH2_HUMAN	inhibitor complex component II) (Serum-derlved hyaluronan-associated protein) (SHAP) - Homo saplens (Human) Thymidine phosphorylase precursor (EC 2.4.2.4) (TdRPase) (TP) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (Gliostatin) -
107	7.5	23.0	P19971 TYPH_HUMAN	Thymidine phosphorylase precursor (EC 2.4.2.4) (TdRPase) (TP) (Platelet-derived endothelial cell growth factor) (PD-ECGF) (Gliostatin) -
416	2.1	8.9	P19971 TYPH_HUMAN	Homo sapiens (Human)
100 97	7.8 11.5	27.6 26.1	P20700 LMNB1_HUMAN P20700 LMNB1_HUMAN	Lamin-B1 - Homo sapiens (Human) Lamin-B1 - Homo sapiens (Human)
214 358	5.2 7.7	7.8 8.4	P20742 PZP_HUMAN P20742 PZP_HUMAN	Pregnancy zone protein precursor - Homo sapiens (Human) Pregnancy zone protein precursor - Homo sapiens (Human)
360	2.0	7.8	P21291 CSRP1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP1) (CRP) - Homo sapiens (Human)
527 36	2.0	7.8	P21291 CSRP1_HUMAN P21333 FLNA_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP1) (CRP) - Homo sapiens (Human) Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin) - Homo
				sapiens (Human) Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin) - Homo
29	10.2	7.9	P21333 FLNA_HUMAN	sapiens (Human) Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin) - Homo
24	27.7	9.4	P21333 FLNA_HUMAN P22314 UBE1_HUMAN	sapiens (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 saplens (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 SFPQ_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 SFPQ_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 saplens (Human)
52	17.2	23.6	P23246 SFPQ_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	(early controlling percent company) (early controlling percent) (incompany) (early controlling percent) (early control
142	2.1	6.7	P23284 PPIB_HUMAN	Septiest (numari) Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophillin B) (S-cyclophillin) (SCYLP) (CYP-S1) - Homo sapiens (Human)
38	18.5	32.7	P23381 SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.2) (TryptophantRNA ligase) (TrpRS) (IFP53) (hWRS) - Homo sapiens (Human)
110 43	3.1 19.9	24.8 32.9	P23381 SYWC_HUMAN P23381 SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.2) (TryptophantRNA ligase) (TrpRS) (IFPS3) (hWRS) - Homo saplens (Human) Tryptophanyl-tRNA synthetase, cytoplasmic (EC 6.1.1.2) (TryptophantRNA ligase) (TrpRS) (IFPS3) (hWRS) - Homo saplens (Human)
54	13.7	60.2	P23528 COF1_HUMAN	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) - Homo sapiens (Human)
42 37	7.2 22.3	29.5 51.8	P23528 COF1_HUMAN P23528 COF1_HUMAN	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) - Homo sapiens (Human) Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) - Homo sapiens (Human)
58 39	13.0 8.0	23.3 30.2	P25774 CATS_HUMAN P25774 CATS_HUMAN	Cathepsin S precursor (EC 3.4.22.27) - Homo sapiens (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 saplens (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 saplens (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 saplens (Human)
187	2.0	6.0	P25787 PSA2_HUMAN	Proteasome subunit alpha type 2 (EC 34.25.1) (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3) - Homo sapiens (Human)
435	2.0	18.4	P25787 PSA2_HUMAN	Subunit C3) - Homo sapiens (Human) 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
147	2.0	12.6	P25789 PSA4_HUMAN	subunit C9) (Proteasome subunit L) - Homo sapiens (Human) Proteasome subunit alpha type 4 (EC 3.4.25.1) (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex
524	2.0	3.8	P25789 PSA4_HUMAN	subunit C9) (Proteasome subunit L) - Homo sapiens (Human) Proteasome subunit alpha type 4 (EC 3.4.25.1) (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex
7	44.9	56.7	P26038 MOES_HUMAN	subunit C9) (Proteasome subunit L) - Homo saplens (Human) Moesin (Membrane-organizing extension spike protein) - Homo saplens (Human)
11 5	20.7 53.4	37.1 55.3	P26038 MOES_HUMAN P26038 MOES_HUMAN	Moesin (Membrane-organizing extension spike protein) - Homo sapiens (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 saplens (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
264	8.2	39.7	P26583 HMGB2_HUMAN	sapiens (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) DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP endonuclease 1) (APEX nuclease) (APEN) (Protein REF-1) - Homo sapiens
159	2.0	28.9	P27695 APEX1_HUMAN	(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 86	6.0	13.9 25.4	P27797 CALR_HUMAN P27797 CALR_HUMAN	Caireticulin precursor (CRP55) (Cairegulin) (HACBP) (ERp60) (grp60) - Homo sapiens (Human) Caireticulin precursor (CRP55) (Cairegulin) (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
149	8.0	21.7	P28062 PSB8_HUMAN	endopeptidase complex subunit C13) - Homo sapiens (Human) Proteasome subunit beta type 8 precursor (EC 3.4.25.1) (Proteasome component C13) (Macropain subunit C13) (Multicatalytic
				endopeptidase complex subunit C13) - Homo saplens (Human) Proteasome subunit alpha type 5 (EC 3.4.25.1) (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta
190	4.0	14.1	P28066 PSA5_HUMAN	chain) - Homo saplens (Human) Proteasome subunit alpha type 5 (EC 3.4.25.1) (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta
169	6.7	26.6	P28066 PSA5_HUMAN	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 saplens (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	Granulins precursor (Proepithelin) (PEPI) [Contains: Acrogranin; Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3
229	2.8	13.2	P28799 GRN_HUMAN	(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	Granulins precursor (Proepithelin) (PEPI) [Contains: Acrogranin; Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3 (Granulin F); Granulin F); Granuli
				(Granulin B); Granulin-4 (Granulin A); Granulin-5 (Granulin-6 (Granulin D); Granulin-7 (Granulin-7); Homo sapiens (Human) Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Leucine aminopeptidase 3) (Proline
32	20.0	37.2	P28838 AMPL_HUMAN	aminopeptidase) (EC 3.4.11.5) (Proly) aminopeptidase) (Peptidase S) - Homo sapiens (Human) Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Leucine aminopeptidase 3) (Proline
84	4.1	22.2	P28838 AMPL_HUMAN	Cytosol aminopeptidase (EC 3.4.11.1) (Ecouine aminopeptidase) (Ler) (Ecouy) aminopeptidase (EC 3.4.11.1) (Evolua minopeptidase) (Peptidase S) (Proline aminopeptidase) (EC 3.4.11.1) (Leucine aminopeptidase) (Leucine aminop
44	19.5	30.1	P28838 AMPL_HUMAN	aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase) (Peptidase S) - Homo saplens (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) (Hematopoletic cell protein-tyrosine phosphatase) (SH-PTP1) (Protein-tyrosine phosphatase SHP-1) - Homo saplens (Human)
128	9.2	25.0	P29350 PTN6_HUMAN	Tyrosine-protein phosphatase non-receptor type 6 (EC 3.1.3.49) (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 saplens (Human)
62 53	5.6 17.1	23.4 30.0	P29401 TKT_HUMAN P29401 TKT_HUMAN	Transketolase (EC 2.2.1.1) (TK) - Homo sapiens (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) Peroxiredoxin-6 (EC 1.11.1.15) (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2)
561	1.7	12.9	P30041 PRDX6_HUMAN	(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
365	2.0	9.3	P30046 DOPD_HUMAN	cells page spot 12) - Homo saplens (Human) D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II) - Homo saplens (Human)
542 331	2.0	9.3 17.0	P30046 DOPD_HUMAN P30050 RL12_HUMAN	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase) (Phenylpyruvate tautomerase II) - Homo sapiens (Human) 60S ribosomal protein L12 - Homo sapiens (Human)
411	2.2	19.4	P30050 RL12_HUMAN	60S ribosomal protein L12 - Homo sapiens (Human)
184	4.0	31.0	P30086 PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (HCNPpp) (Neuropolypeptide h3) (Raf kinase inhibitor protein) (RKIP) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNP)] - Homo sapiens (Human)
102	10.6	55.1	P30086 PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (Prostatic-binding protein) (HCNPpp) (Neuropolypeptide h3) (Raf kinase inhibitor protein) (RKIP) [Contains: Hippocampal cholinergic neurostimulating peptide (HCNP)] - Homo sapiens (Human)
97	8.0	16.4	P30101 PDIA3_HUMAN	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57) (58
61	5.8	17.8	P30101 PDIA3_HUMAN	kDa glucose-regulated protein) - Homo sapiens (Human) Protein disulfide-Isomerase A3 precursor (EC 5.3.4.1) (Disulfide Isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57) (58
63	15.7	23.6	P30101 PDIA3_HUMAN	kDa glucose-regulated protein) - Homo sapiens (Human) Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60) (ERp60) (58 kDa microsomal protein) (p58) (ERp57) (58
270	7.4	30.9	P30508 1C12_HUMAN	kDa glucose-regulated protein) - Homo sapiens (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)
272 155	2.1 7.7	11.3 14.0	P30740 ILEU_HUMAN P30740 ILEU_HUMAN	Leukocyte elastase inhibitor (LEI) (Serpin B1) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI) - Homo sapiens (Human) Leukocyte elastase inhibitor (LEI) (Serpin 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) (Clipin-A) (Tryptophan aspartate-containing coat protein) (TACO) - Homo saplens (Human)
20	13.9	28.2	P31146 COR1A_HUMAN	Coronin-1A (Coronin-like protein p57) (Coronin-like protein A) (Clipin-A) (Tryptophan aspartate-containing coat protein) (TACO) - Homo
26	25.9	41.2	P31146 COR1A_HUMAN	sapiens (Human) Coronin-1A (Coronin-like protein p57) (Coronin-like protein A) (Clipin-A) (Tryptophan aspartate-containing coat protein) (TACO) - Homo
		12.2	P31146 CORTA_HUMAN	sapiens (Human) S-adenosylmethionine synthetase isoform type-2 (EC 2.5.1.6) (Methionine adenosyltransferase 2) (AdoMet synthetase 2) (Methionine
177	4.0			adenosyltransferase II) (MAT-II) - Homo sapiens (Human) S-adenosyltransferase 2) (AdoMet synthetase isoform type-2 (EC 2.5.1.6) (Methionine adenosyltransferase 2) (AdoMet synthetase 2) (Methionine
239	5.0	18.7	P31153 METK2_HUMAN	adenosyltransferase II) (MAT-II) - Homo saplens (Human)
310 189	2.4	37.1 10.5	P31949 S10AB_HUMAN P31949 S10AB_HUMAN	Protein S100-A11 (S100 calcium-binding protein A11) (Protein S100C) (Calgizzarin) (MLN 70) - Homo sapiens (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 saplens (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 saplens (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	Interferor-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) -
84	12.3	35.7	P33241 LSP1_HUMAN	Homo sapiens (Human) Lymphocyte-specific protein 1 (Protein pp52) (52 kDa phosphoprotein) (Lymphocyte-specific antigen WP34) (47 kDa actin-binding protein) -
35	18.9	31.7	P35579 MYH9_HUMAN	Homo sapiens (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) Myosin-9 (Myosin heavy chain 9) (Myosin heavy chain, nonmuscle IIa) (Nonmuscle myosin heavy chain IIa) (NMMHC-II-a) (NMMHC-III-a)
17	36.9	25.6	P35579 MYH9_HUMAN	(Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A) - Homo sapiens (Human) Chitinase-3-like protein 1 precursor (Cartilage glycoprotein 39) (GP-39) (39 kDa synovial protein) (HCgp-39) (YKL-40) - Homo sapiens
104	7.7	18.3	P36222 CH3L1_HUMAN	(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 97	5.4 3.8	51.8 32.7	P37802 TAGL2_HUMAN P37802 TAGL2_HUMAN	Transgelin-2 (SM22-alpha homolog) - Homo sapiens (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)
220 209	3.1 1.4	18.4 6.8	P37837 TALDO_HUMAN P37837 TALDO_HUMAN	Transaldolase (EC 2.2.1.2) - Homo sapiens (Human) Transaldolase (EC 2.2.1.2) - Homo sapiens (Human)
209	1.4 5.9	11.9	P37837 TALDO_HUMAN 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
1				(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) Eukaryotic initiation factor 4A-III (EC 3.6.1) (Eukaryotic translation initiation factor 4A isoform 3) (ATP-dependent RNA helicase eIF4A-3)
428	2.0	3.9	P38919 IF4A3_HUMAN	(ATP-dependent RNA helicase DDX48) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Nuclear matrix protein 265)
72	10.1	30.2	P40121 CAPG_HUMAN	(hNMP 265) - Homo sapiens (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 63	6.4 12.0	19.3 26.3	P40121 CAPG_HUMAN P40925 MDHC_HUMAN	Macrophage-capping protein (Actin-regulatory protein CAP-G) - Homo sapiens (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 71	2.1 14.1	17.2 42.6	P40926 MDHM_HUMAN P40926 MDHM_HUMAN	Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Homo sapiens (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 58	4.1 16.7	11.2 19.1	P42224 STAT1_HUMAN P42224 STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84) - Homo saplens (Human) Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84) - Homo saplens (Human)
55	13.4	20.2	P43490 NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase (EC 2.4.2.12) (NAmPRTase) (Nampt) (Pre-B cell-enhancing factor) (Pre-B-cell colony-enhancing
			P43490 NAMPT_HUMAN	factor 1) (Visfatin) - Homo sapiens (Human) Nicotinamide phosphoribosyltransferase (EC 2.4.2.12) (NAmPRTase) (Nampt) (Pre-B cell-enhancing factor) (Pre-B-cell colony-enhancing
341 244	2.3	6.3 24.9	P46777 RL5_HUMAN	factor 1) (Visfatin) - Homo sapiens (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)
162	5.8 4.4	28.4 11.2	P46781 RS9_HUMAN P46940 QGA1_HUMAN	40S ribosomal protein S9 - Homo sapiens (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)
329 473	2.0	10.3 14.4	P48739 PIPNB_HUMAN P48739 PIPNB_HUMAN	Phosphatidylinositol transfer protein beta isoform (PtdIns transfer protein beta) (PtdInsTP) (PI-TP-beta) - Homo sapiens (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 91	12.2 8.1	23.9	P49368 TCPG_HUMAN	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRiC5) - Homo sapiens (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 GDIB_HUMAN P50395 GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2) - Homo sapiens (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 GDIB_HUMAN	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2) - Homo saplens (Human)
379 209	1.7 6.0	12.2 14.9	P50453 SPB9_HUMAN P50453 SPB9_HUMAN	Serpin B9 (Cytoplasmic antiproteinase 3) (CAP-3) (CAP3) (Protease inhibitor 9) - Homo saplens (Human) Serpin B9 (Cytoplasmic antiproteinase 3) (CAP-3) (CAP3) (Protease Inhibitor 9) - Homo saplens (Human)
138	5.8	21.1	P50552 VASP_HUMAN	Vasodilator-stimulated phosphoprotein (VASP) - Homo sapiens (Human)
83 113	12.7 2.9	31.8 7.3	P50552 VASP_HUMAN P50990 TCPQ_HUMAN	Vasodilator-stimulated phosphoprotein (VASP) - Homo sapiens (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 TCPQ_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)
362 208	3.0	29.6	P51149 RAB7A_HUMAN P51991 ROA3_HUMAN	Ras-related protein Rab-7a - Homo saplens (Human) Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3) - Homo saplens (Human)
162	7.4	39.7	P51991 ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3) - Homo sapiens (Human)
50 121	15.5 2.4	26.3 10.8	P52209 6PGD_HUMAN P52209 6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) - Homo saplens (Human) 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) - Homo saplens (Human)
414	2.2	13.5	P52209 6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) - Homo sapiens (Human)
86 82	8.8 4.1	51.0 26.0	P52565 GDIR_HUMAN P52565 GDIR_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) - Homo sapiens (Human) Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) - Homo sapiens (Human)
28	24.6	49.0	P52565 GDIR_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) - Homo sapiens (Human)
269	2.1	49.3 49.8	P52566 GDIS_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI) - Homo sapiens (Human)
101	12.0		P52566 GDIS_HUMAN	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI) - Homo sapiens (Human)
230	2.7	12.3	P5259/ HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (nnknp F) (Nucleolin-like protein mcsy4-1) - Homo sapiens (Human)
230 334	2.7 6.0	12.3 20.7	P52597 HNRPF_HUMAN P52597 HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo sapiens (Human)
334 282	6.0 2.1	20.7 15.4	P52597 HNRPF_HUMAN P52907 CAZA1_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-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)
334 282 166 233	6.0 2.1 2.0 5.3	20.7 15.4 19.2 19.9	P52597 HNRPF_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase)
334 282 166	2.1 2.0	20.7 15.4 19.2	P52597 HNRPF_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human)
334 282 166 233	6.0 2.1 2.0 5.3	20.7 15.4 19.2 19.9	P52597 HNRPF_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipoptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipoptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin D) (Dipoptidyl-peptidase 1 exclusion domain chain): Dipoptidyl-peptidase 1 heavy chain (Dipoptidyl-peptidase 1 light chain) - Homo saplens (Human)
334 282 166 233	6.0 2.1 2.0 5.3	20.7 15.4 19.2 19.9	P52597 HNRPF_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP1) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 light chain) 1 - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-pe
334 282 166 233 311	6.0 2.1 2.0 5.3 2.0	20.7 15.4 19.2 19.9 3.7	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I exclusion domain chain): Dipeptidyl-peptidase I exclusion domain chain (Dipeptidyl-peptidase I exclusion domain chain): Dipeptidyl-peptidase I heavy chain (Dipeptidyl-peptidase I light chain)] - Homo saplens (Human) Dipeptidyl-peptidase I rocursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I rocursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I rocursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I rocursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I rocursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I rocursor (EC 3.4.14.1) (Dipeptidyl-peptidase I rocursor (EC 3.4.14.1) (Dipeptidyl-peptidase I rocursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I rocursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPPI) (DPP
334 282 166 233 311	2.0 5.3	20.7 15.4 19.2 19.9	P52597 HNRPF_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN P53634 CATC_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP1) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 light chain) 1 - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-pe
334 282 166 233 311 101 126 118 189	2.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EG 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 laght chain): Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 laght chain) [Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EG 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin D) (Dipeptidyl-peptidase I) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin D) (Dipeptidyl-peptidase I)
334 282 166 233 311 101 126 118	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5	P52597 HNRPF_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN P52907 CAZA1_HUMAN P53634 CATC_HUMAN P53634 CATC_HUMAN P53634 CATC_HUMAN P54819 KAD2_HUMAN P54819 KAD2_HUMAN P54819 KAD2_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 recursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase I exclusion domain chain): Dipeptidyl-peptidase I heavy chain (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I heavy chain) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (DPPI) (Cathepsin C) (Cathepsin J) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (DPPI) (Cathepsin C) (Cathepsin J) (DPPI) (Cathepsin C) (
334 282 166 233 311 101 126 118 189	2.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase resclusion domain chain): Dipeptidyl-peptidase resclusion domain chain): Dipeptidyl-peptidase I heavy chain (Dipeptidyl-peptidase I heavy chain): Dipeptidyl-peptidase I light chain (Dipeptidyl-peptidase I light chain)] - Homo saplens (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 I) (DPP-I) (DPPI) (
334 282 166 233 311 101 126 118 189 61 45	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3	P525971 HNRPF _ HUMAN P52907 [CAZA1_HUMAN P52907] CAZA1_HUMAN P52907 [CAZA1_HUMAN P53634] CATC_HUMAN P53634 [CATC_HUMAN P53634] CATC_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P55072] TERA_HUMAN P55072 [TERA_HUMAN P55072] TERA_HUMAN P55072 [TERA_HUMAN P55079] NP1L1_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase I light chain)] - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (Deptidyl-peptidase I) (DPP-I) (DPPI)
334 282 166 233 311 101 126 118 189 61	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 leave) chain (Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 leave) Contains: Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 caccusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase 1 leave) chain (Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase 1 leave) chain (Dipeptidyl-peptidase 1 heavy chain): Dipeptidyl-peptidase 1 leave) chain (Dipeptidyl-peptidase 1 heavy chain): Dipeptidyl-peptidase 1 leave) Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo saplens (Human) Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo saplens (Human) Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP) - Homo saplens (Human)
334 282 166 233 311 101 126 118 189 61 45 187 98 198	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7	P525971 HNRPF_HUMAN P52907 [CAZA1_HUMAN P52907] CAZA1_HUMAN P52907 [CAZA1_HUMAN P52907] CAZA1_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P55072 [TERA_HUMAN P55072 [TERA_HUMAN P5509 [NP1L1_HUMAN P55209 [NP1L1_HUMAN P5520 [NP1L1_HUMAN P552	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase I light chain): Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I heavy chain): Dipeptidyl-peptidase I light chain): Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (D
334 282 166 233 311 101 126 118 189 61 45 187 98	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P552091NP1L1_HUMAN P552091NP1L1_HUMAN P552091NP1L1_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (D
334 282 166 233 311 101 126 118 189 61 45 187 98 198 198 198 198 197 327	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8	P525971 HNRPF_HUMAN P52907 [CAZA1_HUMAN P52907] CAZA1_HUMAN P52907 [CAZA1_HUMAN P52907] CAZA1_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P5502] [TERA_HUMAN P5502] [TERA_HUMAN P55209 [NP1L1_HUMAN P55209 [NP1L1_HUMAN P55206] [P5A_HUMAN P55786] [P5A_HUMAN P5786] [P5A_HUMAN P55786] [P5A_HUMAN P55786] [P5A_HUMAN]	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 heavy chain) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 heavy chain) (Dipeptidyl-peptidase 1 heavy chain): Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (
334 282 166 233 311 101 126 118 189 61 45 187 98 198 181 152 407	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.0	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P55091NP111_HUMAN P55091NP111_HUMAN P557861PSA_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 leave) chain (Dipeptidyl-peptidase 1 leave) chain (Dipeptidyl-peptidase 1 leave) chain (Dipeptidyl-peptidase 1 light chain)] - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 leave) chain (Dipeptidyl-peptidase 1 light chain)] - Homo saplens (Human) Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo saplens (Human) Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo saplens (Human) Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo saplens (Human) Transitional endoplasmic reticulum ATPase (TER ATPase) (TSS Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP) - Homo saplens (Human) Transitional endoplasmic reticulum ATPase (TER ATPase) (TSS Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP) - Homo saplens (Human) Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (NNRP) - Homo saplens (Human) Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (NNRP) -
334 282 166 233 311 101 126 118 189 61 45 187 98 181 152 407 327 123 129 40	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.0 2.3 6.0 18.1	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0	P525971 HNRPF_HUMAN P52907 [CAZA1_HUMAN P52907] CAZA1_HUMAN P52907 [CAZA1_HUMAN P52907] CAZA1_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P55072 [TERA_HUMAN P55072 [TERA_HUMAN P5509 [NP1L1_HUMAN P5509 [NP1L1_HUMAN P55786 [PSA_HUMAN P55786 [PSA_HUMAN P55786 [PSA_HUMAN P55998] [ARPC4_HUMAN P59998] [ARPC4_HUMAN P5998] [ARPC4_HUMAN P59998] [ARPC4_HUMAN]	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP1) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 light chain) I - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 heavy chain (Dipeptidyl-peptidase 1 light chain) (Dipeptidyl-peptidase 1 light chain)] - Homo saplens (Human) Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo saplens (Human) Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo saplens (Human) Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase) - Homo saplens (Human) Transitional endoplasmic reticulum ATPase (TER ATPase) (TSS Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP) - Homo saplens (Human) Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (NNRP) - Homo saplens (Human) Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (NNRP) - Homo
334 282 166 233 311 101 126 118 189 61 45 187 198 181 198 181 297 407 327 123 197 40 13	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.3 2.0 2.3 6.0 18.1 18.3	20 7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7	P525971 HNRPF _ HUMAN P529071 (CAZA1 _ HUMAN P529071 (CAZA1 _ HUMAN P529071 (CAZA1 _ HUMAN P529071 (CAZA1 _ HUMAN P536341 (CATC _ HUMAN P536341 (CATC _ HUMAN P536341 (CATC _ HUMAN P548191 (KAD2 _ HUMAN P548191 (KAD2 _ HUMAN P548191 (KAD2 _ HUMAN P55072 TERA _ HUMAN P55072 TERA _ HUMAN P55072 TERA _ HUMAN P55081 P54 _ HUMAN P557861 P5A _ HUMAN P557861 P5A _ HUMAN P557861 P5A _ HUMAN P59981 ARPC4 _ HUMAN P599981 ARPC4 _ HUMAN P599981 ARPC4 _ HUMAN P599981 ARPC4 _ HUMAN P599981 ARPC4 _ HUMAN P60714 TIPIS _ HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (D
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334 282 166 233 311 101 126 118 189 61 45 187 98 181 192 407 327 407 327 407 327 407 327 407 327 407 327 407 327 407 407 407 407 407 407 407 407 407 40	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.3 2.0 18.1 18.3 28.0 6.1	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7 61.0	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P59981ARPC4_HUMAN P59981ARPC4_HUMAN P59981ARPC4_HUMAN P50781TES_HUMAN P607141TPIS_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 keukusin domain chain): Dipeptidyl-peptidase 1 keukusin domain chain): Dipeptidyl-peptidase I light chain) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I)
334 282 166 233 311 101 126 118 189 61 45 187 98 181 152 407 327 407 327 407 327 407 327 407 327 407 327 407 407 407 407 407 407 407 407 407 40	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.3 2.0 2.3 6.0 18.1 18.3 28.0 6.1	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7 61.0 50.3 31.1	P525971 HNRPF _ HUMAN P529071 (CAZA1_HUMAN P529071 (CAZA1_HUMAN P529071 (CAZA1_HUMAN P529071 (CAZA1_HUMAN P536341 (CATC_HUMAN P536341 (CATC_HUMAN P536341 (CATC_HUMAN P536341 (CATC_HUMAN P548191 (KAD2_HUMAN P548191 (KAD2_HUMAN P55072 TERA_HUMAN P55072 TERA_HUMAN P55072 TERA_HUMAN P557861 PSA_HUMAN P557861 PSA_HUMAN P557861 PSA_HUMAN P557861 PSA_HUMAN P557861 PSA_HUMAN P557861 PSA_HUMAN P59981 ARPC4_HUMAN P599981 ARPC4_HUMAN P599981 ARPC4_HUMAN P601741 TPIS_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EG 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 procursor (EG 3.4.14.1) (Dipeptidyl-peptidase I) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (DPPI)
334 282 166 233 311 101 126 118 189 61 45 187 98 181 152 407 327 407 327 407 327 407 327 407 327 407 407 407 407 407 407 407 407 407 40	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.0 2.3 2.0 18.1 18.3 28.0 6.1 5.2	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7 61.0	P525971 HNRPF _ HUMAN P529071 (CAZA1 _ HUMAN P536341 (CATC _ HUMAN P536341 (CATC _ HUMAN P536341 (CATC _ HUMAN P548191 (KAD2 _ HUMAN P548191 (KAD2 _ HUMAN P548191 (KAD2 _ HUMAN P55072 TERA _ HUMAN P55072 TERA _ HUMAN P55072 TERA _ HUMAN P557861 PSA _ HUMAN P557861 PSA _ HUMAN P557861 PSA _ HUMAN P557861 PSA _ HUMAN P59981 ARPC4 _ HUMAN P599981 ARPC4 _ HUMAN P60174 TPIS _ HUMAN P60660 MYL6 _ HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (D
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334 282 166 233 311 101 126 118 189 61 45 187 98 181 152 407 327 407 327 407 327 407 327 407 327 407 407 407 407 407 407 407 407 407 40	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.0 2.3 2.0 18.1 18.3 28.0 6.1 5.2	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7 61.0	P525971 HNRPF _ HUMAN P529071 (CAZA1 _ HUMAN P536341 (CATC _ HUMAN P536341 (CATC _ HUMAN P536341 (CATC _ HUMAN P548191 (KAD2 _ HUMAN P548191 (KAD2 _ HUMAN P548191 (KAD2 _ HUMAN P55072 TERA _ HUMAN P55072 TERA _ HUMAN P55072 TERA _ HUMAN P557861 PSA _ HUMAN P557861 PSA _ HUMAN P557861 PSA _ HUMAN P557861 PSA _ HUMAN P59981 ARPC4 _ HUMAN P599981 ARPC4 _ HUMAN P60174 TPIS _ HUMAN P60660 MYL6 _ HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (D
334 282 166 233 311 101 126 118 189 61 45 187 98 198 181 152 407 123 197 40 13 27 123 127 123 125 125 126 127 127 128 129 129 129 129 129 129 129 129	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 2.0 2.3 2.0 2.3 2.0 6.1 18.3 28.0 6.1 5.2 10.0 31.5 54.1 2.0 2.0	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 66.7 61.0 50.3 31.1 50.3 66.4 69.9 5.2	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P597861PSA_HUMAN P597861PSA_HUMAN P597861PSA_HUMAN P597861PSA_HUMAN P597861PSA_HUMAN P597861PSA_HUMAN P597861PSA_HUMAN P597861PSA_HUMAN P597861PSA_HUMAN P607861PSA_HUMAN P607861PSA_HUMAN P607861PSA_HUMAN P607861PSA_HUMAN P607861PSA_HUMAN P607861PSA_HUMAN P607861PSA_HUMAN P607861PSA_HUMAN P607861PSA_HUMAN P607891ATB_HUMAN P5151531RAC2_HUMAN	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase 1 individual protein (Dipeptidyl-peptidase 1 leavy chain): Dipeptidyl-peptidase 1 leavy chain (Dipeptidyl-peptidase 1 light chain) 1 - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 exclusion domain chain (Dipeptidyl-peptidase 1 leavy chain) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 leavy chain (Dipeptidyl-peptidase 1 leavy chain) (Dipeptidyl-peptidase 1 leavy chain (Dipeptidyl-peptidase 1 leavy chain) (Dipeptidyl-peptidase 1 leavy chain (Dipeptidyl-peptidase 1 leavy chain) (Dipeptidyl-peptidase 1 leavy chain) (Dipeptidyl-peptidase 1 leavy chain) (Dipeptidyl-peptidase (Dipeptidyl-peptidase (Dipeptidyl-peptidase (Dipeptidyl-pe
334 282 166 233 311 101 126 118 189 61 45 187 98 181 152 407 327 40 123 197 40 13 23 122 65 112 5 449 356	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.0 2.3 2.0 2.3 2.0 18.1 18.3 28.0 6.1 5.2	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7 61.0 50.3 31.1 50.3 66.4 69.9 5.2	P525971 HNRPF_HUMAN P52907 [CAZA1_HUMAN P52907] CAZA1_HUMAN P52907 [CAZA1_HUMAN P52907] CAZA1_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P53634 [CATC_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P54819 [KAD2_HUMAN P55072 [TERA_HUMAN P55072 [TERA_HUMAN P55706 [PSA_HUMAN P55706 [PSA_HUMAN P55706 [PSA_HUMAN P55706 [PSA_HUMAN P59908] ARPC4_HUMAN P59908 [ARPC4_HUMAN P59908] ARPC4_HUMAN P60174 [TPIS_HUMAN P60176 [TRIS_HUMAN P60176 [T	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 procursor (EC 3.4.14.1) (Dipeptidyl-peptidase I) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I) (Dipept
334 282 166 233 311 101 126 118 189 61 45 187 98 198 181 152 407 327 123 197 40 13 23 122 65 112 5 449 356 304 231 449 356 304 231 449 356 304 231 316 317 317 318 318 318 318 318 318 318 318	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 2.0 2.3 2.0 6.0 18.1 18.3 28.0 6.1 15.2 10.0 31.5 54.1 2.0 2.7 2.1	20 7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 66.7 67.6 61.0 50.3 31.1 50.3 66.4 69.9 5.2 9.4 12.3 10.8	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P597861PSA_HUMAN P59781ARCA_HUMAN P607961ATTB_HUMAN P606601MYL6_HUMAN P606601MYL6_HUMAN P606601MYL6_HUMAN P606601MYL6_HUMAN P606601MYL6_HUMAN P60791ACTB_HUMAN P60791ACTB_HUMAN P60791ACTB_HUMAN P608661RSC2_HUMAN P608421F4A1_HUMAN P608661RSC2_HUMAN	F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo saplens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase) (DPP-1) (DPP-1) (DPP) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase) (Contains: Dipeptidyl-peptidase 1 exclusion domain chain): Dipeptidyl-peptidase 1 (Dipeptidyl-peptidase) (Dipeptidyl-pepti
334 282 166 233 311 101 126 118 189 61 45 187 98 198 181 152 407 327 40 13 23 122 65 112 5 449 356 364 231 428 439 449 356 354	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.3 2.0 2.3 2.0 6.0 18.1 18.3 28.0 6.1 15.2 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7 61.0 50.3 31.1 50.3 66.4 66.9 5.2 9.4 12.3 10.8 29.4	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P507031ATPIS_HUMAN P507031ATPIS_HUMAN P607071TPIS_HUMAN P607071ATPIS_HUMAN P607071ATTPIS_HUMAN P6070	F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1 (DPP-1) (DPP-1) (DPP-1) (DPP-1) (Dethepsin D) (Dipeptidyl-peptidase 1 oxclusion domain chain (Dipeptidyl-peptidase 1 (Dipeptidy
334 282 166 233 311 101 126 118 189 61 45 187 98 198 181 152 407 327 123 197 40 13 23 122 65 112 5 449 356 354 94	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.3 2.0 2.3 2.0 6.1 18.3 28.0 6.1 5.2 10.0 31.5 54.1 2.0 2.7 2.1 4.4 3.2 8.1	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 66.7 61.0 50.3 31.1 50.3 36.4 69.9 5.2 9.4 24.8	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P597861RAFC4_HUMAN P597861RAFC4_HUMAN P597861RAFC4_HUMAN P597861RAFC4_HUMAN P607741TPIS_HUMAN P607741TPIS_HUMAN P607741TPIS_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P6061P14TPIS_HUMAN P608121F4A1_HUMAN P609101PSA6_HUMAN	Heterogeneous nuclear ribonucleoprotein E (nnRNP E) (Nucleolin-like protein mes94-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) Dispetityl-peptidase 1 procursor (EG. 3.4.14.1) (Dispetityl-peptidase 1) (DPP-I) (DPPI) (Cathepsin C) (Cathepsin J) (Dispetityl-peptidase 1 exclusion domain chain): Dispetityl-peptidase 1 heavy chain): Dispetityl-peptidase 1 heavy chain; Dispetityl-peptidase 1 heavy chain; Dispetityl-peptidase 1 heavy chain; Dispetityl-peptidase 1 procursor (EG. 3.4.14.1) (Dispetityl-peptidase 1) (DPP-I) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dispetityl-peptidase 1 heavy chain): Dispetityl-peptidase 1 procursor (EG. 3.4.14.1) (Dispetityl-peptidase 1) (DPP-I) (DPPI) (DPPI) (DPPI) (Cathepsin C) (Cathepsin J) (Dispetityl-peptidase 1 heavy chain): Dispetityl-peptidase 1 he
334 282 166 233 311 101 126 118 189 61 45 187 98 198 181 152 407 327 40 13 23 122 65 112 5 449 356 364 231 428 439 449 356 354	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.3 2.0 2.3 2.0 6.0 18.1 18.3 28.0 6.1 15.2 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7 61.0 50.3 31.1 50.3 66.4 66.9 5.2 9.4 12.3 10.8 29.4	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P507031ATPIS_HUMAN P507031ATPIS_HUMAN P607071TPIS_HUMAN P607071ATPIS_HUMAN P607071ATTPIS_HUMAN P6070	Helterogeneous nuclear ribonucleoprotein E (nnRNP E) (Nucleolin-like protein mcs94-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) Dipeptidyl-peptidase 1 precursor (EG. 3.4.1.4.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1 heavy chain): Dipeptidyl-peptidase 1 heavy chain 1 heavy chain): Dipeptidyl-peptidase 1 heavy chain 1 heavy chain 1
334 282 166 233 311 101 126 118 189 61 45 187 98 198 181 152 407 327 123 197 40 13 23 122 65 112 5 449 356 354 94	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.3 2.0 2.3 2.0 6.1 18.3 28.0 6.1 5.2 10.0 31.5 54.1 2.0 2.7 2.1 4.4 3.2 8.1	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 66.7 61.0 50.3 31.1 50.3 36.4 69.9 5.2 9.4 24.8	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P597861RAFC4_HUMAN P597861RAFC4_HUMAN P597861RAFC4_HUMAN P597861RAFC4_HUMAN P607741TPIS_HUMAN P607741TPIS_HUMAN P607741TPIS_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P60601MYL6_HUMAN P6061P14TPIS_HUMAN P608121F4A1_HUMAN P609101PSA6_HUMAN	F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase 1) (DPP-1) (DPP) (DP
334 282 166 233 311 101 126 118 189 61 45 187 98 181 152 407 327 407 327 407 327 407 327 407 327 407 327 407 327 407 327 407 327 407 407 407 407 407 407 407 40	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.0 2.3 2.0 2.3 2.0 3.5 6.0 18.1 18.2 19.1 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7 61.0 50.3 31.1 50.3 66.4 69.9 5.2 9.4 12.3 10.8 21.8 22.8 24.8 8.5 40.2 18.5	P525971 HNRPF_HUMAN P529071 (CAZA1_HUMAN P529071 (CAZA1_HUMAN P529071 (CAZA1_HUMAN P529071 (CAZA1_HUMAN P529071 (CAZA1_HUMAN P536341 (CATC_HUMAN P536341 (CATC_HUMAN P536341 (CATC_HUMAN P536341 (CATC_HUMAN P548191 (KAD2_HUMAN P548191 (KAD2_HUMAN P548191 (KAD2_HUMAN P55072 (TERA_HUMAN P55072 (TERA_HUMAN P55072 (TERA_HUMAN P55072 (NP1L1_HUMAN P50072 (NP1L1_HUMAN P50072 (NP1L1_HUMAN P60072 (NP1L1_HUMAN P600	Heterogeneous nuclear ribonucleoprotein F (neRW P f) (Mucleolin-like protein mss94-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) Dipeptidyl-peptidase I precursor (EC 3.4.1.1.) (Dipeptidyl-peptidase I (DPP-1) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I precursor (EC 3.4.1.1.) (Dipeptidyl-peptidase I (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I neavy chain) (Dipeptidyl-peptidase I (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I precursor (EC 3.4.1.4.1) (Dipeptidyl-peptidase I (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I neavy chain) (Dipeptidyl-peptidase I (DPP-1) (DPP) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I neavy chain) (Dipetidyl-peptidase I neavy chain) (Dipetidyl-pept
334 282 166 233 311 101 126 118 189 61 45 187 87 198 181 152 407 327 123 197 40 13 23 122 65 112 5 449 356 428 1428 150 354 94 180 69	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 3.8 6.0 4.0 2.3 2.0 2.3 6.0 18.1 18.3 28.0 6.1 54.1 2.0 2.7 2.1 4.4 2.7 2.1 4.1 2.0 2.1 2.0 2.1 2.0 2.1 2.0 2.1 2.0 2.1 2.0 2.0 2.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	20.7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 23.8 29.8 57.0 66.7 61.0 50.3 31.1 50.3 31.1 50.3 31.1 50.3 31.1 50.3 31.1 50.3 31.1 50.3 31.1 50.3 31.1 50.3 31.1 50.3 50.4 50.4 50.4 50.4 50.4 50.4 50.4 50.4 50.4 50.4 50.4 50.4 60.9 50.4 50.4 60.9 50.4 60.9	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550201P111_HUMAN P50001P111_HUMAN P50001P111_HUMAN P50001P111_HUMAN P50001P111_HUMAN P60001P111_HUMAN P60001P111_HUMAN P6001P111S_HUMAN P601741TP1S_HUMAN P60601P116_HUMAN P60601P116_HUMAN P60601P116_HUMAN P60601P116_HUMAN P60601P16A1_HUMAN P60601P16A1_HUMAN P60801P168C2_HUMAN P60801P168C2_HUMAN P60801P36_HUMAN P609001P5A6_HUMAN P609001P5A6_HUMAN P609001P5A6_HUMAN	Heterogeneous nuclear ribonucleoprotein F. (hnRMP F.) (Nucleolin-like protein mss94-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) F-actin capping protein subunit alpha-1 (CapZ alpha-1) - Homo sapiens (Human) Dipeptidyl-peptidase I procurs (EC 3.4.1.1.1) (Dipeptidyl-peptidase I (CapZ alpha-1) - Homo sapiens (Human) Dipeptidyl-peptidase I procurs (EC 3.4.1.1.1) (Dipeptidyl-peptidase I (DPP-1) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I exclusion domain chain (Dipeptidyl-peptidase I exclusion domain chain): Dipeptidyl-peptidase I procursor (EC 3.4.1.4.1) (Dipeptidyl-peptidase I (DPP-1) (DPPI) (Cathepsin C) (Cathepsin J) (Dipeptidyl-peptidase I exclusion domain chain (Dipeptidyl-peptidase I exclusion domain chain). Dipeptidyl-peptidase I exclusion domain chain (Dipeptidyl-peptidase I exclusion domain chain
334 282 166 233 311 101 126 118 189 61 45 187 98 198 181 152 407 327 123 197 40 13 23 122 65 112 5 449 356 354 94 180 69 79 181 180 69 79 180 69 69 69 69 69 69 69 69 69 69	6.0 2.1 2.0 5.3 2.0 3.5 6.0 2.6 6.1 12.8 19.1 4.0 2.3 2.0 2.3 2.0 2.3 6.0 18.1 18.3 28.0 6.1 15.2 10.0 31.5 54.1 2.0 2.7 2.1 4.4 3.2 8.1 4.0 2.0 2.1 4.0 2.0 4.0 2.0 4.0 2.0 4.0 2.0 4.0 2.0 4.0 2.0 4.0 4.0 2.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4	20 7 15.4 19.2 19.9 3.7 11.9 28.9 30.5 34.7 18.7 25.3 10.0 10.2 10.5 6.7 7.5 3.8 19.0 66.7 61.0 50.3 31.1 50.3 66.4 69.9 5.2 9.4 24.8 8.5 40.2 18.9 40.2 18.9 40.2 4	P525971HNRPF_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P529071CAZA1_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P536341CATC_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P548191KAD2_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P550721TERA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P557861PSA_HUMAN P597861PSA_HUMAN P59781ARCA_HUMAN P60781ATTPS_HUMAN P60781ATTPS_HUMAN P60781ATTPS_HUMAN P60781ATTPS_HUMAN P608661MYL6_HUMAN P608661MYL6_HUMAN P608661RSC2_HUMAN P608661RSC2_HUMAN P608661RSC2_HUMAN P608661RSC2_HUMAN P608661RSC2_HUMAN P608661RSC2_HUMAN P608661RSC2_HUMAN P608661RSC2_HUMAN P608661RSC2_HUMAN P608661RSC3_HUMAN	Featin capping protein subunit alpha-1 (CapZ alpha-1) - Home sapiens (Human)

1				
63 73	5.5 14.0	16.3 30.7	P61247 RS3A_HUMAN P61247 RS3A_HUMAN	40S ribosomal protein S3a - Homo sapiens (Human) 40S ribosomal protein S3a - Homo sapiens (Human)
271	2.1	29.7	P61254 RL26_HUMAN	60S ribosomal protein L26 - Homo sapiens (Human)
374	1.9	15.2 26.5	P61254 RL26_HUMAN P61604 CH10_HUMAN	60S ribosomal protein L26 - Homo sapiens (Human) 10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (CPN10) (Early-pregnancy factor) (EPF) - Homo sapiens (Human)
3/4	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 41	12.6 20.4	81.1 81.8	P61626 LYSC_HUMAN P61626 LYSC_HUMAN	Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) - Homo sapiens (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 pl 5.3] - Homo sapiens (Human)
53	6.1	26.1	P61769 B2MG_HUMAN	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pl 5.3] - Homo sapiens (Human)
94 386	11.7	49.6 10.6	P61769 B2MG_HUMAN P61916 NPC2_HUMAN	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin variant pl 5.3] - Homo sapiens (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)
237 169	5.2 4.1	36.9 52.9	P62158 CALM_HUMAN P62241 RS8_HUMAN	Calmodulin (CaM) - Homo sapiens (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) 40S ribosomal protein S15a - Homo sapiens (Human)
296 68	10.9	21.5 52.1	P62244 RS15A_HUMAN P62249 RS16_HUMAN	40S ribosomal protein S16a - Homo sapiens (Human) 40S ribosomal protein S16 - Homo sapiens (Human)
106	3.3	35.6	P62249 RS16_HUMAN	40S ribosomal protein S16 - Homo sapiens (Human)
159 256	7.4 3.5	47.3 18.8	P62249 RS16_HUMAN P62258 1433E_HUMAN	40S ribosomal protein S16 - Homo sapiens (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)
164 240	7.2 2.4	34.9 33.9	P62269 RS18_HUMAN P62273 RS29_HUMAN	40S ribosomal protein S18 (Ke-3) (Ke3) - Homo sapiens (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 82	4.9 12.8	25.3 39.2	P62280 RS11_HUMAN P62280 RS11_HUMAN	40S ribosomal protein S11 - Homo sapiens (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)
311 333	2.0	28.4 19.8	P62310 LSM3_HUMAN P62318 SMD3_HUMAN	U6 snRNA-associated Sm-like protein LSm3 - Homo sapiens (Human) Small nuclear ribonucleoprotein Sm D3 (snRNP core protein D3) (Sm-D3) - Homo sapiens (Human)
207	6.0	19.8 38.9	P62318 SMD3_HUMAN P62318 SMD3_HUMAN	Small nuclear ribonucleoprotein Sm D3 (SnRNP core protein D3) (Sm-D3) - Homo sapiens (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) (Fx) [Contains: Hematopoletic system regulatory peptide (Seraspenide)] - Homo sapiens (Human)
29 179	24.5	97.7 15.8	P62328 TYB4_HUMAN P62633 CNBP_HUMAN	Thymosin beta-4 (T beta 4) (Fx) [Contains: Hematopoletic system regulatory peptide (Seraspenide)] - Homo sapiens (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 linger protein 9) - Homo sapiens (Human)
93 195	8.1 6.0	28.1 21.7	P62701 RS4X_HUMAN P62701 RS4X_HUMAN	40S ribosomal protein S4, X isoform (Single copy abundant mRNA protein) (SCR10) - Homo sapiens (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 31	20.7	27.3 88.3	P62753 RS6_HUMAN P62805 H4_HUMAN	40S ribosomal protein S6 (Phosphoprotein NP33) - Homo sapiens (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 90	5.0 4.0	20.4	P62826 RAN_HUMAN P62826 RAN_HUMAN	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4) (Androgen receptor-associated protein 24) - Homo sapiens (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)
178 222	2.0 5.7	29.6 51.3	P62854 RS26_HUMAN P62854 RS26_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human) 40S ribosomal protein S26 - Homo sapiens (Human)
222 363	5.7 2.0	51.3 3.8	P62854 RS26_HUMAN P62873 GBB1_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human)
363 534	5.7 2.0 2.0	51.3 3.8 3.8	P62854 RS26_HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN	40S ribosomal protein S26 - Homo saplens (Human) Guarine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guarine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human)
222 363 534 87	5.7 2.0 2.0 8.7	51.3 3.8 3.8 45.5	P62854 RS26_HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human)
363 534	5.7 2.0 2.0	51.3 3.8 3.8	P62854 RS26_HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human) Guanine nucleotide-binding protein S(I)/S(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl dis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human)
222 363 534 87	5.7 2.0 2.0 8.7	51.3 3.8 3.8 45.5	P62854 RS26_HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/C(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens
222 363 534 87 17	5.7 2.0 2.0 8.7 16.0	51.3 3.8 3.8 45.5 57.0	P62854 RS26_HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin
222 363 534 87 17 27	5.7 2.0 2.0 8.7 16.0 24.9	51.3 3.8 3.8 45.5 57.0 81.8	P62854 RS26_HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN	40S ribosomal protein S26 - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1 A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1 A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin
222 363 534 87 17 27 191	5.7 2.0 2.0 8.7 16.0 24.9 4.0	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7	P62854 RS26_ HUMAN P62873 GBB1_ HUMAN P62873 GBB1_ HUMAN P62937 PPIA_ HUMAN P62937 PPIA_ HUMAN P62937 PPIA_ HUMAN P62942 FKB1A_ HUMAN P62942 FKB1A_ HUMAN	Guanien nucleotide-binding protein G(I)/C(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/C(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophillin FKBP12) - Homo sapiens (Human) FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophillin FKBP12) - Homo sapiens (Human)
222 363 534 87 17 27 191 174 215	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6	P62854 RS26_HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN	Guanine nucleotide-binding protein G()/C(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G()/C(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKS06-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKS06-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human)
222 363 534 87 17 27 191	5.7 2.0 2.0 8.7 16.0 24.9 4.0	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7	P62854 RS26_ HUMAN P62873 GBB1_ HUMAN P62873 GBB1_ HUMAN P62937 PPIA_ HUMAN P62937 PPIA_ HUMAN P62937 PPIA_ HUMAN P62942 FKB1A_ HUMAN P62942 FKB1A_ HUMAN	40S ribosomal protein S26 - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (PEptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin PKS06-binding protein 1A (EC 5.2.1.8) (PEptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FK
222 363 534 87 17 27 191 174 215 157 372 56	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3	51.3 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 51.4	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62979 RS27A_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN	Guanien nucleotide-binding protein G(I)/C(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/C(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKS06-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) FKS06-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) 405 ribosomal protein S27a - Homo sapiens (Human) 405 ribosomal protein S27a - Homo sapiens (Human) 14-3-3 protein 224/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human)
222 363 534 87 17 27 191 174 215 157 372 56	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 51.4 35.1	P62854 [RS26_HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62947 [RS27A_HUMAN P62979 [RS27A_HUMAN P63104] 1433Z_HUMAN P63104 [1433Z_HUMAN	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) HKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) HKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) HKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) HKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human)
222 363 534 87 17 27 191 174 215 157 372 56 67 34	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.0 56.0 57.0	P62854 RS26_ HUMAN P62873 GB81_HUMAN P62873 GB81_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PESSOs-binding protein 1A (EC 5.2.1.8) (Pplase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKSOs-binding protein 1A (EC 5.2.1.8) (Ppltidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOs-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOs-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOs-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOs-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOs-binding protein 1A (EC ft 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOs-binding protein 527a - Homo sapiens (Human) FKSOs-binding protein 527a - Homo sapiens (Human) FKSOs-binding protein 527a - Homo sapie
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.1 65.7 8.5	P62854 [RS26_HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62979 [RS27A_HUMAN P63104] 1433Z_HUMAN P63104 [1433Z_HUMAN P63104] 1433Z_HUMAN P63104 [1433Z_HUMAN P63104] [1433Z_HUMAN P63104] [1433Z_HUMAN	Guanien nucleotide-binding protein G()/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G()/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKS0C-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS0P-12) - Homo sapiens (Human) FKS0C-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS0P-12) - Homo sapiens (Human) FKS0C-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS0P-12) - Homo sapiens (Human) 40S ribosomal protein S27a - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human)
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 51.4 35.1 65.7 8.5	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62941 RS27_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63104 GBLP_HUMAN P63244 GBLP_HUMAN P63244 GBLP_HUMAN	Guanien nucleotide-binding protein G()/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G()/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PESSOG-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOG-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOG-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) 40S ribosomal protein S27a - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human)
222 363 534 87 17 27 191 174 215 157 372 56 67 382 533	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.1 4.35.1 65.7 8.5 4.1	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P63942 FKB1A_HUMAN P63941 RS27A_HUMAN P63104 1433Z_HUMAN P63204 GBLP_HUMAN P63	Guanine nucleotide-binding protein G()/C(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G()/C(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PKS00-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKS00-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKS00-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKS00-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKS00-binding protein S27a
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 51.4 35.1 65.7 8.5	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62941 RS27_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63104 GBLP_HUMAN P63244 GBLP_HUMAN P63244 GBLP_HUMAN	Guanien nucleotide-binding protein G()/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G()/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PESSO-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSO-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSO-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) 40S ribosomal protein S27a - Homo sapiens (Human) 41-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 41-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 41-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 41-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 41-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 41-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 41-3-3 protein
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.0 40.7 65.7 8.5 4.1 69.1 66.4	P62854 [RS26_ HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62979 [RS27A_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63244 [GBLP_HUMAN P63244 [GBLP_HUMAN P63261 [ACTG_HUMAN P63261 [ACTG_HUMAN P63261 [ACTG_HUMAN P63261 [ACTG_HUMAN P63261 [ACTG_HUMAN P63261 [ACTG_HUMAN P63261 [ACTG_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PESSO6-binding protein 1A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PESSO6-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PESSO6-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PESSO6-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PESSO6-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PESSO6-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PESSO6-binding protein PSZPa - Homo sapiens (Human) PESSO6-bin
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 51.4 35.1 65.7 8.5 4.1 69.9 15.8	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63244 GBLP_HUMAN P63241 GBLP_HUMAN P63241 GBLP_HUMAN P63241 GBLP_HUMAN P63261 ACTG_HUMAN P63261 ACTG_	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PESGO-binding protein 1A (EC 5.2.1.8) (Pplase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKSDO-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSDO-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSDO-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSDO-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSDO-binding protein FSZPa - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Pr
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 51.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63244 GBLP_HUMAN P63244 GBLP_HUMAN P63241 ACTG_HUMAN P63261 ACTG_HUMAN P63261 ACTG_HUMAN P63261 ACTG_HUMAN P63279 UBC9_HUMAN P63279 UBC9_	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (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) PRSGO-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) PKSGO-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) PKSGO-binding protein 1A (EC 6.5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) 40S ribosomal protein S27a - Homo sapiens (Human) 414-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor p
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 51.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 49.6	P62854 [RS26_ HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62979 [RS27A_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63244 [GBLP_HUMAN P63261 [ACTG_HUMAN P63261 [ACTG_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PESGO-binding protein 1A (EC 5.2.1.8) (Pplase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKSDO-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSDO-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSDO-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSDO-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSDO-binding protein FSZPa - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Pr
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 57 78	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 2.0 2.0 2.0 2.0 3.1 4.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 51.4 35.1 65.7 8.5 4.1 66.4 69.9 15.8 7.0 49.6	P62854 RS26, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62947 FKB1A, HUMAN P62979 RS27A, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63261 ACTG, HUMAN P63261 ACTG, HUMAN P63261 ACTG, HUMAN P63279 UBC9, HUMAN P6328 TPM4, HUMAN P67936 TPM4, HUMAN P67	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PERSOG-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) FKSOG-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) FKSOG-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) FKSOG-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) 14-3-3 protein protein 527a - Homo sapiens (Human) 14-3-3 protein zeta/deta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/deta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/deta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/deta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/deta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/deta (Protein kinase C
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 78	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 51.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 49.6	P62854 RS26, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62873 FPIA, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62979 RS27A, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63261 ACTG, HUMAN P63274 GBLP, HUMAN P63279 UBC, HUMAN P67306 TPM4, HUMAN P67306 TPM4, HUMAN P67930 TPM4, H	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (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) PESGO-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) FKSO-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) PKSO-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) 40S ribosomal protein S27a - Homo sapiens (Human) 414-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/detta (Protein kinase C inhibitor prote
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 57 78	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 2.0 2.0 2.0 2.0 3.1 4.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 51.4 35.1 65.7 8.5 4.1 66.4 69.9 15.8 7.0 49.6	P62854 RS26, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62947 FKB1A, HUMAN P62979 RS27A, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63261 ACTG, HUMAN P63261 ACTG, HUMAN P63261 ACTG, HUMAN P63279 UBC9, HUMAN P6328 TPM4, HUMAN P67936 TPM4, HUMAN P67	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKSD6-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSD6-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSD6-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSD6-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSD6-binding protein FKBP12 - Homo sapiens (Human) FKSD6-binding protein FKBP12 - Homo sapiens (Human) 14-3-3 protein protein S27a - Homo sapiens (Human) 14-3-3 protein protein S27a - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 57 78 39	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 4.5 2.0 2.0 3.7 3.7 4.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 51.4 35.1 65.7 8.5 4.1 69.9 15.8 7.0 49.6 44.4 45.6 22.1	P62854 RS26, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62873 FPIA, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62979 RS27A, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63104 1435Z, HUMAN P63261 ACTG, HUMAN P63261 ACTG, HUMAN P63261 ACTG, HUMAN P63261 ACTG, HUMAN P63279 UBC9, HUMAN P63279 UBC9, HUMAN P63279 UBC9, HUMAN P63279 UBC9, HUMAN P67306 TPM4, HUMAN P68104 FF1A1, HUMAN P68104 F	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) FKS0-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKS0-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKS0-binding protein TA (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) 40S ribosomal protein S27a - Homo sapiens (Human) 40S ribosomal protein S27a - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protei
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 78 39	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 2.0 31.4 54.2 2.0 31.4 54.2 31.4 54.2 31.4 31.4 31.4 31.4 31.4 31.4 31.4 31.4	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.0 40.7 49.6 44.4 45.6 22.1	P62854 RS26, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62979 RS27A, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63104 1433Z, HUMAN P63104 1435Z, HUMAN P63104 1435Z, HUMAN P63261 ACTG, HUMAN P63261 ACTG, HUMAN P63261 ACTG, HUMAN P63279 UBC9, HUMAN P67360 TPM4, HUMAN P67360 TPM4, HUMAN P67936 TPM4, HUMAN P68104 EF1A1, HUMAN P68104 EFTA1, HUMAN P6	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (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) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKSDG-binding protein 17 A(EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKSDG-binding protein 17 A(EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) A0S ribosomal protein S27a - Homo sapiens (Human) A14-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/detta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/detta (Protein ki
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 4 173 497 90 129	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 2.0 2.0 31.4 54.2 2.0 2.0 31.4 54.2 31.4 54.2 31.6 31.6 31.6 31.6 31.6 31.6 31.6 31.6	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6	P62854 [RS26_ HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62937] PPIA_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62942] FKB1A_HUMAN P62942 [FKB1A_HUMAN P62979] RS27A_HUMAN P63979 [RS27A_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63261 [ACTG_HUMAN P63261] ACTG_HUMAN P63261] ACTG_HUMAN P63261] ACTG_HUMAN P63261] ACTG_HUMAN P63261] ACTG_HUMAN P63261] TPM4_HUMAN P67936 [TPM4_HUMAN P67936] TPM4_HUMAN P67936] TPM4_HUMAN P67936 [TPM4_HUMAN P67936] TPM4_HUMAN P67936] TPM4_HUMAN P67936 [TPM4_HUMAN P67936] TPM4_HUMAN P679	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PESOS-binding protein 1A (EC 5.2.1.8) (Ppltidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKSOS-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKSOS-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKSOS-binding protein S27a - Homo sapiens (Human) A0S ribosomal protein S27a - Homo sapiens (Human) A0S ribosomal protein S27a - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 57 78 39 90 129 91 49 49 33 31 112	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 2.0 8.2 2.0 13.3 5.1 2.0 8.7 2.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 51.4 35.1 65.7 8.5 4.1 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6 37.5	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62873 FPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62979 RS27A_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63261 ACTG_HUMAN P63261 TMAH_HUMAN P63261 TMAH_HUMAN P63261 TMAH_HUMAN P63261 TMAH_HUMAN P63261 TMAH_HUMAN P63263 TBAH_HUMAN P68363 TBAH_HUMAN P68363 TBAK_HUMAN P68363 TBAK_HUMAN P68363 TBAK_HUMAN P68363 TBAK_HUMAN P68363 TBAK_HUMAN P68363 TBAK_HUMAN	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKS06-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKS06-binding protein 1A (EC 6.5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKS06-binding protein S27a - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibi
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 4 173 497 90 129	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 2.0 2.0 31.4 54.2 2.0 2.0 31.4 54.2 31.4 54.2 31.6 31.6 31.6 31.6 31.6 31.6 31.6 31.6	51.3 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6	P62854 RS26, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62979 RS27A, HUMAN P63104 1433Z, HUMAN P63261 ACTG, HUMAN P63261 TPM4, HUMAN P67936 TPM4, HUMAN P	Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanien nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PESOS-binding protein 1A (EC 5.2.1.8) (Ppltidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKSOS-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKSOS-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PKSOS-binding protein S27a - Homo sapiens (Human) A0S ribosomal protein S27a - Homo sapiens (Human) A0S ribosomal protein S27a - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) A
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 57 78 39 90 129 91 49 33 112 139 146 146	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 4.5 2.0 2.0 13.2 4.6 2.0 2.0 13.2 14.5 15.5 16.0 16.	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 51.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 40.4 45.6 22.1 10.2 21.4 29.9 38.6 37.5 19.1 41.2 28.6	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62873 FPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62979 RS27A_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63244 GBLP_HUMAN P63241 ACTG_HUMAN P63261 ACTG_HUMAN P63261 ACTG_HUMAN P63279 UBC9_HUMAN P63279 UBC9_HU	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PERSOS-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOS-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOS-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOS-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) FKSOS-binding protein S27a - Homo sapiens (Human) FKSOS-binding protein subunit beta - Homo sapiens (Human) FKSOS-binding protein subunit bet
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 78 39 90 129 91 49 33 112 132 133	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 4.5 21.0 8.2 2.3 12.0 8.2 2.3 12.0 8.2 2.3 12.0 8.2 2.3 12.0 8.2 2 2.0 8.0 8.2 2 2.0 8.2 2 2.0 8.2 2 2.0 8.2 2.0 8.2 2 2.0 8.2 2 2 2 2 2 3.0 8.2 2 2 3.0 8.2 2 2 2 2 2 3 2 3 2 3 2 3 2 2 3 2 3 2 3	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.0 41.1 65.7 8.5 4.1 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6 37.5 19.1 41.2	P62854 [RS26_ HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62873 [PBB1_HUMAN P62937] PPIA_HUMAN P62937] PPIA_HUMAN P62937 [PPIA_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62979] RS27A_HUMAN P639104 [14332_HUMAN P63104] 14332_HUMAN P63104] 14332_HUMAN P63104] 14332_HUMAN P63201 [ACTG_HUMAN P63201 [ACTG_HUMAN P63261 [ACTG_HUMAN P63	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB0-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB0-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB0-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB0-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB0-binding protein S27a - Homo sapiens (Human) 405 ribosomal protein S27a - Homo sapiens (Human) 405 ribosomal protein S27a - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C imhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C imhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C imhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C imhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C imhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C imhibitor prote
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 57 78 39 90 129 91 49 33 112 139 112 139 1146 188 369 304	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 4.5 2.0 2.0 13.3 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6 3.7.5 19.1 41.2 28.6 3.3 1.4 5.6 3.3	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62873 FPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62941 FKB1A_HUMAN P62979 RS27A_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63261 ACTG_HUMAN P63261 ACTG_HUMAN P63261 ACTG_HUMAN P63279 UBC9_HUMAN P63279 UBC9_H	Guanine nucleotide-binding protein G(I)/G(S)/G(I) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(I) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PERSO6-binding protein 1A (EC 5.2.1.8) (PPlatyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Ppltdyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Ppptdyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Ppptdyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Pptdyl-protyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Pptdyl-protyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 27/a - Homo sapiens (Human) 405 ribosomal protein 527a - Homo sapiens (Human) 405 ribosomal protein 527a - Homo sapiens (Human) 414-3-3 protein zetar/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 144-3-3 protein zetar/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 143-3-3 protein zetar/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo s
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 4 173 39 90 129 91 49 33 112 49 33 113 154 149 149 154 168 168 168 168 168 168 168 168 168 168	5.7 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 4.5 21.0 8.2 2.3 12.3 4.5 2.3 12.3 4.5 2.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6 37.5 19.7 11.2 28.6 3.3 14.5 54.1 19.7	P62854 [RS26_HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62937] PPIA_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62979 [RS27A_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63261 [ACTG_HUMAN P63261] ACTG_HUMAN P63261 [ACTG_HUMAN P63261] ACTG_HUMAN P63261 [ACTG_HUMAN P63261] TPM4_HUMAN P63261 [TPM4_HUMAN P63261] TPM4_HUMAN P63261 [TPM4_HUMAN] P	Guanine nucleotide-binding protein G(I)/G(G)/G(I) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Cuanine nucleotide-binding protein G(I)/G(G)/G(I) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidy-protyl cis-trans isomerase A (EC 5 2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidy-protyl cis-trans isomerase A (EC 5 2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidy-protyl cis-trans isomerase A (EC 5 2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidy-protyl cis-trans isomerase A (EC 5 2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidy-protyl cis-trans isomerase A (EC 5 2.1.8) (PPlate) - Protein IA (EC 5 2.1.8) (Ppetidy-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB06-binding protein IA (EC 5 2.1.8) (Ppetidyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB06-binding protein IA (EC 5 2.1.8) (Ppetidyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB06-binding protein IA (EC 5 2.1.8) (Ppetidyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB06-binding protein IA (EC 5 2.1.8) (Ppetidyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKB06-binding protein S27a - Homo sapiens (Human) 405 ribosomal protein S27a - Homo sapiens (Human) 405 ribosomal protein S27a - Homo sapiens (Human) 405 ribosomal protein S27a - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 14-3-3 protein zeta/delt
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 57 78 39 90 129 91 49 33 112 139 112 139 1146 188 369 304	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 4.5 2.0 2.0 13.3 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 1.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6 3.7.5 19.1 41.2 28.6 3.3 1.4 5.6 3.3	P62854 RS26_ HUMAN P62873 GBB1_HUMAN P62873 GBB1_HUMAN P62873 FPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62937 PPIA_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62942 FKB1A_HUMAN P62941 FKB1A_HUMAN P62979 RS27A_HUMAN P62979 RS27A_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63104 1433Z_HUMAN P63261 ACTG_HUMAN P63261 ACTG_HUMAN P63261 ACTG_HUMAN P63279 UBC9_HUMAN P63279 UBC9_H	Guanine nucleotide-binding protein G(I)/G(S)/G(I) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guanine nucleotide-binding protein G(I)/G(S)/G(I) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Peptidyl-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Peptidyl-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PERSO6-binding protein 1A (EC 5.2.1.8) (PPlatyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Ppltdyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Ppptdyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Ppptdyl-protyl cis-trans isomerase) (PPlase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Pptdyl-protyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 1A (EC 5.2.1.8) (Pptdyl-protyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKS06-binding protein 27/a - Homo sapiens (Human) 405 ribosomal protein 527a - Homo sapiens (Human) 405 ribosomal protein 527a - Homo sapiens (Human) 414-3-3 protein zetar/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 144-3-3 protein zetar/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) 143-3-3 protein zetar/delta (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo s
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 90 129 91 129 91 149 133 112 139 146 148 188 369 304 148 148 159 169 179 189 189 189 189 189 189 189 189 189 18	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 4.5 21.0 8.2 2.3 12.0 8.2 2.0 2.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 51.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6 37.5 19.1 41.2 28.6 3.3 14.5 54.1 19.7 52.5 46.3 37.8	P62854 RS26, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62979 RS27A, HUMAN P631041 1433Z, HUMAN P63104 IA33Z, HUMAN P63104 IA33Z, HUMAN P63201 ACTG, HUMAN P63201 TPM4, HUMAN P63201 TPM4, HUMAN P63201 TPM4, HUMAN P63201 TPM4, HUMAN P63203 TRM5, HUMAN P63203 TRM5, HUMAN P63205 TPM1, HUMAN P63205 TPM1	dos ribosomal protein 526 - Homo sapleins (Human) Guarine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapleins (Human) Guarine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapleins (Human) Reptidy-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapleins (Human) Paptidy-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclophilin A) chaining protein) - Homo sapleins (Human) Paptidy-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclophilin A) chaining protein - Homo sapleins (Human) Paptidy-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cy
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 57 78 39 90 129 91 49 33 112 139 130 146 188 369 304 188 369 304 188 369 304 188 369 304 304 304 304 304 304 304 304 304 304	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 4.5 21.0 8.2 2.3 12.0 12.0 12.0 13.1 14.5 15.1 16.0 17.0 18.0	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 55.4 35.1 65.7 8.5 4.1 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6 37.5 19.1 41.2 28.6 3.3 14.5 54.1 19.7 52.5 46.3 3.8 3.5 54.1 19.7 52.5 46.3 3.8 3.5	P62854 [RS26_ HUMAN P62873 [GBB1_HUMAN P62873 [GBB1_HUMAN P62937 [PPIA_HUMAN P62937 [PPIA_HUMAN P62947 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62942 [FKB1A_HUMAN P62947 [RS27A_HUMAN P62979 [RS27A_HUMAN P63104] 1433Z_HUMAN P63104] 1433Z_HUMAN P63104 [1433Z_HUMAN P63104] 1433Z_HUMAN P63261 [ACTG_HUMAN P63261 [ACTG_HUMAN P63	405 ribosomal protein 526 - Homo sapiens (Human) Guarnier nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Guarnier nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapiens (Human) Papitaly-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) Papitaly-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclophilin A) cip- Human) Papitaly-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human) PEKSO-binding protein 11 (EC 5.2.1.8) (Pplase) Papitaly-protyl cis-trans isomerase (EC 5.2.1.8) (Pplase) Papitaly-protyl cis-trans isomerase (Plase) (Human) PEKSO-binding protein 12 (EC 5.2.1.8) (Pplatiyl-protyl cis-trans isomerase) (Plase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PEKSO-binding protein 12 (EC 5.2.1.8) (Pplatiyl-protyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PEKSO-binding protein 12 (EC 5.2.1.8) (Pplatiyl-protyl cis-trans isomerase) (Pplase) (Rotamase) (12 kDa FKBP) (FKBP-12) (Immunophilin FKBP12) - Homo sapiens (Human) PEKSO-binding protein S27a - Homo sapiens (Human) PESO-binding protein S27a - Homo sapiens (Human) PL-3-3 protein zata/dista (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) PL-3-3 protein zata/dista (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) PL-3-3 protein zata/dista (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) PL-3-3 protein zata/dista (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) PL-3-3 protein zata/dista (Protein kinase C inhibitor protein 1) (KCIP-1) - Homo sapiens (Human) PL-3-3 protein protein S27a - Homo sapiens (Human) PL-3-3 protein protein S27a - Homo sapiens (Human) PL-3-3 protein prot
222 363 534 87 17 27 191 174 215 157 372 56 67 34 382 533 5 154 4 173 497 90 129 91 129 91 149 133 112 139 146 148 188 369 304 148 148 159 169 179 189 189 189 189 189 189 189 189 189 18	5.7 2.0 2.0 2.0 8.7 16.0 24.9 4.0 2.0 6.0 4.6 2.8 13.3 5.1 22.8 1.7 2.0 50.7 31.4 54.2 2.0 2.0 13.2 4.5 21.0 8.2 2.3 12.0 8.2 2.0 2.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4	51.3 3.8 3.8 3.8 45.5 57.0 81.8 25.0 40.7 29.6 55.0 55.0 51.4 35.1 65.7 8.5 4.1 69.1 66.4 69.9 15.8 7.0 49.6 44.4 45.6 22.1 10.2 21.4 29.9 38.6 37.5 19.1 41.2 28.6 3.3 14.5 54.1 19.7 52.5 46.3 37.8	P62854 RS26, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62873 GBB1, HUMAN P62937 PPIA, HUMAN P62937 PPIA, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62942 FKB1A, HUMAN P62979 RS27A, HUMAN P631041 1433Z, HUMAN P63104 IA33Z, HUMAN P63104 IA33Z, HUMAN P63201 ACTG, HUMAN P63201 TPM4, HUMAN P63201 TPM4, HUMAN P63201 TPM4, HUMAN P63201 TPM4, HUMAN P63203 TRM5, HUMAN P63203 TRM5, HUMAN P63205 TPM1, HUMAN P63205 TPM1	dos ribosomal protein 526 - Homo sapleins (Human) Guarine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapleins (Human) Guarine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1) - Homo sapleins (Human) Reptidy-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapleins (Human) Paptidy-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclophilin A) chaining protein) - Homo sapleins (Human) Paptidy-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclophilin A) chaining protein - Homo sapleins (Human) Paptidy-protyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cy

255 119	2.2 9.6	7.9 8.6	Q01082 SPTB2_HUMAN Q01082 SPTB2_HUMAN	Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1) (Beta-II spectrin) (Fodrin beta chain) - Homo sapiens (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 I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I) (HLA-DR-associated protein II) (PHAPII) (Inhibitor of granzyme A-activated DNase) (IGAAD) - Homo sapiens (Human)
61	16.1	15.2	Q01105 SET_HUMAN	Protein SET (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template-activating factor I) (TAF-I) (HLA-DR-associated protein II) (PHAPII)
226	2.9	31.9	Q01469 FABPE_HUMAN	(Inhibitor of granzyme A-activated DNase) (IGAAD) - Homo sapiens (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	
110	7.1	21.1	Q01518 CAP1_HUMAN	Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) - Homo sapiens (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 saplens (Human)
121 312	9.6 2.0	16.2 16.8	Q01518 CAP1_HUMAN Q01844 EWS_HUMAN	Adenylyl cyclase-associated protein 1 (CAP 1) - Homo sapiens (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 saplens (Human)
268 150	4.1	25.8 23.4	Q01844 EWS_HUMAN Q02818 NUCB1_HUMAN	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) - Homo sapiens (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 ITIH3_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 ITIH3_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 ITIH3_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)
50	12.0	24.1	OOV 2021DOMET LILIMAN	Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease
59	12.9	34.1	Q06323 PSME1_HUMAN	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) Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease
68	14.7	38.2	Q06323 PSME1_HUMAN	subunit 1) (11S regulator complex subunit alpha) (REG-alpha) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) - Homo
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
25	12.3	52.8	Q06830 PRDX1_HUMAN	protein) (PAG) (Natural killer cell-enhancing factor A) (NKEF-A) - Homo sapiens (Human) Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Proliferation-associated gene
48	18.3	55.3	Q06830 PRDX1_HUMAN	protein) (PAG) (Natural killer cell-enhancing factor A) (NKEF-A) - Homo sapiens (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) Galectin-3-binding protein precursor (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (Mac-2 BP) (MAC2BP)
276	2.1	7.5	Q08380 LG3BP_HUMAN	(Tumor-associated antigen 90K) - Homo sapiens (Human) Galectin-3-binding protein precursor (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (Mac-2-BP) (MAC2BP)
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-bin
436	2.0	9.1	Q08380 LG3BP_HUMAN	(Tumor-associated antigen 90K) - Homo saplens (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) Interleukin enhancer-binding factor 3 (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Double-stranded RNA-binding protein 76)
60	16.5	21.9	Q12906 ILF3_HUMAN	(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-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetylglycerophosphocholine esterase) - Homo
				sapiens (Human) Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47) (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated
529	2.0	3.6	Q13093 PAFA_HUMAN	phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetylglycerophosphocholine esterase) - Homo
346	2.0	8.2	Q13151 ROA0_HUMAN	saplens (Human) Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0) - Homo saplens (Human)
				Understanding of the control of the
591 212	1.4	24.3	Q13151 ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0) - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human)
212 126	3.2 9.3	37.3 50.7	Q14019 COTL1_HUMAN Q14019 COTL1_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human)
212	3.2	37.3	Q14019 COTL1_HUMAN	Coactosin-like protein - Homo sapiens (Human)
212 126 157 85 404	3.2 9.3 4.0 12.2 1.3	37.3 50.7 11.0 35.2 16.4	Q14019 COTL1_HUMAN Q14019 COTL1_HUMAN Q14103 HNRPD_HUMAN Q14103 HNRPD_HUMAN Q14152 IF3A_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (eIF3 p167) (eIF3 p180) (eIF3 p185) (eIF3a) - Homo sapiens (Human)
212 126 157 85	3.2 9.3 4.0 12.2	37.3 50.7 11.0 35.2	Q14019 COTL1_HUMAN Q14019 COTL1_HUMAN Q14103 HNRPD_HUMAN Q14103 HNRPD_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear risbonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear risbonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human)
212 126 157 85 404 137 145 122	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9	014019 COTL1_HUMAN 014019 COTL1_HUMAN 014103 HNRPD_HUMAN 014103 HNRPD_HUMAN 014152 IF3A_HUMAN 014152 IF3A_HUMAN 014152 IF3A_HUMAN 014764 MVP_HUMAN 014764 MVP_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation inititation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Eukaryotic translation inititation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human)
212 126 157 85 404 137 145	3.2 9.3 4.0 12.2 1.3 8.2 5.1	37.3 50.7 11.0 35.2 16.4 16.1 15.8	Q14019 COTL1_HUMAN Q14019 COTL1_HUMAN Q14103 HNRPD_HUMAN Q14103 HNRPD_HUMAN Q14152 IF3A_HUMAN Q14152 IF3A_HUMAN Q14154 MVP_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear risbonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear risbonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vaulti protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human)
212 126 157 85 404 137 145 122	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7	O14019 COTL1_HUMAN O14019 (COTL1_HUMAN O14103 IHNRPD_HUMAN O14103 IHNRPD_HUMAN O14103 IHNRPD_HUMAN O14152 [IF3A_HUMAN O14152 [IF3A_HUMAN O14764 MVP_HUMAN O14764 MVP_HUMAN O14847 [LASP1_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing cotamer-binding protein (NOP) (clare RNA- and DNA-binding protein) (p54(nrb)) (p54nrb)
212 126 157 85 404 137 145 122 124 72	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9	014019 COTL.1_HUMAN 014019 COTL.1_HUMAN 014103 HNRPD_HUMAN 014152 F3A_HUMAN 014152 F3A_HUMAN 014752 F3A_HUMAN 014764 MVP_HUMAN 014764 MVP_HUMAN 01487 LASP1_HUMAN 014847 LASP1_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elf-3 theta) (elf-3 p167) (elf-3 p180) (elf-3 p185) (
212 126 157 85 404 137 145 122 124 72 232 78	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 10.3	014019 (COT.1 , HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear risonucleoprotein D0 (nnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear risonucleoprotein D0 (nnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MINTS5) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human)
212 126 157 85 404 137 145 122 124 72 232 78	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4	014019 COTL.1_HUMAN 014019 COTL.1_HUMAN 014103 HNRPD_HUMAN 014152 F3A_HUMAN 014152 F3A_HUMAN 014752 F3A_HUMAN 014764 MVP_HUMAN 014764 MVP_HUMAN 01487 LASP1_HUMAN 014847 LASP1_HUMAN 015233 NONO_HUMAN 015233 NONO_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MMTS5) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human)
212 126 157 85 404 137 145 122 124 72 232 78 206 406 286 336	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 3.5	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 10.3 9.8 5.9	014019 COTL: J-HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (finRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (finRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (finRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elf-3 theta) (elf-3 p167) (elf-3 p186) (elf-3 p185) (elf-3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non0 protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MMT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non0 protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MMT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human)
212 126 157 85 404 137 145 122 124 72 232 78 206 406 286	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.7 37.9 21.4 33.3 10.3 9.8	014019 COTL.1_HUMAN 014019 COTL.1_HUMAN 014103 HNRPD_HUMAN 014152 F3A_HUMAN 014152 F3A_HUMAN 014754 F3A_HUMAN 014764 MVP_HUMAN 014764 MVP_HUMAN 01487 LASP1_HUMAN 015233 NONO_HUMAN 015233 NONO_HUMAN 016181 SEP17_HUMAN 016181 SEP17_HUMAN 016181 SEP17_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 thata) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 thata) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MIN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MIN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Dihydropyrimidinase-related protein) (25 kDa auclear RNA- homo sapiens (Human) Dihydropyrimidinase-related protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human)
212 126 157 85 404 137 145 122 124 72 232 78 206 406 286 336 344 383 343	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 3.5 2.0 2.5 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 21.4 33.3 10.3 9.8 9.8 9.8 4.7 11.2 4.6	014019 COTL_1HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non Oprotein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non Oprotein) (54 kDa nuclear protein) (p54(nrb)) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Thioredoxin reductase 1, cytoplasmic precursor (EC 1.8.1.9) (R) (R) (R) (R) (R) (R) (R) (R) (R) (R
212 126 157 85 404 137 145 122 124 72 232 78 206 406 286 336 344 383	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 3.5 2.0 2.5	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 10.3 9.8 9.8 5.9 4.7 11.2	014019 (COTL.] HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (eli-3 theta) (eli-3 p167) (eli-3 p180) (eli-3 p185) (eli-3 a) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (eli-3 theta) (eli-3 p167) (eli-3 p180) (eli-3 p185) (eli-3 a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Fascin (Singed-like protein) (55 kDa actin-bundling
212 126 157 85 404 137 145 122 124 72 232 78 206 406 286 336 344 383 392 129	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.7 37.9 21.4 33.3 9.8 9.8 9.8 4.7 11.2 4.6 9.2 39.2 4.7 11.2 4.6 9.2 39.2 4.7 59.2 59.2 59.2 59.2 59.2 59.2 59.2 59.2	014019 COTL.1 HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p189) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (MpO) protein) (54 k Da nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (MpO) protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Fascin (Singed-like protein) (55 kDa actin-bunding protein) (p55) - Homo sapiens (Human) Fiscin (Singed-like protein) (55 kDa actin-bunding protein) (p59) - Homo sapiens (Human) Thioradoxin reductase 1, cytoplasmic precursor (EC 1.8 1.9) (TR) (TR)
212 126 157 85 404 137 145 122 124 72 232 78 206 406 286 336 344 383 343 392	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 3.5 2.0 2.5 2.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 10.3 9.8 5.9 4.7 11.2 4.6 9.2	014019 (COTL.] HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (finRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (finRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (finRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elf-3 theta) (elf-3 p167) (elf-3 p186) (elf-3 p185) (elf-3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non-POU domain-containing octamer-binding protein) (Non-POU domain-containing prote
212 126 157 85 404 137 145 122 124 72 232 206 406 286 336 344 383 392 129 111 112 139	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 2.5 2.0 2.4 4.0 3.1 6.9 2.1 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.3 10.3 9.8 9.8 9.8 9.8 9.2 24.6 9.2 39.2 39.2 39.2 40.4 41.2	014019 COTL.1 HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear risonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear risonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear risonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non Oprotein) (54 k Da nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (NMTS5) (DNA-binding p52p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non Oprotein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (NMTS5) (DNA-binding p52p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Fascin (Singed-like protein) (55 kDa actin-bunding protein) (p55) - Homo sapiens (Human) Thioredoxin reductase 1, cytoplasmic precursor (EC 1.8.1.9) (TR) (TR) - Homo sapiens (
212 126 157 85 404 137 145 122 72 232 78 206 406 286 336 343 343 343 322 129 111 112	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 3.5 2.0 2.5 2.0 3.5 2.0 3.5 2.0 3.5 2.0 3.5 2.0 2.1 3.5 2.0 3.5 2.0 3.5 3.5 3.5 3.5 3.5 3.5 3.5 3.5	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 10.3 9.8 9.8 5.9 4.7 11.2 4.6 9.2 39.2 59.3 37.9	014019 (COTL.] HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elf-3 theta) (elf-3 p167) (elf-3 p180) (elf-3 p185) (elf-3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non-POU domain-containing octamer-binding protein) (Pot-4 (nrb)) (p54 kDa nuclear RNA- and DNA-binding protein) (p54 (nrb)) (p54 nrb) (f55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non-POU domain-containing octamer-binding protein) (P54 (nrb)) (p54 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Pascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Histone H3.2 (H3/m) (H3/O) - Homo sapiens (Human) Histone H3.2 (H3/m) (H3/O) - Homo sapiens (Hu
212 126 157 85 404 137 145 122 72 232 78 206 406 286 334 4383 343 343 392 129 111 112 139 154 319	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 3.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.3 10.3 9.8 5.9 4.7 11.2 4.6 9.2 39.2 39.2 59.2 11.2 4.6 9.2 19.2 19.2 19.2 19.2 19.2 19.2 19.2	014019 COTL.1 HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Mon Oprotein) (S4 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (NMT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonO protein) (S4 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p55 kDa nuclear protein) (NMT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonO protein) (S4 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p55 kDa nuclear protein) (NMT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Ho
212 126 157 85 404 137 145 122 78 206 286 336 406 286 339 341 343 342 129 111 112 139 154 409	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 3.5 2.0 2.5 2.0 3.5 2.0 3.5 2.0 2.5 2.0 3.5 2.0 2.0 3.5 2.0 3.5 2.0 3.5 2.0 3.5 2.0 3.5 3.5 3.5 3.5 3.5 3.5 3.5 3.5	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.7 37.9 21.4 33.3 10.3 9.8 5.9 4.7 11.2 4.6 9.2 23.9 11.2 4.6 9.2 9.2 9.2 9.3 9.3 9.3 9.3 9.3 9.3 9.3 9.3	014019 COTL.1 HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear risonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear risonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear risonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non Oprotein) (S4 kDa nuclear RNA- and DNA-binding protein) (p54 (nrb)) (p54 nrb) (55 kDa nuclear protein) (NMTS5) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non Oprotein) (S4 kDa nuclear RNA- and DNA-binding protein) (p54 (nrb)) (p54 nrb) (55 kDa nuclear protein) (NMTS5) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dibydropyrimidinase-related protein) (P54 (nrb)) (p54 nrb) (p54
212 126 157 85 404 137 145 122 78 206 286 336 406 286 334 343 392 129 111 112 139 149 409 260	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 3.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.3 10.3 9.8 9.8 5.9 4.7 11.2 4.6 9.2 39.2 39.2 10.1 11.2 4.6 9.2 10.1 10.1 10.1 10.1 10.1 10.1 10.1 10	014019 COTL.1 HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (MpO) protein) (54 k Da nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (NMTS5) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (MpO) protein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (NMTS5) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dibydropyrimidinase-related protein) (P54 (NRS)) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Dibydropyrimidinase-related protein (P54 (NRS)) (P54 (NRS)) (P54 (NRS)) - Homo sapiens (Human) Dibydropyrimidinase-related protein) (P55 kDa actin-bunding prote
212 126 157 85 404 137 145 122 124 72 232 206 406 286 336 344 383 392 129 111 112 139 154 319 409 260	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 2.3 2.0 2.5 2.0 2.4 4.0 2.7 2.0 2.1 2.0 2.1 2.0 2.1 2.0 2.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.7 37.9 21.4 33.3 9.8 9.8 9.8 9.8 9.8 9.2 4.7 11.2 9.2 39.2 10.3 10.3 10.3 10.3 10.3 10.3 10.3 10.3	014019 COTL.1 HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elf-3 theta) (elf-3 p167) (elf-3 p180) (elf-3 p185) (elf-3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Mon-POU domain-containing octamer-binding protein (Mon Oprotein) (54 kDa nuclear RNA- and DNA-binding protein) (p54 (nrb)) (p54 nrb) (55 kBa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Mon-POU domain-containing octamer-binding protein (Mon Oprotein) (54 kDa nuclear RNA- and DNA-binding protein) (p54 (nrb)) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Dihydropyrimidinase-related protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Thioradokin reductase 1, cytoplasmic precursor (Ec 1.8.1.9) (IR) (IR) - Ho
212 126 157 85 404 137 145 122 78 206 286 334 343 343 343 343 392 129 111 112 139 409 260 191 191 327	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.3 10.3 9.8 5.9 4.7 11.2 4.6 9.2 39.2 59.2 11.4 11.2 11.2 11.2 11.2 11.2 11.2 11	014019 COTL.1 HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elf-3 theta) (elf-3 p167) (elf-3 p180) (elf-3 p185) (elf-3 p-185) (elf-3 p-185
212 126 157 85 404 137 145 122 124 72 232 206 406 286 336 344 383 392 129 111 112 139 260 191 154 319 409 200 191 327 315	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.3 10.3 10.3 9.8 9.8 9.8 9.8 9.8 9.2 39.2	014019 COTL_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elF-3 theta) (elF3 p167) (elF3 p180) (elF3 p185) (elF3a) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MLN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonOp Oprotein) (54 KDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 KDa nuclear protein) (MNT55) (DNA-binding p52p100 complex, 52 KDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (NonOp Oprotein) (54 KDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 KDa nuclear protein) (MNT55) (DNA-binding p52p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein) (P54 (P54) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Dihydropyrimidinase-related protein) (S5 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Fascin (Singed-like protein) (S5 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Fascin (Singed-like protein) (S5 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Histone H3.2 (H3/m) (H3/0) - Homo sapiens (Human) Histone H3.2 (H3/m) (H3/0) - Homo sapiens (Human) Histone H3.2 (H3/m) (H3/0) - Homo sapiens (Human) Histone H3.
212 126 157 85 404 137 145 122 124 72 232 78 206 406 286 336 344 339 331 312 111 112 139 154 319 260 191 327 315	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 2.3 2.0 2.5 2.0 2.1 6.0 3.5 2.0 2.1 6.0 3.5 2.0 2.0 2.1 6.0 3.5 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 9.8 9.8 9.8 4.7 11.2 9.2 30.2 10.3	014019 COTL1_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (eli-3 theta) (eli-3 p167) (eli-3 p185) (
212 126 157 85 404 137 145 122 124 72 232 78 206 406 286 336 344 383 392 129 111 112 139 260 191 327 315 194 294 294 414	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 2.5 2.0 2.4 4.0 15.9 2.3 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 10.3 9.8 9.8 9.8 9.8 9.2 39.2	014019 COTL.1, HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotit cranslation initiation factor 3 subunit 10 (elf-3 hata) (elf-3 pt-10) (elf-
212 126 127 187 85 404 137 145 122 124 72 232 124 72 232 206 406 286 334 383 392 129 111 112 139 154 319 409 260 191 327 315 194 290 274 148	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 2.5 2.0 2.4 4.0 2.1 6.9 2.1 7.9 2.0 2.1 7.9 2.0 2.1 7.9 2.0 2.1 7.9 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.3 9.8 9.8 9.8 5.9 4.7 11.2 9.2 39.2 10.1 10.7 10.7 10.7 10.7 10.7 10.7 10.7	014019 COTL1_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein (AUP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vault protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MIN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MIN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non Oprotein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Non-POU domain-containing octamer-binding protein (Non Oprotein) (54 kDa nuclear RNA- and DNA-binding protein) (p54(nrb)) (55 kDa nuclear protein) (MNT55) (DNA-binding p52/p100 complex, 52 kDa subunit) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Septin-7 (CDC10 protein homolog) - Homo sapiens (Human) Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3) - Homo sapiens (Human) Dihydropyrimidinase-related protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Fascin (Singed-like protein) (55 kDa actin-bundling protein) (p55) - Homo sapiens (Human) Histone H32 (H3/m) (H3/0) - Homo sapiens (Human) Histone H32 (H3/m) (H3/0) - Homo sapiens (Human) Histone H32
212 126 157 85 404 137 145 122 72 232 78 206 406 286 334 343 343 343 343 349 212 112 139 409 260 191 327 315 194 296	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 2.3 2.0 2.5 2.0 2.4 4.0 2.5 2.0 2.1 6.0 14.1 15.9 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 10.8 9.8 9.8 9.8 9.8 14.0 9.2 39.2	014019 COTL.1_HUMAN	Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein Do (neRNP DD) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein Do (neRNP DD) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein DO (neRNP DD) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein DO (neRNP DD) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (eli-3 theta) (eli-3 pl-16) (eli-3 pl-180) (eli-
212 126 157 85 404 137 145 122 124 72 232 124 72 232 206 406 286 334 333 343 392 129 154 319 154 319 260 191 327 315 194 290 274 188 293	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 2.3 2.0 2.5 2.0 2.4 4.0 2.7 2.9 2.0 2.1 7.9 2.0 2.1 7.9 2.0 2.1 7.9 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.7 37.9 21.4 33.7 37.9 21.4 33.7 37.9 21.4 33.7 37.9 21.4 33.7 37.9 4.7 11.2 4.6 9.2 39.2 39.8 59.9 4.7 11.2 9.9 12.7 16.9 16.7	014019 COTL_HUMAN	Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elf-3 thata) (elf-3 pt-10) (elf-3 pt-18) (elf-3 pt
212 126 157 85 404 137 145 122 78 206 406 286 336 344 383 343 392 129 111 112 139 409 260 191 327 315 194 295 395 293 395 293 395 293 395 293 395 293 395 293 395 395 395 395 395 395 395 395 395 3	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.0 2.1 4.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 10.8 9.8 9.8 9.8 14.2 9.2 39.2	014019 COTL.1_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear irbonucleoprotein D0 (InRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear irbonucleoprotein D0 (InRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear irbonucleoprotein D0 (InRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (elf-3 thata) (elf3 p167) (elf3 p180) (elf3 p180) (elf3 p180) Allor sult protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vaut protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) Major vaut protein (MVP) (Lung resistance-related protein) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MIN 50) - Homo sapiens (Human) LIM and SH3 domain protein 1 (LASP-1) (MIN 50) - Homo sapiens (Human) Non-POU domain-containing octamer-inding protein (Non Oprotein) (54 Nan nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54 Nrb) (55 Nan nuclear protein) (MMT55) (DNA-binding protein) (Non-POU domain-containing octamer-inding protein (Non Oprotein) (54 Nan nuclear RNA- and DNA-binding protein) (p54(nrb)) (p54 Nrb) (55 Nan nuclear protein) (MMT55) (DNA-binding protein) (Non-POU domain-containing octamer-inding protein (Non-POU domain-containing protein (Non-POU domain-containing protein (Non-POU domain-containing protein (Non-POU domain-contain
212 126 127 128 404 137 145 122 124 72 232 128 206 406 286 334 339 2129 111 112 139 260 191 327 315 194 290 274 148 395 223 236 306 2283	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 2.5 2.0 2.5 2.0 2.4 4.0 1.7 2.0 2.2 1.7 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.7 37.9 21.4 33.3 9.8 9.8 9.8 9.8 9.8 9.9 4.7 11.2 4.6 9.2 39.2 39.7 10.3 10.	014019 COTL_HUMAN	Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (neRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (neRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear ribonucleoprotein D0 (neRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Eukaryotic translation initiation factor 3 subunit 10 (eli-3 theta) (eli3 p.16) (eli3 p.180) (eli3
212 126 157 85 404 137 145 122 78 206 286 336 344 383 343 392 129 111 112 139 409 260 191 327 315 194 290 274 48 139 474 395 283 308 253 308 253 347 266 177 206	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.3 2.0 2.5 2.0 2.5 2.0 2.5 2.0 2.2 4.0 3.1 6.9 2.1 7.1 7.2 7.2 7.3 7.3 7.3 7.3 7.3 7.3 7.3 7.3	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 21.4 33.7 37.9 21.4 33.3 10.3 9.8 5.9 4.7 11.2 4.6 9.2 39.2 59.2 59.2 11.2	014019 COTL.1_HUMAN	Coactosin-like protein - Homo sapiens (Human) Heterogeneous nuclear inbonucleoprotein D0 (InRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Heterogeneous nuclear inbonucleoprotein D0 (InRNP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Elekaryotic translation initiation factor 3 subunit 10 (eli-3 theia) (eli-3 pt.16)
212 122 126 157 85 404 137 145 122 124 72 232 78 206 406 286 334 383 343 392 129 111 112 139 260 191 327 315 194 290 274 148 139 263 363 363 363 374 266 177	3.2 9.3 4.0 12.2 1.3 8.2 5.1 9.5 6.0 14.1 2.6 15.9 3.5 2.0 2.5 2.0 2.5 2.0 2.4 4.0 1.7 2.0 2.2 1.7 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0	37.3 50.7 11.0 35.2 16.4 16.1 15.8 13.9 33.7 37.9 21.4 33.3 10.3 9.8 9.8 9.8 9.8 9.8 9.2 39.2	014019 COTL_HUMAN	Coactosin-like protein - Homo sapiens (Human) Coactosin-like protein - Homo sapiens (Human) Reterogeneous nuclear infoructioprotein D0 (InRRP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Reterogeneous nuclear infoructioprotein D0 (InRRP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Reterogeneous nuclear infoructioprotein D0 (InRRP D0) (AU-rich element RNA-binding protein 1) - Homo sapiens (Human) Reterogeneous nuclear inforuction of the Coactor of Subunit 10 (eli-3 thata) (eli-3 pit-0)

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	GTPase 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	GTPase 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	GTPase 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 saplens (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	Q9UQ80 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	Q9UQ80 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 0	CLIC1_HUMAN 9.5	9.5	Chloride i	intracellular cl	hannel prote	ein 1 (Nuclear chloride ion channel 27) AEEQPQVELFVK	(NCC27) (Chloride c 1457.7	hannel ABP) (Re 1458.8	gulatory nuclear	chloride ion channe 1458.7
123.0	9.5	9.5	31.1	2.0	99.0	EEFASTCPDDEEIELAYEQVAK	2572.1	2573.1	2572.1	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	IGNCPFSQR	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 000391 0				0.0 /I oxidase 1 pr		FSAYIK 1.8.3.2) (Quiescin Q6) (hQSOX) - Hor		728.4	727.4	728.4
201.0	6.0	6.0	12.2	2.0	99.0	LAGAPSEDPQFPK	1355.7	1356.7	1355.7	1356.7
201.0	6.0	6.0	12.2	2.0	99.0	NNEEYLALIFEK	1481.8	1482.8	1481.7	1482.7
201.0	6.0	6.0	12.2	2.0	99.0	SFYTAYLOR	1147.6	1148.6	1147.6	1148.6
160.0	2.0	2.0	11.1	2.0	99.0	NNEEYLALIFEK	1481.8	1482.8	1481.7	1482.7
000479	HMGN4_HUMA	N.	High-mob	oility group nu	cleosome-b	inding domain-containing protein 4 (N	lonhistone chromosor	mal protein HMG-	-17-like 3) (Non-l	nistone 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
490.0	TPP1_HUMAN 2.0	2.0	4.6	yl-peptidase 1 2.0	precursor (EC 3.4.14.9) (Tripeptidyl-peptidase I) LYQQHGAGLFDVTR	1603.8	1604.8	1603.8	1604.8
138.0	2.1	2.1	14.9	2.0	99.0	LFGGNFAHQASVAR	1473.7	1474.7	1473.7	1474.8
138.0	2.1	2.1	14.9	0.1	26.0	LYQQHGAGLFDVTR	1603.8	1604.8	1603.8	1604.8
189.0	4.0	4.0	5.0	2.0	99.0	LFGGNFAHQASVAR	1473.7	1474.8	1473.7	1474.8
189.0	4.0	4.0	5.0	2.0	99.0	LYQQHGAGLFDVTR	1603.8	1604.8	1603.8	1604.8
014818	PSA7_HUMAN			me subunit alp	oha type 7 (EC 3.4.25.1) (Proteasome subunit RC6		unit XAPC7) - Ha		nan)
177.0	6.5	6.5	17.3	2.0	99.0	KICALDDNVCMAFAGLTADAR	2311.1	2312.1	2311.1	2312.1
177.0	6.5	6.5	17.3	2.0	99.0	LYQTDPSGTYHAWK	1665.8	1666.8	1665.8	1666.8
177.0	6.5	6.5	17.3	2.0	99.0	YIASLKQR	977.6	978.6	977.6	978.6
177.0	6.5	6.5	17.3		67.0	ICALDDNVCMAFAGLTADAR	2183.0	2184.0	2183.0	2184.0
202.0	3.7	3.7	11.7	2.0	99.0	KICALDDNVCMAFAGLTADAR	2311.1	2312.1	2311.1	2312.1
202.0	3.7	3.7	11.7	1.7	98.0	YIASLKQR	977.6	978.6	977.6	978.6
O14979 I	HNRDL_HUMA	N	Heteroge	neous nuclear	ribonucleor	protein D-like (hnRPD-like protein) (hi	hHNRP-DL) (JKT41-bi	inding protein) (a	AU-rich element F	(RNA-binding factor
452.0	2.0	6.0	9.8	2.0	99.0	RGFCFITYTDEEPVKK GFGFVLFK	1989.0	1990.0	1989.0	1990.0
452.0	2.0	6.0	9.8	0.0	99.0	SRGFGFVLFK	913.5	914.5	913.5	914.5
452.0	2.0	6.0	9.8	0.0	99.0		1156.6	1157.6	1156.6	1157.6
87.0	4.0	4.0	18.8	2.0	99.0	GFGFVLFK	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 O15143	2.1	2.1	19.5	2.0	99.0 /3 complex	GFGFVLFK	913.5	914.5 Homo sapiens (H	913.5	914.5
152.0	8.0	8.0	17.7	2.0	99.0	CSQFCTTGMDGGMSIWDVK	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	VHELKEHNGQVTGIDWAPESNR	2516.2	2517.2	2516.2	2517.2
152.0	8.0	8.0	17.7	2.0	99.0	WAPNENKFAVGSGSR	1618.8	1619.8	1618.8	1619.8
152.0	8.0	8.0	17.7	0.0	99.0	CSQFCTTGMDGGMSIWDVK	2178.9	2179.9	2178.9	2179.9
152.0	8.0	8.0	17.7	0.0	99.0	CSQFCTTGMDGGMSIWDVK	2163.9	2164.9	2163.9	2164.9
128.0	2.3	2.3	24.7	2.0	99.0	CSQFCTTGMDGGMSIWDVK	2161.9	2162.9	2161.9	2162.9
128.0	2.3	2.3	24.7	0.3	48.0	TWKPTLVILR	1225.8	1226.8	1225.8	1226.8
128.0 85.0	2.3 8.9	2.3 8.9	24.7 22.3	0.0	99.0 99.0	CSQFCTTGMDGGMSIWDVK	2178.9 2371.1	2179.9	2178.9 2371.1	2179.9 2372.1
85.0	8.9	8.9	22.3	2.0	99.0	AYHSFLVEPISCHAWNKDR CSQFCTTGMDGGMSIWDVK	2161.9	2372.1 2162.9	2161.9	2162.9
85.0	8.9	8.9	22.3	2.0	99.0	EVEERPAPTPWGSK	1581.8	1582.8	1581.8	1582.8
85.0	8.9	8.9	22.3	2.0	99.0	WAPNENKFAVGSGSR	1618.8	1619.8	1618.8	1619.8
85.0 O15144	8.9	8.9	22.3	0.9	86.0 /3 complex	FSAYIK	727.4	728.4	727.4	728.4
172.0	6.7	6.7	20.7	2.0	99.0	subunit 2 (ARP2/3 complex 34 kDa su DNTINLIHTFR	1342.7	1343.7	1342.7	protein 2/3 comple 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	YFQFQEEGKEGENR	1759.8	1760.8	1759.8	1760.8
172.0	6.7	6.7	20.7	0.7	79.0	MILLEVNNR	1100.6	1101.6	1100.6	1101.6
196.0	1.7	1.7	21.0	1.2	93.0	DNTINLIHTFR	1342.7	1343.7	1342.7	1343.7
196.0	1.7	1.7	21.0	0.5	71.0	YFQFQEEGKEGENR	1757.8	1758.8	1759.8	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
O15145	ARPC3_HUMAI	N	Actin-rela	ated protein 2.	/3 complex	subunit 3 (ARP2/3 complex 21 kDa su	(bunit) (p21-ARC) - B	os taurus (Bovin	e) : 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	SQFKGPAPR	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 O15204	2.3	2.3	15.2	0.0 C1 precursor	31.0	AYLQQLR) (A disintegrin and metalloproteinase	890.5	891.5	890.5	891.5
264.0	4.3	4.3	10.4	2.0	99.0	HLLGPDYTETLYSPR	1760.9	1761.9	1760.9	1761.9
264.0	4.3	4.3	10.4	2.0	99.0	LKPGTDCGGDAPNHTTE	1768.8	1769.8	1768.8	1769.8
264.0	4.3	4.3	10.4	0.3	44.0	GYFTHHHQR	1181.5	1182.5	1181.5	1182.6
81.0	4.2 4.2	4.2	7.7	2.0	99.0 99.0	ECTNLCCEALTCK	1657.7	1658.7	1657.7	1658.7 1761.9
81.0 81.0	4.2	4.2 4.2	7.7 7.7	2.0 0.2	39.0	HLLGPDYTETLYSPR YLLSQKPK	1760.9 975.6	1761.9 976.6	1760.9 975.6	976.6
216.0	3.2	3.2	8.5	2.0	99.0	LKPGTDCGGDAPNHTTE	1768.8	1769.8	1768.8	1769.8
216.0	3.2	3.2	8.5	1.2	93.0	GYFTHHHQR	1181.6	1182.6	1181.5	1182.6
043390 1	HNRPR_HUMA			neous nuclear	ribonucleo					
267.0 267.0	4.2 4.2	4.2	20.7 20.7	2.0 2.0	99.0 99.0	DLYEDELVPLFEK LKDYAFVHFEDR	1538.8	1609.8 1539.8	1608.8 1538.8	1609.8 1539.8
267.0	4.2	4.2	20.7	0.1	26.0	STAYEDYYYHPPPR	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	RGRAGYSQR	1130.5	1131.5	1130.5	1131.5
166.0 O43707	4.3 ACTN4_HUMAI		14.5 Alpha-act		84.0 nuscle alpha				1608.8	1609.8
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	COLEINFNTLOTK	1590.8	1591.8	1590.8	1591.8
10.0	41.3	41.3	35.2	2.0	99.0	DGLAFNALIHR	1225.6	1226.6	1225.7	1226.7
10.0	41.3	41.3	35.2	2.0	99.0	EGLLLWCQR	1173.6	1174.6	1173.6	1174.6
10.0	41.3	41.3	35.2	2.0	99.0	GISQEQMQEFR	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	35.2		99.0	KTFTAWCNSHLR	1519.7	1520.7	1519.7	1520.7
10.0	41.3	41.3	35.2	2.0	99.0	LEDFRDYR	1112.5	1113.5	1112.5	1113.5
10.0	41.3	41.3	35.2	2.0	99.0	LEDFRDYRR	1268.6	1269.6	1268.6	1269.6
10.0	41.3	41.3	35.2	2.0	99.0	LSNRPAFMPSEGK	1432.7	1433.7	1432.7	1433.7
10.0	41.3	41.3	35.2	2.0	99.0	QLEAIDQLHLEYAKR	1808.9	1809.9	1808.9	1809.9
10.0	41.3	41.3	35.2	2.0	99.0	RDHALLEEQSKQQSNEHLRR	2473.3	2474.3	2473.3	2474.3
10.0	41.3	41.3	35.2	2.0	99.0	TFTAWCNSHLR	1391.6	1392.7	1391.6	1392.6
10.0	41.3	41.3	35.2	2.0	99.0	TINEVENQILTR	1428.8	1429.8	1428.8	1429.8
10.0	41.3	41.3	35.2	2.0	99.0	TIPWLEDRVPQK	1480.8	1481.8	1480.8	1481.8
10.0	41.3	41.3	35.2	2.0	99.0	VGWEQLLTTIAR	1385.8	1386.8	1385.8	1386.8
	41.3	41.3	35.2	2.0	99.0	VLAGDKNFITAEELRR	1831.0	1832.0	1831.0	1832.0
10.0	41.3	41.3	35.2	2.0	99.0	VLAVNQENEHLMEDYEK	2060.0	2061.0	2060.0	2061.0
10.0	41.3	41.3	35.2	1.5	97.0	ELPPDQAEYCIAR	1560.7	1561.7	1560.7	1561.7
	41.3	41.3	35.2	1.5	97.0	GYEEWLLNEIR	1420.7	1421.7	1420.7	1421.7
10.0			35.2	1.1	92.0	HRPELIEYDKLR	1567.8	1568.8	1567.8	1568.9

10.0 10.0		41.3 41.3	35.2 35.2	1.0 0.2	89.0 30.0	HTNYTMEHIR DAKGISQEQMQEFR	1300.6 1665.8	1301.6 1666.8	1300.6 1665.8	1301.6 1666.8
10.0 44.0	41.3 6.9	41.3 6.9	35.2 13.9	0.0 2.0	99.0 99.0	LEDFRDYRR ELPPDQAEYCIAR	1268.6 1560.7	1269.6 1561.7	1268.6 1560.7	1269.6 1561.7
44.0 44.0 44.0	6.9	6.9 6.9 6.9	13.9 13.9 13.9	2.0 1.7 0.9	99.0 98.0 88.0	VGWEQLLTTIAR LEDFRDYR LSNRPAFMPSEGK	1385.7 1112.5 1432.7	1386.8 1113.5 1433.7	1385.8 1112.5 1432.7	1386.8 1113.5 1433.7
44.0 44.0	6.9	6.9 6.9	13.9 13.9	0.3	44.0 84.0	LEDFRDYRR ELPPDQAEYCIAR	1268.6 1557.7	1269.6 1558.7	1268.6 1560.7	1269.6 1561.7
44.0 22.0 22.0	6.9 22.9 22.9	6.9 22.9 22.9	13.9 32.3 32.3	0.0 2.0 2.0	95.0 99.0 99.0	LEDFRDYR ASFNHFDKDHGGALGPEEFK EGLLLWCQR	1112.5 2202.0	1113.6 2203.0 1174.6	1112.5 2202.0	1113.5 2203.0 1174.6
22.0 22.0 22.0	22.9 22.9 22.9	22.9 22.9 22.9	32.3 32.3 32.3	2.0 2.0 2.0	99.0 99.0	ELPPDQAEYCIAR GISQEQMQEFR	1173.6 1560.7 1351.6	1561.7 1352.6	1173.6 1560.7 1351.6	1561.7 1352.6
22.0 22.0	22.9 22.9	22.9 22.9	32.3 32.3	2.0 2.0	99.0 99.0	HTNYTMEHIR KTFTAWCNSHLR	1300.6 1519.7	1301.6 1520.7	1300.6 1519.7	1301.6 1520.7
22.0 22.0 22.0	22.9 22.9 22.9	22.9 22.9 22.9	32.3 32.3 32.3	2.0 2.0 2.0	99.0 99.0 99.0	LEDFRDYR LSNRPAFMPSEGK TINEVENQILTR	1112.5 1432.7 1428.8	1113.5 1433.7 1429.8	1112.5 1432.7 1428.8	1113.5 1433.7 1429.8
22.0 22.0	22.9 22.9	22.9 22.9	32.3 32.3	2.0	99.0 98.0	VLAGDKNFITAEELRR LEDFRDYRR	1831.0 1268.6	1832.0 1269.6	1831.0 1268.6	1832.0 1269.6
22.0 22.0	22.9 22.9	22.9 22.9	32.3 32.3	0.8 0.4	85.0 56.0	KHEAFESDLAAHQDR EAILAIHKEAQR ASFNHFDKDHGGALGPEEFK	1752.8 1377.8	1753.8 1378.8	1752.8 1377.8	1753.8 1378.8
22.0 22.0 22.0	22.9 22.9 22.9	22.9 22.9 22.9	32.3 32.3 32.3	0.0 0.0 0.0	99.0 20.0 97.0	ASFNHFDRDHGGALGPEEFK ASFNHFDKDHGGALGPEEFK LEDFRDYRR	2203.0 2199.0 1268.6	2204.0 2200.0 1269.6	2203.0 2202.0 1268.6	2204.0 2203.0 1269.6
212.0		6.0	Asparaginyl 9.3	2.0	etase, cytor 99.0	olasmic (EC 6.1.1.22) (AsparaginetRNA ligas EGIDPTPYYWYTDQR	1902.8	mo sapiens (Hur 1903.9	nan) 1902.8	1903.8
212.0 212.0 295.0	6.0	6.0 6.0 2.0	9.3 9.3 6.4	2.0 2.0 2.0	99.0 99.0 99.0	IFDSEEILAGYKR NLMFLVLR NLMFLVLR	1539.8 1004.6 1004.6	1540.8 1005.6 1005.6	1539.8 1004.6 1004.6	1540.8 1005.6 1005.6
O75083	WDR1_HUMAN 10.0	10.0	WD repeat p		tin-interact 99.0	ing protein 1) (AIP1) (NORI-1) - Homo sapier IKDIAWTEDSKR	ns (Human) 1460.8	1461.8	1460.8	1461.8
108.0 108.0	10.0	10.0 10.0	16.5 16.5	2.0	99.0 99.0	MTVDESGQLISCSMDDTVR VFASLPQVER	2142.9 1144.6	2144.0 1145.6	2142.9 1144.6	2143.9 1145.6
108.0 108.0 111.0	10.0	10.0 10.0 6.9	16.5 16.5 14.4	2.0 2.0 2.0	99.0 99.0 99.0	YAPSGFYIASGDVSGKLR YEYQPFAGK IKDIAWTEDSKR	1887.0 1101.5 1460.8	1888.0 1102.5 1461.8	1887.0 1101.5 1460.8	1888.0 1102.5 1461.8
111.0 111.0	6.9	6.9 6.9	14.4 14.4	2.0 1.3	99.0 95.0	YEYQPFAGK VFASLPQVER	1101.5 1144.6	1102.5 1145.6	1101.5 1144.6	1102.5 1145.6
111.0 111.0	6.9	6.9 6.9	14.4 14.4	0.9 0.5	88.0 65.0	FTIGDHSR LATGSDDNCAAFFEGPPFKFK	931.5 2318.1	932.5 2319.1	931.5 2318.1	932.5 2319.1
111.0 075368 320.0	SH3L1_HUMAN	6.9 4.0	14.4 SH3 domair 24.6	0.2 n-binding glu 2.0	33.0 tamic acid- 99.0	YAPSGFYIASGDVSGKLR cich-like protein - Homo sapiens (Human) ENNAVYAFLGLTAPPGSK	1887.0	1888.0 1849.0	1887.0	1888.0 1848.9
320.0 373.0	4.0 2.0	4.0 2.0	24.6 8.8	2.0 2.0	99.0 99.0	GDYDAFFEAR GDYDAFFEAR	1189.5 1189.5	1190.6 1190.5	1189.5 1189.5	1190.5 1190.5
075791 553.0 384.0	2.0	2.0 1.7	GRB2-relate 3.3 11.2	ed adapter p 2.0 1.7	rotein 2 (GA 99.0 98.0	DS protein) (Growth factor receptor-binding p YLOHHHFHQER YLQHHHFHQER	protein) (GRBLC 1530.7 1530.7	G) (Grf40 adapter 1531.7 1531.7	protein) (Grf-40 1530.7 1530.7	0) (GRB-2-like pr 1531.7 1531.7
	LDHA_HUMAN	11.3	L-lactate de			C 1.1.1.27) (LDH-A) (LDH muscle subunit) (LI GEMMDLQHGSLFLR				Renal carcinoma 1633.8
129.0 129.0	9.1	11.3 11.3	30.4 30.4	2.0 2.0	99.0 99.0	KSADTLWGIQKELQF SADTLWGIQKELQF	1762.9 1634.8	1763.9 1635.8	1762.9 1634.8	1763.9 1635.8
129.0 129.0 129.0	9.1	11.3 11.3 11.3	30.4 30.4 30.4	1.5 1.2 0.2	99.0 99.0 43.0	SADTLWGIQK DLADELALVDVIEDK RVHPVSTMIK	1117.6 1656.8 1166.7	1118.6 1657.8 1167.7	1117.6 1656.8 1166.7	1118.6 1657.9 1167.7
129.0 129.0	9.1	11.3 11.3	30.4 30.4	0.1	25.0 26.0	FRYLMGER OOEGESRLNLVOR	1070.5 1555.8	1071.5 1556.8	1070.5 1555.8	1071.5 1556.8
129.0 156.0	2.0	11.3 4.0	30.4 11.1	0.0 2.0	83.0 99.0	VIGSGCNLDSAR SADTLWGIQKELQF	1247.6 1634.8	1248.6 1635.9	1247.6 1634.8	1248.6 1635.8
156.0 P00491 166.0	PNPH_HUMAN	7.0	Purine nucle 32.9	0.0 eoside phosp 2.0	99.0 horylase (E 99.0	SADTLWGIQK C 2.4.2.1) (Inosine phosphorylase) (PNP) - H FGDRFPAMSDAYDR		1118.6 uman) 1647.7	1117.6	1118.6
166.0 166.0	7.0	7.0 7.0 7.0	32.9 32.9 32.9	2.0 2.0 2.0	99.0 99.0 99.0	FHMYEGYPLWK LGADAVGMSTVPEVIVAR	1646.7 1469.7 1784.0	1470.7 1785.0	1469.7 1784.0	1470.7 1470.7 1785.0
166.0 141.0	7.0 5.7	7.0 5.7	32.9 29.1	1.0 2.0	89.0 99.0	FEVGDIMLIR FEVGDIMLIR	1191.6 1191.6	1192.6 1192.6	1191.6 1191.6	1192.6 1192.6
141.0 141.0		5.7 5.7	29.1 29.1	2.0 1.7 cerate kinas	99.0 98.0 e 1 (EC 2.7.	FHMYEGYPLWK FGDRFPAMSDAYDR 2.3) (Primer recognition protein 2) (PRP 2) (C	1469.7 1646.7	1470.7 1647.7	1469.7 1646.7	1470.7 1647.7
22.0 22.0	28.0 28.0	28.0 28.0	53.0 53.0	2.0 2.0	99.0 99.0	ACANPAAGSVILLENLR AEPAKIEAFR	1767.9 1130.6	1768.9 1131.6	1767.9 1130.6	1768.9 1131.6
22.0 22.0	28.0	28.0 28.0	53.0 53.0	2.0	99.0 99.0 99.0	AHSSMVGVNLPQK ELNYFAK	1366.7 883.4	1367.7 884.5	1366.7 883.4	1367.7 884.5
22.0 22.0 22.0	28.0	28.0 28.0 28.0	53.0 53.0 53.0	2.0 2.0 2.0	99.0 99.0 99.0	FHVEEEGKGKDASGNKVK GCITIIGGGDTATCCAK ITLPVDFVTADKFDENAK	1958.0 1753.8 2022.0	1959.0 1754.8 2023.0	1958.0 1753.8 2022.0	1959.0 1754.8 2023.0
22.0 22.0	28.0	28.0 28.0	53.0 53.0	2.0	99.0 99.0	LGDVYVNDAFGTAHR TGQATVASGIPAGWMGLDCGPESSK	1633.8 2476.1	1634.8 2477.1	1633.8 2476.1	1634.8 2477.1
22.0 22.0	28.0	28.0 28.0	53.0 53.0	2.0 2.0	99.0 99.0	TGQATVASGIPAGWMGLDCGPESSKK VDFNVPMKNNQITNNQR	2604.2 2031.0	2605.2 2032.0	2604.2 2031.0	2605.2 2032.0
22.0 22.0 22.0	28.0	28.0 28.0 28.0	53.0 53.0 53.0	2.0 2.0 2.0	99.0 99.0 99.0	VKAEPAKIEAFR VLNNMEIGTSLFDEEGAK WNTEDKVSHVSTGGGASLELLEGK	1357.8 1965.9 2513.2	1358.8 1966.9 2514.2	1357.8 1965.9 2513.2	1358.8 1966.9 2514.2
22.0 22.0	28.0	28.0 28.0	53.0 53.0	0.0 0.0	99.0 99.0	AEPAKIEAFR AHSSMVGVNLPQK	1130.6 1366.7	1131.6 1367.7	1130.6 1366.7	1131.6 1367.7
22.0 76.0	4.6	28.0 4.6	53.0 30.5	0.0 2.0	99.0 99.0	LGDVYVNDAFGTAHR ITLPVDFVTADKFDENAK	1634.8 2022.0	1635.8 2023.0	1634.8 2022.0	1635.8 2023.0
76.0 76.0 76.0	4.6	4.6 4.6 4.6	30.5 30.5 30.5	2.0 0.3 0.2	99.0 53.0 39.0	LGDVYVNDAFGTAHR VDFNVPMKNNQITNNQR VLNNMEIGTSLFDEEGAK	1633.8 2031.0 1965.9	1634.8 2032.0 1967.0	1633.8 2031.0 1965.9	1634.8 2032.0 1966.9
30.0 30.0		20.8 20.8	45.6 45.6	2.0 2.0	99.0 99.0	ACANPAAGSVILLENLR AEPAKIEAFR	1919.9 1130.6	1920.9 1131.6	1919.9 1130.6	1920.9 1131.6
30.0 30.0	20.8 20.8	20.8 20.8	45.6 45.6	2.0 2.0	99.0 99.0	AHSSMVGVNLPQK ALESPERPFLAILGGAK	1366.7 1768.0	1367.7 1769.0	1366.7 1768.0	1367.7 1769.0
30.0 30.0	20.8 20.8	20.8 20.8	45.6 45.6	2.0 2.0	99.0 99.0	FHVEEEGKGKDASGNKVK GCITIIGGGDTATCCAK ITLPVDFVTADKFDENAK	1958.0 1753.8	1959.0 1754.8	1958.0 1753.8	1959.0 1754.8
30.0 30.0 30.0	20.8 20.8 20.8	20.8 20.8 20.8	45.6 45.6 45.6	2.0 2.0 2.0	99.0 99.0 99.0	LGDVYVNDAFGTAHR SLLGKDVLFLKDCVGPEVEK	2022.0 1633.8 2245.2	2023.0 1634.8 2246.2	2022.0 1633.8 2245.2	2023.0 1634.8 2246.2
30.0 30.0	20.8	20.8 20.8	45.6	2.0	99.0 78.0	VDFNVPMKNNQITNNQR ELNYFAK	2031.0 883.5	2032.0 884.5	2031.0 883.4	2032.0 884.5
30.0 30.0 30.0	20.8	20.0	45.6	0.7				004.5		1700.0
	20.8 20.8 20.8	20.8 20.8	45.6 45.6	0.0 0.0	93.0 99.0	ACANPAAGSVILLENLR LGDVYVNDAFGTAHR	1761.9 1634.8	1762.9 1635.8	1767.9 1634.8	1768.9 1635.8
65.0	20.8 20.8 20.8 20.8 20.8 A2MG_HUMAN	20.8	45.6 45.6 45.6	0.0	99.0 99.0			1762.9 1635.8 2033.0	1767.9	
65.0 65.0	20.8 20.8 20.8 20.8 20.8 [A2MG_HUMAN] 15.3 15.3	20.8 20.8 20.8 15.3 15.3	45.6 45.6 45.6 Alpha-2-ma 11.9 11.9	0.0 0.0 0.0 acroglobulin 2.0 2.0 2.0	99.0 99.0 precursor (A 99.0 99.0 99.0	LGDVYVNDAFGTAHR VDFNVPMKNNQITNNQR IJpha-2-M) - Homo sapiens (Human) AIGYLNTGYOR MVSGFIPLKPTVK NALFCLESAWK	1634.8 2031.9 1310.7 1415.8 1323.6	1762.9 1635.8 2033.0 1311.7 1416.8 1324.6	1767.9 1634.8 2032.0 1310.7 1415.8 1323.6	1635.8 2033.0 1311.7 1416.8 1324.6
65.0 65.0 65.0 65.0	20.8 20.8 20.8 20.8 A2MG_HUMAN 15.3 15.3 15.3 15.3 15.3	20.8 20.8 20.8 15.3 15.3 15.3 15.3 15.3	45.6 45.6 45.6 Alpha-2-ma 11.9 11.9 11.9 11.9	0.0 0.0 0.0 ecroglobulin 2.0 2.0 2.0 2.0 2.0	99.0 99.0 precursor (A 99.0 99.0 99.0 99.0 99.0	LGDVYVNDAFGTAHR VDFNVPMKNNQITNNQR Upha-2-M) - Homo sapiens (Human) AIGYLNTGYOR MYSGFIPLKPTVK NALFCLESAWK SGGRTEHPFTVEEFVLPK VTAAPOSVCALR	1634.8 2031.9 1310.7 1415.8 1323.6 2001.0 1301.7	1762.9 1635.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7	1767.9 1634.8 2032.0 1310.7 1415.8 1323.6 2001.0 1301.7	1635.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7
65.0 65.0 65.0	20.8 20.8 20.8 20.8 15.3 15.3 15.3 15.3 15.3 15.3 15.3	20.8 20.8 20.8 15.3 15.3 15.3 15.3	45.6 45.6 45.6 Alpha-2-ma 11.9 11.9 11.9	0.0 0.0 0.0 acroglobulin 2.0 2.0 2.0 2.0	99.0 99.0 precursor (A 99.0 99.0 99.0 99.0	LGDVYVNDAFGTAHR VDFNVPMKNNQITNNOR Upha-2-M) - Homo sapiens (Human) AIGYLNTGYOR MVSGFIPLKPTVK NALFCLESAWK SGGRTEHPTTVEEFVLPK	1634.8 2031.9 1310.7 1415.8 1323.6 2001.0	1762.9 1635.8 2033.0 1311.7 1416.8 1324.6 2002.0	1767.9 1634.8 2032.0 1310.7 1415.8 1323.6 2001.0	1635.8 2033.0 1311.7 1416.8 1324.6 2002.0
65.0 65.0 65.0 65.0 65.0 65.0 65.0	20.8 20.8 20.8 20.8 15.3 15.3 15.3 15.3 15.3 15.3 15.3 15.3	20.8 20.8 20.8 15.3 15.3 15.3 15.3 15.3 15.3 15.3 15.3	45.6 45.6 45.6 Alpha-2-ma 11.9 11.9 11.9 11.9 11.9 11.9 11.9 11.	0.0 0.0 0.0 0.0 0.0 0.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	LGDVYVNDAFGTAHR VDFNVPMKNNQITNNOR IJDha 2-M) - Homo sapiens (Human) AIGYLNTGVPR MVSGFIPLKPTVK NALFCLESAWK SGGRTEHPFTVEEFVLPK VTAAPOSVCALR YGAATFIRIG NOGNTWLTAFVLK ALLAYAFALGANDK FSGGLNSHGCFYOQVKTK YGAATFIR	1634.8 2031.9 1310.7 1415.8 1323.6 2001.0 1301.7 1043.5 1635.7 1606.8 2056.9 1013.5	1762.9 1635.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7 1044.5 1636.7 1607.9 2057.9 1014.5	1767.9 1634.8 2032.0 1310.7 1415.8 1323.6 2001.0 1301.7 1043.5 1635.7 1606.9 2056.9 1013.5	1635.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7 1044.5 1636.7 1607.9 2057.9
65.0 65.0 65.0 65.0 65.0 65.0 65.0 65.0	20.8 20.8 20.8 20.8 20.8 20.8 20.8 15.3 15.3 15.3 15.3 15.3 15.3 15.3 15.3	20.8 20.8 20.8 15.3 15.3 15.3 15.3 15.3 15.3 15.3 15.3	45.6 45.6 45.6 Alpha-2-ma 11.9 11.9 11.9 11.9 11.9 11.9 11.9 11.	0.0 0.0 0.0 0.0 0.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	LGDVYVNDAFGTAHR VDFNVPMKNNQITNNOR IJDha 2-M) - Homo sapiens (Human) AIGYLNTGYDR MVSGFIPLKPTVK NALFCLESAWK SGGRTEHPFTVEEFVLPK VTAAPOSVCALR VGAATFIRIG NOGNTWLTAFVLK ALLAYAFALAGNODK FSGGLNSHGCFYOOVKTK VGAATFIR AIGYLNTGYDR AIVLNTGYDR ATVLNTLYCR ATVLNTLYCR ATVLNTLYCR	1634.8 2031.9 1310.7 1415.8 1323.6 2001.0 1301.7 1043.5 1635.7 1606.8 2056.9 1013.5 1310.7 1017.6	1762.9 1685.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7 1044.5 1636.7 1607.9 2057.9 1014.5 1311.7	1767.9 1634.8 2032.0 1310.7 1415.8 1323.6 2001.0 1301.7 1043.5 1635.7 1606.9 2056.9 1013.5 1310.7 1017.6	1635.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7 1636.7 1607.9 2057.9 1014.5 1311.7 1018.6
65.0 65.0 65.0 65.0 65.0 65.0 65.0 65.0	20.8 20.8 20.8 20.8 20.8 20.8 20.8 20.8	20.8 20.8 20.8 15.3 15.3 15.3 15.3 15.3 15.3 15.3 15.3	45.6 45.6 45.6 Alpha-2-ma 11.9 11.9 11.9 11.9 11.9 11.9 11.9 11.	0.0 0.0 0.0 0.0 0.0 0.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	LGDVYVNDAFGTAHR VDFNVPMKNNOITNNOR Upha-2-M) - Homo sapiens (Human) AIGYLNTGYOR WYSGFIPLKPTVK NALFCLESAWK NALFCLESAWK VTAAPOSVCALR YGAATFIRG NOGNTWLTAFVLK ALLAYAFALAGNODK FSGQINSHGCFYQOVKTK YGAATFIR AIGYLNTGYOR	1634.8 2031.9 1310.7 1415.8 1323.6 2001.0 1301.7 1043.5 1635.7 1606.8 2056.9 1013.5 1310.7	1762.9 1635.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7 1044.5 1636.7 1607.9 2057.9 1014.5 1311.7	1767.9 1634.8 2032.0 1310.7 1415.8 1323.6 2001.0 1301.7 1043.5 1635.7 1606.9 2056.9 1013.5 1310.7	1635.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7 1044.5 1636.7 1607.9 2057.9 1014.5 1311.7
65.0 65.0 65.0 65.0 65.0 65.0 65.0 65.0	20.8 20.8 20.8 20.8 20.8 20.8 20.8 20.8	20.8 20.8 20.8 15.3 15.3 15.3 15.3 15.3 15.3 15.3 15.3	45.6 45.6 45.6 Alpha-2-ma 11.9 11.9 11.9 11.9 11.9 11.9 11.9 11.	0.0 0.0 0.0 2.0 2.0 2.0 2.0 2.0 2.0 1.5 1.4 0.2 0.1 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	LGDVYVNDAFGTAHR VDFNVPMKNNQITNNOR IJDha 2-M) - Homo sapiens (Human) AIGYLNTGYDR MYSGFIPLKPTVK MAFCLESAWK SGGRTEHPFTVEEFVLPK YTAAPOSVCALR YGAATFTRTG NOGNTWLTAFVLK ALLAYAFALAGNDIK FSGGLINSHGCFYQOVKTK YGAATFTR AIGYLNTGYDR ATVLNITYOR ATVLNITYOR ATVLNITYOR MYSGFIPLKPTVK	1634.8 2031.9 1310.7 1415.8 1323.6 2001.0 1301.7 1043.5 1635.7 1606.8 2056.9 1013.5 1310.7 1017.6 1446.6 1415.8	1762.9 1635.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7 1044.5 1607.9 2057.9 1014.5 1311.7 1018.6 1447.6	1767.9 1634.8 2032.0 1310.7 1415.8 1323.6 2001.0 1301.7 1043.5 1635.7 1606.9 2056.9 1013.5 1310.7 1017.6 1446.7 1415.8	1635.8 2033.0 1311.7 1416.8 1324.6 2002.0 1302.7 1044.5 1636.7 1607.9 2057.9 1014.5 1311.7 1018.6 1447.7

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		30.0	NQGNTWLTAFVLK	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	AIGYLNTGYQR	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	VTAAPQSVCALR	1301.7	1302.7	1301.7	1302.7
18.0	26.1	26.1	17.1	2.0	99.0	VYDYYETDEFAIAEYNAPCSK	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	1606.8	1607.9	1606.9	1607.9
18.0	26.1	26.1	17.1	0.5	70.0	KSGGRTEHPFTVEEFVLPK	2554.4	2555.4	2554.4	2555.4
18.0	26.1	26.1	17.1	0.2	33.0	FSGQLNSHGCFYQQVKTK	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
	26.1 MP1_HUMAN	26.1			99.0 tor 1 precu	NALFCLESAWK rsor (TIMP-1) (Erythroid-potentiating activity				
319.0	4.0	4.0	14.5	2.0	99.0	EPGLCTWQSLR	1345.6	1346.7	1345.6	1346.7
319.0	4.0	4.0	14.5		99.0	LOSGTHCLWTDQLLQGSEK	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		99.0	EPGLCTWQSLR	1345.6	1346.7	1345.6	1346.7
195.0 PO1034 CY 302.0	4.0 /TC_HUMAN 4.0	4.0	13.0 Cystatin-C pr 25.3	2.0 recursor (Cy 2.0	99.0 ystatin-3) (I 99.0	FVYTPAMESVCGYFHR Neuroendocrine basic polypeptide) (Gamma-t ALDFAVGEYNK	1962.9 race) (Post-gam 1225.6	1963.9 ma-globulin) - H 1226.6	1962.9 lomo sapiens (Hu 1225.6	1963.9 iman) 1226.6
302.0 104.0	4.0 4.0 3.4	4.0 4.0 3.4	25.3 25.3 26.0	2.0	99.0 99.0	LVGGPMDASVEEEGVRR ALDFAVGEYNK	1799.9 1225.6	1800.9 1226.6	1799.9 1225.6	1800.9 1226.6
104.0 355.0	3.4	3.4	26.0 13.7	1.4	96.0 99.0	TQPNLDNCPFHDQPHLK ALDFAVGEYNK	2060.0 1225.6	2061.0 1226.6	2060.0 1225.6	2061.0 1226.6
P01834 KA 260.0		4.5		in C region	- Homo sap	ilens (Human) ADYEKHKVYACEVTHQGLSSPVTK	2746.3	2747.3	2746.3	2747.3
260.0	4.5	4.5	37.7	2.0	99.0	VYACEVTHOGLSSPVTK	1874.9	1875.9	1874.9	1875.9
260.0	4.5	4.5	37.7		64.0	SGTASVVCLLNNFYPR	1797.9	1798.9	1797.9	1798.9
188.0	4.0	4.0	31.1	2.0	99.0	SGTASVVCLLNNFYPR	1797.9	1798.9	1797.9	1798.9
188.0	4.0	4.0	31.1		99.0	VYACEVTHQGLSSPVTK	1874.9	1875.9	1874.9	1875.9
	AC_HUMAN 3.7	3.7	I g lambda ch		ns - Homo s 99.0	apiens (Human) YAASSYLSLTPEQW	1677.8	1678.8	1677.7	1678.7
332.0	3.7	3.7	39.0	1.5	97.0	SYSCOVTHEGSTVEK	1710.8	1711.8	1710.8	1711.8
332.0	3.7	3.7	39.0	0.1	29.1	QPKAAPSVTLFP	1256.7	1257.7	1256.7	1257.7
64.0	5.3	5.3	19.0	2.0	99.0	YAASSYLSLTPEOW	1677.8	1678.8	1677.7	1678.7
64.0	5.3	5.3	19.0	2.0	99.0	YAASSYLSLTPEOWK	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 PO1871 MU	3.7	3.7	28.6 Ig mu chain (1.7 C region - F	98.0 Iomo sapier	YAASSYLSLTPEQWK	1742.9	1743.9	1742.9	1743.9
570.0	1.7	1.7	1.8	1.7	98.0	ÒIQVSWLR	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 P02746 C1	7.6 IQB_HUMAN	7.6	17.2 Complement	0.0 C1q subcor	96.0 nponent sul	QIQVSWLR bunit B precursor - Homo sapiens (Human)	1028.6	1029.6	1028.6	1029.6
95.0	4.0	4.0	13.5	2.0	99.0	FDHVITNMNNNYEPR	1862.8	1863.8	1862.8	1863.8
95.0	4.0	4.0	13.5	2.0	99.0	VPGLYYFTYHASSR	1659.8	1660.8	1659.8	1660.8
	2.0 IQC_HUMAN	2.0	14.3 Complement				1659.8	1660.8	1659.8	1660.8
386.0	2.4	2.4	14.7	1.7	98.0	OTHOPPAPNSLIR	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
190.0 354.0	2.0	2.0 2.0	3.7 10.2	2.0	99.0 99.0	FQSVFTVTR QTHQPPAPNSLIR	1083.6 1457.8	1084.6 1458.8	1083.6 1457.8	1084.6 1458.8
P02751 FI	NC_HUMAN 1.4	1.4	Fibronectin p	1.4	N) (Cold-in 96.0	soluble globulin) (CIG) - Homo sapiens (Hum YQCYCYGR	1168.4	1169.5	1168.4	1169.5
22.0	13.3	13.3	13.7	2.0	99.0	GEWTCIAYSQLR	1482.7	1483.7	1482.7	1483.7
22.0	13.3	13.3	13.7		99.0	IGDQWDKQHDMGHMMR	1983.9	1984.9	1983.9	1984.9
22.0 22.0 22.0	13.3 13.3	13.3 13.3	13.7 13.7	2.0 2.0 1.7	99.0 99.0	LLCQCLGFGSGHFR YQCYCYGR	1650.8 1168.4	1651.8 1169.5	1650.8 1168.4 1354.7	1651.8 1169.5
22.0	13.3 13.3	13.3 13.3	13.7 13.7	1.5	98.0 97.0	IYLYTLNDNAR QDGHLWCSTTSNYEQDQK	1354.7 2195.9	1355.7 2196.9	2195.9	1355.7 2196.9
22.0	13.3	13.3	13.7	1.4	96.0	EYLGAICSCTCFGGQR	1877.8	1878.8	1877.8	1878.8
22.0	13.3	13.3	13.7	0.6	72.0	GATYNIIVEALKDQQR	1817.9	1819.0	1818.0	1819.0
22.0	13.3	13.3	13.7	0.1	11.0	TFYSCTTEGR	1220.5	1221.5	1220.5	1221.5
27.0	21.3	21.3	16.4	2.0	99.0	GATYNIIVEALKDQQR	1818.0	1819.0	1818.0	1819.0
27.0	21.3	21.3	16.4		99.0	GEWTCIAYSQLR	1482.7	1483.7	1482.7	1483.7
27.0 27.0 27.0	21.3 21.3 21.3	21.3 21.3 21.3	16.4 16.4	2.0	99.0 99.0	HTSVQTTSSGSGPFTDVR HYQINQQWER	1862.9 1400.7	1863.9 1401.7	1862.9 1400.7	1863.9 1401.7
27.0 27.0 27.0	21.3 21.3	21.3 21.3	16.4 16.4	2.0 2.0	99.0 99.0	LLCQCLGFGSGHFR TYLGNALVCTCYGGSR	1650.8 1790.8	1651.8 1791.8	1650.8 1790.8	1651.8 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		99.0	WLPSSSPVTGYR	1348.7	1349.7	1348.7	1349.7
27.0	21.3	21.3	16.4	2.0	99.0	WSRPQAPITGYR	1430.7	1431.8	1430.7	1431.7
27.0	21.3	21.3	16.4		99.0	YQCYCYGR	1168.4	1169.5	1168.4	1169.5
27.0	21.3	21.3	16.4	1.2	93.0	IGDQWDKQHDMGHMMR	1999.8	2000.9	1999.8	2000.9
27.0	21.3	21.3	16.4		99.0	YQCYCYGR	1171.5	1172.5	1168.4	1169.5
P02792 FR 550.0	RIL_HUMAN 2.0	2.0		chain (Ferr	itin L subur 99.0	hit) - Homo sapiens (Human) LGGPEAGLGEYLFER	1606.8	1607.8	1606.8	1607.8
370.0 P02795 M1	2.0 T2_HUMAN	2.0	8.6 Metallothione	2.0 ein-2 (MT-2	99.0 !) (Metalloth	LGGPEAGLGEYLFER nionein-II) (MT-II) (Metallothionein-2A) - Ho	1606.8 mo sapiens (Hur	1607.8 nan)	1606.8	1607.8
216.0	6.0	6.0	82.0	2.0	99.0	CAQGCICKGASDKCSCCA	2074.7	2075.7	2074.8	2075.8
216.0	6.0	6.0	82.0	2.0	99.0	MDPNCSCAAGDSCTCAGSCK	2249.8	2250.8	2249.8	2250.8
216.0	6.0	6.0	82.0	2.0	99.0	SCCSCCPVGCAK	1444.5	1445.5	1444.5	1445.5
216.0	6.0	6.0	82.0	0.0	99.0	MDPNCSCAAGDSCTCAGSCK	2252.8	2253.8	2252.8	2253.8
216.0	6.0	6.0	82.0	0.0	99.0	MDPNCSCAAGDSCTCAGSCK	2192.7	2193.7	2192.7	2193.7
216.0	6.0	6.0	82.0		99.0	MDPNCSCAAGDSCTCAGSCK	2253.8	2254.8	2253.7	2254.7
216.0	6.0	6.0	82.0	0.0	47.0	MDPNCSCAAGDSCTCAGSCK	2207.7	2208.7	2207.7	2208.8
216.0	6.0	6.0	82.0	0.0	99.0	SCCSCCPVGCAK	1447.5	1448.5	1444.5	1445.5
216.0	6.0	6.0	82.0	0.0	99.0	SCCSCCPVGCAK	1447.5	1448.5	1444.5	1445.5
114.0	6.7	6.7	62.3	2.0	99.0	KSCCSCCPVGCAK	1573.6	1574.6	1572.6	1573.6
114.0	6.7	6.7	62.3	2.0	99.0	MDPNCSCAAGDSCTCAGSCK	2249.8	2250.8	2249.8	2250.8
114.0	6.7	6.7	62.3		99.0	SCCSCCPVGCAK	1444.5	1445.5	1444.5	1445.5
114.0 114.0	6.7 6.7	6.7 6.7	62.3 62.3	0.7	81.0 99.0	MDPNCSCAAGDSCTCAGSCKCKECK MDPNCSCAAGDSCTCAGSCK	2955.0 2250.7	2956.0 2251.8	2955.0 2250.7	2956.0 2251.7
114.0	6.7	6.7	62.3	0.0	99.0	MDPNCSCAAGDSCTCAGSCK	2253.8	2254.8	2253.7	2254.7
114.0	6.7	6.7	62.3		97.0	MDPNCSCAAGDSCTCAGSCK	2265.8	2266.8	2265.8	2266.8
114.0 114.0	6.7 6.7	6.7 6.7	62.3 62.3	0.0 0.0	99.0 99.0	SCCSCCPVGCAK SCCSCCPVGCAK ding factor) (S-protein) (V75) [Contains: Vitr	1446.5 1446.5	1447.5 1447.5 upit: Vitropection	1444.5 1444.5 V10 subupit: So	1445.5 1445.5 matemadia B1 -
P04004 VT 482.0 119.0	7NC_HUMAN 2.0 2.5	2.0 2.5	Vitronectin p 6.1	2.0 2.0	erum-sprea 99.0 99.0	DVWGIEGPIDAAFTR DVWGIEGPIDAAFTR DVWGIEGPIDAAFTR	1645.8 1645.8	1646.8	1645.8 1645.8	1646.8
119.0 119.0 159.0	2.5 2.5 4.5	2.5 2.5 4.5	12.3 12.3 13.6	0.5 2.0	71.0 99.0	SIAQYWLGCPAPGHL DVWGIEGPIDAAFTR	1645.8 1645.8 1645.8	1646.8 1646.8 1646.8	1645.8 1645.8 1645.8	1646.8 1646.8 1646.8
159.0 159.0 159.0	4.5 4.5 4.5	4.5 4.5 4.5	13.6 13.6 13.6	2.0 2.0 0.4	99.0 99.0 59.0	GQYCYELDEK AVRPGYPK	1288.6 886.5	1289.6 887.5	1288.6 886.5	1289.6 887.5
159.0	4.5 4.5 _DOA_HUMAN	4.5 4.5	13.6 13.6 Fructose-bisp	0.1	23.0	AVRPGYPK GSQYWR EC 4.1.2.13) (Muscle-type aldolase) (Lung car	795.4	796.4	795.4	887.5 796.4
16.0 16.0	37.1 37.1	37.1 37.1	57.7 57.7	2.0 2.0 2.0	99.0 99.0	AAQEEYVKR ADDGRPFPQVIK	1092.6 1341.6	1093.6 1342.7	1092.6 1341.7	1093.6 1342.7
16.0 16.0	37.1 37.1 37.1	37.1 37.1 37.1	57.7 57.7 57.7	2.0	99.0 99.0	ALANSLACOGK AWGGKKENLK	1131.6 1129.6	1132.6 1130.6	1131.6 1129.6	1132.6 1130.6
16.0	37.1	37.1	57.7	2.0	99.0	AWGGKKENLKAAQEEYVKR	2204.2	2205.2	2204.2	2205.2
16.0	37.1	37.1	57.7		99.0	CAQYKKDGADFAK	1483.7	1484.7	1483.7	1484.7
		2								

16.0	37.1	37.1	57.7	2.0		DGADFAKWR	1064.5	1065.5	1064.5	1065.5
16.0 16.0	37.1 37.1	37.1 37.1	57.7 57.7	2.0 2.0		IGEHTPSALAIMENANVLAR IVAPGKGILAADESTGSIAKR	2106.1 2053.1	2107.1 2054.2	2106.1 2053.2	2107.1 2054.2
16.0	37.1	37.1	57.7	2.0		KELSDIAHR	1067.6	1068.6	1067.6	1068.6
16.0	37.1	37.1	57.7	2.0		LQSIGTENTEENRR	1645.8	1646.8	1645.8	1646.8
16.0 16.0	37.1 37.1	37.1 37.1	57.7 57.7	2.0		PYQYPALTPEQK PYQYPALTPEQKK	1433.7 1561.8	1434.7 1562.8	1433.7 1561.8	1434.7 1562.8
16.0	37.1	37.1	57.7	2.0		PYQYPALTPEQKKELSDIAHR	2483.3	2484.3	2483.3	2484.3
16.0	37.1	37.1	57.7	2.0		RLQSIGTENTEENRR	1801.9	1802.9	1801.9	1802.9
16.0	37.1	37.1	57.7	2.0		YTPSGQAGAAASESLFVSNHAY	2227.0	2228.0	2227.0	2228.0
16.0 16.0	37.1 37.1	37.1 37.1	57.7 57.7	1.7 1.4		YQYPALTPEQKKELSDIAHR KENLKAAQEEYVKR	2479.2 1704.9	2480.2 1705.9	2479.2 1704.9	2480.2 1705.9
16.0	37.1	37.1	57.7	0.7		ENLKAAQEEYVKR	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		GVVPLAGTNGETTTQGLDGLSER	2272.1	2273.1	2272.1	2273.1
16.0 16.0	37.1 37.1	37.1 37.1	57.7 57.7	0.3		MPYQYPALTPEQKKELSDIAHR LQSIGTENTEENRR	2495.3 1648.8	2496.3 1649.8	2495.3 1645.8	2496.3 1646.8
52.0	6.2	6.2	29.4	2.0		IGEHTPSALAIMENANVLAR	2106.1	2107.1	2106.1	2107.1
52.0	6.2	6.2	29.4	2.0		PYQYPALTPEQKK	1561.8	1562.8	1561.8	1562.8
52.0 52.0	6.2 6.2	6.2 6.2	29.4 29.4	1.5 0.6		LQSIGTENTEENRR YTPSGQAGAAASESLFVSNHAY	1645.8 2227.0	1646.8 2228.0	1645.8 2227.0	1646.8 2228.0
52.0	6.2	6.2	29.4	0.1		FSHEEIAMATVTALRR	1830.9	1832.0	1830.9	1831.9
23.0	22.8	22.8	50.5	2.0		ADDGRPFPQVIK	1341.7	1342.7	1341.7	1342.7
23.0 23.0	22.8 22.8	22.8 22.8	50.5 50.5	2.0 2.0		ALANSLACQGK AWGGKKENLKAAQEEYVKR	1131.6 2204.2	1132.6 2205.2	1131.6 2204.2	1132.6 2205.2
23.0	22.8	22.8	50.5	2.0		CAQYKKDGADFAK	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 23.0	22.8 22.8	22.8 22.8	50.5 50.5	2.0		KENLKAAQEEYVKR LQSIGTENTEENRR	1704.9 1645.8	1705.9 1646.8	1704.9 1645.8	1705.9 1646.8
23.0	22.8	22.8	50.5	2.0		PYQYPALTPEQK	1433.7	1434.7	1433.7	1434.7
23.0	22.8	22.8	50.5	2.0		PYQYPALTPEQKK	1561.8	1562.8	1561.8	1562.8
23.0	22.8	22.8	50.5	2.0		PYQYPALTPEQKKELSDIAHR	2483.3	2484.3	2483.3	2484.3
23.0 23.0	22.8 22.8	22.8 22.8	50.5 50.5	2.0		YTPSGQAGAAASESLFVSNHAY RLQSIGTENTEENRR	2227.0 1801.9	2228.0 1802.9	2227.0 1801.9	2228.0 1802.9
23.0	22.8	22.8	50.5	0.3		GVVPLAGTNGETTTQGLDGLSER	2272.1	2273.1	2272.1	2273.1
23.0	22.8	22.8	50.5	0.0		IGEHTPSALAIMENANVLAR	2107.1	2108.1	2107.1	2108.1
23.0 23.0	22.8 22.8	22.8 22.8	50.5 50.5	0.0		PYQYPALTPEQKK PYQYPALTPEQKKELSDIAHR	1564.8 2484.3	1565.9 2485.3	1561.8 2483.3	1562.8 2484.3
	CYTB_HUMAN	22.0		-B (Stefin-B	3) (Liver thiol pr	oteinase inhibitor) (CPI-B) - Homo sapiens		2400.0	2403.3	
318.0	4.0	4.0	36.7	2.0	99.0	MMCGAPSATQPATAETQHIADQVR	2612.2	2613.2	2612.2	2613.2
318.0 277.0	4.0 2.1	4.0 2.1	36.7 30.6	2.0		VHVGDEDFVHLR VHVGDEDFVHLR	1421.7 1421.7	1422.7 1422.7	1421.7 1421.7	1422.7 1422.7
	2.1 G3P_HUMAN	2.1			99.0 hosphate dehyd	VHVGDEDFVHLR rogenase (EC 1.2.1.12) (GAPDH) - Homo sa		1422./	1421.7	1422.7
30.0	24.2	24.2	49.6	2.0	99.0	DGRGALQNIIPASTGAAK	1738.9	1739.9	1738.9	1739.9
30.0	24.2	24.2	49.6	2.0		GKVKVGVNGFGR	1217.7	1218.7	1217.7	1218.7
30.0 30.0	24.2 24.2	24.2 24.2	49.6 49.6	2.0 2.0		IISNASCTTNCLAPLAK IKWGDAGAEYVVESTGVFTTMEK	1832.9 2517.2	1833.9 2518.2	1832.9 2517.2	1833.9 2518.2
30.0	24.2	24.2	49.6	2.0		LEKPAKYDDIKK	1446.8	1447.8	1446.8	1447.8
30.0	24.2	24.2	49.6	2.0		LISWYDNEFGYSNR	1762.8	1763.8	1762.8	1763.8
30.0 30.0	24.2 24.2	24.2 24.2	49.6 49.6	2.0		VGVNGFGR VIISAPSADAPMFVMGVNHEK	805.4	806.4	805.4 2212.1	806.4 2213.1
30.0	24.2	24.2	49.6	2.0		VIISAPSADAPMFVMGVNHEK VIISAPSADAPMFVMGVNHEKYDNSLK	2212.1 2932.4	2213.1 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		WGDAGAEYVVESTGVFTTMEK	2276.1	2277.1	2276.0	2277.0
30.0 30.0	24.2 24.2	24.2 24.2	49.6 49.6	1.3 0.5		VIPELNGKLTGMAFR LTGMAFR	1645.9 794.4	1646.9 795.4	1645.9 794.4	1646.9 795.4
30.0	24.2	24.2	49.6	0.4		LTGMAFRVPTANVSVVDLTCR	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		GKVKVGVNGFGR	1217.7	1218.7	1217.7	1218.7
30.0 30.0	24.2 24.2	24.2 24.2	49.6 49.6	0.0		LISWYDNEFGYSNR LISWYDNEFGYSNR	1764.8 1778.8	1765.8 1779.8	1762.8 1778.8	1763.8 1779.8
30.0	24.2	24.2	49.6	0.0		LISWYDNEFGYSNR	1763.8	1764.8	1763.8	1764.8
74.0	4.7	4.7	25.4	2.0		LISWYDNEFGYSNR	1762.8	1763.8	1762.8	1763.8
74.0 74.0	4.7 4.7	4.7 4.7	25.4 25.4	2.0 0.5		VPTANVSVVDLTCR VIISAPSADAPMFVMGVNHEK	1529.8 2212.1	1530.8 2213.1	1529.8 2212.1	1530.8 2213.1
74.0	4.7	4.7	25.4	0.3		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		LISWYDNEFGYSNR	1754.7	1755.8	1762.8	1763.8
34.0 34.0	19.3 19.3	19.3 19.3	40.3 40.3	2.0		GALQNIIPASTGAAK IISNASCTTNCLAPLAK	1410.8 1832.9	1411.8 1833.9	1410.8 1832.9	1411.8 1833.9
34.0	19.3	19.3	40.3	2.0		IKWGDAGAEYVVESTGVFTTMEK	2517.2	2518.2	2517.2	2518.2
34.0	19.3	19.3	40.3	2.0		LEKPAKYDDIKK	1446.8	1447.8	1446.8	1447.8
34.0 34.0	19.3 19.3	19.3 19.3	40.3 40.3	2.0 2.0		LISWYDNEFGYSNR VPTANVSVVDLTCR	1762.8 1529.8	1763.8 1530.8	1762.8 1529.8	1763.8 1530.8
34.0	19.3	19.3	40.3	2.0		VVDLMAHMASKE	1329.6	1330.7	1329.6	1330.6
34.0	19.3	19.3	40.3	2.0	99.0	WGDAGAEYVVESTGVFTTMEK	2276.0	2277.0	2276.0	2277.0
34.0	19.3	19.3	40.3	1.4		VIISAPSADAPMFVMGVNHEK	2212.1	2213.1	2212.1	2213.1
34.0 34.0	19.3 19.3	19.3 19.3	40.3 40.3	1.2 0.7		LEKPAKYDDIK LTGMAFR	1318.7 794.4	1319.7 795.4	1318.7 794.4	1319.7 795.4
34.0	19.3	19.3	40.3	0.0		LISWYDNEFGYSNR	1763.8	1764.8	1763.8	1764.8
34.0	19.3	19.3	40.3	0.0		LISWYDNEFGYSNR	1778.8	1779.8	1778.8	1779.8
34.0	19.3	19.3	40.3	0.0	98.0	LISWYDNEFGYSNR ding protein A8) (Calgranulin-A) (Migration	1794.8	1795.8	1794.8 (MDD-8) (Cyctic	1795.8
317.0	S10A8_HUMAN 4.0	4.0	25.8	2.0		GNFHAVYRDDLKK	1561.8	1562.8	1561.8	1562.8
317.0	4.0	4.0	25.8	2.0	99.0	LLETECPQYIR	1420.7	1421.7	1420.7	1421.7
161.0 161.0	4.4 4.4	4.4 4.4	25.8 25.8	2.0 2.0		GNFHAVYRDDLKK LLETECPQYIR	1561.8 1420.7	1562.8 1421.7	1561.8 1420.7	1562.8 1421.7
161.0	4.4	4.4	25.8	0.4		GNFHAVYR	962.5	963.5	962.5	963.5
161.0	4.4	4.4	25.8	0.0	33.0	GNFHAVYRDDLKK	1561.8	1562.8	1561.8	1562.8
P05120 F 114.0	PAI 2_HUMAN 10.0	10.0	Plasmino 13.5	ogen activa 2.0		ecursor (PAI-2) (Placental plasminogen ac ITNCILFFGR	ctivator inhibitor) (1239.6	Monocyte Arg-s 1240.7	erpin) (Urokinase 1239.6	inhibitor) - Hon 1240.7
114.0	10.0 10.0	10.0	13.5	2.0		LEEHYELR	1239.6 1087.5	1240.7 1088.5	1239.6 1087.5	1240.7
114.0	10.0	10.0	13.5	2.0	99.0	SASFREEYIR	1256.6	1257.6	1256.6	1257.6
114.0 114.0	10.0 10.0	10.0 10.0	13.5 13.5	2.0		TPVQMMYLR VVSSEROAVDELECAFEAR	1137.6 2263.0	1138.6 2264.0	1137.6	1138.6
114.0	10.0 10.0	10.0	13.5	0.0		YYSSEPQAVDFLECAEEAR SASFREEYIR	2263.0 1256.6	2264.0 1257.6	2263.0 1256.6	2264.0 1257.6
38.0	8.1	8.1	21.2	2.0	99.0	AILQAQAADKIHSSFR	1754.9	1755.9	1754.9	1756.0
38.0	8.1	8.1	21.2	2.0		SASFREEYIR	1256.6	1257.6	1256.6	1257.6
38.0 38.0	8.1 8.1	8.1 8.1	21.2 21.2	2.0		TPVQMMYLR YYSSEPQAVDFLECAEEAR	1137.6 2263.0	1138.6 2264.0	1137.6 2263.0	1138.6 2264.0
17.0	26.4	26.4	37.3	2.0		AILQAQAADKIHSSFR	1754.9	1755.9	1754.9	1756.0
17.0	26.4	26.4	37.3	2.0	99.0	GKIPNLLPEGSVDGDTR	1766.9	1767.9	1766.9	1767.9
17.0	26.4	26.4	37.3	2.0		GSYPDAILQAQAADKIHSSFR	2274.1	2275.1	2274.1	2275.1
17.0 17.0	26.4 26.4	26.4 26.4	37.3 37.3	2.0 2.0		ITNCILFFGR KKINSWVK	1239.6 1001.5	1240.6 1002.6	1239.6 1001.6	1240.7 1002.6
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		MAEDEVEVYIPQFK	1696.8	1697.8	1696.8	1697.8
17.0 17.0	26.4 26.4	26.4 26.4	37.3 37.3	2.0 2.0		MVLVNAVYFK SASFREEYIR	1182.6 1256.6	1183.7 1257.6	1182.6 1256.6	1183.7 1257.6
17.0	26.4	26.4	37.3	2.0		SMGMEDAFNKGR	1341.6	1342.6	1341.6	1342.6
17.0	26.4	26.4	37.3	2.0	99.0	TPVQMMYLR	1137.6	1138.6	1137.6	1138.6
17.0	26.4	26.4	37.3	2.0		YYSSEPQAVDFLECAEEAR	2263.0	2264.0	2263.0	2264.0
17.0 17.0	26.4 26.4	26.4 26.4	37.3 37.3	2.0 0.3		YYSSEPQAVDFLECAEEARK LNGLYPFR	2391.1 961.5	2392.1 962.5	2391.1 961.5	2392.1 962.5
17.0	26.4	26.4	37.3	0.0	99.0	ITNCILFFGR	1240.6	1241.6	1240.6	1241.6
17.0	26.4	26.4	37.3	0.0		LEEHYELR	1088.5	1089.5	1087.5	1088.5
17.0 17.0	26.4 26.4	26.4 26.4	37.3 37.3	0.0		SASFREEYIR SMGMEDAFNKGR	1256.6 1341.6	1257.6 1342.6	1256.6 1341.6	1257.6 1342.6
17.0	26.4	26.4	37.3	0.0	99.0	SMGMEDAFNKGR	1345.6	1346.6	1341.6	1342.6
17.0	26.4	26.4	37.3	0.0	99.0	TPVQMMYLR	1140.6	1141.6	1137.6	1138.6
P05161 U 502.0	UCRP_HUMAN 2.0	2.0	Interfere 12.7	on-induced 2.0		orecursor [Contains: Ubiquitin cross-reactive IGVHAFQQR	ve protein (hUCRP) 1054.6	(Interferon-inc 1055.6	luced 15 kDa prot 1054.6	ein)] - Homo sa _l 1055.6
353.0	2.0	2.0	10.9	2.0		IGVHAFQQR	1054.6	1055.6	1054.6	1055.6
P05362 I	ICAM1_HUMAN		Intercell	lular adhesi	on molecule 1 p	recursor (ICAM-1) (Major group rhinovirus	receptor) (CD54 a	ntigen) - Homo	sapiens (Human)	
569.0	1.7	1.7	2.1 2.1	1.7		TFLTVYWTPER TFLTVYWTPER	1411.7	1412.7	1411.7	1412.7 1412.7
369.0	2.0	2.0	2.1	2.0	99.0	II LIVIWIFER	1411.7	1412.7	1411.7	1412.7

P06576 A	TPB_HUMAN		ATP synthas	e subunit l	oeta, mitocho	ondrial precursor (EC 3.6.3.14) - Homo sapie	ns (Human)			
251.0	2.2	2.2	15.7	2.0	99.0	AHGGYSVFAGVGER	1405.7	1406.7	1405.7	1406.7
251.0	2.2	2.2	15.7	0.2	38.0	IMDPNIVGSEHYDVAR	1814.9	1815.9	1814.9	1815.9
316.0	4.0	4.0	6.6	2.0	99.0	AIAELGIYPAVDPLDSTSR	1987.0	1988.0	1987.0	1988.0
316.0	4.0	4.0	6.6	2.0	99.0	IMDPNIVGSEHYDVAR	1814.9	1815.9	1814.9	1815.9
P06733 Ef	NOA_HUMAN 38.3	38.3	Alpha-enolas 62.9	se (EC 4.2. 2.0	1.11) (2-pho 99.0	ospho-D-glycerate hydro-lyase) (Non-neural AAVPSGASTGIYEALELR	enolase) (NNE) 1803.9	(Enolase 1) (Phos 1804.9	sphopyruvate hyd 1803.9	dratase) (C-myc 1804.9
15.0	38.3	38.3	62.9	2.0	99.0	AGAVEKGVPLYR	1258.7	1259.7	1258.7	1259.7
15.0	38.3	38.3	62.9		99.0	EIFDSRGNPTVEVDLFTSK	2153.1	2154.1	2153.1	2154.1
15.0	38.3	38.3	62.9	2.0	99.0	FTASAGIOVVGDDLTVTNPKR	2188.1	2189.1	2188.1	2189.2
15.0	38.3	38.3	62.9		99.0	IGAEVYHNLK	1142.6	1143.6	1142.6	1143.6
15.0	38.3	38.3	62.9	2.0	99.0	LAKYNQLLR	1117.6	1118.6	1117.7	1118.7
15.0	38.3	38.3	62.9	2.0	99.0	LAMQEFMILPVGAANFR	1907.0	1908.0	1907.0	1908.0
15.0	38.3	38.3	62.9	2.0	99.0	LAQANGWGVMVSHR	1525.7	1526.7	1525.7	1526.8
15.0	38.3	38.3	62.9	2.0	99.0	NFRNPLAK	958.5	959.5	958.5	959.5
15.0	38.3	38.3	62.9	2.0	99.0	SCNCLLLK	1006.5	1007.5	1006.5	1007.5
15.0	38.3	38.3	62.9	2.0	99.0	SGKYDLDFKSPDDPSR	1825.8	1826.9	1825.8	1826.9
15.0	38.3	38.3	62.9		99.0	VNQIGSVTESLQACK	1632.8	1633.8	1632.8	1633.8
15.0	38.3	38.3	62.9	2.0	99.0	VNQIGSVTESLQACKL	1784.8	1785.8	1784.8	1785.8
15.0	38.3	38.3	62.9	2.0	99.0	VVIGMDVAASEFFR	1539.8	1540.8	1539.8	1540.8
15.0	38.3	38.3	62.9	2.0	99.0	YGKDATNVGDEGGFAPNILENK	2308.1	2309.1	2308.1	2309.1
15.0	38.3	38.3	62.9	2.0	99.0	YGKDATNVGDEGGFAPNILENKEGLELLK	3090.6	3091.6	3090.6	3091.6
15.0	38.3	38.3	62.9	2.0	99.0	YISPDQLADLYK	1424.7	1425.7	1424.7	1425.7
15.0	38.3	38.3	62.9	1.3	95.0	AGYTDKVVIGMDVAASEFFR	2175.1	2176.1	2175.1	2176.1
15.0	38.3	38.3	62.9	1.3	95.0	EIFDSR	765.4	766.4	765.4	766.4
15.0	38.3	38.3	62.9	1.1	92.0	AAVPSGASTGIYEALELRDNDKTR	2533.3	2534.3	2533.2	2534.2
15.0	38.3	38.3	62.9	0.6	75.0	GVPLYR	703.4	704.4	703.4	704.4
15.0	38.3	38.3	62.9	0.0	45.0	AGAVEKGVPLYR	1260.7	1261.7	1258.7	1259.7
15.0	38.3	38.3	62.9	0.0	99.0	LAKYNQLLR	1117.7	1118.7	1117.7	1118.7
15.0	38.3	38.3	62.9	0.0	99.0	LAMQEFMILPVGAANFR	1910.0	1911.0	1907.0	1908.0
15.0	38.3	38.3	62.9	0.0	53.0	LAQANGWGVMVSHR	1541.7	1542.8	1541.7	1542.7
15.0	38.3	38.3	62.9		23.0	LAQANGWGVMVSHR	1522.7	1523.8	1522.7	1523.8
15.0	38.3	38.3	62.9	0.0	99.0	NFRNPLAK	958.5	959.5	958.5	959.5
15.0	38.3	38.3	62.9		99.0	YISPDQLADLYK	1420.7	1421.7	1424.7	1425.7
15.0	38.3	38.3	62.9	0.0	57.0	YISPDOLADLYK	1423.7	1424.7	1424.7	1425.7
19.0	14.1	14.1	35.3		99.0	GNPTVEVDLFTSK	1405.7	1406.7	1405.7	1406.7
19.0	14.1	14.1	35.3	2.0	99.0	IGAEVYHNLK	1142.6	1143.6	1142.6	1143.6
19.0	14.1	14.1	35.3	2.0	99.0	LAMQEFMILPVGAANFR	1907.0	1908.0	1907.0	1908.0
19.0	14.1	14.1	35.3	2.0	99.0	LAQANGWGVMVSHR	1525.7	1526.8	1525.7	1526.8
19.0	14.1	14.1	35.3	2.0	99.0	YISPDQLADLYK	1422.7	1423.7	1424.7	1425.7
19.0	14.1	14.1	35.3	1.4	96.0	AAVPSGASTGIYEALELR	1803.9	1804.9	1803.9	1804.9
19.0 19.0	14.1 14.1 14.1	14.1	35.3 35.3	0.8 0.7	83.0 81.0	VNQIGSVTESLQACK LAKYNQLLR	1632.8 1117.6	1633.8	1632.8	1633.8
19.0	14.1	14.1	35.3	0.5	70.0	SGKYDLDFKSPDDPSR	1825.8	1118.6 1826.9	1117.7 1825.8	1118.7 1826.9
19.0	14.1	14.1	35.3	0.4	57.0	NFRNPLAK	958.5	959.5	958.5	959.5
19.0	14.1	14.1	35.3		50.0	YNQLLR	805.5	806.5	805.4	806.5
19.0	14.1	14.1	35.3	0.0	99.0	YISPDQLADLYK	1423.7	1424.7	1424.7	1425.7
12.0	31.0	31.0	55.8	2.0	99.0	AAVPSGASTGIYEALELR	1803.9	1804.9	1803.9	1804.9
12.0 12.0	31.0 31.0	31.0 31.0	55.8 55.8	2.0	99.0 99.0	AGYTDKVVIGMDVAASEFFR DATNVGDEGGFAPNILENKEGLELLK	2175.0 2742.4	2176.0	2175.1 2742.3	2176.1
12.0	31.0	31.0	55.8	2.0	99.0	EIFDSRGNPTVEVDLFTSK	2153.1	2743.4 2154.1	2153.1	2743.3 2154.1
12.0	31.0	31.0	55.8	2.0	99.0	GNPTVEVDLFTSK	1405.7	1406.7	1405.7	1406.7
12.0	31.0	31.0	55.8	2.0	99.0	IGAEVYHNLK	1142.6	1143.6	1142.6	1143.6
12.0	31.0	31.0	55.8	2.0	99.0	LAQANGWGVMVSHR	1525.7	1526.8	1525.7	1526.8
12.0	31.0	31.0	55.8	2.0	99.0	NFRNPLAK	958.5	959.5	958.5	959.5
12.0	31.0	31.0	55.8	2.0	99.0	SGKYDLDFKSPDDPSR	1825.8	1826.8	1825.8	1826.9
12.0	31.0	31.0	55.8	2.0	99.0	VNQIGSVTESLQACK	1632.8	1633.8	1632.8	1633.8
12.0	31.0	31.0	55.8		99.0	VVIGMDVAASEFFR	1539.8	1540.8	1539.8	1540.8
12.0	31.0	31.0	55.8	2.0	99.0	YISPDQLADLYK	1424.7	1425.7	1424.7	1425.7
12.0	31.0	31.0	55.8	1.5	97.0	VNQIGSVTESLQACKL	1784.8	1785.8	1784.8	1785.8
12.0	31.0	31.0	55.8	1.5	97.0	YNQLLR	805.5	806.5	805.4	806.5
12.0	31.0	31.0	55.8	1.3	95.0	SGETEDTFIADLVVGLCTGQIK	2352.2	2353.2	2352.1	2353.1
12.0	31.0	31.0	55.8	1.0	91.0	AAVPSGASTGIYEALELRDNDKTR	2533.3	2534.3	2533.3	2534.3
12.0	31.0	31.0	55.8	0.7	82.0	SCNCLLLK	1006.5	1007.5	1006.5	1007.5
12.0	31.0	31.0	55.8	0.3	49.0	GVPLYR	703.4	704.4	703.4	704.4
12.0	31.0	31.0	55.8	0.2	42.0	LAMQEFMILPVGAANFR	1907.9	1909.0	1907.0	1908.0
12.0	31.0	31.0	55.8	0.2	32.0	LAKYNQLLR	1117.6	1118.6	1117.7	1118.7
12.0	31.0	31.0	55.8	0.1	25.0	AVNEKSCNCLLLK	1562.8	1563.8	1562.8	1563.8
12.0	31.0	31.0	55.8	0.0	48.0	GVPLYR	703.4	704.4	703.4	704.4
12.0	31.0	31.0	55.8	0.0	95.0	IGAEVYHNLK	1142.6	1143.6	1142.6	1143.6
12.0	31.0	31.0	55.8	0.0	99.0	NFRNPLAK	958.5	959.5	958.5	959.5
12.0	31.0	31.0	55.8	0.0	94.0	NFRNPLAK	956.5	957.5	958.5	959.5
12.0	31.0	31.0	55.8	0.0	29.0	NFRNPLAK	959.5	960.5	959.5	960.5
12.0	31.0	31.0	55.8		42.0	YISPDQLADLYK	1420.7	1421.7	1424.7	1425.7
92.0	6PI_HUMAN 11.9	11.9	Glucose-6-ph 18.6	2.0	somerase (E	AALTRDPQFQK	1315.7	1316.7	1315.7	1316.7
92.0	11.9	11.9	18.6	2.0	99.0	MFNGEKINYTEGR	1558.7	1559.7	1558.7	1559.7
92.0	11.9	11.9	18.6	2.0	99.0	MIPCDFLIPVQTQHPIRK	2194.2	2195.2	2192.2	2193.2
92.0	11.9	11.9	18.6	2.0	99.0	SGDWKGYTGK	1097.5	1098.5	1097.5	1098.5
92.0	11.9	11.9	18.6		99.0	VWYVSNIDGTHIAK	1601.8	1602.8	1601.8	1602.8
92.0	11.9	11.9	18.6	1.2	94.0	LQQWYR	892.5	893.5	892.5	893.5
92.0	11.9	11.9	18.6	0.6	75.0	TLAQLNPESSLFIIASK	1831.0	1832.0	1831.0	1832.0
92.0	11.9	11.9	18.6	0.0	93.0	LQQWYR	892.5	893.5	892.5	893.5
103.0	7.7	7.7	15.2	2.0	99.0	AALTRDPQFQK	1315.7	1316.7	1315.7	1316.7
103.0	7.7	7.7	15.2	2.0	99.0	LQQWYR	892.5	893.5	892.5	893.5
103.0	7.7	7.7	15.2	2.0	99.0	MIPCDFLIPVQTQHPIRK	2192.2	2193.2	2192.2	2193.2
103.0	7.7	7.7	15.2	1.7	98.0	FAAYFQQGDMESNGKYITK	2198.0	2199.0	2198.0	2199.0
103.0	7.7	7.7	15.2	0.0	98.0	LQQWYR	892.5	893.5	892.5	893.5
255.0	PM3_HUMAN 4.6	16.4	Tropomyosir 40.8	2.0	hain (Tropor	myosin-3) (Tropomyosin gamma) (hTM5) - H ALKDEEKMELOEIOLKEAK	2273.1	2274.1	2272.2	2273.2
255.0	4.6	16.4	40.8	1.4	96.0	KLVIIEGDLERTEER	1799.0	1800.0	1799.0	1800.0
255.0	4.6	16.4	40.8	1.2	99.0	KLVIIEGDLER	1283.7	1284.8	1283.7	1284.8
255.0	4.6	16.4	40.8	0.0	99.0	HIAEEADRKYEEVAR	1826.9	1827.9	1826.9	1827.9
255.0	4.6	16.4	40.8		99.0	HIAEEADRKYEEVAR	1814.9	1815.9	1814.9	1815.9
255.0	4.6	16.4	40.8	0.0	74.0	HIAEEADRKYEEVAR	1814.9	1815.9	1814.9	1815.9
255.0	4.6	16.4	40.8		99.0	IOLVEEELDR	1242.6	1243.6	1242.6	1243.7
255.0	4.6	16.4	40.8	0.0	99.0	IQLVEEELDRAQER	1726.9	1727.9	1726.9	1727.9
255.0	4.6	16.4	40.8	0.0	99.0	LATALQKLEEAEKAADESER	2201.1	2202.1	2201.1	2202.1
255.0	4.6	16.4	40.8	0.0	89.0	LEEAEKAADESER	1475.7	1476.7	1475.7	1476.7
255.0	4.6	16.4	40.8	0.0	99.0	RIQLVEEELDRAQER	1883.0	1884.0	1883.0	1884.0
391.0	1.5	9.7	21.5	1.5	97.0	KLVIIEGDLER	1279.7	1280.8	1283.7	1284.8
391.0 391.0	1.5	9.7 9.7	21.5 21.5 21.5	0.0	50.0 99.0	HIAEEADRKYEEVAR IQLVEEELDRAQER	1814.9 1726.9	1815.9 1727.9	1814.9 1726.9	1815.9 1727.9
391.0	1.5 1.5	9.7	21.5	0.0	99.0	LATALQKLEEAEKAADESER	2201.1	2202.1	2201.1	2202.1
391.0	1.5	9.7	21.5	0.0	83.0	LEEAEKAADESER	1475.7	1476.7	1475.7	1476.7
391.0	1.5	9.7	21.5	0.0	92.0	RIQLVEEELDR	1398.7	1399.8	1398.7	1399.8
391.0	1.5	9.7	21.5	0.0	99.0	RIQLVEEELDRAQER	1883.0	1884.0	1883.0	1884.0
P07195 LE	DHB_HUMAN		L-lactate der	nydrogena	se B chain (E	CC 1.1.1.27) (LDH-B) (LDH heart subunit) (LD	DH-H) (Renal car	cinoma antigen N	IY-REN-46) - Hor	no sapiens (Hum
56.0	16.9	16.9	32.6	2.0	99.0	FRYLMAEK GEMMDLQHGSLFLQTPK	1056.5	1057.5	1056.5	1057.5
56.0	16.9	16.9	32.6	2.0	99.0		1930.9	1931.9	1930.9	1931.9
56.0	16.9	16.9	32.6	2.0	99.0	GLTSVINQK	958.6	959.6	958.5	959.6
56.0	16.9	16.9	32.6	2.0	99.0	IVVVTAGVR	912.6	913.6	912.6	913.6
56.0	16.9	16.9	32.6	2.0	99.0	IVVVTAGVRQQEGESR	1726.9	1727.9	1726.9	1727.9
56.0	16.9	16.9	32.6	2.0	99.0	SADTLWDIQK	1175.6	1176.6	1175.6	1176.6
56.0	16.9	16.9	32.6	2.0	99.0	SADTLWDIQKDLKDL	1759.9	1760.9	1759.9	1760.9
56.0	16.9	16.9	32.6	2.0	99.0	SLADELALVDVLEDK	1628.8	1629.8	1628.9	1629.9
56.0	16.9	16.9	32.6	0.8	83.0	VIGSGCNLDSAR	1247.6	1248.6	1247.6	1248.6
56.0	16.9	16.9	32.6	0.1	26.0	QQEGESRLNLVQR	1555.8	1556.8	1555.8	1556.8
207.0	1.4	4.0	20.1	1.4	99.0	SADTLWDIQK	1175.6	1176.6	1175.6	1176.6
207.0	1.4	4.0	20.1	0.0	99.0	FRYLMAEK	1056.5	1057.6	1056.5	1057.5
196.0	3.8	3.8	17.4	2.0	99.0	SADTLWDIQKDLKDL	1759.9	1760.9	1759.9	1760.9
196.0	3.8	3.8	17.4	1.3	95.0	QQEGESRLNLVQR	1555.8	1556.8	1555.8	1556.8
196.0	3.8 DI A1_HUMAN	3.8	17.4 Protein disul	0.5	70.0	VIGSGCNLDSAR sor (EC 5.3.4.1) (PDI) (Prolyl 4-hydroxylase:	1247.6	1248.6	1247.6	1248.6
481.0	2.0	2.0	6.5	2.0	99.0	ITEFCHR	961.4	962.5	961.4	962.5
298.0	2.0	2.0	6.7	2.0	99.0	ILFIFIDSDHTDNQR	1832.9	1833.9	1832.9	1833.9

D0722010	ATD HUMAN		Cathonoin	DECO. 150.05	(EC 2 4 22 E	Contains Cathanain D light shain. Catha	noin D books abole	1 Home conton	· (Llumann)	
199.0	ATD_HUMAN 6.0	6.0	18.2	2.0	99.0	[Contains: Cathepsin D light chain; Cather FDGILGMAYPR	psin D neavy chain 1238.6	1239.6	1238.6	1239.6
199.0 199.0	6.0 6.0	6.0 6.0	18.2 18.2	2.0	99.0 99.0	QVFGEATKQPGITFIAAK RISVNNVLPVFDNLMQQK	1905.0 2211.1	1906.0 2212.1	1905.0 2211.1	1906.0 2212.1
70.0	4.9	4.9	20.9	2.0	99.0	AIGAVPLIQGEYMIPCEK	1988.0	1989.0	1988.0	1989.0
70.0 70.0	4.9 4.9	4.9 4.9	20.9 20.9	2.0	99.0 86.0	FDGILGMAYPR YYTVFDRDNNR	1238.6 1462.7	1239.6 1463.7	1238.6 1462.6	1239.6 1463.7
70.0	4.9	4.9	20.9	0.0	81.0	YYTVFDRDNNR	1461.7	1462.7	1461.7	1462.7
149.0 149.0	4.9 4.9	4.9 4.9	16.0 16.0	2.0 2.0	99.0 99.0	AIGAVPLIQGEYMIPCEK FDGILGMAYPR	1988.0 1238.6	1989.0 1239.6	1988.0 1238.6	1989.0 1239.6
149.0	4.9	4.9	16.0	0.7	82.0	YYTVFDRDNNR	1461.7	1462.7	1461.7	1462.7
149.0 PO74371TE	4.9 BB5_HUMAN	4.9	16.0 Tubulin beta	0.1 a chain (Tub	20.0 oulin beta-5	QVFGEATKQPGITFIAAK chain) - Homo sapiens (Human)	1905.0	1906.0	1905.0	1906.0
21.0	28.5	28.5	47.3	2.0	99.0	ALTVPELTQQVFDAK	1658.9	1659.9	1658.9	1659.9
21.0 21.0	28.5 28.5	28.5 28.5	47.3 47.3	2.0 2.0	99.0 99.0	EIVHIQAGQCGNQIGAK FWEVISDEHGIDPTGTYHGDSDLQLDR	1821.9 3101.4	1822.9 3102.4	1821.9 3101.4	1822.9 3102.4
21.0	28.5	28.5	47.3	2.0	99.0	GHYTEGAELVDSVLDVVR	1957.9	1958.9	1958.0	1959.0
21.0 21.0	28.5 28.5	28.5 28.5	47.3 47.3	2.0 2.0	99.0 99.0	ISEQFTAMFR ISVYYNEATGGK	1228.6 1300.6	1229.6 1301.6	1228.6 1300.6	1229.6 1301.6
21.0 21.0	28.5 28.5	28.5 28.5	47.3 47.3	2.0 2.0	99.0 99.0	ISVYYNEATGGKYVPR LAVNMVPFPR	1815.9 1142.6	1816.9 1143.6	1815.9 1142.6	1816.9 1143.6
21.0	28.5	28.5	47.3	2.0	99.0	MSMKEVDEQMLNVQNK	1922.9	1923.9	1922.9	1923.9
21.0 21.0	28.5 28.5	28.5 28.5	47.3 47.3	2.0 2.0	99.0 99.0	NSSYFVEWIPNNVK YLTVAAVFR	1695.8 1038.6	1696.8 1039.6	1695.8 1038.6	1696.8 1039.6
21.0	28.5	28.5	47.3	1.7	98.0	IMNTFSVVPSPK	1318.7	1319.7	1318.7	1319.7
21.0 21.0	28.5 28.5	28.5 28.5	47.3 47.3	1.5 1.3	97.0 95.0	LHFFMPGFAPLTSR IREEYPDRIMNTFSVVPSPK	1619.8 2377.2	1620.8 2378.2	1619.8 2377.2	1620.8 2378.2
21.0	28.5	28.5	47.3	0.9	87.0	RISEQFTAMFR	1384.7	1385.7	1384.7	1385.7
21.0 21.0	28.5 28.5	28.5 28.5	47.3 47.3	0.5 0.5	69.0 66.0	IREEYPDR AILVDLEPGTMDSVR	1076.5 1614.8	1077.5 1615.8	1076.5 1614.8	1077.5 1615.8
21.0	28.5	28.5	47.3	0.1	24.9	GQLNADLR	887.5	888.5	887.4	888.4
26.0 26.0	11.9 11.9	11.9 11.9	22.5 22.5	2.0 2.0	99.0 99.0	ISVYYNEATGGKYVPR KLAVNMVPFPR	1815.9 1270.7	1816.9 1271.7	1815.9 1270.7	1816.9 1271.7
26.0	11.9	11.9	22.5	2.0	99.0	LAVNMVPFPR NECVENTIALIDATIVE	1142.6	1143.6	1142.6	1143.6
26.0 26.0	11.9 11.9	11.9 11.9	22.5 22.5	2.0 2.0	99.0 99.0	NSSYFVEWIPNNVK YLTVAAVFR	1695.8 1038.6	1696.8 1039.6	1695.8 1038.6	1696.8 1039.6
26.0 26.0	11.9 11.9	11.9 11.9	22.5 22.5	1.7 0.1	98.0 26.0	ISEQFTAMFR ALTVPELTQQVFDAK	1228.6 1658.9	1229.6 1659.9	1228.6 1658.9	1229.6 1659.9
47.0	15.8	15.8	30.0	2.0	99.0	ALTVPELTQQVFDAK	1658.9	1659.9	1658.9	1659.9
47.0 47.0	15.8 15.8	15.8 15.8	30.0 30.0	2.0 2.0	99.0 99.0	ISEQFTAMFR ISVYYNEATGGK	1228.6 1300.6	1229.6 1301.6	1228.6 1300.6	1229.6 1301.6
47.0	15.8	15.8	30.0	2.0	99.0	ISVYYNEATGGKYVPR	1815.9	1816.9	1815.9	1816.9
47.0 47.0	15.8 15.8	15.8 15.8	30.0 30.0	2.0 2.0	99.0 99.0	KLAVNMVPFPR LAVNMVPFPR	1270.7 1142.6	1271.7 1143.6	1270.7 1142.6	1271.7 1143.6
47.0	15.8	15.8	30.0	2.0	99.0	YLTVAAVFR	1038.4	1039.5	1038.5	1039.6
47.0 47.0	15.8 15.8	15.8 15.8	30.0 30.0	1.4 0.3	96.0 45.0	NSSYFVEWIPNNVK RISEQFTAMFR	1696.8 1384.7	1697.8 1385.7	1696.8 1384.7	1697.8 1385.7
47.0	15.8	15.8	30.0	0.0	99.0	ISVYYNEATGGKYVPR	1813.9	1814.9	1815.9	1816.9
	15.8 AP_HUMAN	15.8	30.0 Proactivator	0.0 polypeptid		YLTVAAVFR [Contains: Saposin A (Protein A); Saposin I	1038.6 B-Val; Saposin B (5	1039.6 Sphingolipid activ	1038.6 vator protein 1)	1039.6 (SAP-1) (Cerebro
204.0 204.0	6.0 6.0	6.0 6.0	9.7 9.7	2.0 2.0	99.0 99.0	DNGDVCQDCIQMVTDIQTAVR GDVCQDCIQMVTDIQTAVR	2420.1 2208.0	2421.1 2209.0	2420.0 2208.0	2421.0 2209.0
204.0	6.0	6.0	9.7	2.0	99.0	SDVYCEVCEFLVK	1646.7	1647.7	1646.7	1647.7
92.0 92.0	4.0 4.0	4.0 4.0	5.7 5.7	2.0 2.0	99.0 99.0	DVYCEVCEFLVK SDVYCEVCEFLVK	1559.7 1646.7	1560.7 1647.7	1559.7 1646.7	1560.7 1647.7
89.0	8.3	8.3	11.8	2.0	99.0	DNGDVCQDCIQMVTDIQTAVR	2438.1	2439.1	2438.1	2439.1
89.0 89.0	8.3 8.3	8.3 8.3	11.8 11.8	2.0 2.0	99.0 99.0	GDVCQDCIQMVTDIQTAVR NGDVCQDCIQMVTDIQTAVR	2208.0 2323.0	2209.0 2324.0	2208.0 2323.0	2209.0 2324.0
89.0	8.3	8.3	11.8	2.0	99.0	SDVYCEVCEFLVK	1646.7	1647.7	1646.7	1647.7
89.0 89.0	8.3 8.3	8.3 8.3	11.8 11.8	0.1 0.1	27.0 24.0	LGPGMADICK SDVYCEVCEFLVKEVTK	1060.5 2103.9	1061.5 2105.0	1060.5 2104.0	1061.5 2105.0
P07711 C	ATL_HUMAN		Cathepsin L	precursor (EC 3.4.22.15	(Major excreted protein) (MEP) [Contain	is: Cathepsin L hea	vy chain; Cathep	sin L light chain	- Homo sapiens
438.0 438.0	2.0 2.0	2.0 2.0	7.8 7.8	2.0 0.0	99.0 99.0	NSWGEEWGMGGYVK NSWGEEWGMGGYVK	1598.7 1614.7	1599.7 1615.7	1598.7 1614.7	1599.7 1615.7
438.0 210.0	2.0 1.4	2.0 1.4	7.8 5.1	0.0 1.4	99.0 96.0	NSWGEEWGMGGYVK NSWGEEWGMGGYVK	1614.7 1598.7	1615.7 1599.7	1614.7 1598.7	1615.7 1599.7
438.0 210.0 210.0 225.0	2.0 1.4 1.4 2.9	2.0 1.4 1.4 2.9	7.8 5.1 5.1 22.2	0.0 1.4 0.0 2.0	99.0 96.0 94.0 99.0	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK	1614.7 1598.7 1614.7 1598.7	1615.7 1599.7 1615.7 1599.7	1614.7 1598.7 1614.7 1598.7	1615.7 1599.7 1615.7 1599.7
438.0 210.0 210.0 225.0 225.0	2.0 1.4 1.4 2.9 2.9	2.0 1.4 1.4 2.9 2.9	7.8 5.1 5.1 22.2 22.2	0.0 1.4 0.0 2.0 0.9	99.0 96.0 94.0 99.0 86.0	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR	1614.7 1598.7 1614.7 1598.7 1494.7	1615.7 1599.7 1615.7 1599.7 1495.8	1614.7 1598.7 1614.7 1598.7 1494.8	1615.7 1599.7 1615.7 1599.7 1495.8
438.0 210.0 210.0 225.0 225.0 225.0 PO7737 PF	2.0 1.4 1.4 2.9 2.9 2.9 2.9 ROF1_HUMAN	2.0 1.4 1.4 2.9 2.9 2.9	7.8 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P	0.0 1.4 0.0 2.0 0.9 0.0 Profilin I) - H	99.0 96.0 94.0 99.0 86.0 99.0 Homo sapier	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK (HUMAN)	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7
438.0 210.0 210.0 225.0 225.0 225.0	2.0 1.4 1.4 2.9 2.9 2.9	2.0 1.4 1.4 2.9 2.9	7.8 5.1 5.1 22.2 22.2 22.2	0.0 1.4 0.0 2.0 0.9	99.0 96.0 94.0 99.0 86.0 99.0	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK	1614.7 1598.7 1614.7 1598.7 1494.7	1615.7 1599.7 1615.7 1599.7 1495.8	1614.7 1598.7 1614.7 1598.7 1494.8	1615.7 1599.7 1615.7 1599.7 1495.8
438.0 210.0 210.0 225.0 225.0 225.0 PO7737 PF 36.0 36.0 36.0	2.0 1.4 1.4 2.9 2.9 2.9 2.9 ROF1_HUMAN 22.5 22.5 22.5	2.0 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5	7.8 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 Profilin I) - I 2.0 2.0 2.0	99.0 96.0 94.0 99.0 86.0 99.0 Homo sapier 99.0 99.0 99.0	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFOEPLFYEAPR NSWGEEWGMGGYVK S (FUEMAN) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7
438.0 210.0 210.0 225.0 225.0 225.0 PO7737 PF 36.0 36.0	2.0 1.4 1.4 2.9 2.9 2.9 2.9 2.9 2.5 22.5	2.0 1.4 1.4 2.9 2.9 2.9 2.9	7.8 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 Profilin 1) - 1 2.0 2.0	99.0 96.0 94.0 99.0 86.0 99.0 Homo sapien 99.0 99.0 99.0 99.0	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5
438.0 210.0 210.0 225.0 225.0 225.0 PO7737 PF 36.0 36.0 36.0 36.0 36.0	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 22.5 22.5 22.5 22.5 22.5 22.5 22.5	2.0 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 0.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 96.0 94.0 99.0 86.0 99.0 99.0 99.0 99.0 99.0	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK 5 (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFYVNGLTLGGOK	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6
438.0 210.0 210.0 225.0 225.0 225.0 PO7737 Pi 36.0 36.0 36.0 36.0 36.0 36.0 36.0	2.0 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	2.0 1.4 1.4 2.9 2.9 2.9 22.5 22.5 22.5 22.5 22.5 22	7.8 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 96.0 94.0 99.0 86.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 9	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK 5 (HUMAN) CSVIRDSILODGEFSMDLR CYEMASHLR DSILODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFVYNGLTLGGOK STGGAPTENUTVTK	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1146.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7
438.0 210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 22.5 22.5 22.5 22.5 22.5 22.5 22.5 22.	2.0 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 Profilin I) - I 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 96.0 94.0 99.0 86.0 99.0 Homo sapier 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFOEPLFYEAR NSWGEEWGMGGYVK S (HUMAN) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFYWGLILLGGGK STGGAPTFNNTVTKTDK TFWNTFAEKVCKLVGK	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9	1615.7 1599.7 1615.7 1695.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1551.7 1294.6 1471.7 1379.7 1723.9
438.0 210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.5 22	2.0 1.4 1.4 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.5 22	7.8 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 96.0 94.0 99.0 86.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 9	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFVNGLTLGGOK STGGAPTFNVTVTK TFUNITPAEVGVLVGKUR TFVNITPAEVGVLVGKUR TKSTGGAPTFNVTVTK	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1915.1	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1294.6 1471.7 1379.7 1723.9 1643.9 1915.1 1608.9
438.0 210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 22.5 22.5 22.5 22.5 22.5 22.5 22.5 22.	2.0 1.4 1.4 2.9 2.9 2.9 22.5 22.5 22.5 22.5 22.5 22	7.8 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFVNGLTLGGOK STGGAPTFNVTVTK TFVNITPAEVGVLVGKDR TFXNITPAEVGVLVGKDR TKSTGGAPTFNVTVTK CYEMASHLR CYEMASHLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1915.1	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1915.1
438.0 210.0 210.0 225.0 225.0 225.0 225.0 25.0 26.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 3	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 22.5 22.5 22.5 22.5 22.5 22.5 22.5 22.	2.0 1.4 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.5 22	7.8 5.1 5.1 5.1 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFOEPLFYEARR NSWGEEWGMGGYVK VFOEPLFYEARR NSWGEEWGMGGYVK S (HUMAN) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGYHGGLINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TSTGAPTFNYTVTNDK TFVNITPAEVGYLVGKOR TKSTGGAPTFNYTVTK CYEMASHLRR KCYEMASHLRR KCYEMASHLRR KCYEMASHLRR CSVIRDSLUDGEFSMDLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.0	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1915.1 1608.9 1305.6 1450.7 2241.1	1614.7 1598.7 1614.7 1988.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.1	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1915.1 1688.9 1305.6 1480.7 2241.1
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438.0 210.0 210.0 210.0 225.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	2.0 1.4 1.4 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.5 22	7.8 5.1 5.1 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	99.0 94.0 99.0 86.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 9	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (HUMAN) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFVNGLTLGGOK STGGAPTFNVTVTK TFVNITPAEVGVLVGKDR TFVNITPAEVGVLVGKDR TKSTGGAPTFNVTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR SFFVNGLTLGGOK STGGAPTFNVTVTK TKSTGGAPTFNVTVTK TKSTGGAPTFNVTVTK TKSTGGAPTFNVTVTK TYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR SFFVNGLTLGGOK STGGAPTFNVTVTK TKSTGGAPTFNVTVTK TKSTGAPTFNVTVTK TKSTGAPTFNVTTK TKSTGAPTFNVTVTK TKSTGAPTFNVTTK TKSTGAPTFNVTTK TKSTGAPTFNVTVTK TKSTGAPTFNVTVTK TKSTGAPTFNVTTK TKSTGAPTFNVTTK TKSTGAPTFNVTTK TKSTGAPTFNTTTK	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.0 1165.5 1321.6 1470.7 1378.7 1665.5 1321.6	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1915.1 1608.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 1608.9	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.1 1165.5 1321.6 1470.7 1378.7 167.9	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1294.6 1471.7 1294.6 1471.7 1379.7 1723.9 1643.9 1915.1 1608.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 1608.9
438.0 210.0 210.0 225.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 2.2.5 22.5 22.5 22.5 22.5 22.5 22.5 22	20.0 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 1.4 0.0 2.0 0.9 0.0 1.7 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFVYNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGLUGK TFVNITPAEVGLUGK TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLRR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.0 1165.5 1321.6 1470.7 1378.7 1607.9	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1643.9 1915.1 1608.9 1305.6 1450.7 2241.1 1166.5 1322.6	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.1 1165.5 1321.6 1470.7 1378.7 1607.9 16	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1915.1 1608.9 1305.6 1450.7 2241.1 1166.5 1322.6
438.0 210.0 210.0 225.0	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 2.2.5 22.5 22.5 22.5 22.5 22.5 22.5 22	2.0 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 98.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (HUMAN) CSVIRDSILODGEFSMDLR CYEMASHLR DSILODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFVYNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVCYLVGK TFVNITPAEVCYLVGK TFVNITPAEVCYLVGK TKSTGGAPTFNYTVTK CYEMASHLR SSFVYNGLTLGGOK STGGAPTFNYTVTK CYEMASHLR C	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 1304.6 1449.7 1378.7 1607.9 1165.5 1321.6 1624.7 1469.8 1914.0	1615.7 1599.7 1615.7 1615.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1643.9 1643.9 1645.0 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 1608.9 1166.5 1322.6 1471.7 1379.7 1608.9 1166.5 1322.6 1471.7 1379.7 1608.9 1166.5 1322.6 1625.7 1470.8 1915.1 1608.9	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 1224.0 1165.5 1321.6 1470.7 1378.7 1607.9 1654.7 1654.7 1654.7 1655.7 1654.7 1655.7 1654.7 1655.7 1654.7 1655.7 1654.7 1655.7 1654.7 1655.7 1654.7 1655.7 1654.7 1655.7 1654.7 1655.7 1657.9 1654.7 1655.7 1656.7 1656.7 1656.7 1657.7 16	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1294.6 1471.7 1379.7 1643.9 1915.1 1668.9 1395.6 1471.7 1379.7 1668.9 1395.6 1471.7 1379.7 1668.9 166.5 1322.6 1625.7 170.8 1915.1 166.5 1322.6 1625.7 170.8 1915.1 166.9
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438.0 210.0 210.0 210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	2.0 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	99.0 94.0 98.0 98.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR SSEVNOLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGKDR TKSTGGAPTFNYTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR SFYVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLRR SFYVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLRR CYEMASHLRR SFYVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLRR DSLLODGEFSMDLR SSFYVNGLTLGGOK TTSTTGGAPTFNYTVTK CYEMASHLRR DSLLODGEFSMDLR SSFYNGLTLGGOK TFVNITPAEVGVLVGKDR TKSTGGAPTFNYTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CSGRAFTENTYTTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.0 1165.5 1321.6 1470.7 1378.7 149.7 149.7 149.7 149.7 149.7 149.7 149.7 149.8 149.7 149.8 149.7 149.8 149.8 149.8 1914.0 1607.9 1293.6 2240.1 1607.9 1293.6 2240.1 1293.6 2240.1 1293.6 2240.1	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1643.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 166.5 1322.6 1625.7 1470.8 1915.1 1608.9 1625.7 1470.8 1915.1 1608.9 1625.7 1470.8 1915.1 1608.9 1625.7 1470.8 1915.1 1608.9 1625.7 1470.8 1915.1 1608.9 1625.7 1470.8 1915.1 1608.9 1625.7 1470.8 1915.1 1608.9 1625.7 1470.8 1915.1 1608.9 1625.7 1625.7 1625.7 1626.8 1625.7 1626.8 1625.7 1626.8 162	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.1 1165.5 1321.6 1470.7 1378.7 149.7	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1305.6 1450.7 2241.1 1166.5 1322.6 1470.8 14
438.0 210.0 210.0 225.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.5 2.5 2.5	2.0 1.4 1.4 2.9 2.9 2.9 2.5 23.6 24.1 34.4 3	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 94.0 98.0 98.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGLVGK TFVNITPAEVGLVGK TFVNITPAEVGLVGK TKSTGGAPTFNYTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR SFYVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR DSLLODGEFSMDLR SFYVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLRR DSLLODGEFSMDLR SSFYVNGLTLGGOK TTSTGGAPTFNYTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLRR CYEMASHLRR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1642.9 1642.9 1607.9 1304.6 1449.7 1240.0 1165.5 1321.6 1624.7 1469.8 1914.0 1607.9 1293.6	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1643.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 1608.9 1166.5 1322.6 1625.7 1470.8 1915.1 1608.9 1608.9 1608.9 1294.6 2241.1 1222.4 1149.5	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 1240.1 1165.5 1321.6 1470.7 1378.7 149.8 1914.1 1607.9 1293.6 2240.1 2223.0 1448.7 1449.8 1449	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1915.1 1608.9 1305.6 1490.7 1241.1 1166.5 1322.6 1490.7 14
438.0 210.0 210.0 225.0 225.0 225.0 225.0 225.0 225.0 25.0	2.0 1.4 1.4 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	2.0 1.4 1.4 2.9 2.9 2.5 23.6 24.1	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (HUMAN) CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFYNGLTLGGOK STGAPTFNVTVTK STGAPTFNVTVTKTDK TFWNITPAEVCVLVGKDR TFVNITPAEVCVLVGKDR TKSTGGAPTFNVTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR SSFYNGLTLGGOK STGGAPTFNVTVTK TKSTGGAPTFNVTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR SSFYNGLTLGGOK TKSTGGAPTFNVTVTK TKSTGGAPTFNVTVTK CYEMASHLRR CSTGGAPTFNVTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLOGGEFSMDLR CSVIRDSLLOGGEFSMDLR CSVIRDSLLOGGEFSMDLR CYEMASHLRR SFYVNGLTLGGOK	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1914.1 1607.9 1304.6 1449.7 2240.0 1165.5 1321.6 1449.7 1378.7 1607.9 1378.7 1607.9 1378.7 1607.9 1449.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.7 1469.8 1914.0 1607.9 1223.0 1148.5 1304.6 1449.7	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1915.1 1608.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1470.8 14	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.1 1165.5 1321.6 1470.7 1378.7 1607.9 1378.7 1607.9 138.7 148.8 1	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1294.6 1471.7 123.9 1643.9 1915.1 1608.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 166.5 1322.6 1471.7 1379.7 166.5 1322.6 1471.7 1379.7 166.5 1322.6 1470.8
438.0 210.0 210.0 210.0 225.0	2.0 1.4 1.4 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	2.0 1.4 1.4 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.5 22	7.8 5.1 5.1 5.1 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 94.0 98.0 98.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (HUMAN) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGYHGGILNKK KCYEMASHLR SSFYNGLTLGGOK STGAPTFNVTVTK TSTGAPTFNVTVTKTDK TFVNITPAEVGVLVGKR TFVNITPAEVGVLVGKR TFVNITPAEVGVLVGKR KCYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLRR SSFYNGLTLGGOK STGGAPTFNVTVTK TYSTGGAPTFNVTVTK TYSTGGAPTFNVTVTK TYSTGGAPTFNVTVTK TYSTGGAPTFNVTVTK TKSTGGAPTFNVTVTK TKSTGGAPTFNVTTK TKSTGGAPTFNTTVTK TKSTGGAPTFNTTTK TKSTGGAPTFNTTTK TKSTGGAPTFNTTTK TKSTGGAPTFNTTTK TKSTGGAPTFNTTTK	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.0 1165.5 1321.6 1470.7 1378.7 1607.9 1304.6 1470.7 1378.7 1607.9 16	1615.7 1599.7 1615.7 1699.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1470.8 1915.1 1608.9 1915.1 1608.9 1055.7 1470.8 1915.1 1608.9 1166.5 1322.6 1471.7 1470.8 1915.1 1608.9 1915.1 1608.9 1915.1 1608.9 1915.1 1608.9 1915.1 1608.9 1915.1 1608.9 1915.1 1608.9 1915.1 1608.9 1915.1 1608.9 1915.1 1608.9	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.1 1165.5 1321.6 1470.7 1378.7 1607.9 1304.6 1470.7 1378.7 1607.9 1304.6 1470.7 149.8 1914.1 1607.9 1304.6 1470.7 149.8 1914.1 1607.9 1304.6 1470.7 149.8 1914.1 1607.9 1304.6 1470.7 149.8 1914.1 1607.9 1304.6 149.8 14	1615.7 1599.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 1608.9 1305.6 1471.7 1470.8 14
438.0 210.0 2210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 21.0 2	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 2.2.5 22.5 22.5 22.5 22.5 22.5 22.5 22	200 1.4 1.4 2.9 2.9 2.9 2.2.5 22.5 22.5 22.5 22.5 2	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGLVJGK TFVNITPAEVGLVJGK TKNITGAFTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR CSYGRASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSYRDSLLODGEFSMDLR CYEMASHLR CSYRDSLLODGEFSMDLR CYEMASHLR CSYRDSLLODGEFSMDLR CYEMASHLR CYEMASHLR CSYRDSLLODGEFSMDLR CYEMASHLR CYEMASHLR SSFYVNGLTLGGOK SFYVNGLTLGGOK SFYVNGLTLGGOK CYEMASHLR CYEMASHLR CSFYVNGLTLGGOK CYEMASHLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1642.9 1607.9 1304.6 1470.7 1378.7 1607.9 1165.5 1321.6 1624.7 1469.8 1914.0 1607.9 1293.6 2240.1 2223.0 1148.5 1304.6 1470.7 1470.7	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1450.7 1241.1 1166.5 1322.6 1450.7 1471.7 1379.7 1471.7 1471.8 1915.1 1608.9 1224.1 1149.5 1224.1 1149.5 1305.6 1471.7 1379.7 1471.8	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.1 1165.5 1321.6 1470.7 1378.7 1470.7 1378.7 1470.7 1378.7 149.7 149.7 149.8 1914.1 1607.9 1293.6 1293.	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1915.1 1608.9 1305.6 1450.7 2241.1 1166.5 1322.6 1625.7 1470.8 1915.1 1608.9 1400.9 1400.8 14
438.0 210.0 210.0 225.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 2.5 22.5 22.5 22.5 22.5 22.5 22.5 22.5	200 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 98.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLEYEAPR NSWGEEWGMGGYVK 5. (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR ECYHGGIINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGLVJGK TFVNITPAEVGLVJGK TKNITGAFTFNYTVTK CYEMASHLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1642.9 1607.9 1304.6 1449.7 1249.0 1165.5 1321.6 1624.7 14607.9 1165.5 1321.6 1624.7 1460.9 1165.5 1321.6 1624.7 1460.9 1165.5 1321.6 1624.7 1460.9 1165.5 1321.6 1624.7 1460.9 1165.5 1321.6 1624.7 1460.9 1165.5 1321.6 1624.7 1460.9 1165.5 1321.6 1624.7 1460.9 1165.5 1321.6 1624.7 1460.9 1165.5 1321.6 1624.7 1460.8 1914.0 1607.9 1293.6 1240.0 1240.0 1470.7 1	1615.7 1599.7 1615.7 1615.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 1608.9 1166.5 1322.6 1471.7 1379.7 1471.8 1915.1 1608.9 1224.1 1149.5 1305.6 1471.7 1379.7 1471.8 1915.1 1608.9 1294.6 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 1495.6 1625.7 1471.8	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1424.7 1407.7 1378.7 165.5 1321.6 1624.7 1470.7 1378.7 1407.9 1223.0 1148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1624.7 1150.6	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1915.1 1666.5 1322.6 1471.7 1379.7 1668.9 166.5 1322.6 1625.7 1471.7 147
438.0 210.0 210.0 210.0 225.0	2.0 1.4 1.4 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	2.0 1.4 1.4 2.9 2.9 2.9 2.5 2	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 94.0 98.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (HUMAN) CSVIRDSLLODGEFSMDLR CYEMASHLR SSFLOOK STGGAPTFNTVTK STGGAPTFNTVTK STGGAPTFNTVTK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR SSFYVNGLTLGGOK SFFYNGLTLGGOK SFFYNGLTLGGOK CYEMASHLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1914.1 1607.9 1304.6 1449.7 2240.0 1165.5 1321.6 1470.7 1378.7 1607.9 1165.5 1321.6 1470.7 149.8 149	1615.7 1599.7 1615.7 1699.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1305.6 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1470.8 1915.1 1608.9 1224.1 149.5 1305.6 1471.7 1470.8 1915.1 1608.9 1294.6 1625.7	1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.1 1165.5 1321.6 1470.7 1378.7 165.5 1321.6 1470.7 1378.7 149.8 149	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1723.9 1643.9 1305.6 1450.7 2241.1 1166.5 1322.6 165.7 1470.8 166.5 1322.6 166.5 1322.6 166.5 1322.6 166.5 1322.6 166.5 1322.6 166.5 1322.6 166.5 1322.6 166.5 1322.6 166.5 1771.7 1771.7 1771.8 1771.
438.0 210.0 210.0 210.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	200 1.4 1.4 2.9 2.9 2.9 2.5 2	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.1.4 0.0 0.9 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 94.0 98.0 98.0 98.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR SSEVNOLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TKSTGGAPTFNYTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR SFYVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLRR DSLLODGEFSMDLR SYFVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLRR DSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR SSFVNGLTLGGOK TKSTGGAPTFNYTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR SSFVNGLTLGGOK STGGAPTFNTTVTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR SSFVNGLTLGGOK STGGAPTFNTTVTK CYEMASHLR CYEMASHLR SSFVNGLTLGGOK STGVABSHLRR SSFVNGLTLGGOK STGGAPTFNTTVTK	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.0 1165.5 1321.6 167.9 1624.7 149.7 1607.9 1624.7 1607.9 1624.7 149.8 1914.0 1607.9 1607.	1615.7 1599.7 1615.7 1699.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1166.5 1322.6 1471.7 1379.7 1471.8 108.9 1166.5 1322.6 1471.7 1379.7 1471.8 1166.5 1322.6 1471.7 1379.7 1471.8 1379.7 1471.8 1379.7 1471.8 1385.6 1471.7 147	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1642.9 1642.9 171.1 165.5 1321.6 1470.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 149.8 1914.1 1607.9 1165.5 1321.6 1470.7 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 1188.5 1304.6 1470.7 1188.5 1304.6 1470.7 1188.5 1304.6 1470.7 1378.7 1150.6 1470.7 1378.7 1150.6 1470.7 1378.7 1150.6	1615.7 1599.7 1615.7 1615.7 1599.7 1495.8 1615.7 224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1305.6 1450.7 1241.1 1166.5 1322.6 1471.7 1379.7 1608.9 1608.9 1608.9 1608.9 1608.9 1625.7 1471.7 1470.8 1915.1 1608.9 1608.9 1625.7 1471.7 1470.8 1915.1 1608.9 1625.7 1471.7 1470.8 1915.1 1608.9 1294.6 1471.7 1470.8 1915.1 1608.9 1294.6 1471.7 1470.8 1471.7 1470.8 1471.7 1470.8 1471.7 1470.8 1471.7 1470.8 1471.7 1470.8 1471.7 1470.8 1471.7 1470.8 1471.7 1470.8 1471.7 1470.8 1471.7 1470.8 1471.7 1471.7 1470.8 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 1472.9
438.0 210.0 2210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 21.0 2	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 2.5 22.5 22.5 22.5 22.5 22.5 22.5 22.5	200 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 1.4 0.0 2.0 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	99.0 96.0 98.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLEYEAPR NSWGEEWGMGGYVK 5 (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR ECYHGGIINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNVTVTK STGGAPTFNVTVTK TFVNITPAEVGLVJGK TFVNITPAEVGLVJGK TFVNITPAEVGLVJGK TCYEMASHLR CYEMASHLR CYEMASH	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1642.9 1642.9 1607.9 1645.5 1321.6 1470.7 1378.7 1607.9 165.5 1321.6 1624.7 1469.8 1914.0 1607.9 1293.6 1207.9 1293.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 1470.7 1470.7 1470.7 148.5 1304.6 1470.7	1615.7 1599.7 1615.7 1615.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1606.5 1450.7 1608.9 1605.7 1470.8 1915.1 1608.9 1224.1 1149.5 1305.6 1450.7 1471.7 1379.7 1471.7 1379.7 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 1495.6 1625.7 1470.8	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1624.7 1407.9 1165.5 1321.6 1624.7 1470.7 1378.7 1697.9 1148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 1148.5 1304.6 1470.7 1148.5 1304.6 1470.7 1148.5 1304.6 1470.7 1148.5 1304.6 1470.7 1148.5 1304.6 1470.7 1148.5 1304.6 1470.7 1148.5 1304.6 1470.7 1148.5 1304.6 1470.7 1148.5 1304.6 1470.7 1378.7 1722.9 1642.9	1615.7 1599.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1915.1 1668.9 1450.7 2241.1 1166.5 1322.6 1471.7 1379.7 168.9 16
438.0 210.0 2210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 21.0 2	2.0 1.4 1.4 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	200 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 1.4 0.0 2.0 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	99.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFOEPLFYEAPR NSWGEEWGMGGYVK 5 (HUMAN) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK TFVNITPAEVGLVGKDR TKSTGGAPTFNYTVTK TFVNITPAEVGLVGKDR TKSTGGAPTFNYTVTK CYEMASHLR CYEMASHLR CYEMASHLR CYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK TKSTGGAPTFNYTVTK TKSTGGAPTFNYTVTK CYEMASHLR CYEMASHLR SSFYVNGLTLGGOK STGAPTFNYTVTK TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR SSFYVNGLTLGGOK TFVNITPAEVGLVGKDR TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR SSFYVNGLTLGGOK TFVNITPAEVGLVGKDR TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CYEMASHLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1607.9 1165.5 1321.6 1624.7 1470.7 1470.7 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1624.7 150.6	1615.7 1599.7 1615.7 1615.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1643.9 1615.6 1450.7 1224.1 1166.5 1322.6 1450.7 1471.7 1379.7 1608.9	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1165.5 1321.6 1470.7 1378.7 1607.9 1165.5 1321.6 1624.7 1172.7 1469.8 1914.1 1607.9 1293.6 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 142.7 1150.6 1470.7 1378.7 1722.9 1914.1 1607.9	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1450.7 1224.0 1166.5 1322.6 1471.7 1379.7 1608.9 1166.5 1322.6 1471.7 1379.7 1608.9 1294.6 1471.7 1471.7 1479.7 1508.9 1294.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1305.6 1471.7 1471.7 1495.7 1495.7 14
438.0 210.0 2210.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 21	2.0 1.4 1.4 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	200 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 94.0 98.0 98.0 98.0 98.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CCYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGLVJGK TFVNITPAEVGLVJGK TFVNITPAEVGLVJGK TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CYEMASHLR SFYVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLR DSLLODGEFSMDLR SYFVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLR DSLLODGEFSMDLR SSFVNGLTLGGOK TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR SSFVNGLTLGGOK TKSTGGAPTFNYTVTK CYEMASHLR SSFVNGLTLGGOK STGGAPTFNTTYTK CYEMASHLR SSFVNGLTLGGOK STGGAPTFNTTYTK CYEMASHLR SSFVNGLTLGGOK STGGAPTFNTTYTK CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR SSFVNGLTLGGOK STGGAPTFNTTYTK SSFVNGLTLGGOK STGVAMSHLR CYEMASHLR SSFVNGLTLGGOK STGVAMSHLR SSFVNGLTLGGOK STGVAMSHLR SSFVNGLTLGGOK STGVAMSHLR SSFVNGLTLGGOK STGVAMSHLR SSFVNGLTLGGOK STGGAPTFNTYTTK STGGAPTFNTYTK STGGAPTFNTYTK STGGAPTFNTYTK STGGAPTFNTYTK STGGAPTFNTYTK STGGAPTFNTYTK STGGAPTFNTYTK STGGAPTFNTYTK STGGAPTGNTYTK STGGAPTGNTYTK STGGAPTGNTYTK STGGAPTGNTYTK STGGAPTGNTYTK STGAPTGNTYTK STGAPTGNTYTC STGAPTGNTTT STGAPTGNTTT STGAPTGNTT STGAPTGNTT STGAPTGNTT STGAPTGNTT STGAPTGNT STGAPTGNT STGAPTGNT STGAPTGNT STGAPTGNT STGAPTGNT STGAPTGN	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 2240.0 1165.5 1321.6 167.9 160	1615.7 1599.7 1615.7 1699.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1166.5 1322.6 1450.7 1471.7 1379.7 1470.8 1166.5 1322.6 1450.7 1471.7 1471.7 1479.5 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 1723.9 1643.9 1915.1	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 1499.8 1914.1 1607.9 1165.5 1321.6 1470.7 1378.7 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 1378.7 1506.8	1615.7 1599.7 1615.7 1615.7 1599.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1608.9 1608.9 1608.9 170.8 17
438.0 210.0 210.0 210.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 2.5 22.5 22.5 22.5 22.5 22.5 22.5 22.5	200 1.4 1.4 2.9 2.9 2.9 2.2.5 22.5 22.5 22.5 22.5 2	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 94.0 98.0 98.0 88.0 88.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TCYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLOGEFSMDLR CYEMASHLR CYEMASHLR SFYVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR SFYVNGLTLGGOK TFVNITPAEVGVLVGKDR TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR SSFVVNGLTLGGOK TFVNITPAEVGVLVGKDR TKSTGGAPTFNYTVTK KCYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR SSFVVNGLTLGGOK SFFVNGLTLGGOK SFFVNTTYTK STGGAPTFNTTYTK STGGAPTFNTTYTK STGGAPTFNTTYTK STGGAPTFNTYTTK STGGAPTFNTTYTK STGGAPT	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1642.9 1642.9 165.5 1321.6 167.7 1378.7 1607.9 1165.5 1321.6 1624.7 149.7 1	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1450.7 1471.7 1379.7 1470.8 1915.1 1608.9 1166.5 1322.6 1625.7 1470.8 1915.1 1608.9 1166.5 1322.6 1471.7 1379.7 1471.7 1379.7 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 149.5 1305.6 1471.7 149.5 1305.6 1471.7 149.5 1305.6 1471.7 149.5 1305.6 1471.7 149.5 1305.6 1471.7 149.5 1305.6 1471.7 149.5 1305.6 1471.7 149.5 1305.6 1471.7 149.9 149.9 149.0 1	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 149.8 1914.1 1607.9 1293.6 1470.7 1378.7 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 1378.7 1223.9 1642.9 1944.1	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1915.1 1666.5 1322.6 1625.7 1471.8 1915.1 1668.9 1166.5 1322.6 1625.7 1471.7 1379.7 1471.7 149.5 168.9 1166.5 1322.6 1625.7 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.9 1643.9 1915.1 1608.9 1450.7 1471.7 149.9 1643.9 1915.1 1608.9 1450.7 1429.9
438.0 210.0 2210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0	2.0 1.4 1.4 2.9 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	200 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 1.4 0.0 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFOEPLFYEAPR NSWGEEWGMGGYVK s (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR EGVHGGLINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTENVTVTK TFVNITPAEVCVLVGK TFVNITPAEVCVLVGK TFVNITPAEVCVLVGK TCYMASHLR CYEMASHLR CYEMASHLR CYEMASHLR CYEMASHLR SSFYVNGLTLGGOK STGGAPTENVTVTK CYEMASHLR CYEMASHLR CYEMASHLR SSFYVNGLTLGGOK TSTGGAPTFNVTVK CYEMASHLR	1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 1378.7 1607.9 1321.6 1624.7 1469.8 1914.0 1607.9 1293.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 1470.7 1470.7 1470.7 1470.7 1378.7 1722.9 1914.1 1607.8 1449.7	1615.7 1599.7 1615.7 1615.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1450.7 1224.1 1166.5 1322.6 1471.7 1379.7 1608.9 11608.9 1294.6 1471.7 1379.7 1470.8 1915.1 1608.9 1294.6 1471.7 1	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1203.6 1	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1625.7 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 149.5 1305.6 1471.7 1471.7 1471.7 148.5 1395.6 1625.7 1151.7 1471.7 1471.7 149.5 1305.6 1625.7 1151.7 1471.7 1471.7 149.5 1305.6 1628.7 1151.7 1471.7 1471.7 1479.7 1723.9 1915.1 1608.9 1450.7 1471.7 1471.7 1471.7 1471.7 1472.9 1915.1 1608.9 1450.7 1643.9 1915.1 1608.9
438.0 210.0 2210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 21.0 2	2.0 1.4 1.4 2.9 2.9 2.9 2.5 2.5 2.2.	200 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	7.8 5.1 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 1.4 0.0 2.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 94.0 98.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFOEPLFYEAPR NSWGEEWGMGGYVK SULUTION SOURCESTON OF THE STANDARD CSYLROSLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR ECYHGGLINKK KCYEMASHLR SSFYNKITLGGOK STGGAPTENTYTK TFVNITPAEVCYLVGK TFVNITPAEVCYLVGK TFVNITPAEVCYLVGK TKSTGGAPTENTYTK CYEMASHLR CYEMASHLR CYEMASHLR SSFYNKILLOGGESMDLR CYEMASHLR SSFYNKILLOGGESMDLR CYEMASHLR SSFYNKILLOGGESMDLR CYEMASHLR CYEMASHLR SSFYNKILLOGGESMDLR CSYLROSLOGGESMDLR CSYLROSLOGGESMDLR CSYLROSLOGGESMDLR CSYLROSLOGGESMDLR CSYLROSLOGGESMDLR CYEMASHLR	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 1607.9 1148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 1148.5 1304.6 1470.7 117	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 12224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1450.7 1224.1 166.5 1471.7 1379.7 1470.8 1915.1 1608.9 1224.1 1149.5 1305.6 1471.7 1379.7 1471.7 1479.8 1915.1 1608.9 1294.6 1471.7 14	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1449.7 1221.6 1470.7 1378.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 149.9 1293.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 148.5 148.5 148.5 148.5 148.5 148.5 148.5 148.5 148.5 148.5 148.5	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1450.7 1241.1 166.5 1322.6 1471.7 1379.7 1608.9 1605.9 1605.9 1605.7
438.0 210.0 210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 2.5 22.5 22.5 22.5 22.5 22.5 22.5 22.5	200 1.4 1.4 2.9 2.9 2.9 2.5 22.9 20.9 2	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.1.4 0.0 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK S (HUMAN) CSVIRDSLLODGEFSMDLR CYEMASHLR SSFYVNGLTLGGOK STGGAPTFNTYTK STGGAPTFNTYTKTDK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGKDR TKSTGGAPTFNTYTK CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR SFYVNGLTLGGOK STGGAPTFNTYTK CYEMASHLRR DSLLODGEFSMDLR SFYVNGLTLGGOK STGGAPTFNTYTK CYEMASHLRR DSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLRR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLRR SSFVNGLTLGGOK STGGAPTFNTYTK KCYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CYEMASHLR CYEMASHLR SSFVNGLTLGGOK STGGAPTFNTTYTK TSTGGAPTFNTTYTK TSTGGAPTGAPTGAPT TSTGAPTGAPTGAPT TSTGAPTGAPT TSTGAPTGAPT TSTGAPTGAPT TSTGAPTGAPT TSTGAPT	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 1469.8 1914.0 1607.9 1148.5 1304.6 1470.7 1378.7 1469.8 1914.0 1607.9 1148.5 1304.6 1470.7 1378.7 1470.7 1378.7 1722.9 1642.9 1914.1 1607.8 1449.7 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.8 1449.7 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.8 1485.5 1166.5 1166.5 1166.5 1166.5 1166.5 1166.5 1166.5 1166.5 1166.5 1166.5	1615.7 1599.7 1615.7 1699.7 1615.7 1699.7 1495.8 1615.7 1224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1305.6 1450.7 1241.1 166.5 1322.6 1625.7 1471.7 1379.7 1608.9 1608.9 1608.9 1605.7 1608.9 1608.9 171.7 171.9 1668.9 1655.7 161.7 171.7	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1222.9 1914.1 1607.9 1304.6 1449.7 1240.1 1165.5 1321.6 1470.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 1607.9 1165.5 1321.6 1470.7 1378.7 149.8 1914.1 1607.9 1165.5 1321.6 1470.7 1378.7 149.8 1914.1 1607.9 149.8 1914.1 1607.9 149.8 1914.1 1607.9 149.8 1914.1 1607.9 149.8 1914.1 1607.9 149.8 1914.1 1607.9 149.8 1914.1 1607.9 149.8 1914.1 1607.9 149.8 1914.1 1607.9 149.8 1914.1 1607.9 149.8 148.5 150.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1448.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 149.5 163.9 1305.6 1450.7 1241.1 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 166.5 1322.6 1625.7 1471.7 1379.7 1471.
438.0 210.0 2210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.0 21.	2.0 1.4 1.4 2.9 2.9 2.9 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5	200 1.4 1.4 29 29 22.5 22.9 20.9 2	7.8 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 94.0 98.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFOEPLFYEAPR NSWGEEWGMGGYVK S (HUMAN) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR ECVHGGIINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGLVJGK TFVNITPAEVGLVJGK TKNTGGAPTFNYTVTK CYEMASHLR CSVIRDSLUDGEFSMDLR CSVIRDSLUDGEFSMDLR CSVIRDSLUDGEFSMDLR CYEMASHLR	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1607.9 1165.5 1321.6 1624.7 1469.8 1914.0 1607.9 1293.6 1470.7 1378.7 1470.7 1378.7 1470.7 1378.7 1722.9 1622.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.9 1914.1 1607.8 1440.7 1293.6 1741.8 1642.9 1914.1 1607.8 1144.5 1165.5 1165.5 1165.5 1165.5 1165.5	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 12224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 123.9 1643.9 1915.1 1608.9 1305.6 1450.7 1241.1 1166.5 1322.6 1471.7 1379.7 1471.7 1379.7 1471.7 1379.7 1471.7 14	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1607.9 165.5 1321.6 1624.7 1470.7 1378.7 149.8 1914.1 1607.9 1203.6 1470.7 1378.7 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 1304.6 1470.7 148.5 150.6 1470.7 148.5 150.6 1470.7 148.5 150.6 1470.7 148.5 165.5 165.5 165.5 165.5 165.5 1473.5	1615.7 1599.7 1615.7 1615.7 1615.7 1699.7 1495.8 1615.7 2224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1915.1 1666.5 1322.6 1625.7 1470.8 1915.1 1608.9 1450.7 1471.7 1379.7 1471.7 1379.7 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 1471.7 149.5 1608.9 1625.7 1471.7 1471.7 1471.7 1471.7 1471.7 149.5 1305.6 1625.7 1471.7 1471.7 149.5 1305.6 1625.7 1471.7 1471.7 149.5 1305.6 1625.7 1471.7 149.5 1305.6 1625.7 1471.7 149.5 1305.6 1625.7 1471.7 149.5 1305.6 1625.7 1471.7 149.5 1305.6 1625.7 1471.7 1471.7 149.5 1305.6 1625.7 1471.7 149.5 1305.6 166.5 166.5 166.5 166.5 166.5 166.5
438.0 210.0 210.0 210.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 2.5 22.5 22.5 22.5 22.5 22.5 22.5 22.5	200 1.4 1.4 29 29 29 22.5 22.9 20.	7.8 5.1 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	99.0 96.0 96.0 98.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFOEPLFYEAPR NSWGEEWGMGGYVK 5 (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR ECVHGGLINKK KCYYMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGLVJGK TFVNITPAEVGLVJGK TKNTGGAPTFNYTVTK CYEMASHLR CYEMASHL	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1470.7 1378.7 1470.7 1378.7 1470.7 1378.7 1470.7 1378.7 1462.9 1914.1 1607.9 165.5 1321.6 1624.7 1470.7 1378.7 1722.9 162.9 1914.1 1607.9 165.5 1321.6 1624.7 1470.7 1470.7 148.5 1304.6 1624.7 1470.7 1378.7 1722.9 1642.9 1914.1 1607.8 1449.7 1293.6 1741.8 1148.5 1165.5 11660.7 1470.7	1615.7 1599.7 1615.7 1615.7 1495.8 1615.7 12224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1450.7 1221.1 1166.5 1322.6 1471.7 1379.7 1608.9 1608.5 1608.5 1608.5 1668.5 1668.5	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1624.7 149.7 149.7 149.7 149.7 149.7 149.7 149.8 1914.1 1607.9 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1642.9 1914.1 1607.9 1652.5 1304.6 1470.7 148.5 1304.6 1624.7 1506.6 1470.7 148.5 1304.6 1624.7 1506.6 1470.7 148.5 1304.6 1624.7 1180.6 1470.7 148.5 1304.6 1624.7 1180.6 1470.7 1485.5 1304.6 1624.7 1180.6 1470.7 1489.7 1180.6 1470.7 1489.7 1180.6 1470.7 1489.7 1470.7 1470.7 1470.7 1470.7 1470.7	1615.7 1599.7 1615.7 1615.7 1615.7 1699.7 1495.8 1615.7 1224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1643.9 1643.9 1665.6 1471.7 1379.7 1608.9 16
438.0 210.0 210.0 225.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.9 2.5 22.5 22.5 22.5 22.5 22.	200 1.4 1.4 2.9 2.9 2.9 2.5 22.9 20.9 2	7.8 5.1 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 1.4 0.0 0.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	99.0 96.0 94.0 98.0 98.0 98.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGGYVK VFQEPLFYEAPR NSWGEEWGMGWYK VFQEPLFYEAPR NSWGEEWGMGWYK S (Human) CSVIRDSLLODGEFSMDLR CEVHGGIINKK KCYEMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TFVNITPAEVGVLVGK TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CYEMASHLR SFYVNGLTLGGOK STGGAPTFNYTVTK CYEMASHLR DSLLODGEFSMDLR SFYVNGLTLGGOK TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR SFYVNGLTLGGOK TFVNITPAEVGVLVGKDR TKSTGGAPTFNYTVTK CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR CSVIRDSLLODGEFSMDLR CYEMASHLR SFYVNGLTLGGOK SFYVNGLTLGGOK SFYVNGLTLGGOK SFYVNGLTLGGOK STGGAPTFNYTVTK TYMTPAEVGVLVGKDR TKSTGGAPTFNYTYTK TYMTPAEVGVLVGKDR TKSTGGAPTFNYTYTK TYMTPAEVGVLVGKDR TKSTGGAPTFNYTYTK TYMTPAEVGVLVGKDR TKSTGGAPTFNYTYTK SSFYVNGLTLGGOK STGGAPTFNYTYTK SSFYVNGLTLGGOK STGGAPTFNYTYTK STGGAPTFNYTYT	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 1223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1607.9 1165.5 1321.6 1624.7 1469.8 1914.0 1607.9 1304.6 1470.7 1378.7 1607.9 1165.5 1321.6 1624.7 1470.7 1378.7 1607.9 1165.5 1321.6 1624.7 1470.7 1378.7 1722.9 1642.9 1642.9 17470.7 1378.7 1722.9 1642.9 1914.1 1607.8 1449.7 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.8 1449.7 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.8 1449.7 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.8 1449.7 1293.6 1449.7 1293.6 1470.7 1378.7 1722.9 1642.9 1642.9 1914.1 1607.8 1449.7 1293.6 1470.7 1473.6 1640.7 1473.6 1640.7 1470.7 1165.5 1165.5 1165.5 1165.5 1165.5 1163.8	1615.7 1599.7 1615.7 1699.7 1615.7 1699.7 1495.8 1615.7 12224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1166.5 1322.6 1450.7 1294.6 1471.7 1379.7 1471.7 1471.7 149.5 1608.9 16	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1607.9 1304.6 1470.7 1378.7 1607.9 1642.9 1642.9 1714.1 1607.9 18	1615.7 1599.7 1615.7 1615.7 1699.7 1495.8 1615.7 1294.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1471.7 1379.7 1608.9 16
438.0 210.0 210.0 225.0 225.0 225.0 225.0 225.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	2.0 1.4 1.4 2.9 2.9 2.9 ROF1_HUMAN 2.5 22.5 22.5 22.5 22.5 22.5 22.5 22.5	200 1.4 1.4 29 29 29 22.5 22.9 20.	7.8 5.1 5.1 5.1 5.1 22.2 22.2 22.2 Profilin-1 (P 82.1 82.1 82.1 82.1 82.1 82.1 82.1 82.1	0.0 0.0 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	99.0 96.0 96.0 98.0 99.0 99.0 99.0 99.0 99.0 99.0 99	NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK NSWGEEWGMGGYVK VFOEPLFYEAPR NSWGEEWGMGGYVK 5 (Human) CSVIRDSLLODGEFSMDLR CYEMASHLR DSLLODGEFSMDLR ECVHGGLINKK KCYYMASHLR SSFYVNGLTLGGOK STGGAPTFNYTVTK STGGAPTFNYTVTK TFVNITPAEVGLVJGK TFVNITPAEVGLVJGK TKNTGGAPTFNYTVTK CYEMASHLR CYEMASHL	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.7 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1470.7 1378.7 1470.7 1378.7 1470.7 1378.7 1470.7 1378.7 1462.9 1914.1 1607.9 165.5 1321.6 1624.7 1470.7 1378.7 1722.9 162.9 1914.1 1607.9 165.5 1321.6 1624.7 1470.7 1470.7 148.5 1304.6 1624.7 1470.7 1378.7 1722.9 1642.9 1914.1 1607.8 1449.7 1293.6 1741.8 1148.5 1165.5 11660.7 1470.7	1615.7 1599.7 1615.7 1615.7 1495.8 1615.7 12224.0 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1305.6 1450.7 1221.1 1166.5 1322.6 1471.7 1379.7 1608.9 1608.5 1608.5 1608.5 1668.5 1668.5	1614.7 1598.7 1614.7 1598.7 1614.7 1598.7 1494.8 1614.7 2223.0 1148.5 1624.7 1150.6 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1304.6 1470.7 1378.7 1607.9 165.5 1321.6 1624.7 149.7 149.7 149.7 149.7 149.7 149.8 1914.1 1607.9 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1293.6 1470.7 1378.7 1722.9 1642.9 1914.1 1607.9 1642.9 1914.1 165.5 1304.6 1624.7 1150.6 1470.7 1378.7 1722.9 1914.1 1607.9 1642.9 1914.1 165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1165.5 1173.6	1615.7 1599.7 1615.7 1615.7 1615.7 1698.7 1495.8 1615.7 1294.6 1149.5 1625.7 1151.7 1294.6 1471.7 1379.7 1608.9 1166.5 1322.6 1625.7 1470.8 1915.1 1668.9 1471.7 14

51.0 51.0	17.4 17.4	17.4 17.4	38.3 38.3	2.0 2.0	99.0 99.0	LCGTFLGGPKPPQR LPASFDAR	1526.8 875.5	1527.8 876.5	1526.8 875.5	1527.8 876.5
51.0 51.0	17.4 17.4	17.4 17.4	38.3 38.3	2.0 2.0	99.0 99.0	SGVYQHVTGEMMGGHAIR VMFTEDLKLPASFDAR	1928.9 1838.9	1929.9 1839.9	1928.9 1838.9	1929.9 1839.9
51.0	17.4	17.4	38.3	1.5	97.0	EQWPQCPTIK	1285.6	1286.6	1285.6	1286.6
51.0 51.0	17.4 17.4	17.4 17.4	38.3 38.3	1.2 0.5	94.0 67.0	ILRGQDHCGIESEVVAGIPR DQGSCGSCWAFGAVEAISDR	2205.1 2171.9	2206.1 2172.9	2205.1 2171.9	2206.1 2172.9
51.0 71.0	17.4 4.9	17.4 4.9	38.3 28.0	0.1 2.0	26.0 99.0	RLCGTFLGGPKPPQR EQWPQCPTIKEIR	1682.9 1683.8	1683.9 1684.8	1682.9 1683.8	1683.9 1684.8
71.0	4.9	4.9	28.0	2.0	99.0	SGVYQHVTGEMMGGHAIR EQWPQCPTIK	1928.9	1929.9	1928.9	1929.9
71.0 48.0	4.9 15.7	4.9 15.7	28.0 34.2	0.9 2.0	86.0 99.0	DQGSCGSCWAFGAVEAISDR	1285.6 2171.9	1286.6 2172.9	1285.6 2171.9	1286.6 2172.9
48.0 48.0	15.7 15.7	15.7 15.7	34.2 34.2	2.0 2.0	99.0 99.0	EQWPQCPTIKEIR ICEPGYSPTYKQDK	1683.8 1684.8	1684.8 1685.8	1683.8 1684.8	1684.8 1685.8
48.0 48.0	15.7 15.7	15.7 15.7	34.2 34.2	2.0 2.0	99.0 99.0	ILRGQDHCGIESEVVAGIPR LPASFDAR	2205.1 875.5	2206.1 876.5	2205.1 875.5	2206.1 876.5
48.0	15.7	15.7	34.2	2.0	99.0	SGVYQHVTGEMMGGHAIR	1928.9	1929.9	1928.9	1929.9
48.0 48.0	15.7 15.7	15.7 15.7	34.2 34.2	2.0 1.7	99.0 98.0	VMFTEDLKLPASFDAR EQWPQCPTIK	1838.9 1285.6	1839.9 1286.6	1838.9 1285.6	1839.9 1286.6
P07900 75.0	HS90A_HUMAN 4.7	4.7	Heat shock p 23.5	protein HSP 2.0	90-alpha (F 99.0	ISP 86) (Renal carcinoma antigen NY-REN-3 HIYYITGETK	8) - Homo sapien 1223.6	s (Human) 1224.6	1223.6	1224.6
75.0 75.0	4.7 4.7	4.7 4.7	23.5	2.0 0.6	99.0 73.0	SLTNDWEDHLAVK RAPFDLFENR	1526.7 1263.6	1527.7 1264.7	1526.7 1263.6	1527.7 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 20.0	29.4 29.4	29.4 29.4	29.9 29.9	2.0 2.0	99.0 99.0	ALLFVPR AQALRDNSTMGYMAAK	814.5 1726.8	815.5 1727.8	814.5 1726.8	815.5 1727.8
20.0 20.0	29.4 29.4	29.4 29.4	29.9 29.9	2.0 2.0	99.0 99.0	FYEQFSK HFSVEGQLEFR	947.4 1347.7	948.4 1348.7	947.4 1347.7	948.4 1348.7
20.0 20.0	29.4 29.4	29.4 29.4	29.9 29.9	2.0 2.0	99.0 99.0	HIYYITGETK HIYYITGETKDQVANSAFVER	1223.6 2440.2	1224.6 2441.2	1223.6 2440.2	1224.6 2441.2
20.0	29.4	29.4	29.9	2.0	99.0	KHLEINPDHSIIETLR	1914.0	1915.0	1914.0	1915.0
20.0 20.0	29.4 29.4	29.4 29.4	29.9 29.9	2.0 2.0	99.0 99.0	LVTSPCCIVTSTYGWTANMER NPDDITNEEYGEFYK	2445.1 1832.8	2446.1 1833.8	2445.1 1832.8	2446.1 1833.8
20.0 20.0	29.4 29.4	29.4 29.4	29.9 29.9	2.0 2.0	99.0 99.0	RAPFDLFENR VILHLKEDQTEYLEER	1263.6 2014.0	1264.6 2015.0	1263.6 2014.0	1264.6 2015.0
20.0	29.4 29.4	29.4 29.4	29.9 29.9	2.0	99.0 99.0	YIDQEELNK YIDQEELNKTKPIWTR	1150.6 2033.1	1151.6 2034.1	1150.6 2033.1	1151.6 2034.1
20.0	29.4	29.4	29.9	2.0	99.0	YYTSASGDEMVSLKDYCTR	2245.0	2246.0	2245.0	2246.0
20.0 20.0	29.4 29.4	29.4 29.4	29.9 29.9	1.4 0.0	96.0 99.0	AQALRDNSTMGYMAAKK HIYYITGETK	1854.9 1235.6	1855.9 1236.6	1854.9 1235.6	1855.9 1236.6
20.0 P07910	29.4 HNRPC_HUMAN	29.4	29.9 Heterogeneo	0.0 ous nuclear i	99.0 ribonucleop	YIDQEELNK proteins C1/C2 (hnRNP C1 / hnRNP C2) - Hor	1152.5	1153.5	1150.6	1151.6
241.0	5.0	5.0	8.8	2.0	99.0	GFAFVQYVNER	1328.6	1329.7	1328.7	1329.7
241.0 241.0	5.0	5.0 5.0	8.8 8.8	2.0 0.6	99.0 72.0	SYPARVPPPPPIAR MYSYPARVPPPPPIAR	1516.8 1811.0	1517.9 1812.0	1516.9 1811.0	1517.9 1812.0
241.0 213.0	5.0 3.2	5.0 3.2	8.8 27.5	0.4 2.0	63.0 99.0	VPPPPPIAR GFAFVQYVNER	942.6 1328.6	943.6 1329.6	942.6 1328.7	943.6 1329.7
213.0 P08107	3.2 HSP71_HUMAN	3.2	27.5 Heat shock	1.2 70 kDa prote	93.0 ein 1 (HSP70	VPPPPPIAR 0.1) (HSP70-1/HSP70-2) - Homo sapiens (H	942.6 uman)	943.6	942.6	943.6
127.0 127.0	9.2 9.2	14.3 14.3	29.2 29.2	2.0 2.0	99.0 99.0	FEELCSDLFR LLQDFFNGRDLNK	1314.6 1579.8	1315.6 1580.8	1314.6 1579.8	1315.6 1580.8
127.0	9.2	14.3	29.2	2.0	99.0	MVQEAEKYKAEDEVQRER	2237.1	2238.1	2237.1	2238.1
127.0 127.0	9.2 9.2	14.3 14.3	29.2 29.2	1.7 1.2	98.0 99.0	ARFEELCSDLFR ATAGDTHLGGEDFDNR	1541.7 1674.7	1542.7 1675.7	1541.7 1674.7	1542.7 1675.7
127.0 127.0		14.3 14.3	29.2 29.2	0.3 0.0	46.0 45.0	DAGVIAGLNVLR LDKAQIHDLVLVGGSTR	1196.7 1837.0	1197.7 1838.0	1196.7 1837.0	1197.7 1838.0
127.0 127.0	9.2	14.3 14.3	29.2 29.2	0.0	99.0 99.0	TTPSYVAFTDTER VEHANDQGNR	1486.7 1227.6	1487.7 1228.6	1486.7 1227.6	1487.7 1228.6
126.0	2.3	5.0	23.2	1.5	97.0	AFYPEEISSMVLTK	1613.8	1614.8	1613.8	1614.8
126.0 126.0		5.0 5.0	23.2 23.2	0.5 0.2	80.0 43.0	IINEPTAAAIAYGLDR FEELCSDLFR	1686.9 1314.6	1687.9 1315.6	1686.9 1314.6	1687.9 1315.6
126.0	2.3	5.0	23.2	0.0	47.0	ATAGDTHLGGEDFDNR	1690.7	1691.7	1690.7	1691.7
126.0 126.0	2.3 2.3	5.0 5.0	23.2 23.2	0.0 0.0	39.0 99.0	NALESYAFNMK TTPSYVAFTDTER	1302.6 1486.7	1303.6 1487.7	1302.6 1486.7	1303.6 1487.7
126.0 126.0 P08571 0 548.0	2.3 2.3 CD14_HUMAN 2.0	5.0 5.0	23.2 23.2 Monocyte di 4.8	0.0 0.0 fferentiation 2.0	39.0 99.0 n antigen CE 99.0	NALESYAFNMK TTPSYVAFTDTER D14 precursor (Myeloid cell-specific leucine-r VLSIAOAHSPAFSCEQVR	1302.6 1486.7 rich glycoprotein) 1999.0	1303.6 1487.7 [Contains: Mon- 2000.0	1302.6 1486.7 ocyte differentiat 1999.0	1303.6 1487.7 ion antigen CD1- 2000.0
126.0 126.0 P08571 548.0 145.0 182.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0	5.0 5.0 2.0 2.1 4.0	23.2 23.2 Monocyte di 4.8 16.3 18.1	0.0 0.0 fferentiation 2.0 2.0 2.0	39.0 99.0 n antigen CE 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTDTER 214 precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEOVR VLSIAQAHSPAFSCEOVR AFPALTSLDLSONPGLGER	1302.6 1486.7 "ich glycoprotein) 1999.0 1999.0 1972.0	1303.6 1487.7 [Contains: Mon- 2000.0 2000.0 1973.0	1302.6 1486.7 ocyte differentiat 1999.0 1999.0 1972.0	1303.6 1487.7 Sion antigen CD1- 2000.0 2000.0 1973.0
126.0 126.0 P08571 i 548.0 145.0 182.0 P08575 i	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 4.0 CD45_HUMAN	5.0 5.0 2.0 2.1 4.0 4.0	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1	0.0 0.0 fferentiation 2.0 2.0 2.0 2.0	39.0 99.0 n antigen CE 99.0 99.0 99.0 99.0 gen precurs	NALESYAFNMK TTPSYVAFTDTER 114 precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEOVR VLSIAQAHSPAFSCEOVR AFPALTSLDLSDMPGLGER VLSIAQAHSPAFSCEOVR or (EC 3.1.3.48) (L-CA) (T200) (CD45 antige	1302.6 1486.7 rich glycoprotein) 1999.0 1992.0 1999.0 en) - Homo sapier	1303.6 1487.7 [Contains: Mon- 2000.0 2000.0 1973.0 2000.0 as (Human)	1302.6 1486.7 ocyte differentiat 1999.0 1999.0 1972.0 1999.0	1303.6 1487.7 ion antigen CD1- 2000.0 2000.0 1973.0 2000.0
126.0 126.0 P08571 0 548.0 145.0 182.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 4.0 CD45_HUMAN	5.0 5.0 2.0 2.1 4.0	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1	0.0 0.0 fferentiation 2.0 2.0 2.0 2.0	39.0 99.0 n antigen CE 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 014 precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEOVR VLSIAQAHSPAFSCEOVR AFPALTSLDLSDNPGLGER VLSIAQAHSPAFSCEOVR	1302.6 1486.7 ich glycoprotein) 1999.0 1999.0 1972.0 1999.0	1303.6 1487.7 [Contains: Mon- 2000.0 2000.0 1973.0 2000.0	1302.6 1486.7 ocyte differentiat 1999.0 1999.0 1972.0	1303.6 1487.7 Sion antigen CD1- 2000.0 2000.0 1973.0
126.0 126.0 PO8571 i 548.0 145.0 182.0 PO8575 i 250.0 250.0	2.3 2.3 2.0 2.0 2.1 4.0 4.0 CD45_HUMAN 4.7 4.7	5.0 5.0 2.0 2.1 4.0 4.0 4.7 4.7	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 Leukocyte co 3.7 3.7 3.7	0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 ommon antig 2.0 2.0 2.0	39.0 99.0 n antigen CE 99.0 99.0 99.0 gen precurs 99.0 99.0 80.0	NALESYAFNMK TTPSYVAFTOTER 7)14 precursor (Myeloid cell-specific leucine-r VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLDLSDNPGLGER VLSIAOAHSPAFSCEOVR 67 (C 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAFFOSIPR TDFGSPGEPOLIFCR	1302.6 1486.7 1499.0 1999.0 1999.0 1972.0 1999.0 en) - Homo sapier 1403.7 1319.7 1722.8	1303.6 1487.7 [Contains: Mon- 2000.0 2000.0 1973.0 2000.0 Is (Human) 1404.7 1320.7 1723.8	1302.6 1486.7 1486.7 1999.0 1999.0 1972.0 1999.0 1403.7 1319.7	1303.6 1487.7 ion antigen CD1- 2000.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8
126.0 126.0 P08571 548.0 145.0 182.0 P08575 250.0 250.0 250.0 323.0 P08670	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 4.0 CD45_HUMAN 4.7 4.7 4.7 2.0 VIME_HUMAN	5.0 5.0 2.0 2.1 4.0 4.0 4.7 4.7 4.7 2.0	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 Leukocyte co 3.7 3.7 3.7 6.7	0.0 0.0 fferentiatior 2.0 2.0 2.0 common antig 2.0 2.0 0.7 2.0 domo sapien	39.0 99.0 99.0 99.0 99.0 99.0 gen precurs 99.0 99.0 80.0 99.0	NALESYAFNMK TTPSYVAFTOTER 7)14 precursor (Myeloid cell-specific leucine-r VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLDLSDNPGLGER VLSIAOAHSPAFSCEOVR OF (EC. 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTOYEK LFLAEFOSIPR TDFGSPGEPOLIFCR LFLAEFOSIPR	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1972.0 199.0 en) - Homo sapier 1403.7 1319.7 1722.8 1319.7	1303.6 1487.7 [Contains: Mon- 2000.0 2000.0 1973.0 2000.0 s: (Human) 1404.7 1320.7 1723.8 1320.7	1302.6 1486.7 ocyte differentiat 1999.0 1999.0 1972.0 1999.0 1403.7 1319.7 1722.8 1319.7	1303.6 1487.7 ion antigen CD1- 2000.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7
126.0 126.0 P08571 548.0 145.0 182.0 P08575 250.0 250.0 250.0 323.0 P08670 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 CD45_HUMAN 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4	5.0 5.0 2.0 2.1 4.0 4.0 4.7 4.7 4.7 2.0	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 Leukocyte ci 3.7 3.7 3.7 6.7 Vimentin - H 70.0	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 gen precurs 99.0 99.0 80.0 99.0 s (Human) 99.0	NALESVAFNMK TTPSYVAFTOTER 714 Precursor (Myeloid cell-specific leucine-r V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR AFPALTSLID SONVEGLER V.SIAOAHSPAFSCEOVR Or (EC 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTQUEK LFLAEFOSIPR TDFGSPGEPOLIFOR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLOREEAENTLOSFR	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1992.0 1999.0 en) - Homo sapier 1403.7 1319.7 1722.8 1319.7	1303.6 1487.7 [Contains: Mon- 2000.0 1973.0 2000.0 1973.0 2000.0 os (Human) 1404.7 1320.7 1723.8 1320.7	1302.6 1486.7 ocyte differential 1999.0 1999.0 1972.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3	1303.6 1487.7 ion antigen CD1- 2000.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3
126.0 126.0 PO8571 i 548.0 145.0 182.0 182.0 250.0 250.0 250.0 323.0 PO8670 i 3.0 3.0 3.0	2.3 2.3 2.0 2.1 4.0 4.0 4.0 CD45_HUMAN 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4	5.0 5.0 2.0 2.1 4.0 4.0 4.7 4.7 4.7 2.0	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 Leukocyte ci 3.7 3.7 6.7 Vimentin - H 70.0 70.0 70.0	0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 0.7 2.0 domosapien 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 214 Precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEQVR VLSIAQAHSPAFSCEQVR AFPALTSLDLSDNPGLGER VLSIAQAHSPAFSCEQVR or (EC. 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTQVEK FLAEFGSIPR TDFGSPGEPOIIFCR LFLAEFGSIPR EEAENTLOSFRODVDNASLAR EKLQEEMLOREEAENTLQSFR EMEENFAVEAANYQDTIGR FADLSEAAMNRNDALR	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1972.0 1999.0 en) - Homo sapier 1403.7 1319.7 1722.8 1319.7 2392.1 2607.2 2186.0 1775.9	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 is (Human) 1404.7 1320.7 1723.8 1320.7	1302.6 1486.7 1999.0 1999.0 1972.0 1999.0 1403.7 1319.7 1722.8 1319.7	1303.6 1487.7 ion antigen CD1- 2000.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9
126.0 126.0 P08571]I 548.0 145.0 182.0 182.0 250.0 250.0 250.0 323.0 P08670]I 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 CD45_HUMAN 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 Leukocyte ci 3.7 3.7 3.7 (70.0 70.0 70.0 70.0 70.0 70.0	0.0 0.0 fferentiation 2.0 2.0 2.0 common antig 2.0 0.7 2.0 0.7 2.0 2.0 0.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFMMK TTPSYVAFTOTER 714 Precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEOVR AFPALTSLDLSONPGLGER VLSIAQAHSPAFSCEOVR AFPALTSLDLSONPGLGER VLSIAQAHSPAFSCEOVR OF (EC 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR TDFGSSPGEPOHECR LFLAEFOSIPR EEABTILQSFRODVDNASLAR EKLOEBMLOREAENTLQSFR EMEENFAVEAANYQDTIGR FADLSEAANRNNDALR FANYIDKVR	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1999.0 1999.0 1999.0 rin) - Homo sapier 1403.7 1319.7 1722.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6	1302.6 1486.7 poyte differential 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6	1303.6 (1487.7 (1500 antigen CD1) (1500.0 (150
126.0 126.0 PO8571 548.0 182.0 PO8575 250.0 250.0 250.0 323.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 CD45_HUMAN 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 5.7 6.7 Vimentin - F 70.0 70.0 70.0 70.0 70.0 70.0 70.0 70.	0.0 0.0 fferentiation 2.0 2.0 2.0 common antig 2.0 0.7 2.0 common sapien 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 71.4 precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEOVR AFPALTSLLSSNDPGLGER VLSIAQAHSPAFSCEOVR AFPALTSLLSSNDPGLGER VLSIAQAHSPAFSCEOVR OF (EC 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR TDFGSSPGEPOLIFCR LFLAEFQSIPR EEAENTLOSFRODVDNASLAR EKLQEEMLQREEAENTLQSFR EMEENFAVEANYQDTIGR FADLSEAANRNNDALR FANTIGKYR FSLADAINTEFKKT FSLADAINTEFKKT FSLADAINTEFKT	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1972.0 1999.0 1999.0 1319.7 1319.7 1722.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 1723.8 1320.7 2393.1 2688.3 2187.0 1776.9 1125.6 1355.7 1726.9	1302.6 1486.7 poyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9	1303.6 1487.7 2000.0 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9
126.0 P08571] 548.0 145.0 182.0 P08575] 250.0 250.0 250.0 250.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 5.7 3.7 3.7 6.7 Vimentin - F 70.0 70.0 70.0 70.0 70.0 70.0 70.0 70.	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 common antig 2.0 2.0 0.7 2.0 domo sapien 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 714 Precursor (Myeloid cell-specific leucine-r VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLLISNOPGLGER VLSIAOAHSPAFSCEOVR FOLHDCTOVEK LELAEFOSIPR TDFGSPGEPOLIFCR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEMLOREEAENTLOSFR EMEENFAVEAANYODTIGR FADLSEAANRINDDALR FANTIDKVER FSLADAINTEFKHT HLREYODLLNVK KLHEEFIGLOOGIOEOHVOID	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2884.3	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 1723.8 1320.7 2993.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3	1302.6 1486.7 poyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3	1303.6 (1487.7 ion antigen CD1. 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3
126.0 126.0 P08571 548.0 145.0 145.0 182.0 P08575 250.0 250.0 230.0 P086702 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 CD45_HUMAN 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 20.0 3.7 3.7 3.7 3.7 4.7 Vimentin - H 70.0 70.0 70.0 70.0 70.0 70.0 70.0 70.	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 0.7 2.0 0.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 714 Precursor (Myeloid cell-specific leucine-f VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLLISNOPGIGER VLSIAOAHSPAFSCEOVR FOLHDCTOVEK LELAFOSIPR TDFGSPGEPOIIFCR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEFMLOFREAENTLOSFR EMEENFAVEAANYODTIGR FADLSEAANRNDALR FANTIDKVR FSLADAINTEFKNT HLREYODLLNVK KLHEETIGELOAOIGEOHVOID KVESLOEELAFLK KVESLOEELAFLKK KVESLOEELAFLKK	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1873.0 2000.0 18.5(Human) 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1562.0	1302.6 1486.7 cyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9	1303.6 (1487.7 ion antigen CD1. 2000.0 (1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 (1355.7 1726.9 1527.8 2685.3 1533.9 1661.9
126.0 126.0 PO8571 548.0 145.0 182.0 182.0 250.0 250.0 250.0 323.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 CD45_HUMAN 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 Leukocyte di 3.7 3.7 3.7 Vimentin - H 70.0	0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 714 Precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEOVR VLSIAQAHSPAFSCEOVR AFPALTSLDLSDNPGLGER VLSIAQAHSPAFSCEOVR or (EC 3.1.3.48) (L-CA) (T200) (CD45 antige- FOLHDCTOVEK LFLAEFOSIPR TDFGSPGEPOLIFICR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLOREFAENTLOSFR EMEENFAVEANYODTIGR FADLSEAANRNNDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KLHEEFIOELONG	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1972.0 1999.0 1999.0 1-Homo sapler 1403.7 1219.7 1722.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1973.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8	1302.6 1496.7 poyte differentiat 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8	1303.6 1487.7 ion antigen CD1. 2000.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.9
126.0 126.0 PO8571 548.0 145.0 182.0 182.0 250.0 250.0 250.0 33.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 CD45_HUMAN 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 70.0 70.0 70.0 70.0 70.0 70.0 70.0 70	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 0.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 71.4 precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEOVR AFPALTSLDLSONPGLGER VLSIAQAHSPAFSCEOVR AFPALTSLDLSONPGLGER VLSIAQAHSPAFSCEOVR OF (EC 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR TDFGSSPGEPOLIFCR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEBMLOREAENTLOSFR EMEENFAVEAMYODTIGR FADLSEAAMRNIDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK HLREYODLLNVK KLHEETIGELOAGIGEOHVOID KVESLOEEIAFLK KVESLOEEIAFLK KVESLOEEIAFLK LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1972.0 1999.0 1999.0 1403.7 17122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1753.6 1651.8 1807.9	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1973.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9	1302.6 1486.7 poyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8	1303.6 (1487.7 (1500 antigen CD1) (1500.0 (150
126.0 126.0 PO8571 548.0 145.0 182.0 182.0 250.0 250.0 250.0 323.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 4.0 CD45_HUMAN 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 18.1 70.0 70.0 70.0 70.0 70.0 70.0 70.0 70	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 0.7 2.0 0.7 2.0 0.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 71.4 precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEOVR AFPALTSLDLSONPGLGER VLSIAQAHSPAFSCEOVR AFPALTSLDLSONPGLGER VLSIAQAHSPAFSCEOVR FOLHDCTOVEK LFLAEFOSIPR TDGCSPGEPOLIFCR LFLAEFOSIPR EEABTILOSFPODVDNASLAR EKLOEEMLOREAENTLOSFR EMEENFAVEAMYODTIGR FADLSEAANRNIDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KLHEELIOCLOQIOGEOHVOID KVESLOELIAFLK KVESLOEELIAFLK LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LHEELIOGLOQOIOCHVOID LYEELIORLORGHEENER LHEELIOLOGIOCHVOID LYEELIORLORGHEENER LHEELIOLOGIOCHVOID LYEELIORLORGHEENER LHEELIOLOGIOCHVOID LOVEREMRELR LHEELIORLORGHEENER LHORGHEENER LHEELIORLORGHEENER LHORGHEENER LHORGHEENE	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 120.8 1319.7 122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1973.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2	1302.6 1496.7 poyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8	1303.6 1487.7 2000.0 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1527.8 2685.3 1533.9 1661.9 1254.6 1652.8 1808.9 2557.3 1734.8
126.0 126.0 PO8571 548.0 145.0 145.0 182.0 182.0 250.0 250.0 250.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 18.1 19.1 19.1 19.1	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 714 Precursor (Myeloid cell-specific leucine-r VLSIAOAHSPAFSCEOVR AFPALTSLLDSNDPGLGER VLSIAOAHSPAFSCEOVR AFPALTSLLDSNDPGLGER VLSIAOAHSPAFSCEOVR FOLHDCTOVEK LELAEFOSIPR TDGCSPGEPOLIFCR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEMLOREAENTLOSFR EMEENFAVEANYODTIGR FADLSEANARNINDALR FANTIDKVR FSLADAINTEFK FSLADAINTEFK HLREYODLLNVK KLHEELIGELOAGIGEOHVOID KVESLOELIAFLK KVESLOEELIAFLK KUSDLYEEMR LGDLYEEMREL LGDLYEEMREL LGDLYEEMREL LGDLYEEMRELR LHEELIGLAGIGEOHVOID LODEIONMKEEMAR LODEEMLOREAENTLOSFR HHEROBLERAER LHEELIGLOGIGEOHVOID LODEIONMKEEMAR LODEMLOREAENTLOSFR HHEROBLERAER LHEELIGLOGIGEOHVOID LODEIONMKEEMAR LOGEMLOREAENTLOSFR HHEROBLERAENSSSR	1302.6 1486.7 16th glycoprotein) 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 1319.7 1722.8 1319.7 122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1973.0 1404.7 1320.7 1723.8 1320.7 2993.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 22851.1 1494.7	1302.6 1486.7 poyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1526.8 2884.3 1532.8 1560.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7	1303.6 1487.7 2000.0 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1527.8 2685.3 1535.7 1726.9 1527.8 2685.3 1533.9 1661.9 1254.6 1652.8 1808.9 2557.3 1734.8 2351.1 1494.7
126.0 126.0 P08571 548.0 145.0 145.0 182.0 182.0 250.0 250.0 250.0 33.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 19.1	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 714 Precursor (Myeloid cell-specific leucine-r VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLLISNOPFGLER VLSIAOAHSPAFSCEOVR AFPALTSLLISNOPFGLER VLSIAOAHSPAFSCEOVR FOLHDCTOVEK LELAEFOSIPR TDFGSPGEPOIIFCR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEMLOREEAENTLOSFR EMEENFAVEAANYODTIGR FADLSEAANRINDALR FANTIOKVR FSLADAINTEFKTR HLRYODLLNVK KLHEETIGLOAGIGEOHVOID KVESLOELIAFLK KVESLOEELIAFLK LGDLYEEEMRELR LGDLYEEMRELR LG	1302.6 1486.7 1599.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 120.7 1219.7 122.8 1319.7 122.8 1319.7 124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7	1303.6 1487.7 [Contains: Mon 2000.0 1973.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 1723.8 1320.7 2993.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1309.6	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7	1303.6 1487.7 2000.0 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 293.1 1 2608.3 2187.0 1776.9 1527.8 2685.3 1533.9 1661.9 1254.6 1652.8 1808.9 2557.3 1734.8 2351.1 1494.7 1309.6 1524.7
126.0 126.0 126.0 126.0 126.0 126.0 126.0 126.0 127.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 CD45_HUMAN 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 Leukocyte di 7.0 70.0 70.0 70.0 70.0 70.0 70.0 70.0	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 0.7 2.0 0.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNIK TTPSYVAFTOTE 7)14 precursor (Myeloid cell-specific leucine-r V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR OF (EC 3.1 3.48) (I.CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR TDFGSPGEPOIIFCR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLOREEAENTLOSFR EMEENFAVEAANYODTIGR FADLSEAANRINDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KVESLOEELAFLK KVESLOEELAFLK KVESLOEELAFLK LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGELGEAEONTOSFR MFGGPGTASRPSSSR NLOEEMEVK NLOEAEEWYK NLOEAEWY NLOEAEWY NLOEAEWY NLOEAEWY NLOEAEW	1302.6 1486.7 rich glycoprotein) 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 1222.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1308.6	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1125.6 1125.7 1726.9 1527.8 2685.3 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1309.6 1524.7	1302.6 1496.7 poyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1308.6	1303.6 1487.7 2000.0 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1527.8 2685.3 1533.9 1661.9 1254.6 1652.8 1808.9 2557.3 1734.8 2351.1 1494.7 1309.6 1524.7
126.0 126.0 126.0 126.0 126.0 126.0 126.0 126.0 125.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 2.1 4.0 CD45_HUMAN 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 4.7 4.7 2.0 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 18.1 18.1 18.1 70.0 70.0 70.0 70.0 70.0 70.0 70.0 70	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 0.7 2.0 10msapien 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFMIK TTPSYVAFTOTER 2)14 precursor (Myeloid cell-specific leucine-r V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR OF (EC 3.13.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR TDFGSPGEPOIIFCR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLOREEAENTLOSFR EMEENFAVEAANYODTIGR FADLSEAANRINDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KVESLOFELIAFLK KVESLOFELIAFLK KVESLOFELIAFLK KVESLOFELIAFLK LGDLYEEEMRELR LGDLYEEMRELR LGDLY	1302.6 1486.7 16th glycoprotein) 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 1722.8 1319.7 1722.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1269.6 2359.1 1442.8	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1973.0 1404.7 1320.7 1223.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1444.7 1309.6 1524.7 1270.6 2360.1 1443.8	1302.6 1486.7 poyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1269.6 2359.1 1442.8	1303.6 1487.7 2000.0 1973.0 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1527.8 2685.3 1533.9 1661.9 1254.6 1652.8 1808.9 2557.3 1734.8 2351.1 1494.7 1309.6 1524.7 1270.6 2360.1 1443.8
126.0 126.0 P08571 548.0 145.0 145.0 182.0 182.0 250.0 250.0 250.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23.2 23.2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 18.1 70.0 70.0 70.0 70.0 70.0 70.0 70.0 70	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 0.7 2.0 0.7 2.0 0.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 71.4 precursor (Myeloid cell-specific leucine-r VLSIAQAHSPAFSCEOVR AFPALTS.LD.SDNPGLGER VLSIAQAHSPAFSCEOVR AFPALTS.LD.SDNPGLGER VLSIAQAHSPAFSCEOVR FOLHDCTOVEK LFLAEFOSIPR TDGCSPGEPOIHECR LFLAEFOSIPR EEARTILQSFRODVDNASLAR EKLOEEMLOREARNTQSFR EMEENFAVEAMYODTIGR FADLSEAANRNIDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KVESLOEELAFLK KUHEELOLOGIOEOHVOID KVESLOEELAFLK LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LHEELIOLAGIOEOHVOID LODEIONMEEMAR LOEEMLOREAENTLOSFR MFGGPGTASRSPSSR NLOEAEEWYK NLOEAEEWYKSK QVDQLTNDKAR QVOSLTCEVDALKGTNESLER ROVDQLTNDKAR SVALOES SPRICK SVALOES SPRICK ROVDQLTNDKAR SVALOES SPRICK ROVDQLTNDKAR SVALOES SPRICK SVALOES SPRICK ROVDQLTNDKAR SVALOES SPRICK SVALOES SPRICK SVALOES SPRICK ROVDQLTNDKAR SVALOES SPRICK SVALO	1302.6 1486.7 16th glycoprotein) 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 120	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1973.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1309.6 1524.7 1270.6 1362.0 1270.6 1383.8 1483.8 1484.7 1309.6 1524.7 1270.6 1362.0 1284.8 1488.7 1270.6 1388.9	1302.6 1486.7 poyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1269.6 2359.1 1442.8 1427.7 1269.6	1303.6 1487.7 2000.0 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.9 1661.9 1254.6 1652.8 1808.9 2557.3 1734.8 2351.1 1494.7 1309.6 1524.7 1270.6 2360.1 1443.8 1428.7 2052.0
126.0 126.0 P08571 548.0 142.	2.3 2.3 2.1 4.0 2.1 4.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.0 0.0 70.0 70.0 70.0 70.0 70.0 70.0 70	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 714 Precursor (Myeloid cell-specific leucine-f VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLLISDNPGIGER VLSIAOAHSPAFSCEOVR FOLHDCTOVEK LELAEFOSIPR TDFGSPGEPOIIFCR LELAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLGREEAENTLOSFR EMEENFAVEAANYODTIGR FANDISVARNINDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KLHEEEIOELOAOIGEOHVOID KVESLOEEIAFLK KVESLOEEIAFLK LGDLYEEEMR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEMRELR LGDLYEMRELR LGD	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2881.3 1532.8 1660.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1253.7 1269.6 1523.7 1269.6 2359.1 1442.8	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 1723.8 1320.7 2993.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 1608.3 1838.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1200.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1354.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1270.6 1364.7 1370.6 1370	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2380.1 1493.7 1308.6 1523.7 1269.6 1523.7 1269.6	1303.6 (1487.7 ion antigen CD1. 2000.0 (1973.0 (1404.7 1320.7 1723.8 1320.7 1723.8 1320.7 1726.9 1527.8 (1661.9 1254.6 (1652.8 1808.9 1254.6 (1652.8 1808.9 1254.7 134.8 2351.1 1494.7 1309.6 1524.7 1270.6 (2360.1 1443.8 7
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126.0 126.0 PO8571 548.0 145.0 145.0 182.0 182.0 182.0 250.0 250.0 33.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 2.3 2.3 2.1 4.0 2.0 4.0 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 7 7 7 Vimentin - F 7 7 Vimentin - F 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 0.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 2)14 precursor (Myeloid cell-specific leucine-f VLSIAQAHSPAFSCEOVR VLSIAQAHSPAFSCEOVR VLSIAQAHSPAFSCEOVR VLSIAQAHSPAFSCEOVR VLSIAQAHSPAFSCEOVR AFPALTSLD SDNIPGLGER VLSIAQAHSPAFSCEOVR OF (CC 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLORECAENTLOSFR EMERNAVEANNYODTIGR FADLSEANANRNIDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KFSLADEIAFLK KVESLOEEJAFLK KUSELOEEJAFLK KUSELOEEJAFLK KUSELOEEJAFLK KUSELOEGJAFLK KUSELOEGJAFL KUS	1302.6 1486.7 1699.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 1269.6 1239.1 1442.8 1427.7 2051.0 1586.8 2423.1 1114.6 1404.7 1687.8 1120.6	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1973.0 1404.7 1320.7 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1399.6 1524.7 1206.2 2360.1 1443.8 1428.7 2052.0 1887.8 2424.1 1115.6 1405.8 1688.8 1121.6 1405.8	1302 6 1486 7 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1403 7 1319 7 1722 8 1319 7 2392 1 2607 3 2186 0 1775 9 1124 6 1354 7 1725 9 1526 8 2684 3 1532 8 2684 3 1532 8 1660 9 1253 6 1651 8 1807 9 1253 6 1651 8 1807 9 1253 6 1651 8 1807 9 1253 6 1651 8 1807 9 1253 6 1651 8 1807 9 1253 6 1651 8 1807 9 1253 6 1551 8 1807 9 1253 6 1551 8 1807 9 1253 6 1551 8 1807 9 1253 6 1551 8 1807 9 1253 6 1551 8 1807 9 1253 6 1551 8 1807 9 1253 6 1551 8 1807 9 1556 2 1733 8 1807 9 1556 2 1733 8 1807 9 1556 2 1733 8 1807 9 1556 8 1407 9 1568 8 1427 7 1568 8 1427 7 1568 8 1428 1 1114 6 1404 8 1404 8 1409 5	1303.6 (1487.7 ion antigen CD1-2000.0 2000.0 1973.0 2000.0 1973.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1557.8 2685.3 1533.9 1254.6 1955.8 1808.9 2557.3 1734.8 2351.1 1494.7 1270.6 2360.1 1443.8 1428.7 2052.0 1587.8 2424.1 1115.6 1405.8 1688.8 1115.6 1405.8 1688.8 1115.6 1405.8
126.0 126.0 PO8571 548.0 145.0 145.0 182.0 182.0 250.0 250.0 250.0 33.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 2D14_HUMAN 2.0 2.1 4.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 19.1	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 0.7 2.0 0.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 2)14 precursor (Myeloid cell-specific leucine-f V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR OF (EC. 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLOREEAENTLOSFR EMERNEAVEAANYODTIGR FADLSEAANRNDALR FANYIDKVR FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK KVESLOEEIAFL KVESLOEEIAFL KVESLOEEIAFL KVESLOEEIAFL KUSLYEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGELOEGOAOIGOHVOID LODEIONMKEEMAR LOEEMLOREAENTLOSFR MFGGPGTASRPSSSR NLOEAEEWK NLOEAEEWK NLOEAEEWK NLOEAEEWK NLOEAEEWK NLOEAEEWK SLOADEIAFL SVASSPGGVYATR SRICDLYEEMRELR TINEVELOELNDR VESLOEIAFLK VESLOEEIAFL SLYASSPGGVYATR SRICDLYEEMRELR TINEVELOELNDR VESLOEIAFLK VEVENDIALEGHERER TINEVELOELNDR VESLOEIAFLK VEVENDIALEGHIR VEVENDILANGEN VESLOEEIAFLK VEVENDIALEGHIR VEVENDILANGEN VESLOEEIAFLK VEVENDILAGEIMR VEVENDILANGEN VESLOEEIAFLK VEVENDILANGEN VESLOEEIAFLK VEVENDILANGEN VESLOEEIAFLK VEVENDILANGEN VESLOELIAFL VESLOELIA	1302 6 1486 7 1699 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 10	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1309.6 1524.7 1270.6 2360.1 1443.8 1428.7 2052.0 1587.8 2424.1 1115.6 1688.8 1121.6 1693.5 1688.8 1121.6 1693.5 1688.8 1121.6	1302 6 1486 7 1999.0 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 126.9 12	1303.6 1487.7 2000.0 2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.9 1661.9 1254.6 1652.8 1808.9 2557.3 1734.8 2351.1 1494.7 1309.6 1524.7 1270.6 2360.1 1443.8 1428.7 2052.0 1587.8 2424.1 1115.6 1405.8 1688.8 1121.6
126.0 126.0 PO8571 548.0 145.0 145.0 182.0 182.0 250.0 250.0 250.0 33.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 10.0 10.0 10.0 10.0 10	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 71.4 precursor (Myeloid cell-specific leucine-f VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLLISNOPFGUER VLSIAOAHSPAFSCEOVR FOLHDCTOVEK LELAEFOSIPR TDFGSPGEPOIIFCR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEMLOREEAENTLOSFR EMEENFAVEAANYODTIGR FADLSEAANRINDALR FANTIDKVR FSLADAINTEFKHTR HLREYODLLNVK KLHEEFIGELOAGIGEOHVOID KVESLOEELAFLK KCSLUFEEMR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEMRELR LHEEFIGLOAGIGEOHVOID LODEIONMKEEMAR LOEEMLOREAENTLOSFR MFGGGFTASFSSS NLOEAEEWYK NLOEAEEWYKSK OVDOLTNDKAR SVASSOVSTANDAKAR SVASSOVSTANDAKAR SVASSOVSTANDAKAR SVASSOVSTANDAKAR SVASSOVSTANDAKAR SVASSOVSTANDAKAR VSSLOEELAFLK KOVELOEAEWYKSK OVDOLTNDKAR SVASSOVSTANDAKAR SVASSOVSTANDAKAR TVETROGOVINETSOHHDDLE VELOELNDR TVETROGOVINETSOHHDDLE VELOELNDR TVETROGOVINETSOHHDDLE VELOELNDR TVETROGOVINETSOHHDDLE VELOELNDR VESUGEELAFLK VEVERDILAEDINK FADLSEAANR LOEEMICR TVETROGOVINETSOHHDDLE VELOELNDR VESUGEELIAFLK VEVERDILAEDINK FADLSEAANR LOEEMICOR EEAENTLOSFR	1302.6 1486.7 16th glycoprotein) 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 120.7 1219.7 122.8 1319.7 122.8 1319.7 124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1651.8 1807.9 2556.9 1242.1 1142.8 1242.7 1269.6 1586.8 1427.7 1269.6 1586.8 1427.7 1269.6 1651.8 1442.8 1427.7 1686.8 1421.1 1114.6 1404.7 1687.8 1120.6 1092.5 1322.6 1045.5 1322.6 1291.0	1303.6 1487.7 [Contains: Mon 2000.0 1973.0 2000.0 1973.0 2000.0 18. (Human) 1404.7 1320.7 1723.8 1320.7 2993.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 1808.9 2557.2 1734.8 1242.1 1399.6 1524.7 1270.6 1523.8 1428.7 1443.8 1428.7 1443.8 1428.7 1443.8 1428.7 1443.8 1428.7 1443.8 1428.7 1443.8 1428.7 1444.8 1438.8 1428.7 1444.8 1438.8 1428.7 1444.8 1458.8 1428.7 1444.8 1458.8 145	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 122.8 1319.7 2392.1 2406.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1269.6 1269	1303.6 (1487.7 ion antigen CD1. 2000.0 (1973.0 (1404.7 1320.7 1723.8 1320.7 1723.8 1320.7 1726.9 1527.8 (1661.9 1254.6 1855.7 1726.9 1527.8 1808.9 1254.6 1808.9 1254.7 1270.6 1852.7 1726.9 1527.8 1808.9 1254.7 1254.6 1808.9 1254.7 1270.6 1808.9 1254.7 1270.6 1808.9 1809.9 18
126.0 126.0 P08571 548.0 142.	2.3 2.3 2.3 2.1 4.0 2.1 4.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 19.1	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 2.0 domosapien 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNMK TTPSYVAFTOTER 714 precursor (Myeloid cell-specific leucine-f VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR FOLHDCTOVEK LELAEFOSIPR TDFGSPGEPOIIFCR LELAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLGREEAENTLOSFR EMEENFAVEAANYODTIGR FADLISFAANARNNDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KLHEEEIOELOAOIGEOHVOID KVESLOEEIAFLK KUSLOEELAFLK LGDLYEEMRELR ROVPOLITNDKAR VOSLICEVDALKGTNESLER ROVPOLITNDKAR SLVASSPGGVVATR SRLGDLYEEMRELR THERFIGLOAOIGEOHVOID VSSLOEDHALR SLVASSPGGVVATR SRLGDLYEELRR THERFIGLOAOIGEOHVOID VSSLOEDHALR VSTROEGENVESK VOVOLITNDKAR SLVASSPGGVVATR SRLGDLYEEEMRELR THERFICALOELORD VESLOELIAFLK VEVERONLAEDHM EYODLINVK FADLSEANTA LOEBLORECHNOR VESLOELIAFLK VEVERONLAEDHM EYODLINVK FADLSEANTA LOEBLORECHNOR VESLOELIAFLK VEVERONLAEDHM EYODLINVK FADLSEANTA LOEBLORE EMEENFAVEAANYODTIGR OVOSLICEVDALKGTNESLER TNEKVELOELINDR VESLOELIAFLK FADLSEANTA LOEBLORE EMEENFAVEAANYODTIGR OVOSLICEVDALKGTNESLER TNEKVELOELINDR	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1269.6 1523.7 1526.6 1527.7 1526.6 1527.7 1526.6 1527.7 1526.6 1527.7 152	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 123.8 1320.7 2993.1 2608.3 2187.0 1176.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1200.6 1524.6 1652.8 1808.9 2557.2 1734.8 2481.1 1494.7 1270.6 1524.7 1525.7 1527.8 1628.8	1302.6 1486.7 1599.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1423.7 1269.6 142.8 142.7 1269.6 1523.7 1524.6 1640.7 1640.	1303.6 (1487.7 ion antigen CD1-2000.0 1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 2393.1 2608.3 2187.0 1776.9 1527.8 2685.3 1535.7 1726.9 1527.8 1661.9 1254.6 1355.7 1726.9 1527.8 1608.9 1652.8 1808.9 1254.7 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1524.7 1270.5 1527.7 1270.5 1527.7 1270.7 1527.7
126.0 126.0 P08571 548.0 142.0 142.0 125.0 250.0 250.0 33.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 2.3 2.1 4.0 2.1 4.0 2.1 4.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 10.0 10.0 10.0 10.0 10	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 0.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNIK TTPSYVAFTOTER 714 precursor (Myeloid cell-specific leucine-f VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLDLSDNPGLGER VLSIAGAHSPAFSCEOVR FOLHDCTOVEK LELAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLOREEAENTLOSFR EEAENTLOSFRODVDNASLAR EKLOEEMLOREEAENTLOSFR EMEENFAVEAANYODTIGR FADLSEAAANRNIDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KUHEELIOELOAOIOEOHVOID KVESLOEEIAFLK KUSLOEEJAFLK KUSLOEEJA	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1269.6 1523.7 1586.8 1586.8 1587.8 1586.8 1587.8	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 123.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 1582.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 1256.1 1494.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1688.8 1128.7 1255.0 1254.6 1405.8 1428.7 1255.0 1254.6 1405.8 1255.1 1115.6 1405.8 1263.0 1270.6 1270.	1302.6 1486.7 1599.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1269.6 1523.7 1524.6 1525.6 1526.8 1526.8 1527.8	1303.6 (1487.7 ion antigen CD1. 2000.0 (1973.0 2000.0 1973.0 2000.0 1973.0 (1404.7 1320.7 1723.8 1320.7 1723.8 1320.7 1726.9 1527.8 1355.7 1726.9 1527.8 1661.9 1254.6 1355.7 1726.9 1527.8 1688.3 1533.9 1254.6 1254.7 1270.6 1255.7 125
126.0 126.0 POS571 548.0 145.0 182.	2,3 2,3 2,3 2,3 2,3 2,1 4,0 2,1 4,0 2,1 4,0 4,7 4,7 4,7 4,7 2,0 VIME_HUMAN 63,4 63,4 63,4 63,4 63,4 63,4 63,4 63,4	5.0 5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 19.1	0.0 0.0 0.0 ffer entiation 2.0 2.0 2.0 2.0 0.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNIK TTPSYVAFTOTER 214 Precursor (Myeloid cell-specific leucine-f V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR OF (EC. 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR EFACTOVEK LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLOREAENTLOSFR EMERNAVEAANYODTIGR FADLSEAANRNIDALR FANYIDKVR FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KVESLOELAFLK KVESLOELAFLK KVESLOELAFLK LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGEBLOEGAOOLOGOHVOID LODEIONMKEEMAR LOEEMLOREAENTLOSFR MFGGFGTASRPSSSR NLOEAEGWYK NLOEAEGWYC NLOEAEGWY NLOEA	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1269.6 1551.8 142.7 1269.6 152.8 142.7 1269.6 152.8 142.7 1269.6 152.8 142.7 1442.8 142.7 1493.7 1442.8 142.7 1493.7 1442.8 142.7 1493.7 1586.8 1427.7 1687.8 1140.4 1404.7 1687.8 1120.6 1092.5 1045.5 1322.6 1191.0 2376.1 1586.8 2423.1 1114.6 1404.7 1687.8 1120.6 1092.5 1045.5 1322.6 1191.0 2376.1 1586.8 1587.8 1286.0 1775.8	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 123.8 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 1582.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1524.7 1270.6 1688.8 1121.6 1093.5 1046.5 1121.6 1093.5 1046.5 1121.6 1093.5 1046.5 1123.6 12192.0 22377.2 2387.8 1588.8 1121.6 1093.5 1046.5 1123.6 12192.0 2377.2 1587.8 1588.8 1121.6 1093.5 1046.5 1123.6 11776.9 11776.9 11776.9	1302.6 1486.7 1599.0 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1289.6 1551.8 1807.9 1526.8 1807.9 1526.8 1807.9 1526.8 1807.9 1526.8 1807.9 1526.8 1807.9 1526.8 1807.9 1526.8 1807.9 1526.6 1551.8 1807.9 1556.2 1733.8 160.9 1733.8 160.9 1733.8 160.9 1733.8 1807.9 1807.9 1808.6 1807.9 1808.6 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1808.8 1809.9 1775.9 1856.8 1886.8	1303.6 (1487.7 ion antigen CD1. 2000.0 (1973.0 2000.0 1973.0 2000.0 1404.7 1320.7 1723.8 1320.7 1723.8 1320.7 1726.9 1527.8 1661.9 1254.6 1355.7 1726.9 1527.8 1808.9 1254.6 1652.8 1808.9 1254.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 12360.1 1443.8 1235.1 115.6 1405.8 1428.7 1270.6 1287.8 1288.8 1428.7 1270.6 1287.8 1288.8 1121.6 1287.8 1287.8 1288.8 1287.0 1776.9 1355.7
126.0 126.0 126.0 126.0 126.0 126.0 126.0 126.0 126.0 125.0	2.3 2.3 2.3 2D14_HUMAN 2.0 2.1 4.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 10.0 10.0 10.0 10.0 10	0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNIK TTPSYVAFTOTER 214 Precursor (Myeloid cell-specific leucine-f V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR V.SIAOAHSPAFSCEOVR OF (EC 3.13.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR EEACHTLOSFRODVDINASLAR EKLOEEMLOREAENTLOSFR EMERIFAVEANNYODTIGR FADLSEAANRINDALR FANYIDKVR FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK KVESLOELIAFLK KVESLOELIAFLK KVESLOELIAFLK KVESLOELIAFLK KVESLOELIAFLK LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR LGDLYEEEMRELR NICEMELORSF MFGGGTASRPSSSR NLOEMEGAENT NLOEMEGNEK NUCAEEWYK NLOEAEEWYK NLOEAEEWY NLOEAEEW	1302.6 1486.7 1619.9 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 120.7 1219.7 122.8 1319.7 122.8 1319.7 122.8 1319.7 122.8 1319.7 125.9 1526.8 166.9 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1253.7 1269.6 1269.6 1279.0 1586.8 1223.7 1206.6 1299.0 1236.8 1226.6 1299.0 12376.1 1186.8 1226.6 1299.0 1775.8 1354.7 1538.9	1303.6 1487.7 [Contains: Mon 2000.0 1973.0 2000.0 1973.0 2000.0 15 (Human) 1404.7 1320.7 1238.8 1320.7 2933.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1309.6 1524.7 1270.6 2360.1 1443.8 1287.0 2552.0 1587.8 1288.7 1290.6 1155.8 1688.8 1428.7 1290.6 1355.7 1115.6 1688.8 1121.6 1093.5 1093.5 1125.8 1688.8 1121.6 1093.5 1233.6 1233.6 1237.2 1377.6 1323.6 1237.2 1587.8 1588.8 1121.6 1093.5 1125.7 1176.9 1155.7 1155.9 1155.7 1155.9	1302.6 1486.7 poyte differential 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1526.8 2884.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1651.8 1807.9 2556.9 1124.6 1352.7 1269.6 1651.8 142.8 1427.7 12051.0 1586.8 1427.7 12051.0 1586.8 1427.7 12051.0 1586.8 1427.7 12051.0 1586.8 1427.7 12051.0 1586.8 1427.7 12051.0 1586.8 1427.7 12051.0 1586.8 1427.7 12051.0 1586.8 1427.7 12051.0 1586.8 1427.7 12051.0 1586.8 1427.7 1404.8 1687.8 1120.6 1092.5 1322.6 1286.0 1286.0 1286.8 1887.8 1120.6 11775.9 11554.7 1538.9	1303.6 (1487.7 ion antigen CD1. 2000.0 (1973.0 2000.0 1973.0 2000.0 1973.0 (1404.7 1320.7 1723.8 1320.7 1726.9 1527.8 2685.3 1535.7 1726.9 1527.8 1808.9 2557.3 1734.8 1235.7 1726.9 1524.6 (165.2 8 1808.9 2557.3 1734.8 1235.1 1494.7 1309.6 (1443.8 1428.7 1494.7 1309.6 (1443.8 1428.7 1494.7 1309.6 (1443.8 1428.7 1494.7 1309.6 (1443.8 1428.7 1494.7 1309.6 (1443.8 1428.7 1494.7 1309.6 (1443.8 1428.7 1494.7 1309.6 (1443.8 1428.7 1494.7 1309.6 (1443.8 1428.7 1494.7 1309.6 (1443.8 1428.7 1494.7 1309.6 (1443.8 1428.7 1495.8 1443.
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126.0 126.0 PO8571 548.0 145.0 145.0 162.0 PO8575 250.0 250.0 233.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 2.3 2D14_HUMAN 2.0 2.1 4.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 10.0 10.0 10.0 10.0 10	0.0 0.0 0.0 0.0 fferentiation 2.0 2.0 2.0 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 2.0 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNIK TTPSYVAFTOTER 214 Precursor (Myeloid cell-specific leucine-f VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLLISNOPGIGER VLSIAOAHSPAFSCEOVR FOLHDCTOVEK LELAEFOSIPR TDFGSPGEPOIIFCR LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEFILOREAENTLOSFR EMEENFAVEAANVODTIGR FADLSEAANRINDALR FANDISKY FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK FSLADAINTEFK KLHEERIOELOAOIOEOHVOID KVESLOELIAFLK KVESLOEELAFLK KGDLYEEMRELR LGDLYEEMRELR LGDLYEEMRELR LGDLYEEMRELR LGDLYEEMRELR LGDLYEEMRELR LGEMLOREAENTLOSFR MFGGGGTASRSPSSSR NLOEAEEWYK KVOSLOELIAFLK KVOSLOELIAFLK KVESLOEELIAFLK KUSLOELIAFLK KNESLOEELIAFLK KNESLOEE	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 122.8 1319.7 122.8 1319.7 124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1808.6 1651.8 1807.9 1808.6 181.3 1838.6 1858.8 1828.6 1807.9 1808.6 1808.8 181.8 181.8 1886.8 1888.8 1886.8 1888.8 1886.8 1888.8 1886.8 1888.8 1886.8 1888.8 1886.8 1888.8 1886.8 1888.8 1886.8 1888.8 1886.8 1888.8 1886.8 1888.8 1888.8 1886.8 1888.8 1888.8 1888.8 1888.8 1888.8 1888.8 1888.8 1888.8 1888.8 1888.8 1888.8 1888.8 1888.8 1888.8	1303.6 1487.7 [Contains: Mon 2000.0 1973.0 2000.0 1973.0 2000.0 18. (Human) 1404.7 1320.7 1723.8 1320.7 2993.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1533.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 1242.4 1115.6 1443.8 1428.7 2052.0 1587.8 1443.8 1428.7 2052.0 1587.8 1443.8 1428.7 2052.0 1587.8 1688.8 1121.6 1093.5 1121.6 1093.5 1123.6 1093.5 1125.7 1539.9 1254.6 1176.9 1155.7 1153.9 1124.8 1139.6 1134.8 1139.6 1134.8 1139.6 1134.8	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 120.7 1219.7 122.8 1319.7 122.8 1319.7 124.6 1354.7 1725.9 1526.8 160.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1523.7 1269.6 1651.8 1100.6 1002.5 1328.6 1338.8 1386.8 1887.8 1286.0 1775.9 1354.7 1538.9 1253.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8	1303.6 (1487.7 (1500 antigen CD1). (2000.0 (1573.0 (1687.8 (16
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126.0 126.0 PO8571 548.0 145.0 145.0 125.0 250.0 250.0 323.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 2.3 2.3 2.3 2.1 4.0 2.1 4.0 4.0 4.7 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 10.0 10.0 10.0 10.0 10	0.0 (1) (1) (1) (2) (2) (2) (2) (2) (2) (2) (2) (2) (2	39.0 99.0 99.0 99.0 99.0 99.0 80.0 99.0 99	NALESYAFNMK TTPSYVAFTOTER 2)14 precursor (Myeloid cell-specific leucine-f VI.SIAOAHSPAFSCEOVR VI.SIAOAHSPAFSCEOVR VI.SIAOAHSPAFSCEOVR VI.SIAOAHSPAFSCEOVR VI.SIAOAHSPAFSCEOVR VI.SIAOAHSPAFSCEOVR AFPALTSIALDSONPGLIGER VI.SIAOAHSPAFSCEOVR OF (EC. 3.1.3.48) (L-CA) (T200) (CD45 antige FOLHDCTOVEK LFLAEFOSIPR EEAENTLOSFRODVDNASLAR EKLOEEMLOREEAENTLOSFR EMERIFAVEAANYODTIGR FADLSEAANRNIDALR FANYIDKVR FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK FSIADAINTEFK KVESLOEEIAFLK KVESLOEEIAFLK KVESLOEEIAFLK KUSLYEEMRELRR LGDLYEEEMRELRR LGDLYEEEMRELRR LGDLYEEEMRELRR LGDLYEEEMRELRR LGDLYEEMRELRR NOEMCHOEAEANTLOSFR MFGGPGTASRPSSSR NLOEAECWK NLO	1302 6 1486 7 1499 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1999 0 1319 7 2392.1 2607.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 160.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1253.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1308.6 1523.7 1538.8 1427.7 1538.8 1120.6 1733.8 1358.8 1358.8 1358.7 1358.8 1358.7 1358.8 1358.7 1358.8 1358.7 1358.8 1358.7 1358.8 1358.7 1338.9 1253.6 1733.8 1308.6 12359.1 1687.8 1125.9 1253.6 1733.8 1308.6 12359.1 1687.8 1725.9 1253.6 1725.9 1253.6 1725.9 1253.6 1725.9 1253.6 1725.9	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 18 (Human) 1404.7 1320.7 1320.7 2393.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 2685.3 1633.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 2351.1 1494.7 1309.6 1524.7 1309.6 1524.7 1309.6 1524.7 1309.6 1524.7 1115.6 1405.8 1608.8 1121.6 1605.8 1608.8 1121.1 1494.7 1524.7 1524.7 1525.7 1734.8 1624.7 1734.8 1624.7 1745.8 1624.7 1746.8 1624.7 1747.8 1624.7 1747.8 1854.8 1748.8	1302 6 1486 7 1999.0 1999.0 1999.0 1999.0 1999.0 1403.7 1319.7 1722.8 1319.7 2392.1 2607.3 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 2684.3 1532.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1807.9 2556.2 1733.8 1822.6 2859.1 1442.8 1427.7 2051.0 1586.8 2423.1 1114.6 1404.8 1120.6 2186.0 2376.2 1886.8 2186.0 2376.2 1886.8 2186.0 2376.2 1586.8 2186.0 2376.2 1586.8 2186.0 2376.2 1586.8 2186.0 2376.2 2359.1 1143.7 1538.9 1253.6 1733.8 1308.6 2359.1 1687.8 1725.9 1253.6 1733.8 1308.6 2359.1 1687.8 1725.9	1303.6 (1487.7 c) 1303.6 (1487.7 c) 1303.6 (1487.7 c) 1404.7 c) 1320.7 c) 1404.7 c) 1320.7 c) 13
126.0 126.0 PO8571 548.0 145.0 145.0 125.0 250.0 250.0 250.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0 3.0	2.3 2.3 2.3 CD14_HUMAN 2.0 2.1 4.0 2.1 4.0 4.7 4.7 4.7 4.7 2.0 VIME_HUMAN 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	5.0 5.0 5.0 2.0 2.1 4.0 4.7 4.7 4.7 2.0 63.4 63.4 63.4 63.4 63.4 63.4 63.4 63.4	23. 2 23. 2 Monocyte di 4.8 16.3 18.1 18.1 18.1 18.1 19.1 19.1 19.1 10.0 10.0 10.0 10.0 10	0.0 0.0	39.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	NALESYAFNIK TTPSYVAFTOTER 714 precursor (Myeloid cell-specific leucine-f VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR VLSIAOAHSPAFSCEOVR AFPALTSLLISNDYBGLER VLSIAOAHSPAFSCEOVR FOLHDCTOVEK LELAEFOSIPR EEAENTLOSFRODVDNASLAR EELAENTLOSFRODVDNASLAR EELAENTAVEAANYODTIGR FADLISTAANNINDALR FANYIDKVR FSLADAINTEFKNTR HLREYODLLNVK KLHEEIGLOAOIGEOHVOID KVESLOEEIAFLK KUSLOEEIAFLK KUSLOEEIAFLK KUSLOEEIAFLK KUSLOEEIAFLK KUSLOEEIAFLK LOELYEEMRELR LOELYEEMRELR LOELOELOAOIGEOHVOID LODEIONMKEEMAR LOEAEWWKSK OVOSLICEVDALKGTNESLER ROVPOOLTNDKAR SVLASSPGGTASRPSSSR NLOEAEEWYKSK OVOSLICEVDALKGTNESLER ROVOOLTNDKAR SULVASSPGGVVATR SRLODLYEEMRELR THEKVELOELNDR VESTOEEIAFLK VEVERDLAEDHIN VESTOEEIAFLK VEVERDLAEDHIN VESTOEEIAFLK VEVERDNLAEDHIN FENDELNVK FADLSEAANNYDDTIGR OVOSSICEVDALKGTNESLER THEKVELOELNDR TNEKVELOELNDR	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 122.8 1319.7 2392.1 2407.2 2186.0 1775.9 1124.6 1354.7 1725.9 1526.8 1660.9 1253.6 1651.8 1807.9 2556.2 1733.8 2350.1 1493.7 1308.6 1523.7 1269.6 1442.8 142.7 12051.0 1586.8 1427.7 1687.8 142.8 1120.6 1092.5 1322.6 1404.7 1687.8 1120.6 1092.5 1322.6 1404.7 1588.8 1120.6 1092.5 1322.6 1404.7 1588.8 1120.6 1092.5 1322.6 1491.0 2376.1 1588.8 1587.8 1386.8 1587.8 1386.8 1385.4 1775.8 1384.7 1538.9 1258.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6 1733.8 1308.6	1303.6 1487.7 [Contains: Mon 2000.0 2000.0 1973.0 2000.0 18. (Human) 1404.7 1320.7 1723.8 1320.7 2993.1 2608.3 2187.0 1776.9 1125.6 1355.7 1726.9 1527.8 1688.8 1662.0 1254.6 1652.8 1808.9 2557.2 1734.8 1309.6 1270.6 1887.8 1428.7 2052.0 1887.8 1428.7 2052.0 1887.8 1428.7 1776.9 1827.8 1838.8 1428.7 1770.6 1827.8 1838.8 1428.7 1770.6 1843.8 1428.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1854.7 1770.6 1855.7 1859.9 1776.9 1776.9 1355.7 1839.9 1254.6 1774.8 1309.6 1776.9 1355.7 1339.9 1254.6 1734.8 1309.6 1776.9	1302.6 1486.7 1999.0 1999.0 1999.0 1999.0 1999.0 1319.7 120.7 1219.7 122.8 1319.7 122.8 1319.7 124.6 1354.7 125.9 1526.8 160.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1651.8 1807.9 1253.6 1653.8 1807.9 1253.6 1853.8 1858.8 1858.8 1868.8 1878.8 1886.8 1886.8 1886.8 1886.8 1887.8 1886.8	1303.6 (1487.7 ion antigen CD1. 2000.0 (1973.0 2000.0 1973.0 2000.0 1973.0 (1404.7 1320.7 1723.8 1320.7 1724.8 1320.7 1726.9 1527.8 1661.9 1254.6 1652.8 1808.9 2557.3 1734.8 2351.1 1494.7 1309.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1808.9 1254.7 1270.6 1652.8 1809.6 1552.8 1428.7 1270.6 1652.8 1428.7 1270.6 1652.8 1428.7 1270.9 1555.7 1559.9 1255.7 1559.9 1255.7 1539.9 1255.7 1539.9 1255.7 1539.9 1255.7 1539.9 1255.7 1539.9 1255.7 1539.9 1255.7 1539.9 1254.6 1734.8 1309.6 1888.8 1726.9 126.9 126.9 176.9 176.9 126.9 176.8 176.8 176.8 176.8 176.8 176.8 176.8 176.8 176.8 176.9 176

8.0 8.0	22.8 22.8	22.8 22.8	70.6 70.6	0.1 0.1	28.0 18.0	HLREYQDLLNVK FANYIDKVR	1526.8 1124.6	1527.8 1125.6	1526.8 1124.6	1527.8 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 8.0	22.8 44.3	22.8 44.3	70.6 62.2	0.0 2.0	56.0 99.0	TNEKVELQELNDR DGQVINETSQHHDDLE	1586.8 1835.8	1587.8 1836.8	1586.8 1835.8	1587.8 1836.8
8.0	44.3	44.3	62.2	2.0	99.0	EEAENTLQSFRQDVDNASLAR	2392.1	2393.1	2392.1	2393.1
8.0 8.0	44.3 44.3	44.3 44.3	62.2 62.2	2.0 2.0	99.0 99.0	EKLQEEMLQR EKLQEEMLQREEAENTLQSFR	1302.7 2607.3	1303.7 2608.3	1302.7 2607.3	1303.7 2608.3
8.0	44.3	44.3	62.2	2.0	99.0	EMEENFAVEAANYQDTIGR	2185.9	2186.9	2186.0	2187.0
8.0 8.0	44.3 44.3	44.3 44.3	62.2 62.2	2.0 2.0	99.0 99.0	FADLSEAANRNNDALR FANYIDKVR	1775.9 1124.6	1776.9 1125.6	1775.9 1124.6	1776.9 1125.6
8.0	44.3	44.3	62.2	2.0	99.0	FSLADAINTEFK	1354.7	1355.7	1354.7	1355.7
8.0 8.0	44.3 44.3	44.3 44.3	62.2 62.2	2.0	99.0 99.0	FSLADAINTEFKNTR HI REYODI I NVK	1725.9 1526.8	1726.9 1527.8	1725.9 1526.8	1726.9 1527.8
8.0	44.3	44.3	62.2	2.0	99.0	LGDLYEEEMR	1253.6	1254.6	1253.6	1254.6
8.0 8.0	44.3 44.3	44.3 44.3	62.2 62.2	2.0 2.0	99.0 99.0	LGDLYEEEMRELRR LQDEIQNMKEEMAR	1807.9 1733.8	1808.9 1734.8	1807.9 1733.8	1808.9 1734.9
8.0	44.3	44.3	62.2	2.0	99.0	LQEEMLQR	1045.5	1046.5	1045.5	1046.5
8.0 8.0	44.3 44.3	44.3 44.3	62.2 62.2	2.0	99.0 99.0	NLQEAEEWYK QVQSLTCEVDALKGTNESLER	1308.6 2359.1	1309.6 2360.2	1308.6 2359.1	1309.6 2360.1
8.0	44.3	44.3	62.2	2.0	99.0	RQVDQLTNDKAR	1442.8	1443.8	1442.8	1443.8
8.0 8.0	44.3 44.3	44.3 44.3	62.2 62.2	2.0	99.0 99.0	TNEKVELQELNDR TVETRDGQVINETSQHHDDLE	1586.8 2423.1	1587.8 2424.1	1586.8 2423.1	1587.8 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 8.0	44.3 44.3	44.3 44.3	62.2 62.2	1.7 1.2	98.0 93.0	EYQDLLNVK VELQELNDR	1120.6 1114.6	1121.6 1115.6	1120.6 1114.6	1121.6 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 8.0	44.3 44.3	44.3 44.3	62.2 62.2	0.3 0.2	46.0 42.0	EEAENTLQSFR QVDQLTNDKAR	1322.6 1286.7	1323.6 1287.7	1322.6 1286.7	1323.6 1287.7
8.0	44.3	44.3	62.2	0.0	99.0	FADLSEAANRNNDALR	1777.9	1778.9	1775.9	1776.9
8.0 8.0	44.3	44.3	62.2 62.2	0.0	42.0 32.0	FSLADAINTEFK OVER TARRIAD	1350.6	1351.6	1354.7	1355.7
8.0	44.3 44.3	44.3 44.3	62.2	0.0	99.0	QVDQLTNDKAR QVQSLTCEVDALKGTNESLER	1270.6 2376.1	1271.7 2377.2	1270.6 2376.2	1271.6 2377.2
8.0	44.3	44.3	62.2	0.0	94.0	TNEKVELQELNDR	1586.8	1587.8	1586.8	1587.8
8.0 P09211 G	44.3 STP1_HUMAN	44.3	62.2 Glutathione	0.0 S-transfera	22.0 se P (EC 2.5	TVETRDGQVINETSQHHDDLE 1.18) (GST class-pi) (GSTP1-1) - Homo sapi	2422.1 ens (Human)	2423.1	2422.1	2423.1
96.0	11.7	11.7	37.6	2.0	99.0	AFLASPEYVNLPINGNGKQ	2033.0	2034.0	2033.0	2034.0
96.0 96.0	11.7 11.7	11.7 11.7	37.6 37.6	2.0 2.0	99.0 99.0	ALPGQLKPFETLLSQNQGGK FQDGDLTLYQSNTILR	2125.2 1882.9	2126.2 1883.9	2125.2 1882.9	2126.2 1883.9
96.0	11.7	11.7	37.6	2.0	99.0	MLLADQGQSWK	1275.7	1276.7	1275.6	1276.6
96.0 96.0	11.7 11.7	11.7 11.7	37.6 37.6	2.0 1.7	99.0 98.0	PPYTVVYFPVR PPYTVVYFPVRGR	1336.7 1549.8	1337.7 1550.8	1336.7 1549.8	1337.7 1550.8
96.0	11.7	11.7	37.6	0.0	47.0	PPYTVVYFPVRGR	1552.8	1553.8	1549.8	1550.8
47.0 47.0	6.6 6.6	6.6 6.6	23.3 23.3	2.0 2.0	99.0 99.0	ALPGQLKPFETLLSQNQGGK PPYTVVYFPVR	2125.2 1336.7	2126.2 1337.7	2125.2 1336.7	2126.2 1337.7
47.0	6.6	6.6	23.3	2.0	99.0	PPYTVVYFPVRGR	1549.8	1550.8	1549.8	1550.8
47.0 99.0	6.6 8.0	6.6 8.0	23.3 18.6	0.6 2.0	72.0 99.0	FQDGDLTLYQSNTILR ASCLYGQLPK	1882.9 1135.6	1883.9 1136.6	1882.9 1135.6	1883.9 1136.6
99.0	8.0	8.0	18.6	2.0	99.0	FQDGDLTLYQSNTILR	1882.9	1883.9	1882.9	1883.9
99.0 99.0	8.0 8.0	8.0 8.0	18.6 18.6	2.0	99.0 99.0	PPYTVVYFPVR PPYTVVYFPVRGR	1336.7 1549.8	1337.7 1550.8	1336.7 1549.8	1337.7 1550.8
P09382 LE	G1_HUMAN		Galectin-1 (I	Lectin galac	toside-bindi	ng soluble 1) (Beta-galactoside-binding lecti	n L-14-I) (Lacto	se-binding lectin	1) (S-Lac lectin	1) (Galaptin) (14
99.0 99.0	11.2 11.2	11.2 11.2	61.5 61.5	2.0 2.0	99.0 99.0	ACGLVASNLNLKPGECLR DSNNLCLHFNPR	2013.0 1485.7	2014.0 1486.7	2013.0 1485.7	2014.0 1486.7
99.0	11.2	11.2	61.5	2.0	99.0	FNAHGDANTIVCNSK	1646.8	1647.8	1646.7	1647.8
99.0 99.0	11.2 11.2	11.2 11.2	61.5 61.5	2.0 2.0	99.0 99.0	LNLEAINYMAADGDFK LPDGYEFKFPNR	1783.8 1481.7	1784.9 1482.7	1783.8 1481.7	1784.9 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 68.0	11.2 4.9	11.2 4.9	61.5 61.5	0.0 2.0	71.0 99.0	LPDGYEFKFPNR ACGLVASNLNLKPGECLR	1480.7 2013.0	1481.7 2014.0	1481.7 2013.0	1482.7 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 68.0	4.9 4.9	4.9 4.9	61.5 61.5	0.7 0.2	81.0 38.0	FNAHGDANTIVCNSK LPDGYEFKFPNR	1646.8 1481.7	1647.8 1482.7	1646.7 1481.7	1647.8 1482.7
		4.7				ACGLVASNLNLKPGECLR				2014.0
142.0	5.7	5.7	29.6	2.0	99.0		2013.0	2014.0	2013.0	2014.0
142.0	5.7	5.7	29.6	2.0	99.0	LPDGYEFKFPNR	1481.7	1482.7	1481.7	1482.7
142.0 142.0 P09429 HI	5.7 5.7 MGB1_HUMAN	5.7 5.7	29.6 29.6 High mobilit	2.0 1.7 y group pro	99.0 98.0 tein B1 (Hig	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo	1481.7 1075.5 sapiens (Human	1482.7 1076.5	1481.7 1075.5	1482.7 1076.5
142.0 142.0 P09429 HI 42.0	5.7 5.7 MGB1_HUMAN 20.0	5.7 5.7 20.0	29.6 29.6 High mobilit 45.6	2.0 1.7 y group pro 2.0	99.0 98.0 tein B1 (Hig 99.0	LPDGYEFKFPNR DGGAWGTEGR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR	1481.7 1075.5 sapiens (Humar 1680.8	1482.7 1076.5 1)	1481.7 1075.5 1680.8	1482.7 1076.5 1681.8
142.0 142.0 PO9429 HI 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0	5.7 5.7 20.0 20.0 20.0	29.6 29.6 High mobilit 45.6 45.6 45.6	2.0 1.7 sy group pro 2.0 2.0 2.0	99.0 98.0 tein B1 (Hig 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCREEHKK KHPDASVNFSEFSKK	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9	1482.7 1076.5 1) 1681.8 2333.1 1720.9	1481.7 1075.5 1680.8 2332.1 1719.9	1482.7 1076.5 1681.8 2333.1 1720.9
142.0 142.0 PO9429 HI 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0	5.7 5.7 20.0 20.0 20.0 20.0 20.0	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6	2.0 1.7 ty group pro 2.0 2.0 2.0 2.0	99.0 98.0 tein B1 (Hig 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEOR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTOR GKMSSYAFFVOTOREHKK KHPDASVNFSEFSKK KLGEMWNTAADDKGPYEK	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0
142.0 142.0 P09429 HI 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0	5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 2.9 group pro 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 1tein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCREHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0
142.0 142.0 P09429 H 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 2y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 1tein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEKVENDAAVR	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9	1481.7 1075.5 1680.8 2332.1 17179.9 2237.0 2108.9 2237.0 1625.9	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9
142.0 142.0 142.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 2.0 group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 99.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKEPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCRE GKMSSYAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPVEK LGEMWNNTAADDKOPVEK LGEMWNNTAADDKOPVEK LKEKYEKDIAAVR MSSVAFFVOTCREHKK	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 17179.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0	1481.7 1075.5 1680.8 2332.1 17179.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0	1482.7 1076.5 1081.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0
142.0 142.0 142.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 2.0 group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 98.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR GKMSSVAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKQPYEK LGEMWNNTAADDKQPYEK LGEMWNNTAADDKQPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCREHKK YEKDIAAVR	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6
142.0 142.0 142.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 2.0 group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 98.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR GKMSSVAFFVOTCR GKMSSVAFFVOTCREEHKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1625.9	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 110.0 2238.0 1126.6 9 1496.7 2148.0 1128.6 1499.7 1626.9	1481.7 1075.5 1680.8 2332.1 17179.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 1626.9
142.0 142.0 142.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 40.0 40.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 2.0 group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 14ein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKEPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCREHKK KHPDASVNFSEFSKK KKEDEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAYR MSSYAFFVOTCR MSSYAFVOTCR MSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR	1481.7 10755 Sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 1625.9 1495.7 2147.0 1127.6 1498.7 1625.9 1495.7	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 1625.9 1495.7	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 1626.9 1496.7
142.0 PO9429 HI 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 40.0 40.0 40.0 40.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 2.9 group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKEPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR LKEKYEKDIAAVR MSSYAFFVOTCR LKEKYEKDIAAVR MSSVAFFVOTCR LKEKYEKDIAAVR MSSVAFFVOTCR LKEKYEKDIAAVR MSSVAFFVOTCR LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCREHKK KLGEMWNTAADDKOPVEK	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 2147.0 2337.0 1495.7 2147.0 2337.0 1495.7 2147.0 2337.0 1495.7 2147.0 2337.0	1482.7 1076.5 10) 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 2338.1	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 1495.7 2147.0 2337.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 1496.7 2148.0 238.0
142.0 PO94.29 HI 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 40.0 40.0 40.0 40.0 40.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 2y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKEPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR EHKK KHPDASVNFSEFSKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAYR MSSVAFFVOTCREHKK YEKDIAAYR MSSVAFFVOTCREHKK YEKDIAAYR MSSVAFFVOTCREHKK KYEKDIAAYR MSSVAFFVOTCR LKEKYEKDIAAYR MSSVAFFVOTCR KSSYAFFVOTCR KSSYAFFVOTCR KSSYAFFVOTCR KSSYAFFVOTCR KSSYAFFVOTCR KKSKAFFVOTCR KKLGEMWNNTAADDKOPYEK KLGEMWNNTAADDKOPYEK YEKDIAAYR	1481.7 1075.5 Saplens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1625.9 1495.7 2147.0 2237.0 1127.6	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 238.1 1128.6	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 1495.7 1495.7 1495.7	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 1626.9 1496.7 148.0 238.0 1128.6
142.0 PO9429 HI 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 40.0 40.0 40.0 40.0 73.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 tein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKEPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCREHKK KHPDASVNFSEFSKK KKHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR KSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR GKMSSYAFFVOTCR	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1625.9 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8	1482.7 1076.5 1) 1 188.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 2238.1 1128.6 1681.8	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 1495.7 2147.0 1127.6 1495.7 1495.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 1248.0 2238.0 1128.6 1681.8 1520.8
142.0 142.0 PO9429 H 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 40.0 40.0 40.0 40.0 73.0 73.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1,7 y group pro 2,0 2,0 2,0 2,0 2,0 2,0 2,0 2,0 2,0 2,0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCREEHKK KHPDASVNFSEFSKK KKEDMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KGEHPGLSIGOVAK LKEKYEKDIAAVR KLGEMWNNTAADDKOPYEK YEKDIAAVR KGKMSSVAFFVOTCR KGEHPGLSIGOVAK LKKEKYEKDIAAVR	1481.7 1075.5 sapiens (Human 1880.8 2332.1 17179.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9	1482.7 1076.5 10 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1499.7 1496.7 2148.0 1128.6 1499.7 2148.0 2238.1 1128.6 1681.8 1520.8	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1681.8 1626.9
142.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1,7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 98.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCR GKMSSYAFFVOTCREHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR KKEKYEKDIAAYR MSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR KSSYAFFVOTCR KKEKYEKDIAAYR KSSYAFFVOTCR KKEKYEKDIAAYR KKLGEMWNNTAADDKOPYEK YEKDIAAYR KKLGEMWNNTAADDKOPYEK YEKDIAAYR KKEKYEKDIAAYR RPPSAFFLFCSEVRPK YEKDIAAYR RPPSAFFLFCSEVRPK YEKDIAAYR RPPSAFFLFCSEVRPK YEKDIAAYR	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1495.7 2147.0 1127.6 1498.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6	1482.7 1076.5 10 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1499.7 1248.0 1128.6 1499.7 1248.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1681.8 1626.9 2002.0 1128.6
142.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 7.5 7.5 7.5 7.5 10.0 10.0 10.0 10.0 10.0	5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1,7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 99.0 90.0 90.0 90.0 90.0 90.0 90.0	LPDGYEFKEPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTOR GKMSSYAFFVOTOREHKK KHPDASVNFSEFSKK KKHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMVNNTAADDKOPYEK LKEKYEKDIAAVR MSSVAFFVOTOR MSSVAFVOTOR MSSVAFFVOTOR LKEKYEKDIAAVR MSSVAFFVOTOR LKEKYEKDIAAVR MSSVAFFVOTOR MSSVAFFVOTOR MSSVAFFVOTOR LKEKYEKDIAAVR KLGEMWNTAADDKOPYEK YEKDIAAVR GKMSSVAFFVOTOR KGEHPGLSIGDVAK LKEKYEKDIAAVR KLEKYEKDIAAVR KLGEMWNTAADDKOPYEK YEKDIAAVR KLGEMWSTAFFVOTOR KGEHPGLSIGDVAK LKEKYEKDIAAVR LKEKYEKDIAAVR KLEKYEKDIAAVR KLEKYEKDIAAVR KLEKYEKDIAAVR	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1625.9 1495.7 2147.0 2337.0 1127.6 1680.8 1651.8 1625.9 2001.0	1482.7 1076.5 1) 1 188.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 2238.1 1128.6 1681.8 1620.9 1620.9	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 1495.7 2147.0 1127.6 1495.7 1495.7 2147.0 2237.0 1127.6 1625.9 1495.7 2147.0 1127.6 1680.8 1619.8	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1626.9 1496.7 2148.0 1128.6 1626.9 1626.9 1626.9
142.0 142.0 20.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0 73.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 10	5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1,7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 99.0 90.0	LPDGYEFKEPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCREHKK KHPDASVNFSEFSKK KKEDMWNATAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNATAADDKOPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR LKEKYEKDIAAVR MSSVAFFVOTCR LKEKYEKDIAAVR MSSVAFFVOTCR LKEKYEKDIAAVR MSSVAFFVOTCR LKEKYEKDIAAVR MSSVAFFVOTCR KGEHPGLSIGDVAK LKEHPGLSIGDVAK LKEKYEKDIAAVR KREHPGLSIGDVAK LKEKYEKDIAAVR RPPSAFFLFCSEVRFK YEKDIAAVR REKYEKDIAAVR RPPSAFFLFCSEVRFK YEKDIAAVR LKEKYEKDIAAVR RPSAFFLFCSEVRFK YEKDIAAVR AEKAFVENDIAGNR AAELSAFVENDIAGNR AAELSAFVENDIDESSPGTEWER	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 2147.0 2237.0 1127.6 1598.8 1519.8 1519.8 1625.9 2001.0 1127.6 1127.6 1127.6 2337.0	1482.7 1076.5 10 1681.8 2333.1 1720.9 2238.0 2110.0 1238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 1128.6 1626.9 2020.0 1128.6 1620.9 2038.1	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1626.9 1496.7 2148.0 1128.6 1626.9 1496.7 2148.0 1128.6 1626.9 16
142.0 142.0 P094.29 H 42.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20	5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 98.0 98.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSVAFFVOTCR CKMSVAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYKENDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYENDIAAVR MSSVAFFVOTCR KKEKYENDIAAVR MSSVAFFVOTCR KKEKYENDIAAVR MSSVAFFVOTCR KKEKYENDIAAVR KLGEMWNNTAADDKOPYEK KLGEMWNNTAADDKOPYEK KLGEMWNNTAADDKOPYEK KLGEMWNNTAADDKOPYEK YEKDIAAVR GKMSSVAFFVOTCR IKGEHPGLSIGDVAK LKEKYENDIAAVR RPPSAFFLFCSEVRK YEKDIAAVR LFEKNEAVR LFEKNEAVR LFEKNEAVR LFEKNEAVR LFEKNEKYENDIAAVR LFEKNEAVR	1481.7 1075.5 sapiens (Human 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8	1482.7 1076.5 10 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1499.7 1248.0 2238.1 1128.6 1881.8 1520.8 1626.9 2002.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1880.8 1519.8 1625.9 2001.0 1127.6 1622.8	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1620.9 2002.0 1128.6
142.0 142.0	5.7 5.7 MGB1_HUMAN 20.0 20	5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 10.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 98.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR KKSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKLGEMWNNTAADDKOPYEK VEKDIAAVR GKMSSVAFFVOTCR KKEGEHGEISGIOVAK LKEKYEKDIAAVR RPSAFFLFCSEVPRK YEKDIAAVR RPSAFFLFCSEVPRK YEKDIAAVR LKEKYEKDIAAVR SSPAFFLFCSEVPRK YEKDIAAVR AKELEEWYAR AKELEWYAR AKELEEWYAR AKELEEWYAR AKELEEWYAR AKELEEWYAR AKELEEWYAR AKE	1481.7 1075.5 sapiens (Human 1690.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1680.8 1625.9 201.0 1127.6 1680.8 1625.9 201.0 1127.6 1680.8 1625.9 201.0 1127.6 1680.8 1625.9 201.0 1127.6 1680.8 1625.9 201.0 1127.6 1680.8 1625.9 201.0 1127.6 1680.8 2551.0 1406.7	1482.7 1076.5)) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8	1481.7 1075.5 1680.8 2332.1 17119.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 2351.0 1406.7 1406.7	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 1407.7 1407.7 1407.7
142.0 142.0 22.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20	5.7 5.7 5.7 20.0 20.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1,7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 98.0 99.0 99.0 99.0 99.0 99.0	LPDGYEFKEPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo CKMSSYAFFVOTCR CKMSSYAFFVOTCREEHKK KHPDASVNFSEFSKK KKEDMWNATAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR LKEKYEKDIAAVR MSSYAFFVOTCR LKEKYEKDIAAVR MSSYAFFVOTCR KSSVAFFVOTCR KKEKYEKDIAAVR MSSYAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR KLEEMWATAADDKOPYEK YEKDIAAVR KLEEMVAFKOTCR KKEKYEKDIAAVR KKEKYEKDIAAVR KKEKYEKDIAAVR KKEKYEKDIAAVR KKEKYEKDIAAVR KKEKYEKDIAAVR KKEKYEKDIAAVR KKEKYEKDIAAVR KRENSAFFVOTCR KKEKYEKDIAAVR KKEKYEKDIAAVR KRENSAFFVOTCR KKEKYEKDIAAVR KRENSAFFVOTCR KKEKYEKDIAAVR KAKEKEKYEKDIAAVR KAKELEEWVAR AKKELEEWVAR	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 1128.6 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 nding protein) (t	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1619.8 1625.9 2001.0 1127.6 1622.8 2351.0 1127.6 1622.8	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1128.6 1623.8
142.0 142.0 22.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20	5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 10.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1,7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 98.0 10 1 1 1 1 1 1 1 1 1	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo CKMSSYAFFVOTCR CKMSSYAFFVOTCREHKK KHPDASVNFSEFSKK KKHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR KLKEKYEKDIAAYR MSSYAFFVOTCR KLKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR KLEKYKEKDIAAYR KLEEMWNTAADDKOPYEK YEKDIAAYR KLEGMWNNTAADDKOPYEK YEKDIAAYR KLEKYKEKDIAAYR KREJEBOYAK LKEKYEKDIAAYR AREALEEWYAR AKELEEWYAR AKELEEWYAR AIKELEEWYAR AIKELEEWYAR ALSKOEMASASSSORGR AVSREDSORPGAHLTVKK EDSORPGAHLTVKK EDSORPGAHLTVKK EDSORPGAHLTVKK EDSORPGAHLTVKK EDSORPGAHLTVKK EDSORPGAHLTVKK	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1496.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8	1482.7 1076.5 101 1681.8 2333.1 1720.9 2238.0 2110.0 2138.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1128.6 1623.8	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1519.8 1625.9 2001.0 1127.6 1622.8	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1128.6 1623.8
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142.0 142.0 242.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 20.0 20.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1,7 y group pro 20 20 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 98.0 1tein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR GKMSSVAFFVOTCR GKMSSVAFFVOTCR GKMSSVAFFVOTCR GKMSSVAFFVOTCR KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNTAADDKOPYEK LKEKYEKOIAAVR MSSVAFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKOIAAVR MSSVAFFVOTCR KKEKYEKOIAAVR MSSVAFFVOTCR KKEKYEKOIAAVR MSSVAFFVOTCR KKEKYEKOIAAVR MSSVAFFVOTCR KKEKYEKOIAAVR KSSVAFFVOTCR KKEKYEKOIAAVR KLEKYEKOIAAVR KLGEMWNNTAADDKOPYEK YEKDIAAVR KLEKYEKOIAAVR SSPAFFVOTCR KKEHPGLSIGDVAK LKEKYEKOIAAVR SSPAFFVOTCR SSPAFFVOTCR KKEHPGLSIGDVAK KK	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1625.9 1495.7 2147.0 1127.6 1237.0 1127.6 125.9 2001.0 1127.6 1262.9 2351.0 1406.7 1406.7 1406.7 1406.7 1436.7 2281.1 1436.7 2280.1	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2138.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 1128.6 1626.9 2002.0 1128.6 1628.9 2002.0 1128.6 1628.9 2002.0 1128.6 1629.9 1497.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1437.8 2281.2 1950.0 1694.7	1481.7 1075.5 1680.8 2332.1 17119.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1682.8 2351.0 1406.7 10RNP core prote 1820.9 1978.1 1436.7 2280.1 1949.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 1128.6 1623.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1437.7 2881.1 1950.0 1694.7
142.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 1.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 20 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.	99.0 98.0 98.0 98.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCR GKMSSYAFFVOTCR GKMSSYAFFVOTCR GKMSSYAFFVOTCR GKMSSYAFFVOTCR KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR KKEKYEKDIAAYR MSSYAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR KKEGEMWNNTAADDKOPYEK YEKDIAAYR GKMSSYAFFVOTCR KGEHPGLSIGDVAK LKEKYEKDIAAYR RESPAFFLFCSEVREY YEKDIAAYR LKEKYEKDIAAYR ARELEEWYAR AKELEEWYAR AKELEEWYAR AKELEEWYAR AKELEEWYAR ALSKOEMASASSSORGR AVSREDSORPGAHLTVK GFAFVIFDDHOSVDKIVIOK KALSKOEMASASSSORGR NOGGYGGSSSSSSVGSGR RAVSREDSORPGAHLTVK KALSKOEMASASSSORGR NOGGYGGSSSSSSVGSGR RAVSREDSORPGAHLTVK	1481.7 1075.5 Sapiens (Human 1680.8 2332.1 17179.9 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 2147.0 2237.0 1127.6 1680.8 1519.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1406.7 1406.7 1406.7 12280.1 1343.7 2280.1	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2138.0 1626.9 1496.7 2148.0 1128.6 1499.7 1248.0 2238.1 1128.6 1496.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1409.0 1693.7 2280.1 11949.0 1693.7 2134.2	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.7 1407.7 1407.7 1281.1 1437.7 2281.1 1950.0 1694.7 2135.2
142.0 142.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 20.0 20.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1.7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 98.0 98.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR CKMSSVAFFVOTCREEHKK KHPDASVNFSEFSKK KKEDMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYKENDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYENDIAAVR KLEKEYKENDIAAVR KLEKEYKENDIAAVR KLEKEYKENDIAAVR KLEKEYKENDIAAVR KLEKEYKENDIAAVR AREAEPUNDIDESSPOTEWER AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR KLESKOEMASASSSORGR AVSBENDSORPGAHLTVKK EDSORPGAHLTVK EDSORPGAHLTVK SHEPWOKTEN SCOPYGEOSSPOTSER KALSKOEMASASSSORGR NOGGYGGSSSSSSVGSCR RAVSREDSORPGAHLTVK SHEPWOKTLTDCVWMRDPNTKR SSCOPYGGGOVFAKPR	1481.7 1075.5 sapiens (Human 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1519.8 1525.9 2001.0 1127.6 1622.8 2351.0 1406.7 1406.7 1406.7 1238.0 1820.9 1978.1 1426.7 2280.1 1446.7 2280.1 1449.0 1693.7 2134.2 2676.3 1627.8	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.7 nding protein) (F 1821.9 1497.9 1497.9 1497.9 1497.9 1497.9 1497.7 1407.7 14	1481.7 1075.5 1680.8 2332.1 17179.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1622.8	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 1128.6 1496.7 1128.6 1496.7 1128.6 1626.9 1496.7 1128.6 1628.8 1520.8 1520.8 1625.9 2002.0 1128.6 1623.8 2352.0 1407.7 14
142.0 142.0 242.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 5.7 20.0	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1.7 y group pro 20 20 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 98.0 1tein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKEPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMVNNTAADDKOPYEK LGEMVNNTAADDKOPYEK LKEKYEKDIAAYR MSSYAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR LKEKYEKDIAAYR MSSYAFFVOTCR KGEMPNTAADDKOPYEK KLGEMWNTAADDKOPYEK YEKDIAAYR GKSYAFFVOTCR KIGEHPGLSIGDVAK LKEKYEKDIAAYR KLGEMWNTAADDKOPYEK YEKDIAAYR GKMSSYAFFVOTCR KKGEHPGLSIGDVAK LKEKYEKDIAAYR RPPSAFFLFCSEYRK YEKDIAAYR LKEKYEKDIAAYR LKEKYEKDIAAYR AERAFVADIDESSPGTEWER AKELEEWYAR ROTEIN (HUMBA) ALSACMASASSSORGR AVSREDSORPGAHLTVK GFAFVTFDDHDSVDKIVIOK KALSKOEMASASSSORGR RONGGYGGSSSSSSYCSGR RAVSREDSORPGAHLTVK FFAFVTFDDHDSVDKIVIOK KALSKOEMASASSSORGR RONGGYGGSSSSSSYCSGR RAVSREDSORPGAHLTVK FFAFVTFDDHDSVDKIVIOK KALSKOEMASASSSORGR RONGGYGGSSSSSSYCSGR RAVSREDSORPGAHLTVK	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1625.9 1495.7 2147.0 2237.0 1127.6 127.6 127.	1482.7 1076.5 1) 1681.8 2333.1 1720.9 2238.0 2110.0 2138.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 1418.2 1590.0 1124.8 1520.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 1407.9 1821.9 1999.1 1437.8 2281.2 1950.0 1694.7 2135.2 2677.3	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2337.0 1127.6 1495.7 2147.0 1127.6 1880.8 1519.8 1625.9 2001.0 1127.6 1625.9 201.0 1127.6 1880.8 1625.9 201.0 1127.6 1820.9 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1230.9 1406.7	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1626.9 1496.7 2148.0 1128.6 1626.9 2002.0 1128.6 1626.9 2002.0 1128.6 1620.8 1
142.0 142.0 142.0 22.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 5.7 5.7 20.0	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1,7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 1tein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo CKMSSYAFFVOTCR CKMSSYAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR KEKYEKDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR KEKYEKDIAAYR MSSYAFFVOTCR KEKPEDIAAYR MSSYAFFVOTCR KEKPEDIAAYR MSSYAFFVOTCR KGEHPGLSIGDVAK LKEKYEKDIAAYR KLGEMWNTAADDKOPYEK YEKDIAAYR CKMSSYAFFVOTCR KKGEHPGLSIGDVAK LKEKYEKDIAAYR ROMSSYAFFVOTCR KKEKPENDIAAYR ARELEEWYAR ARELEEWYAR AIKELEEWYAR AIKELEEWYAR AIKELEEWYAR AIKELEEWYAR AIKELEEWYAR COTEIN AI (Helix-destabilizing protein) (Singi ALSKOEMSASSSORGR AVSREDSORPGAHLTVK GFAFVIFODHOSVOBKIVIOK KALSKOEMSASSSORGR NOGGYGGSSSSSSYGSGR RAVSREDSORPCAHLTVK SHFEOWGTLTDCVVMRDPNTKR SSGPYGGGOVFAKPR YHTVNGHNOEVR	1481.7 1075.5 sapiens (Humar 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8	1482.7 1076.5 101681.8 2333.1 1720.9 2238.0 2110.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1418.9 1437.8	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1694.7 2437.7 2281.1 1950.0 1694.7 2135.2 2677.2 1628.8 1485.7 1218.6
142.0 142.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 20.0 20.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 17 y group pro 20 20 20 20 20 20 20 20 20 20 20 20 20	99.0 98.0 98.0 1cin B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR GKMSSVAFFVOTCR GKMSSVAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNTAADDKOPYEK LGEMWNTAADDKOPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR KLGEMWNNTAADDKOPYEK VEKDIAAVR LKEKYEKDIAAVR KLGEMWNTAADDKOPYEK VEKDIAAVR KLGEHPOLSIGDVAK LKEKYEKDIAAVR AKELEEWVAR AKELEEWVAR AKELEEWVAR AKELEEWVAR AKELEEWVAR AKELEEWVAR KKSCEMASASSSORGR AVSREDSGPCAHLTVK EDSORPCAHLTVK EDSORPCAHLTVK EDSORPCAHLTVK SHORGEN KALGEMSASSSSORGR RAVSREDSGPCAHLTVK SHEPCWGTLTDEVMRDPNTKR SSCHYGGGSSTSSSYGGR RAVSREDSGRPCAHLTVK SHEPCWGTLTDEVMRDPNTKR SSCHYGGGSGSTSSSYGGR RAVSREDSGROFAHEPT HTVNGHNCEVR LEIGELSFETTDESLR LEIGELSFETTDESLR LEIGGLSFETTDESLR	1481.7 1075.5 Sapiens (Human 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1682.8 2351.0 1406.7 1406.7 1406.7 1406.7 1498.0 1978.1 1414.6 1782.0 1978.1 1446.7 1499.0 1693.7 12134.2 2676.3 1484.7 1217.6 1883.9 1912.0	1482.7 1076.5)) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1128.6 1499.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7	1481.7 1075.5 1680.8 2332.1 17179.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 2237.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1625.9 1127.6 1880.8 1519.8 1625.9 2001.0 1107.6 1820.9 2001.0 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 122.8 1436.7 122.8 1436.7 1236.2 1436.7 1249.0 1499.0 1493.7 1214.2 1627.8 1484.7 1217.6 1783.9 1912.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1626.9 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 1128.6 1623.8 2352.0 1407.7 14
142.0 142.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 20.0 20.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1.7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 1ein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKQPYEK LGEWNNTAADDKQPYEK LGEWNNTAADDKQPYEK LGEWNNTAADDKQPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR RSSVAFFVOTCR KKEGENGENGENGENGENGENGENGENGENGENGENGENGEN	1481.7 1075.5 sapiens (Human 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1127.6 1498.7 2147.0 2237.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1625.9 2001.0 1127.6 1680.8 1625.9 2001.0 1127.6 1680.8 1625.9 201.0 1127.6 1622.8 2351.0 1406.7 1 e-strand RNA-bi 1820.9 1931.1 1436.7 2280.1 1949.0 1627.8 1648.7 1217.6 183.9 1949.0 1693.7 2134.2 2676.3 1627.8 1484.7 1217.6 1783.9 1912.0 1683.9 1912.0 1683.9	1482.7 1076.5)) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 2238.1 1128.6 1499.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7	1481.7 1075.5 1680.8 2332.1 17119.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 2351.0 1406.7 170RNP core prote 1820.9 1	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1626.9 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1623.8 1623.8 2352.0 1407.7 14
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142.0 142.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 20.0 20.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 17 y group pro 20 20 20 20 20 20 20 20 20 20 20 20 20	99.0 98.0 1ein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEWNNTAADDKOPYEK LGEWNNTAADDKOPYEK LGEWNNTAADDKOPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR RSSVAFFVOTCR KKELEGWANTAADDKOPYEK YEKDIAAVR LKEKYEKDIAAVR RSSVAFFVOTCR KKEHPGISIGDVAK LKEKYEKDIAAVR RSSVAFFVOTCR KKEHPGISIGDVAK LKEKYEKDIAAVR RSPSAFFLFCSEYRPK YEKDIAAVR LKEKYEKDIAAVR RSPSAFFLFCSEYRPK YEKDIAAVR AKELEEWVAR AKELEEWVAR AKELEEWVAR AKELEEWVAR KKELEEWVAR KKELEEWVAR KKSCEMASASSSORGR AVSREDSORPGAHLTVKK EDSORPGAHLTVK EDSORPGAHLTVK SSGPYGGGGOYFAKPR HTVNCHNOEVR LFIGGLSEETTDESLR KKJGISEGTEDHILR KKJGISKESTEHDESLR KKJSERPSORPGAHLTVK IFVGGIKEDTEEHHLR IFVGGIKEDTEHHLR	1481.7 1075.5 sapiens (Human 1690.8 2332.1 1719.9 2237.0 2109.0 2237.0 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1625.9 1495.7 2147.0 2237.0 1127.6 1680.8 1625.9 2351.0 1127.6 1680.8 1625.9 2351.0 1406.7 2- c-strand RNA-bi 1436.7 2280.1 1496.7 1498.1 1436.7 2280.1 1499.0 1693.7 2134.2 2676.3 1627.8 1484.7 1217.6 1783.9 1978.1 1436.7 2134.2 2676.3 1627.8	1482.7 1076.5 1) 1481.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7	1481.7 1075.5 1680.8 2332.1 17119.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 2351.0 1127.6 1622.8 2351.0 1406.7	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 1128.6 1682.8 235.0 1128.6 1623.8 235.0 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1281.1 1950.0 1694.7 2135.2 2677.2 1628.8 1485.7 1218.6 1784.9 1913.0 1684.9 1913.0 1684.9 1913.0 1684.9 1851.0 1880.0 2008.1 1628.8
142.0 142.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 10	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 y group pro 20 20 20 20 20 20 20 20 20 20 20 20 20	99.0 98.0 1ein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GCMSTEQR h mobility group protein 1) (HMG-1) - Homo GCMSSVAFFVOTCR GCMSSVAFFVOTCR GCMSSVAFFVOTCR KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNTAADDKOPYEK LKEKYEKOIAAVR MSSVAFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKLGEMWNNTAADDKOPYEK YEKDIAAVR GKMSSVAFFVOTCR KKLGEMWNNTAADDKOPYEK YEKDIAAVR ASSPAFFVOTCR KKEEPIGLSGVAR LKEKYEKDIAAVR SSPAFFVOTCR KKEEPIGLSGVAR LKEKYEKDIAAVR SSPEDSORFUGENEV YEKDIAAVR AKELEEWWAR AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR SVSREDSORPGAHLTVK EDSORPGAHLTVK EDSORPGAHLTVK SGAPVTEDDHOSVDKIVIOK KALSKOEMASASSSORGR RAVSREDSORPGAHLTVK SGAPVTEDDHOSVDKIVIOK KALSKOEMASASSSORGR RAVSREDSORPGAHLTVK SGAPVTEDDHOSVDKIVIOK KALSKOEMASASSSORGR RAVSREDSORPGAHLTVK SGAPVEGGGOYFAKPR YHTNNCHNCEVR LEVIGGIKEDTEEHHLR KIFVGGIKEDTEEHHLR KIFVGGIKEDTEHHLR	1481.7 1075.5 sapiens (Human 1690.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1625.9 1495.7 2147.0 2237.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1680.8 1625.9 2001.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1680.8 1690.1 1495.7 1214.1 1496.7 2280.1 1494.0 1693.7 2134.2 2676.3 1627.8 1484.7 1217.6 1783.9 1912.0 1683.9 1879.0	1482.7 1076.5 101 1481.8 2333.1 1720.9 2238.0 2110.0 2238.0 1496.7 2148.0 1128.6 1499.7 1426.9 1496.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.	1481.7 1075.5 1680.8 2332.1 17119.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 2351.0 1127.6 1680.8 2351.0 1127.6 1692.8 201.0 1127.6 1693.7 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2147.0 2149.0 1127.6 1680.8 1519.8 1625.9 1040.7 1127.6 1682.9 1040.7 1127.6 1683.9 1040.7 1140.7 1	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1881.8 1520.8 1626.9 1128.6 16823.8 235.0 1407.7 14
142.0 142.0 142.0 142.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 10.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 20 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.	99.0 98.0 98.0 98.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR CKMSSYAFFVOTCREEHKK KHPDASVNFSFFSKK KLEEMWNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNTAADDKOPYEK LKEKYKENDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR KKEKYENDIAAYR MSSYAFFVOTCR KKEKYENDIAAYR MSSYAFFVOTCR KKEKYENDIAAYR MSSYAFFVOTCREHKK KLGEMWNITAADDKOPYEK KKEKYENDIAAYR MSSYAFFVOTCR KKEKYENDIAAYR MSSYAFFVOTCREHKK KLGEMWNITAADDKOPYEK YENDIAAYR KLEKEYKENDIAAYR KLEKEYKENDIAAYR KLEKEYKENDIAAYR ASSAFFVOTCREHKK KLGEMWNITAADDKOPYEK YENDIAAYR KLEKEYKENDIAAYR ASSAFFVOTCREHKK KLGEMWNITAADDKOPYEK YENDIAAYR LKEKYENDIAAYR ARELEEWYAR AKELEEWYAR AIKELEEWYAR RAVSREDSORPGAHLTVK EDSORPGAHLTVK SHEOWGTEDEN KLIGGLSFETTDESLR KLIGGLSF	1481.7 1075.5 sapiens (Human 1680.8 2332.1 17179.9 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1406.7 1406.7 1406.7 1406.7 1406.7 14106.	1482.7 1076.5 101 1681.8 2333.1 1720.9 2238.0 2110.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 181.8 2281.2 1950.0 1694.7 1318.6 1784.9 1881.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1886.7 1412.7 1851.0	1481.7 1075.5 1680.8 2332.1 1717.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1406.7 1406.7 1406.7 1406.7 1406.7 123.0 1406.7 1406.7 123.1 1436.7 1234.2 1427.8 1484.7 1217.6 1783.9 1891.0 1893.7 1217.6 1783.9 1891.0 1893.0 1899.0 1895.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1626.9 1496.7 2148.0 2238.0 1128.6 1628.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 12135.2 2677.2 281.1 1950.0 1694.7 2135.2 2677.2 2677.2 1628.8 1485.7 1218.6 1784.9 1913.0 1684.9 1913.0 1684.9 1913.0 1684.9 1913.0 1684.9 1913.0 1684.9 1951.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1880.0 1886.6 1412.7 1851.0
142.0 142.0 142.0 142.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 10.	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 20 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.	99.0 98.0 98.0 98.0 99.0 99.0 99.0 99.0	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR KLGEMWNNTAADDKQPYEK LGEMWNNTAADDKQPYEK LGEMWNTAADDKQPYEK LKEKYKENDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYENDIAAVR KLEKEYENDIAAVR KLEKEYENDIAAVR KLEKEYENDIAAVR AVENDIAAVR LKEKYENDIAAVR LKEKYENDIAAVR ARELEEWVAR AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR AIKELEEWVAR AVSENDSORPGAHLTVK EDSORPGAHLTVK CFAFVTFDDHDSVDKIVIOK KALSKOEMASASSSORGR NOGGYGSSSSSSYCSCR RAVSREDSORPGAHLTVK SHEPOWGTLTDCVVMRDPNTKR SSCHYGGGKDTEEHHLR KIFVGGIKEDTEEHHLR KIFVGGI	1481.7 1075.5 sapiens (Human 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1406.7 1606.7 1606.7 1606.7 1607.8 1628.8 1618.8 1625.9 178.8 1819.8 1	1482.7 1076.5 101 1681.8 2333.1 1720.9 2238.0 2110.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.	1481.7 1075.5 1680.8 2332.1 17179.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1622.8 2351.0 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1209.1 1217.6 1820.9 1978.1 1436.7 1217.6 1820.9 1978.1 1436.7 1217.6 1830.9 1979.0 1879.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1626.9 1496.7 2148.0 2238.0 1128.6 1628.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 1
142.0 142.0 142.0 22.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 10	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1.7 y group pro 20 20 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 98.0 1cin B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GCMSTEQR h mobility group protein 1) (HMG-1) - Homo GCMSSVAFFVOTCR ECKMSSVAFFVOTCR ECKMSSVAFFVOTCR KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNTAADDKOPYEK LKEKYEKOIAAVR MSSVAFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR GKMSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR SSVAFFVOTCR KKEKYEKDIAAVR SSVAFFVOTCR KKELEKYEKDIAAVR SSVAFFVOTCR KKELEKYEKDIAAVR SSPAFFVOTCR KKELEKYEKDIAAVR ASSPAFFVOTCR KKELEWAR ALKELEWAR AIKELEEWYAR AIKELEEWYAR AIKELEEWYAR AIKELEEWYAR AIKELEEWYAR AIKELEEWYAR AIKELEEWYAR HIELDEWSCHALLTVK EDSORPGAHLTVK EDSORPGAHLTVK EDSORPGAHLTVK SGAPVTEDDHOSVDKIVIOK KALSKOEMASASSSORGR RAVSREDSORPGAHLTVK SSGPYGGGGOYFAKPR YHTNNGHNCEVR LIFIGGLSFETTDESLR KLEIGGLSFETTDESLR KSESPKEPEOLIK AVSREDSORPGAHLTVK IFVGGIKEDTEEHHLR IFVGGIKEDTEEHHLR IFVGGIKEDTEEHHLR KIFVGGIKEDTEEHHLR KIFVGGI	1481.7 1075.5 sapiens (Human 1680.8 2332.1 1719.9 20237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1622.8 201.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1623.9 199.0 199.	1482.7 1076.5) 1681.8 2333.1 1720.9 2238.0 2110.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1881.0 1880.0	1481.7 1075.5 1680.8 2332.1 17119.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1680.8 1619.8 1625.9 2001.0 1127.6 1680.8 1625.9 2001.0 1127.6 1680.8 1625.9 2001.0 1127.6 1680.8 1625.9 2001.0 1127.6 1680.8 1625.9 2001.0 1127.6 1680.8 1627.6 2134.2 2076.2 1627.8 1484.7 1217.6 1783.9 1912.0 1890.0 1890.0 1899.0 1899.0 1899.0 1899.0 1899.0 1899.0 2007.1 1627.8 1485.6	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 1128.6 16823.8 2352.0 1128.6 1623.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1507.1 1407.7 1608.8 1486.7 1218.6 1784.9 1913.0 1684.9 1880.0
142.0 142.0 142.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 10.0	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1.7 y group pro 200 200 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 1cin B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCR GKMSSYAFFVOTCREEHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR KLKEKYEKDIAAYR MSSVAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR MSSYAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR IKGEHPGLSIGDVAK LKEKYEKDIAAYR GKMSSYAFFVOTCR IKGEHPGLSIGDVAK LKEKYEKDIAAYR RESPAFFLFCSEVTREY YEKDIAAYR LKEKYEKDIAAYR AKKELEEWYAR AKKELEEWYAR AKKELEEWYAR LKEKYEKDIAAYR LKEKYEKOR LKEKYEKDIAAYR LKEKYEKOR LKEKYEKOR LKEKYEKDIAAYR LKEKYEKOR L	1481.7 1075.5 sapiens (Human 1680.8 2332.1 1719.9 2107.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 1237.0 1127.6 1498.7 1495.7 2147.0 1227.6 1495.7 2147.0 1227.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 2351.0 1127.6 1622.8 1519.8 1625.9 2001.0 1127.6 1622.8 1519.8 1625.9 201.0 1127.6 1622.8 1127.6 1486.7 1280.1 129.9 1978.1 1436.7 1280.1 149.9 1978.1 1436.7 1280.1 1893.7 1217.6 1893.7 1217.6 1893.7 1893.9 1912.0 1879.0	1482.7 1076.5) 1681.8 2333.1 1720.9 2238.0 2110.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2352.0 1128.6 1623.8 2452.0 1128.6 1623.8 2552.0 1128.6 1623.8 2452.0 1128.6 1623.8 2552.0 1128.6 1623.8 2552.0 1128.6 1623.8 2452.0 1128.6 1623.8 2452.0 1694.7 1407.7 1213.5 1218.6 1784.9 1913.0 1880.0	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 1237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1406.7 1406.7 1406.7 1406.7 1237.0 1127.6 1622.8 2351.0 1494.0 1493.7 1217.6 1820.9 1978.1 1436.7 1280.1 1949.0 1693.7 1217.6 1693.7 1217.6 1783.9 1912.0 1683.9 1899.0 1879.0	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1681.8 1520.8 1628.9 2002.0 1128.6 1628.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 1213.6 1681.8 1628.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1821.9 1979.1 1437.7 2281.1 1950.0 1694.7 1213.6 2677.2 1628.8 1485.7 1218.6 1784.9 1913.0 1684.9 1851.0 2008.1 1628.8 1486.6 1412.7 1851.0 2007.1 1628.8 1486.6 1412.7 1851.0 2007.1 1628.8 1486.6 1412.7 1851.0 2007.1 1628.8 1486.6 1412.7 1851.0 2007.1 1628.8 1486.6 1412.7
142.0 142.0 142.0 142.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 5.7 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0 10.0	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	2.0 1.7 y group pro 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 1cin B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR KLGEMWNNTAADDKQPYEK LGEMWNTAADDKQPYEK LGEMWNTAADDKQPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR KKELEWWAR AKELEEWVAR AKELEEWVAR AKELEEWVAR AKELEEWVAR KKELEEWVAR KKELEEWAR KKELEEWVAR KKE	1481.7 1075.5 Sapiens (Human 16808 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1406.7 1406.7 1406.7 1406.7 141.0	1482.7 1076.5 101 1681.8 2333.1 1720.9 2238.0 2110.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1128.6 1499.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1521.9 1979.1 1979.	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 2237.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 2351.0 1127.6 1622.8 2351.0 1406.7 170RNP core prote 1820.9 1978.1 1436.7 1249.0 1495.7 1217.6 1820.9 1978.1 1436.7 1718.9 1820.9 1879.0 1879	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1626.9 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 1128.6 1623.8 1626.9 1128.6 1623.8 1407.7 1
142.0 142.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 5.7 5.7 20.0	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 20 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.	99.0 98.0 1ein B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GCMSSTAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR CKMSSVAFFVOTCR LGEMWNNTAADDKQPYEK LGEMWNTAADDKQPYEK LGEMWNTAADDKQPYEK LKEKYEKDIAAVR MSSVAFFVOTCR MSSVAFFVOTCR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KKEKYEKDIAAVR MSSVAFFVOTCR KIKEKYEKDIAAVR MSSVAFFVOTCR KIKEKYEKDIAAVR KSCHMSLSIGDVAK LLEKKYEKDIAAVR RSSVAFFVOTCR KIKEHPELSIGDVAK LKEKYEKDIAAVR RSPSAFFLCSEVRFK VEKDIAAVR SSPAFFLCSEVRFK VEKDIAAVR SSPIENS (HUMBA) AAELAFVNDIDESSPGTEWER AIKELEEWVAR KIKELEWVAR KIKELEWVAR KIKELEWVAR KIKELEWVAR KIKELEWVAR KIKELEWVAR KIKELEWVAR KIKELEWVAR KIKELESWORG ROGGYGGSSSSSSVSGG ROGGYGKSSSSSSVSGG RAVSREDSGRGAHLTVK EDSGRPGAHLTVK EDSGRPGAHLTVK EDSGRPGAHLTVK ENGGIKEDTEEHHLR KIFVGGIKEDTEEHHLR KIFVGGIKEDT	1481.7 1075.5 Sapiens (Human 1680.8 2332.1 1719.9 2237.0 2109.0 2237.0 1625.9 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 1406.7 1622.8 2351.0 1406.7 1622.8 1480.7 1491.7 1	1482.7 1076.5) 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1128.6 1499.7 2148.0 2238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1619.8 1625.9 2001.0 1127.6 1680.8 1519.8 1625.9 2001.0 1127.6 1680.8 2351.0 1406.7 170RNP core prote 1820.9 1879.0 1879.0 1879.0 1879.0 1879.0 1879.0 1879.0 1879.0 1879.0 1879.0 2007.1 1850.0 1879.0 2007.1 1850.0 1879.0 2007.1 1850.0 1879.0 2007.1 1850.0 1879.0 2007.1 1850.0 1879.0 2007.1 1850.0 1879.0 2007.1 1850.0 1879.0 2007.1 1850.0 1879.0 2006.1 1627.8 1485.6 1411.7 1885.0 2134.2	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 2238.0 2162.8 1496.7 2148.0 1128.6 1496.7 2148.0 2238.0 1128.6 1496.7 2148.0 2238.0 1128.6 1626.9 1496.7 2148.0 2238.0 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1682.8 2352.0 1407.7 1
142.0 142.0 142.0 42.0 42.0 42.0 42.0 42.0 42.0 42.0	5.7 5.7 MGB1_HUMAN 20.0 20.0 20.0 20.0 20.0 20.0 20.0 20.	5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7	29.6 29.6 High mobilit 45.6 45.6 45.6 45.6 45.6 45.6 45.6 45.6	20 1.7 y group pro 200 200 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 98.0 1cin B1 (Hig 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	LPDGYEFKFPNR DGGAWGTEQR h mobility group protein 1) (HMG-1) - Homo GKMSSYAFFVOTCR GKMSSYAFFVOTCR GKMSSYAFFVOTCREHKK KHPDASVNFSEFSKK KLGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LGEMWNNTAADDKOPYEK LKEKYEKDIAAYR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR MSSYAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR MSSYAFFVOTCR MSSYAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR KKEKYEKDIAAYR MSSVAFFVOTCR KKEKYEKDIAAYR KLGEMWNNTAADDKOPYEK YEKDIAAYR KKEGMANTAADDKOPYEK YEKDIAAYR KKEKYEKDIAAYR AKELEBWAR AKELEBWAR AKELEEWYAR AIKELEEWYAR	1481.7 1075.5 sapiens (Human 1880.8 2332.1 1719.9 2109.0 2237.0 1102.5 1495.7 2147.0 1127.6 1498.7 1495.7 2147.0 1127.6 1495.7 2147.0 1127.6 1495.7 2147.0 1127.6 1680.8 1519.8 1519.8 1625.9 2001.0 1127.6 1622.8 2351.0 1127.6 160.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1406.7 1820.9 1978.1 1436.7 2280.1 1979.0 1879.0 1	1482.7 1076.5 101618.8 2333.1 1720.9 2238.0 2110.0 2110.0 2238.0 1626.9 1496.7 2148.0 1128.6 1499.7 1626.9 1496.7 2148.0 1238.1 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7	1481.7 1075.5 1680.8 2332.1 1719.9 2237.0 2108.9 2237.0 1625.9 1495.7 2147.0 1127.6 1495.7 2147.0 2237.0 1127.6 1680.8 1519.8 1652.9 2001.0 1127.6 1680.8 1622.8 2351.0 1127.6 1622.8 2351.0 1406.7	1482.7 1076.5 1681.8 2333.1 1720.9 2238.0 2110.0 1626.9 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 2148.0 1128.6 1496.7 1496.7 1496.7 1128.6 1681.8 1520.8 1626.9 2002.0 1128.6 1623.8 2352.0 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1407.7 1851.0 1694.7 1218.6 1684.9 189.0 1694.7 1218.6 1684.9 1913.0 1684.9 1913.0 1684.9 1913.0 1684.9 1913.0 1684.9 1913.0 1686.6 16185.1 1628.8 1486.6 1412.7 1851.0 2007.1 1628.8 1486.6 1412.7 1851.0 2007.1 1628.8 1486.6 1461.7 2677.3 2135.2

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		99.0	IFVGGIKEDTEEHHLR	1879.0	1880.0	1879.0	1880.0
P09874 125.0	PARP1_HUMAN	9.4	Poly [ADP-rib			2.4.2.30) (PARP-1) (ADPRT) (NAD(+) ADP-ril NREELGFRPEYSASOLK			ribose] synthetas 2023.0	
125.0	9.4	9.4	16.2	2.0	99.0	SDAYYCTGDVTAWTK VGHSIRHPDVEVDGFSELR	1736.8	1737.8	1736.7	1737.7
125.0 125.0	9.4	9.4 9.4	16.2 16.2	2.0	99.0 99.0	WYHPGCFVK	2148.2 1192.5	2149.2 1193.6	2148.1 1192.5	2149.1 1193.6
125.0		9.4	16.2	0.7	79.0	MVDPEKPQLGMIDR	1627.8	1628.8	1627.8	1628.8
125.0		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	WYHPGCFVK	1192.5	1193.6	1192.5	1193.6
224.0	2.9	2.9	3.9	1.4	96.0	MAESSDKLYR	1214.6	1215.6	1214.6	1215.6
	LKHA4_HUMAN 2.0	2.0	Leukotriene A			6) (LTA-4 hydrolase) (Leukotriene A(4) hydro MQEVYNFNAINNSEIR				1941.9
115.0	9.9	9.9	14.1	2.0	99.0	HFNALGGWGELQNSVK	1755.9	1756.9	1755.9	1756.9
115.0	9.9	9.9	14.1	2.0	99.0	MQEVYNFNAINNSEIR	1940.9	1941.9	1940.9	1941.9
115.0		9.9	14.1	2.0	99.0	PEIVDTCSLASPASVCR	1860.9	1861.9	1860.9	1861.9
115.0		9.9	14.1	2.0	99.0	TLTGTAALTVQSQEDNLR	1917.0	1918.0	1917.0	1918.0
115.0		9.9	14.1	1.7	98.0	APLPLGHIKR	1100.7	1101.7	1100.7	1101.7
115.0 P101241	9.9 PGSG_HUMAN	9.9	14.1 Secretory are	0.2	34.0	MKFTRPLFK protein precursor (Platelet proteoglycan core	1166.7	1167.7	1166.7	1167.7
179.0	6.4	6.4	39.2	2.0	99.0	GPMFELLPGESNKIPR	1783.9	1784.9	1783.9	1784.9
179.0	6.4	6.4	39.2	2.0	99.0	NLPSDSQDLGQHGLEEDFML	2244.0	2245.0	2244.0	2245.0
179.0		6.4	39.2	2.0	99.0	YQLVDESDAFHDNLR	1820.8	1821.8	1820.8	1821.8
179.0 179.0		6.4 6.4	39.2 39.2	0.4	61.0 99.0	ARYQWVR YQLVDESDAFHDNLR	977.5 1820.8	978.5 1821.8	977.5 1820.8	978.5 1821.8
48.0	6.5	6.5	39.2	2.0	99.0	GPMFELLPGESNKIPR	1783.9	1784.9	1783.9	1784.9
48.0	6.5	6.5	39.2	2.0	99.0	NLPSDSQDLGQHGLEEDFML	2244.0	2245.0	2244.0	2245.0
48.0	6.5	6.5	39.2	1.5	97.0	YQLVDESDAFHDNLR	1820.8	1821.8	1820.8	1821.8
48.0	6.5	6.5	39.2		86.0	ARYQWVR	977.5	978.5	977.5	978.5
48.0	6.5	6.5	39.2	0.1	23.0	YOWVR	750.4	751.4	750.4	751.4
82.0	9.0	9.0	39.2	2.0	99.0	GPMFELLPGESNKIPR	1783.9	1784.9	1783.9	1784.9
82.0	9.0	9.0	39.2	2.0	99.0	NLPSDSQDLGQHGLEEDFML	2244.0	2245.0	2244.0	2245.0
82.0	9.0	9.0	39.2	2.0	99.0	SLDRNLPSDSQDLGQHGLEEDFML	2715.3	2716.3	2715.2	2716.3
82.0	9.0	9.0	39.2	2.0	99.0	YQLVDESDAFHDNLR	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 P101451	9.0 IL8_HUMAN	9.0	39.2 Interleukin-8	0.0 precursor (99.0 (IL-8) (CXCL	YQLVDESDAFHDNLR 8) (Monocyte-derived neutrophil chemotactic	1820.8	1821.8	1820.8	1821.8
133.0	8.4	8.4 8.4	49.5 49.5	2.0	99.0 99.0	ELCLDPKENWVQR	1685.8	1686.8	1685.8 2214.1	1686.8 2215.1
133.0 133.0	8.4	8.4	49.5	2.0	99.0	LSDGRELCLDPKENWVQR TYSKPFHPK	2214.1 1103.6	2215.1 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	49.5	0.2	40.0	ENWVQR	830.4	831.4	830.4	831.4
133.0		8.4	49.5	0.1	27.0	FIKELR	804.5	805.5	804.5	805.5
133.0		8.4	49.5	0.0	99.0	VIESGPHCANTEIIVK	1765.9	1766.9	1765.9	1766.9
133.0 133.0	8.4	8.4 8.4	49.5 49.5	0.0	99.0 99.0	VIESGPHCANTEIIVK VIESGPHCANTEIIVK	1917.9 1767.9	1918.9 1768.9	1917.8 1765.9	1918.9 1766.9
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	ELCLDPKENWVQR	1685.8	1686.8	1685.8	1686.8
73.0	4.8	4.8	43.4	0.2	36.0	TYSKPFHPK	1103.6	1104.6	1103.6	1104.6
73.0	4.8	4.8	43.4	0.0	24.0	VIESGPHCANTEIIVK	1765.9	1766.9	1765.9	1766.9
105.0	7.7	7.7	56.6	2.0	99.0	ELCLDPKENWVQR	1685.8	1686.8	1685.8	1686.8
105.0	7.7	7.7	56.6		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		96.0	TYSKPFHPK	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 P10319		7.7				VIESGPHCANTEIIVK n, B-58 alpha chain precursor (MHC class I an				1766.9
107.0		3.2	41.7	2.0	99.0	WAAVVVPSGEEQR	1426.7	1427.7	1426.7	1427.7
107.0		3.2	41.7	0.7	79.0	AYLEGLCVEWLR	1507.8	1508.8	1507.7	1508.8
107.0		3.2	41.7	0.3	55.0	APWIEQEGPEYWDGETR	2061.9	2062.9	2061.9	2062.9
107.0		3.2	41.7	0.1	22.0	YFYTAMSRPGRGEPR	1786.8	1787.9	1786.9	1787.9
160.0 160.0	7.4	12.3 12.3	40.6 40.6	2.0	99.0 99.0	APWIEQEGPEYWDGETR DGEDQTQDTELVETRPAGDRTFQK	2061.9 2735.3	2062.9 2736.3	2061.9 2735.3	2062.9 2736.3
160.0	7.4	12.3	40.6	2.0	99.0	YTCHVQHEGLPKPLT	1778.9	1779.9	1778.9	1779.9
160.0	7.4	12.3	40.6	1.2	99.0	MYGCDVGPDGR	1225.5	1226.5	1225.5	1226.5
160.0		12.3	40.6	0.2	38.0	AYLEGLCVEWLR	1507.8	1508.8	1507.7	1508.8
160.0 160.0		12.3 12.3	40.6 40.6	0.0	99.0 99.0	FIAVGYVDDTQFVR WAAVVVPSGEEQR	1628.8 1426.7	1629.8 1427.7	1628.8 1426.7	1629.8 1427.7
P10412 74.0	H14_HUMAN 14.0	14.0	Histone H1.4 18.3	(Histone H ²	1b) - Homo s 99.0	apiens (Human) 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 74.0	14.0	14.0	18.3	2.0	99.0 99.0	SETAPAAPAAPAAEKTPVK SETAPAAPAAPAAPAFKTPVKK	1945.0	1946.0 2074.1	1945.0	1946.0 2074.1
74.0	14.0 14.0	14.0 14.0	18.3 18.3	2.0	99.0	SETAPAAPAAPAEKTPVKKK	2073.1 2201.2	2202.2	2073.1 2201.2	2202.2
74.0	14.0	14.0	18.3	2.0	99.0	SETAPAAPAAPAEKTPVKKKAR	2428.4	2429.4	2428.3	2429.4
74.0	14.0	14.0	18.3	0.0	99.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
74.0	14.0	14.0	18.3	0.0	20.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
160.0	4.4	7.7	24.2	2.0	99.0	SETAPAAPAAPAAEKTPVKK	2073.1	2074.1	2073.1	2074.1
160.0	4.4	7.7	24.2	1.2	99.0	SETAPAAPAAPAEKTPVK	1945.0	1946.0	1945.0	1946.0
160.0		7.7	24.2	1.2	99.0	SETAPAAPAAPAEKTPVKKK	2201.2	2202.2	2201.2	2202.2
160.0	4.4	7.7	24.2	0.0	98.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
	THIO_HUMAN	7.7	24.2 Thioredoxin (ALAAAGYDVEKNNSR r) (ADF) (Surface-associated sulphydryl prote		1578.8 Iomo sapiens (Hu	1577.8 uman)	1578.8
113.0	10.0	10.0	42.9	2.0	99.0	CMPTFQFFK	1187.5	1188.5	1187.5	1188.6
113.0		10.0	42.9	2.0	99.0	CMPTFQFFKK	1332.6	1333.6	1332.6	1333.6
113.0		10.0	42.9	2.0	99.0	CMPTFQFFKKGQK	1628.8	1629.8	1628.8	1629.8
113.0		10.0	42.9	2.0	99.0	MIKPFFHSLSEK	1462.8	1463.8	1462.8	1463.8
113.0 113.0	10.0	10.0 10.0	42.9 42.9	2.0	99.0 99.0	VGEFSGANKEKLEATINELV CMPTFOFFK	2147.1 1204.5	2148.1 1205.5	2147.1 1204.5	2148.1 1205.5
113.0 113.0	10.0	10.0 10.0	42.9 42.9	0.0	85.0 63.0	CMPTFQFFK CMPTFQFFKK	1187.6 1315.6	1188.6 1316.6	1187.6 1315.6	1188.6 1316.6
80.0	4.3	4.3	33.3	2.0	99.0	CMPTFQFFK	1159.5	1160.5	1159.5	1160.5
80.0	4.3	4.3	33.3	2.0	99.0	MIKPFFHSLSEK	1462.8	1463.8	1462.8	1463.8
80.0	4.3	4.3	33.3	0.3	51.0	CMPTFQFFKK	1315.6	1316.6	1315.6	1316.6
80.0	4.3	4.3	33.3	0.0	99.0	CMPTFQFFK CMPTFQFFK	1204.5	1205.5	1204.5	1205.5
80.0	4.3	4.3	33.3	0.0	99.0		1187.5	1188.5	1187.5	1188.6
80.0	4.3	4.3	33.3	0.0	79.0	CMPTFQFFK	1203.5	1204.5	1203.5	1204.5
80.0	4.3	4.3	33.3		41.0	CMPTFQFFK	1220.5	1221.5	1220.5	1221.5
81.0	9.1	9.1	42.9	2.0	99.0	CMPTFQFFK	1187.5	1188.5	1187.5	1188.6
81.0	9.1	9.1	42.9		99.0	CMPTFQFFKKGQK	1628.8	1629.8	1628.8	1629.8
81.0	9.1	9.1	42.9	2.0	99.0	MIKPFFHSLSEK	1478.8	1479.8	1478.8	1479.8
81.0	9.1	9.1	42.9	2.0	99.0	VGEFSGANKEKLEATINELV	2147.1	2148.1	2147.1	2148.1
81.0	9.1	9.1	42.9	1.1	92.0	CMPTFQFFKK	1315.6	1316.6	1315.6	1316.6
81.0	9.1	9.1	42.9	0.0	99.0	CMPTFQFFK	1204.5	1205.5	1204.5	1205.5
81.0	9.1	9.1	42.9		99.0	CMPTFQFFK	1189.5	1190.5	1189.5	1190.6
81.0 P11021	9.1 GRP78_HUMAN	9.1	42.9 78 kDa glucos	0.0 se-regulated	99.0 d protein pre	MIKPFFHSLSEK ecursor (GRP 78) (Heat shock 70 kDa protein	1462.8	1463.8	1462.8 in-binding proteir	1463.8
104.0	10.4	13.3	22.3	2.0	99.0	IEIESFYEGEDFSETLTR	2164.0	2165.0	2164.0	2165.0
104.0		13.3	22.3	2.0	99.0	KSDIDEIVLVGGSTR	1587.8	1588.9	1587.8	1588.9
104.0	10.4	13.3	22.3	2.0	99.0	TFAPEEISAMVLTK	1535.8	1536.8	1535.8	1536.8
104.0	10.4	13.3	22.3	2.0	99.0	TWNDPSVQQDIK	1429.7	1430.7	1429.7	1430.7
104.0		13.3	22.3	1.0	99.0	IINEPTAAAIAYGLDKR	1815.0	1816.0	1815.0	1816.0
104.0		13.3	22.3	0.8	85.0	SDIDEIVLVGGSTR	1459.8	1460.8	1459.8	1460.8
104.0		13.3	22.3	0.5	67.0	AKFEELNMDLFR	1511.7	1512.7	1511.7	1512.8
104.0 104.0	10.4	13.3 13.3	22.3 22.3	0.0	88.0 82.0	TWNDPSVQQDIK TWNDPSVQQDIK	1427.7 1429.7	1428.7 1430.7	1429.7 1429.7	1430.7 1430.7
104.0 105.0	10.4	13.3	22.3 22.3 20.6	0.0	99.0 99.0	VEHANDGNR AKFEELNMDLFR	1227.6 1511.7	1228.6 1512.7	1227.6 1511.7	1228.6 1512.8
105.0	3.4	3.5	20.6	1.3	95.0	TWNDPSVQQDIK	1429.7	1430.7	1429.7	1430.7
83.0	9.0	10.6	15.3	2.0	99.0	AKFEELNMDLFR	1511.7	1512.8	1511.7	1512.8
83.0	9.0	10.6	15.3		99.0	IEIESFYEGEDFSETLTR	2164.0	2165.0	2164.0	2165.0
83.0	9.0	10.6	15.3	2.0	99.0	ITPSYVAFTPEGER	1565.8	1566.8	1565.8	1566.8
83.0	9.0	10.6	15.3	2.0	99.0	TWNDPSVQQDIK	1429.7	1430.7	1429.7	1430.7

83.0 83.0 83.0 P11142	9.0 9.0 9.0 HSP7C_HUMAN	10.6 10.6 10.6	15.3 15.3 15.3 Heat shock o	1.0 0.0 0.0	92.0 36.0 96.0 <mark>kDa protein</mark>	FEELNMDLFR FEELNMDLFR VEIIANDQGNR (Heat shock 70 kDa protein 8) - Homo sapiens	1312.6 1252.6 1227.6	1313.6 1253.6 1228.6	1312.6 1252.6 1227.6	1313.6 1253.6 1228.6
9.0	43.1	43.1	46.0	2.0 2.0	99.0 99.0	ARFEELNADLFR ATVEDEKLOGKINDEDKOK	1479.7 2229.1	1480.8	1479.7	1480.8 2230.2
9.0 9.0	43.1 43.1	43.1 43.1	46.0 46.0	2.0	99.0	FEELNADLFR	1252.6	2230.2 1253.6	2229.1 1252.6	1253.6
9.0	43.1	43.1	46.0	2.0	99.0	HWPFMVVNDAGRPK	1652.8	1653.8	1652.8	1653.8
9.0	43.1	43.1	46.0	2.0	99.0	LDKSQIHDIVLVGGSTR	1837.0	1838.0	1837.0	1838.0
9.0	43.1	43.1	46.0	2.0	99.0	LLQDFFNGKELNK	1565.8	1566.8	1565.8	1566.8
9.0	43.1	43.1	46.0	2.0	99.0	MVNHFIAEFK	1234.6	1235.6	1234.6	1235.6
9.0	43.1	43.1	46.0	2.0	99.0	MVNHFIAEFKR	1390.7	1391.7	1390.7	1391.7
9.0	43.1	43.1	46.0	2.0	99.0	MVQEAEKYKAEDEKQR	1980.0	1981.0	1981.0	1982.0
9.0	43.1	43.1	46.0	2.0	99.0	MVQEAEKYKAEDEKQRDKVSSK	2625.3	2626.3	2625.3	2626.3
9.0	43.1	43.1	46.0	2.0	99.0	NQVAMNPTNTVFDAK	1648.8	1649.8	1648.8	1649.8
9.0 9.0	43.1	43.1	46.0	2.0	99.0 99.0	NQVAMNPTNTVFDAKR	1805.0	1806.0	1804.9	1805.9
9.0	43.1 43.1	43.1 43.1	46.0 46.0	2.0 2.0	99.0	NSLESYAFNMK SFYPEEVSSMVLTK	1302.6 1615.8	1303.6 1616.8	1302.6 1615.8	1303.6 1616.8
9.0	43.1	43.1	46.0	2.0	99.0	SQIHDIVLVGGSTR	1480.8	1481.8	1480.8	1481.8
9.0	43.1	43.1	46.0	2.0	99.0	STAGDTHLGGEDFDNR	1690.7	1691.7	1690.7	1691.7
9.0	43.1	43.1	46.0	2.0	99.0	TTPSYVAFTDTER TVTNAVVTVPAYFNDSQR	1486.7	1487.7	1486.7	1487.7
9.0	43.1	43.1	46.0	2.0	99.0		1981.0	1982.0	1981.0	1982.0
9.0	43.1	43.1	46.0	2.0	99.0	VEIIANDQGNR	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	RFDDAVVQSDMK	1409.7	1410.7	1409.7	1410.7
9.0	43.1	43.1	46.0	1.3	95.0	MVQEAEKYKAEDEKQRDK	2224.1	2225.1	2224.1	2225.1
9.0	43.1	43.1	46.0	0.0	79.0	MVQEAEKYKAEDEKQR	1981.0	1982.0	1981.0	1982.0
9.0	43.1	43.1	46.0		99.0	STAGDTHLGGEDFDNR	1693.8	1694.8	1690.7	1691.7
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	MVNHFIAEFK	1234.6	1235.6	1234.6	1235.6
15.0	16.6	16.6	32.5	2.0	99.0	MVNHFIAEFKR	1390.7	1391.7	1390.7	1391.7
15.0	16.6	16.6	32.5	2.0	99.0	SFYPEEVSSMVLTK	1615.7	1616.7	1615.8	1616.8
15.0	16.6	16.6	32.5	2.0	99.0	STAGDTHLGGEDFDNR	1690.7	1691.7	1690.7	1691.7
15.0	16.6	16.6	32.5	2.0	99.0	TTPSYVAFTDTER TVTNAVVTVPAYFNDSQR	1486.7	1487.7	1486.7	1487.7
15.0	16.6	16.6	32.5	1.4	96.0		1981.0	1982.0	1981.0	1982.0
15.0	16.6	16.6	32.5	1.2	93.0	NQVAMNPTNTVFDAKR	1804.9	1805.9	1804.9	1805.9
15.0	16.6	16.6	32.5	1.0	91.0	MVQEAEKYKAEDEKQR	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		34.0	DAGTIAGLNVLR	1198.7	1199.7	1198.7	1199.7
26.0	21.5	21.5	28.8	2.0	99.0	DAGTIAGLNVLR	1198.7	1199.7	1198.7	1199.7
26.0	21.5	21.5	28.8	2.0	99.0	LDKSQIHDIVLVGGSTR	1837.0	1838.0	1837.0	1838.0
26.0	21.5 21.5 21.5	21.5 21.5	28.8 28.8	2.0	99.0 99.0	MVNHFIAEFK	1234.6 1804.8	1235.6	1234.6 1804.9	1235.6 1805.9
26.0 26.0	21.5	21.5	28.8	2.0	99.0	NQVAMNPTNTVFDAKR QATKDAGTIAGLNVLR	1609.9	1805.8 1610.9	1609.9	1610.9
26.0	21.5	21.5	28.8	2.0	99.0	SFYPEEVSSMVLTK	1615.8	1616.8	1615.8	1616.8
26.0	21.5	21.5	28.8	2.0	99.0	STAGDTHLGGEDFDNR	1690.7	1691.7	1690.7	1691.7
26.0	21.5	21.5	28.8	2.0	99.0	TTPSYVAFTDTER	1486.7	1487.7	1486.7	1487.7
26.0	21.5	21.5	28.8	2.0	99.0	TVTNAVVTVPAYFNDSQR	1981.0	1982.0	1981.0	1982.0
26.0	21.5	21.5	28.8	1.4	96.0	VEIIANDOGNR	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	MVNHFIAEFKR	1390.7	1391.7	1390.7	1391.7
26.0	21.5	21.5	28.8		99.0	STAGDTHLGGEDFDNR	1694.8	1695.8	1690.7	1691.7
26.0 26.0	21.5 21.5 21.5	21.5 21.5	28.8 28.8	0.0	99.0 99.0	STAGDTHLGGEDFDNR STAGDTHLGGEDFDNR	1693.8 1688.7	1694.8 1689.7	1690.7 1690.7	1691.7 1691.7
P11413	G6PD_HUMAN		Glucose-6-pl	hosphate 1	-dehydroger	ase (EC 1.1.1.49) (G6PD) - Homo sapiens (Hun	nan)			
100.0	11.1	11.1	20.8	2.0	99.0	DGLLPENTFIVGYAR	1663.9	1664.9	1663.9	1664.9
100.0		11.1	20.8	2.0	99.0	LKLEDFFAR	1137.6	1138.6	1137.6	1138.6
100.0	11.1	11.1	20.8	2.0	99.0	LNSHMNALHLGSQANR	1761.9	1762.9	1761.9	1762.9
100.0		11.1	20.8	2.0	99.0	NIHESCMSQIGWNR	1730.8	1731.8	1730.8	1731.8
100.0		11.1	20.8	2.0	99.0	NSYVAGQYDDAASYQR	1806.8	1807.8	1806.8	1807.8
100.0		11.1	20.8	0.6	74.0	WDGVPFILR	1101.6	1102.6	1101.6	1102.6
100.0		11.1	20.8	0.5	69.0	LQFHDVAGDIFHQQCKR	2098.0	2099.0	2098.0	2099.0
205.0		1.5	6.8	1.0	89.0	LKLEDFFAR	1137.6	1138.6	1137.6	1138.6
205.0		1.5	6.8	0.5	70.0	LOFHDVAGDIFHQQCKR	2098.0	2099.0	2098.0	2099.0
101.0		7.7	22.9	2.0	99.0	LKLEDFFAR	1137.6	1138.6	1137.6	1138.6
101.0 101.0	7.7 7.7	7.7 7.7	22.9	2.0	99.0 99.0	LQFHDVAGDIFHQQCK NSYVAGQYDDAASYQR	1941.9 1806.8	1942.9 1807.8	1941.9 1806.8	1942.9 1807.8
101.0	7.7	7.7	22.9	1.7	98.0	DGLLPENTFIVGYAR	1663.9	1664.9	1663.9	1664.9
101.0	7.7	1.5	22.9	0.0	99.0	NSYVAGQYDDAASYQR	1807.8	1808.8	1807.8	1808.8
P11717	MPRI_HUMAN		Cation-indep	pendent ma	nnose-6-pho	osphate receptor precursor (CI Man-6-P receptor	or) (CI-MPR) ((M6PR) (Insulin-li	ke growth factor	2 receptor) (In:
201.0	1.5		6.2	1.5	97.0	GHQAFDVGQPR	1210.6	1211.6	1210.6	1211.6
322.0 P11940	2.0	2.0	2.5	2.0	99.0	GHQAFDVGQPR Oly(A)-binding protein 1) (PABP 1) - Homo sapi	1210.6	1211.6	1210.6	1211.6
194.0	6.0	6.0	21.2	2.0	99.0	GFGFVSFER	1044.5	1045.5	1044.5	1045.5
194.0	6.0	6.0	21.2	2.0	99.0	QAHLTNQYMQR	1371.6	1372.6	1371.6	1372.6
194.0		6.0	21.2	2.0	99.0	SLGYAYVNFQQPADAER	1927.9	1928.9	1927.9	1928.9
194.0	2.6	6.0	21.2	0.0	99.0	QAHLTNQYMQR	1388.7	1389.7	1388.7	1389.7
117.0		2.6	18.4	1.4	96.0	SLGYAYVNFQQPADAER	1927.9	1928.9	1927.9	1928.9
117.0	2.6	2.6	18.4	1.2	94.0	GFGFVSFER	1044.5	1045.5	1044.5	1045.5
199.0	3.7	3.7	11.9	2.0	99.0	GFGFVSFER	1044.5	1045.5	1044.5	1045.5
199.0 P12955	3.7 PEPD_HUMAN	3.7	11.9 Xaa-Pro dipe	1.7 eptidase (E	98.0 C 3.4.13.9) (GYGFVHFETQEAAER X-Pro dipeptidase) (Proline dipeptidase) (Proli	1739.8 dase) (I midoo	1740.8 dipeptidase) - Hor	1739.8 no sapiens (Hum	1740.8 an)
572.0	2.0	1.5	3.4	1.5	97.0	AFTPFSGPK	950.5	951.5	950.5	951.5
367.0		2.0	2.0	2.0	99.0	VPLALFALNR	1112.7	1113.7	1112.7	1113.7
49.0	KU70_HUMAN 18.0	18.0	ATP-depende 20.2	2.0	99.0	unit 1 (ATP-dependent DNA helicase II 70 kDa : DTGIFLDLMHLK	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	ILELDQFKGQQGQKR	1787.0	1788.0	1787.0	1788.0
49.0	18.0	18.0	20.2	2.0	99.0	IMATPEQVGK	1072.6	1073.6	1072.6	1073.6
49.0	18.0	18.0	20.2	2.0	99.0	IMLFTNEDNPHGNDSAK	1901.9	1902.9	1901.9	1902.9
49.0 49.0	18.0 18.0	18.0 18.0	20.2	2.0	99.0 99.0	NIYVLOELDNPGAKR SDSFENPVLOOHFR	1728.9 1702.8	1729.9 1703.8	1728.9 1702.8	1729.9 1703.8
49.0 49.0	18.0 18.0	18.0 18.0	20.2 20.2 20.2	2.0 2.0	99.0 99.0	SGWESYYK VHFEESSKLEDLLR	1060.5 1700.9	1061.5 1701.9	1060.5 1700.9	1061.5 1701.9
49.0	18.0	18.0	20.2	0.0	99.0	SDSFENPVLQQHFR	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
545.0		2.0	4.2	2.0	99.0	mal thiol reductase precursor (Gamma-interfer GMQLMHANAQR	1255.6	1256.6	1255.6	1256.6
545.0	2.0	2.0	4.2	0.0	99.0	GMQLMHANAQR	1256.6	1257.6	1255.6	1256.6
545.0		2.0	4.2	0.0	99.0	GMQLMHANAQR	1256.6	1257.6	1256.6	1257.6
183.0	2.0	2.0	8.8	2.0	99.0	GMQLMHANAQR	1255.6	1256.6	1255.6	1256.6
366.0	2.0	2.0	4.2	2.0	99.0	GMQLMHANAQR	1255.6	1256.6	1255.6	1256.6
366.0	2.0	2.0	4.2	0.0	99.0	GMQLMHANAQR	1271.6	1272.6	1271.6	1272.6
366.0	2.0	2.0	4.2		99.0	GMQLMHANAQR	1256.6	1257.6	1256.6	1257.6
366.0 P134891	2.0 RINI_HUMAN	2.0	4.2 Ribonuclease	0.0 e inhibitor	99.0 (Ribonuclea:	GMQLMHANAQR se/angiogenin inhibitor 1) (RAI) (Placental ribo	1256.6 pnuclease inhi	1257.6 bitor) (RNase inh	1256.6 ibitor) (RL) - Hor	1257.6
232.0	5.3	5.3	15.0	2.0	99.0	SLDIOSLDIOCEELSDAR	2133.0	2134.0	2133.0	2134.0
232.0		5.3	15.0	2.0	99.0	TLWIWECGITAK	1476.8	1477.8	1476.7	1477.8
232.0 232.0 300.0		5.3 2.0	15.0 6.9	1.3 2.0	95.0 99.0	LDDCGLTEAR SCSFTAACCSHFSSVLAQNR	1148.5 2289.0	1149.5 2290.0	1148.5 2289.0	1149.5 2290.0
	EF2_HUMAN 22.8	22.8	Elongation fa				2142.1	2143.1	2142.1	2143.1
35.0	22.8	22.8	20.3	2.0	99.0	AYLPVNESFGFTADLR	1798.9	1799.9	1798.9	1799.9
35.0 35.0	22.8 22.8	22.8 22.8	20.3	2.0	99.0 99.0	CELLYEGPPDDEAAMGIK FAAKGEGOLGPAER	1989.9 1429.7	1990.9 1430.8	1989.9 1429.7	1990.9 1430.7
35.0	22.8	22.8	20.3	2.0	99.0	GHVFEESQVAGTPMFVVK	1961.0	1962.0	1961.0	1962.0
35.0	22.8	22.8	20.3	2.0	99.0	IMGPNYTPGKKEDLYLKPIQR	2460.3	2461.3	2460.3	2461.3
35.0	22.8	22.8	20.3	2.0	99.0	TFCQLILDPIFK	1493.8	1494.8	1493.8	1494.8
35.0	22.8	22.8	20.3	2.0	99.0	VNFTVDQIR	1090.6	1091.6	1090.6	1091.6
35.0	22.8	22.8	20.3	2.0	99.0	YEWDVAEAR	1137.5	1138.5	1137.5	1138.5
35.0	22.8	22.8	20.3	2.0	99.0	YLAEKYEWDVAEAR	1741.8	1742.8	1741.8	1742.8
35.0	22.8	22.8	20.3	1.7	98.0	TILMMGR	820.4	821.4	820.4	821.4
35.0	22.8	22.8	20.3	0.8	83.0	FYAFGR	759.4	760.4	759.4	760.4
35.0	22.8	22.8	20.3	0.3	50.0	GGGOIIPTARR	1124.6	1125.7	1124.6	1125.6
33.0	9.8	9.8	18.4	2.0	99.0	AYLPVNESFGFTADLR	1798.9	1799.9	1798.9	1799.9
33.0	2.5	2.0	10.4	2.0	77.0					

33.0	9.8	9.8	18.4	2.0	99.0	CLYASVLTAQPR	1377.7	1378.7	1377.7	1378.7
33.0	9.8	9.8	18.4	2.0	99.0	GHVFEESQVAGTPMFVVK	1961.0	1962.0	1961.0	1962.0
33.0	9.8	9.8	18.4		99.0	YLAEKYEWDVAEAR	1741.8	1742.8	1741.8	1742.8
33.0	9.8	9.8	18.4	1.3	95.0	YEWDVAEAR	1137.5	1138.5	1137.5	1138.5
33.0	9.8	9.8	18.4		42.0	FSVSPVVR	889.5	890.5	889.5	890.5
33.0	9.8	9.8	18.4	0.2	37.0	CELLYEGPPDDEAAMGIK	1989.9	1990.9	1989.9	1990.9
51.0	15.4	15.4	27.2	2.0	99.0	CLYASVLTAQPR	1360.7	1361.7	1360.7	1361.7
51.0	15.4	15.4	27.2	2.0	99.0	GHVFEESQVAGTPMFVVK	1961.0	1962.0	1961.0	1962.0
51.0	15.4	15.4	27.2	2.0	99.0	IMGPNYTPGKKEDLYLKPIQR	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	YEWDVAEAR	1137.5	1138.5	1137.5	1138.5
51.0	15.4	15.4	27.2	2.0	99.0	YLAEKYEWDVAEAR	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	1763.9	1764.9
51.0	15.4	15.4	27.2		30.0	FAAKGEGQLGPAER	1429.7	1430.7	1429.7	1430.7
51.0	15.4	15.4	27.2	0.1	22.0	GGGQIIPTARR	1124.6	1125.7	1124.6	1125.6
P13640 460.0	2.0	4.0	Metallothion 53.2	2.0	99.0	othionein-IG) (MT-IG) (Metallothionein- MDPNCSCAAAGVSCTCASSCK	2334.8	2335.8	2334.8	2335.9
460.0 460.0	2.0	4.0 4.0	53.2 53.2	0.0	99.0 99.0	SCCSCCPVGCAK SCCSCCPVGCAK	1444.5 1447.5	1445.5 1448.5	1444.5 1444.5	1445.5 1445.5
460.0		4.0	53.2	0.0	99.0	SCCSCCPVGCAK	1447.5	1448.5	1444.5	1445.5
182.0		2.0	53.2	2.0	99.0	SCCSCCPVGCAK	1444.5	1445.5	1444.5	1445.5
305.0		6.0	54.8	2.0	99.0	MDPNCSCAAAGVSCTCASSCK	2334.8	2335.9	2334.8	2335.9
305.0		6.0	54.8	0.0	99.0	KSCCSCCPVGCAK	1573.6	1574.6	1572.6	1573.6
305.0 305.0	2.0	6.0 6.0	54.8 54.8	0.0	99.0 99.0	MDPNCSCAAAGVSCTCASSCK SCCSCCPVGCAK	2338.8 1444.5	2339.9 1445.5	2338.8 1444.5	2339.8 1445.5
305.0 305.0	2.0	6.0 6.0	54.8 54.8	0.0	99.0	SCCSCCPVGCAK SCCSCCPVGCAK	1446.5 1446.5	1447.5 1447.5	1444.5 1444.5	1445.5 1445.5
	PPA5_HUMAN	4.9	Tartrate-res	istant acid	phosphatase 99.0					
247.0 247.0	4.9	4.9 4.9	12.3 12.3	2.0	99.0 86.0	FVAVGDWGGVPNAPFHTAR WNFPSPFYR	1997.0 1212.6	1998.0 1213.6	1997.0 1212.6	1998.0 1213.6
144.0	2.1	2.1	15.7	2.0	99.0	FVAVGDWGGVPNAPFHTAR	1997.0	1998.0	1997.0	1998.0
	PLSL_HUMAN	2.0	6.5 Plastin-2 (L-		99.0 ymphocyte c	FQETFEDVFSDR ytosolic protein 1) (LCP-1) (LC64P) - Hor		1519.7	1518.7	1519.7
25.0	26.0	26.0	32.2	2.0	99.0	AECMLQQAER	1234.5	1235.6	1234.5	1235.6
25.0	26.0	26.0	32.2	2.0	99.0	FSLVGIGGQDLNEGNR	1674.8	1675.8	1674.8	1675.8
25.0	26.0	26.0	32.2	2.0	99.0	GDEEGVPAVVIDMSGLR	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	KLENCNYAVELGKNQAK	1978.0	1979.0	1978.0	1979.0
25.0	26.0	26.0	32.2	2.0	99.0	LENCNYAVELGKNQAK	1849.9	1850.9	1849.9	1850.9
25.0	26.0	26.0	32.2	2.0	99.0	MINLSVPDTIDER	1501.7	1502.8	1501.7	1502.8
25.0	26.0	26.0	32.2		99.0	QFVTATDVVR	1134.6	1135.6	1134.6	1135.6
25.0	26.0	26.0	32.2	2.0	99.0	VNDDIIVNWVNETLR	1798.9	1799.9	1798.9	1799.9
25.0	26.0	26.0	32.2	2.0	99.0	VYALPEDLVEVNPK	1584.8	1585.8	1584.8	1585.8
25.0	26.0	26.0	32.2		99.0	YAFVNWINK	1153.6	1154.6	1153.6	1154.6
25.0	26.0	26.0	32.2	2.0	99.0	YTLNILEEIGGGQK	1533.8	1534.8	1533.8	1534.8
25.0	26.0	26.0	32.2	1.4	96.0	VNKPPYPK	941.5	942.5	941.5	942.5
25.0	26.0	26.0	32.2	0.6	75.0	TFRNWMNSLGVNPR	1690.8	1691.8	1690.8	1691.8
25.0	26.0	26.0	32.2	0.0	99.0	KLENCNYAVELGKNQAK	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	1153.6	1154.6
18.0	14.2	14.2	31.4	2.0	99.0	FSLVGIGGQDLNEGNR	1674.8	1675.8	1674.8	1675.8
18.0	14.2	14.2	31.4	2.0	99.0	GDEEGVPAVVIDMSGLR	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 99.0	KLENCNYAVELGKNQAK	1978.0	1979.0	1977.9	1979.0
18.0 18.0	14.2 14.2	14.2 14.2	31.4 31.4	2.0	99.0	NWMNSLGVNPR VYALPEDLVEVNPK	1286.6 1584.8	1287.6 1585.8	1286.6 1584.8	1287.6 1585.8
18.0	14.2	14.2	31.4	1.0	91.0	QFVTATDVVR	1134.6	1135.6	1134.6	1135.6
18.0	14.2	14.2	31.4	0.6	72.0	VNDDIIVNWVNETLR	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	MINLSVPDTIDER	1501.7	1502.8	1501.7	1502.8
18.0	14.2	14.2	31.4	0.1	23.0	QFVTATDVVRGNPK	1530.8	1531.8	1530.8	1531.8
18.0	14.2	14.2	31.4	0.1	21.2	DLLKTENLNDDEK	1562.7	1563.8	1562.7	1563.7
18.0	14.2	14.2	31.4	0.0	83.0	KLENCNYAVELGKNQAK	1978.0	1979.0	1978.0	1979.0
18.0	14.2	14.2	31.4		83.0	QFVTATDVVR	1130.6	1131.6	1134.6	1135.6
24.0	22.6	22.6	37.5	2.0	99.0	AECMLQQAER	1234.5	1235.6	1234.5	1235.6
24.0	22.6	22.6	37.5	2.0	99.0	FSLVGIGGQDLNEGNR	1674.8	1675.8	1674.8	1675.8
24.0	22.6	22.6	37.5	2.0	99.0	GDEEGVPAVVIDMSGLR	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	KLENCNYAVELGKNQAK	1978.0	1979.0	1978.0	1979.0
24.0	22.6	22.6	37.5	2.0	99.0	QFVTATDVVR	1134.6	1135.6	1134.6	1135.6
24.0	22.6	22.6	37.5	2.0	99.0	TFRNWMNSLGVNPR	1690.8	1691.8	1690.8	1691.8
24.0	22.6	22.6	37.5	2.0	99.0	VNDDIIVNWVNETLR	1798.9	1799.9	1798.9	1799.9
24.0	22.6	22.6	37.5	2.0	99.0	VYALPEDLVEVNPK	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	EGICAIGGTSEQSSVGTQHSYSEEEK	2769.2	2770.2	2769.2	2770.2
24.0	22.6	22.6	37.5	0.8	84.0	YTLNILEEIGGGQK	1533.8	1534.8	1533.8	1534.8
24.0	22.6	22.6	37.5	0.1	23.0	RYTLNILEEIGGGQK	1689.9	1690.9	1689.9	1690.9
24.0	22.6 MIF_HUMAN	22.6	37.5	0.0	99.0	QFVTATDVVR ctor (MIF) (Phenylpyruvate tautomerase	1117.6	1118.6	1117.6	1118.6
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	22.6	2.0	99.0	PMFIVNTNVPR	1286.7	1287.7	1286.7	1287.7
193.0 193.0	6.0	6.0	22.6 22.6	2.0	99.0 99.0	SYSKLLCGLLAER PMFIVNTNVPR	1508.8 1298.7	1509.8 1299.7	1508.8 1298.7	1509.8 1299.7
193.0 193.0 193.0	6.0	6.0 6.0	22.6 22.6 22.6	0.0 0.0 0.0	92.0 90.0	PMFIVNTNVPR PMFIVNTNVPR	1296.7 1289.7 1314.7	1290.7 1290.7 1315.7	1296.7 1286.7 1314.7	1297.7 1287.7 1315.7
94.0	4.0	4.0	17.4	2.0	99.0	LLCGLLAER PMFIVNTNVPR	1043.6	1044.6	1043.6	1044.6
94.0 94.0	4.0	4.0	17.4 17.4	2.0 0.0	99.0 99.0	PMFIVNTNVPR	1286.7 1298.7	1287.7 1299.7	1286.7 1298.7	1287.7 1299.7
94.0	4.0	4.0	17.4	0.0	98.0	PMFIVNTNVPR	1287.7	1288.7	1287.7	1288.7
94.0		4.0	17.4	0.0	75.0	PMFIVNTNVPR	1289.7	1290.7	1286.7	1287.7
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	17.4	2.0	99.0	PMFIVNTNVPR	1286.7	1287.7	1286.7	1287.7
194.0 P143171	4.0 HCLS1_HUMAN	4.0	17.4 Hematopoie	0.0 tic lineage o	99.0 cell-specific	PMFIVNTNVPR protein (Hematopoietic cell-specific LYN	1298.7 substrate 1) (LckBP1)	1299.7 (p75) - Homo	1298.7 sapiens (Human)	1299.7
130.0		8.7	13.8	2.0	99.0	EHPVPLLPIR	1169.7	1170.7	1169.7	1170.7
130.0		8.7	13.8	2.0	99.0	GFGGQYGIQK	1053.5	1054.5	1053.5	1054.5
130.0 130.0	8.7	8.7 8.7	13.8 13.8	2.0	99.0 99.0	RSPEAPQPVIAMEEPAVPAPLPK TEHINIHQLR	2423.3 1259.7	2424.3 1260.7	2423.3 1259.7	2424.3 1260.7
130.0	8.7	8.7	13.8	0.5	71.0	TIEGSGRTEHINIHQLR	1960.0	1961.0	1960.0	1961.0
130.0		8.7	13.8	0.2	36.0	GFGGQYGIQKDR	1324.7	1325.7	1324.7	1325.7
130.0	8.7	8.7	13.8	0.0	99.0	TEHINIHQLR	1259.7	1260.7	1259.7	1260.7
137.0	4.6	2.1	30.0	2.0	99.0	GFGGQYGIQK	1053.5	1054.5	1053.5	1054.5
153.0		4.6	17.9	2.0	99.0	EHPVPLLPIR	1169.7	1170.7	1169.7	1170.7
153.0	4.6	4.6	17.9	2.0	99.0	TEHINIHQLR	1259.7	1260.7	1259.7	1260.7
153.0		4.6	17.9	0.5	68.0	ASHGYGGRFGVER	1391.7	1392.7	1391.7	1392.7
153.0		4.6	17.9	0.1	29.0	GFGGQYGIQKDRVDK C 2.7.1.40) (Pyruvate kinase muscle iso	1666.8	1667.9	1666.8	1667.8
14.0	38.4	38.4	54.6	2.0	99.0	APIIAVTRNPQTAR	1506.9	1507.9	1506.9	1507.9
14.0		38.4	54.6	2.0	99.0	CDENILWLDYK	1450.6	1451.6	1450.6	1451.7
14.0 14.0	38.4	38.4 38.4	54.6 54.6	2.0	99.0 99.0	CDENILWLDYKNICK EAEAAIYHLQLFEELR	1983.0 1931.0	1984.0 1932.0	1982.9 1931.0	1983.9 1932.0
14.0 14.0 14.0	38.4	38.4 38.4	54.6 54.6	2.0	99.0 99.0	FDEILEASDGIMVAR FGVEQDVDMVFASFIR	1664.8 1858.9	1665.8 1859.9	1664.8 1858.9	1665.8 1859.9
14.0	38.4	38.4	54.6	2.0	99.0	GDLGIEIPAEKVFLAQK	1827.0	1828.0	1827.0	1828.0
14.0 14.0	38.4	38.4 38.4	54.6 54.6	2.0	99.0 99.0	GIFPVLCKDPVQEAWAEDVDLR IISKIENHEGVR	2556.2 1393.8	2557.2 1394.8	2556.3 1393.8	2557.3 1394.8
14.0	38.4	38.4	54.6	2.0	99.0	ITLDNAYMEK	1196.6	1197.6	1196.6	1197.6
14.0		38.4	54.6	2.0	99.0	IYVDDGLISLQVK	1461.8	1462.8	1461.8	1462.8
14.0		38.4	54.6	2.0	99.0	KGVNLPGAAVDLPAVSEKDIQDLK	2476.3	2477.3	2476.4	2477.4
14.0		38.4	54.6	2.0	99.0	LAPITSDPTEATAVGAVEASFK	2175.1	2176.1	2174.1	2175.1
14.0	38.4	38.4	54.6	2.0	99.0	LNFSHGTHEYHAETIK	1882.9	1883.9	1882.9	1883.9
14.0	38.4	38.4	54.6	2.0	99.0	LNFSHGTHEYHAETIKNVR	2252.1	2253.1	2252.1	2253.1
14.0 14.0	38.4	38.4 38.4	54.6 54.6	2.0	99.0 99.0	NTGIICTIGPASR RFDEILEASDGIMVAR	1358.7 1820.9	1359.7 1821.9	1358.7 1820.9	1359.7 1821.9
14.0	55.4	50.7	51.5	2.5	77.0		.020.7		.020.7	. 32

14.0 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	38.4 38.4	54.6 54.6	1.0 0.7	91.0 81.0	SGRSAHQVAR YRPRAPIIAVTR	1070.6 1411.8	1071.6 1412.8	1070.6 1411.8	1071.6 1412.8
14.0 14.0	38.4 38.4	38.4 38.4	54.6 54.6	0.6	72.0 55.0	EAEAAIYHLQLFEELRR TATESFASDPILYRPVAVALDTKGPEIR	2087.1	2088.1 3017.6	2087.1	2088.1 3017.6
14.0	38.4	38.4	54.6	0.0	99.0	CDENILWLDYK	3016.6 1467.7	1468.7	3016.6 1467.7	1468.7
14.0 14.0	38.4 38.4	38.4 38.4	54.6 54.6	0.0	99.0 99.0	CDENILWLDYKNICK LAPITSDPTEATAVGAVEASFK	1965.9 2174.1	1966.9 2175.1	1965.9 2174.1	1966.9 2175.1
14.0	38.4	38.4	54.6	0.0	58.0	LAPITSDPTEATAVGAVEASFK	2174.1	2171.2	2170.1	2171.1
49.0 49.0	6.4 6.4	6.4 6.4	37.1 37.1	2.0 1.5	99.0 97.0	LNFSHGTHEYHAETIK CDENILWLDYK	1882.8 1467.7	1883.8 1468.7	1882.9 1467.7	1883.9 1468.7
49.0	6.4	6.4	37.1	1.4	96.0	GDLGIEIPAEKVFLAQK	1827.0	1828.0	1827.0	1828.0
49.0 49.0	6.4 6.4	6.4 6.4	37.1 37.1	1.2 0.2	94.0 32.0	LAPITSDPTEATAVGAVEASFK IISKIENHEGVR	2174.1 1393.8	2175.1 1394.8	2174.1 1393.8	2175.1 1394.8
16.0	27.4	27.4	51.2	2.0	99.0	APIIAVTRNPQTAR	1506.9	1507.9	1506.9	1507.9
16.0 16.0	27.4 27.4	27.4 27.4	51.2 51.2	2.0 2.0	99.0 99.0	CDENILWLDYK CDENILWLDYKNICK	1450.6 1965.9	1451.6 1966.9	1450.6 1965.9	1451.7 1966.9
16.0	27.4	27.4	51.2	2.0	99.0	EAEAAIYHLQLFEELR	1931.0	1932.0	1931.0	1932.0
16.0 16.0	27.4 27.4	27.4 27.4	51.2 51.2	2.0 2.0	99.0 99.0	FGVEQDVDMVFASFIR IISKIENHEGVR	1858.9 1393.8	1859.9 1394.8	1858.9 1393.8	1859.9 1394.8
16.0	27.4	27.4	51.2	2.0	99.0	LAPITSDPTEATAVGAVEASFK	2174.1	2175.1	2174.1	2175.1
16.0 16.0	27.4 27.4	27.4 27.4	51.2 51.2	2.0 2.0	99.0 99.0	LDIDSPPITAR LNFSHGTHEYHAETIK	1196.6 1882.9	1197.6 1883.9	1196.6 1882.9	1197.6 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 16.0	27.4 27.4	27.4 27.4	51.2 51.2	2.0 2.0	99.0 99.0	NTGIICTIGPASR RFDEILEASDGIMVAR	1358.7 1820.9	1359.7 1821.9	1358.7 1820.9	1359.7 1821.9
16.0	27.4	27.4	51.2	1.1	92.0	GDLGIEIPAEKVFLAQK	1827.0	1828.0	1827.0	1828.0
16.0 16.0	27.4 27.4	27.4 27.4	51.2 51.2	1.0 0.7	91.0 81.0	MQHLIAR FDEILEASDGIMVAR	867.5 1664.8	868.5 1665.8	867.5 1664.8	868.5 1665.8
16.0	27.4	27.4	51.2	0.5	68.0	TATESFASDPILYRPVAVALDTK	2464.3	2465.3	2464.3	2465.3
16.0 16.0	27.4 27.4	27.4 27.4	51.2 51.2	0.0	99.0 99.0	NTGIICTIGPASR RFDEILEASDGIMVAR	1359.7 1818.9	1360.7 1819.9	1358.7 1820.9	1359.7 1821.9
P14625 E	ENPL_HUMAN		Endoplasmir	n precursor	(Heat shock	protein 90 kDa beta member 1) (94 kDa g	lucose-regulated p	rotein) (GRP94)	(gp96 homolog)	(Tumor rejection
467.0 316.0	2.0 2.0	2.0 2.0	5.5 8.8	2.0	99.0 99.0	FAFQAEVNR FAFQAEVNR	1080.5 1080.5	1081.5 1081.5	1080.5 1080.5	1081.5 1081.5
P14780 N	MMP9_HUMAN		Matrix metal	Hoproteinas	e-9 precurs	or (EC 3.4.24.35) (MMP-9) (92 kDa type IV	collagenase) (92	kDa gelatinase)	(Gelatinase B) (G	ELB) [Contains:
8.0 8.0	44.0 44.0	44.0 44.0	50.2 50.2	2.0 2.0	99.0 99.0	AFALWSAVTPLTFTR AVIDDAFAR	1679.9 976.5	1680.9 977.5	1679.9 976.5	1680.9 977.5
8.0	44.0	44.0	50.2	2.0	99.0	FGFCPSER	998.4	999.4	998.4	999.4
8.0 8.0	44.0 44.0	44.0 44.0	50.2 50.2	2.0 2.0	99.0 99.0	FGNADGAACHFPFIFEGR FTEGPPLHKDDVNGIR	2011.9 1794.9	2012.9 1795.9	2011.9 1794.9	2012.9 1795.9
8.0	44.0	44.0	50.2	2.0	99.0	GDGRLWCATTSNFDSDKK	2056.9	2057.9	2056.9	2057.9
8.0 8.0	44.0 44.0	44.0 44.0	50.2 50.2	2.0 2.0	99.0 99.0	GKMLLFSGR GSRPQGPFLIADKWPALPR	1007.6 2105.1	1008.6 2106.2	1007.6 2105.2	1008.6 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 8.0	44.0 44.0	44.0 44.0	50.2 50.2	2.0	99.0 99.0	LWCATTSNFDSDKK MFPGVPLDTHDVFQYREK	1671.8 2150.0	1672.8 2151.0	1671.8 2150.0	1672.8 2151.0
8.0	44.0	44.0	50.2	2.0	99.0	QLAEEYLYR	1166.6	1167.6	1166.6	1167.6
8.0 8.0	44.0 44.0	44.0 44.0	50.2 50.2	2.0 2.0	99.0 99.0	QLSLPETGELDSATLK QSTLVLFPGDLR	1700.9 1327.7	1701.9 1328.7	1700.9 1327.7	1701.9 1328.7
8.0	44.0	44.0	50.2	2.0	99.0	QVWVYTGASVLGPR	1531.8	1532.8	1531.8	1532.8
8.0 8.0	44.0 44.0	44.0 44.0	50.2 50.2	2.0 2.0	99.0 99.0	SDGLPWCSTTANYDTDDR SLGPALLLLQK	2072.8 1151.7	2073.8 1152.7	2072.8 1151.7	2073.8 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 8.0	44.0 44.0	44.0 44.0	50.2 50.2	1.4 1.2	96.0 94.0	QRQSTLVLFPGDLR MLLFSGR	1611.9 822.4	1612.9 823.4	1611.9 822.4	1612.9 823.4
8.0	44.0	44.0	50.2	1.2	93.0	DGNADGKPCQFPFIFQGQSYSACTTDGR	3123.3	3124.3	3123.3	3124.4
8.0 8.0	44.0 44.0	44.0 44.0	50.2 50.2	1.2 0.8	93.0 83.0	LFGFCPTR LFFFSGR	996.5 872.5	997.5 873.5	996.5 872.5	997.5 873.5
8.0	44.0	44.0	50.2	0.7	81.0	WCATTANYDRDK	1499.6	1500.7	1499.6	1500.7
8.0 8.0	44.0 44.0	44.0 44.0	50.2 50.2	0.6 0.5	76.0 69.0	RLDKLGLGADVAQVTGALR CGVPDLGR	1952.0 872.4	1953.1 873.4	1952.1 872.4	1953.1 873.4
8.0	44.0	44.0	50.2	0.1	28.8	QNYSEDLPR	1273.5	1274.5	1273.5	1274.5
8.0 8.0	44.0 44.0	44.0 44.0	50.2 50.2	0.1 0.1	27.0 27.0	AYFCQDRFYWR GVVVPTR	1610.7 726.4	1611.7 727.4	1610.7 726.4	1611.7 727.4
8.0	44.0	44.0	50.2	0.0	99.0	FGNADGAACHFPFIFEGR	2012.9	2013.9	2011.9	2012.9
8.0 8.0	44.0 44.0	44.0 44.0	50.2 50.2	0.0	99.0	QLAEEYLYR	1183.6	1184.6	1183.6	1184.6
8.0	44.0 44.0	44.0	50.2	0.0 0.0	43.0 99.0	QLAEEYLYR QLSLPETGELDSATLK	1166.6 1683.9	1167.6 1684.9	1166.6 1683.9	1167.6 1684.9
8.0	44.0 31.5	44.0 31.5	50.2	0.0	96.0 99.0	QVWVYTGASVLGPR	1514.8	1515.8 977.5	1514.8	1515.8 977.5
6.0 6.0	31.5	31.5	42.9 42.9	2.0 2.0	99.0	AVIDDAFAR FGNADGAACHFPFIFEGR	976.5 2014.9	2015.9	976.5 2011.9	2012.9
6.0	31.5 31.5	31.5 31.5	42.9 42.9	2.0	99.0 99.0	FQTFEGDLK FTEGPPLHKDDVNGIR	1083.5 1794.9	1084.5 1795.9	1083.5 1794.9	1084.5 1795.9
6.0 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	31.5 31.5	42.9 42.9	2.0	99.0 99.0	GSRPQGPFLIADKWPALPR KLEEFSGR	2105.2 1000.5	2106.2 1001.6	2105.2 1000.5	2106.2 1001.6
6.0 6.0	31.5	31.5	42.9	2.0	99.0	LFGFCPTR	996.5	997.5	996.5	997.5
6.0 6.0	31.5 31.5	31.5 31.5	42.9 42.9	2.0 2.0	99.0 99.0	LWCATTSNFDSDKK QLAEEYLYR	1671.7 1166.6	1672.7 1167.6	1671.8 1166.6	1672.8 1167.6
6.0	31.5	31.5	42.9	2.0	99.0	QSTLVLFPGDLR	1327.7	1328.7	1327.7	1328.7
6.0 6.0	31.5 31.5	31.5 31.5	42.9 42.9	2.0 2.0	99.0 99.0	QVWVYTGASVLGPR SDGLPWCSTTANYDTDDR	1531.8 2067.8	1532.8 2068.9	1531.8 2072.8	1532.8 2073.8
6.0	31.5	31.5	42.9	2.0	99.0	SLGPALLLLQK	1151.7	1152.7	1151.7	1152.7
6.0 6.0	31.5 31.5	31.5 31.5	42.9 42.9	1.2 1.1	93.0 92.0	LFFFSGR FGFCPSER	872.5 998.4	873.5 999.4	872.5 998.4	873.5 999.4
6.0	31.5	31.5	42.9	0.6	74.0	QLSLPETGELDSATLK	1700.9	1701.9	1700.9	1701.9
6.0 6.0	31.5 31.5	31.5 31.5	42.9 42.9	0.5 0.1	70.0 24.0	MLLFSGR AFALWSAVTPLTFTR	822.5 1679.9	823.5 1680.9	822.4 1679.9	823.4 1680.9
6.0	31.5	31.5	42.9	0.0	99.0	AVIDDAFAR	976.5	977.5	976.5	977.5
6.0 6.0	31.5 31.5	31.5 31.5	42.9 42.9	0.0 0.0	99.0 99.0	FGNADGAACHFPFIFEGR FTEGPPLHKDDVNGIR	2011.9 1793.9	2012.9 1794.9	2011.9 1793.9	2012.9 1794.9
6.0	31.5	31.5	42.9	0.0	89.0	FTEGPPLHKDDVNGIR	1794.9	1795.9	1794.9	1795.9
6.0 6.0	31.5 31.5	31.5 31.5	42.9 42.9	0.0 0.0	99.0 20.0	QLAEEYLYR QLAEEYLYR	1183.6 1166.6	1184.6 1167.6	1183.6 1166.6	1184.6 1167.6
6.0	31.5	31.5	42.9	0.0	97.0	QSTLVLFPGDLR	1327.7	1328.7	1327.7	1328.7
6.0 6.0	31.5 31.5	31.5 31.5	42.9 42.9	0.0 0.0	45.0 97.0	QSTLVLFPGDLR QVWVYTGASVLGPR	1341.7 1514.8	1342.7 1515.8	1341.7 1514.8	1342.7 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 6.0	46.9 46.9	46.9 46.9	48.9 48.9	2.0 2.0	99.0 99.0	AVIDDAFAR EKAYFCQDR	976.5 1215.5	977.5 1216.5	976.5 1215.5	977.5 1216.5
6.0	46.9	46.9	48.9	2.0	99.0	FGNADGAACHFPFIFEGR	2012.9	2013.9	2011.9	2012.9
6.0 6.0	46.9 46.9	46.9 46.9	48.9 48.9	2.0 2.0	99.0 99.0	FQTFEGDLK FTEGPPLHKDDVNGIR	1083.5 1794.9	1084.5 1795.9	1083.5 1794.9	1084.5 1795.9
6.0	46.9	46.9	48.9	2.0	99.0	GSRPQGPFLIADKWPALPR	2105.1	2106.2	2105.2	2106.2
6.0 6.0	46.9 46.9	46.9 46.9	48.9 48.9	2.0 2.0	99.0 99.0	KLDSVFEEPLSKK LFGFCPTR	1518.8 996.5	1519.8 997.5	1518.8 996.5	1519.8 997.5
6.0	46.9	46.9	48.9	2.0	99.0	LGLGADVAQVTGALR	1439.8	1440.8	1439.8	1440.8
6.0 6.0	46.9 46.9	46.9 46.9	48.9 48.9	2.0 2.0	99.0 99.0	LWCATTSNFDSDKK MFPGVPLDTHDVFQYR	1671.8 1920.9	1672.8 1921.9	1671.8 1920.9	1672.8 1921.9
6.0	46.9	46.9	48.9	2.0	99.0	MFPGVPLDTHDVFQYREK	2178.1	2179.1	2178.1	2179.1
6.0 6.0	46.9 46.9	46.9 46.9	48.9 48.9	2.0 2.0	99.0 99.0	MLLFSGR QLAEEYLYR	822.4 1183.6	823.5 1184.6	822.4 1183.6	823.4 1184.6
6.0	46.9	46.9	48.9	2.0	99.0	QLSLPETGELDSATLK	1700.9	1701.9	1700.9	1701.9
6.0 6.0	46.9 46.9	46.9 46.9	48.9 48.9	2.0 2.0	99.0 99.0	QSTLVLFPGDLR QVWVYTGASVLGPR	1327.7 1514.8	1328.7 1515.8	1327.7 1514.8	1328.7 1515.8
6.0	46.9	46.9	48.9	2.0	99.0	RLDKLGLGADVAQVTGALR	1952.1	1953.1	1952.1	1953.1
6.0 6.0	46.9 46.9	46.9 46.9	48.9 48.9	2.0 2.0	99.0 99.0	SDGLPWCSTTANYDTDDR SLGPALLLLQK	2072.8 1151.7	2073.8 1152.7	2072.8 1151.7	2073.8 1152.7
6.0	46.9	46.9	48.9	1.5	97.0	FGFCPSER	998.4	999.4	998.4	999.4
6.0 6.0	46.9 46.9	46.9 46.9	48.9 48.9	1.5 1.3	97.0 95.0	LFFFSGR KLDSVFEEP	872.5 1121.5	873.5 1122.5	872.5 1121.6	873.5 1122.6
6.0	46.9	46.9	48.9	1.0	91.0	KLDSVFEEPLSK	1390.7	1391.7	1390.7	1391.7
6.0 6.0	46.9 46.9	46.9 46.9	48.9 48.9	0.5 0.5	70.0 67.0	SDGYRWCATTANYDRDK IFQGQSYSACTTDGR	2077.9 1689.8	2078.9 1690.8	2077.9 1689.7	2078.9 1690.7
6.0	46.9	46.9	48.9	0.4	64.0	WCATTANYDRDKLFGFCPTR	2478.1	2479.1	2478.1	2479.1

Part	6.0	46.9	46.9	48.9	0.0	99.0	FGNADGAACHFPFIFEGR	2011.9	2012.9	2011.9	2012.9
Column							QLAEEYLYR				
Part						99.0	QSTLVLFPGDLR		1328.7	1327.7	1328.7
March	P14854	CX6B1_HUMAN		Cytochrome	c oxidase su	ıbunit VI b	soform 1 (EC 1.9.3.1) (COX VIb-1) - Hom	no sapiens (Human)			
1968 1968 1969	344.0	3.4	3.4	31.4	1.4	96.0	TAPFDSRFPNQNQTR	1777.8	1778.9	1777.8	1778.9
Mathematical Math	155.0	4.6	4.6	65.1	2.0	99.0	VYQSLCPTSWVTDWDEQR	2269.0	2270.0	2269.0	2270.0
Section Sect	155.0	4.6		65.1	0.3	44.0	TAPFDSRFPNQNQTR	1777.9	1778.9	1777.8	
March Marc	304.0	4.0		9.4	2.0	99.0	AKWFPEVR	1031.6	1032.6	1031.6	
A	356.0	2.0		5.2	2.0	99.0	YLECSALTQR				
March 190 191 19	46.0	19.0		41.1	2.0	99.0	EVWYFGLHYVDNK				
A	46.0	19.0	27.2	41.1	2.0	99.0	KENPLQFKFR	1305.7	1306.7	1305.7	1306.7
A	46.0	19.0	27.2	41.1	2.0	99.0	RKEDEVEEWQHR	1639.8	1640.8	1639.8	1640.8
140 140 170 171	46.0	19.0	27.2	41.1	2.0	99.0	THNDIIHNENMR	1492.7	1493.7	1492.7	1493.7
Section 1.0	46.0	19.0	27.2	41.1	1.4	99.0	IQVWHAEHR	1174.6	1175.6	1174.6	1175.6
A	46.0	19.0	27.2	41.1	0.1	26.0	RITEAEKNERVQR	1670.9	1671.9	1670.9	1671.9
Add	46.0	19.0	27.2	41.1	0.0	99.0	IGFPWSEIR	1103.6	1104.6	1103.6	1104.6
Aug. 19.0	46.0	19.0	27.2	41.1	0.0	99.0	KAPDFVFYAPR	1309.7	1310.7	1309.7	1310.7
1920 2.3	46.0	19.0	27.2	41.1	0.0	97.0	RKEDEVEEWQHR	1639.8	1640.8	1639.8	1640.8
1220 2.3	127.0	2.3	10.3	24.9	0.1	31.0	FGDYNKEVHK	1235.6	1236.6	1235.6	1236.6
130 2.3	127.0	2.3	10.3	24.9	0.0	99.0	APDFVFYAPR	1181.6	1182.6	1181.6	1182.6
127.0 2.3 2.3 2.4 2.5 2.	127.0	2.3	10.3	24.9	0.0	99.0	IGFPWSEIR	1101.6	1102.6	1103.6	1104.6
Fig. 111	127.0	2.3	10.3	24.9	0.0	99.0	LFFLQVK	893.5	894.5	893.5	894.5
Fig. 1.11	67.0	11.1	23.1	38.4	2.0	99.0	FGDYNKEVHKSGYLSSER	2115.0	2116.0	2115.0	2116.0
Fig. 11.1	67.0	11.1	23.1	38.4	2.0	99.0	RKEDEVEEWQHR	1639.8	1640.8	1639.8	1640.8
Fig. 0	67.0	11.1	23.1	38.4	0.9	90.0	FGDYNKEVHK	1235.6	1236.6	1235.6	1236.6
Color	67.0	11.1	23.1	38.4	0.1	20.0	IAQDLEMYGINYFEIK	1946.0	1947.0	1945.9	1947.0
Fig. 11	67.0	11.1	23.1	38.4	0.0	99.0	APDFVFYAPR	1181.6	1182.6	1181.6	1182.6
Fig. 111	67.0	11.1	23.1	38.4	0.0	99.0	IQVWHAEHR	1174.6	1175.6	1174.6	1175.6
11.1 23.1 38.4 30.0 93.0 RREPOTENCOMIK 1627.9 1628.9 1627.9 1628.9 1627.9 1628.9 1627.9 1628.9 1627.9 1628.9 1627.9 1628.0 1627	67.0	11.1	23.1	38.4	0.0	98.0	LFFLQVK	893.5	894.5	893.5	894.5
PIOSOTICO CALL HUMAN CD44 antique mercursor (*Proportoletal *) (*CSP-1) (*CH7CH) (*CH7	67.0	11.1	23.1	38.4	0.0	99.0	RRKPDTIEVQQMK	1627.9	1628.9	1627.9	1628.9
340 0 3 3 3 3 4 0 1.3 95.0 ALSIGEFICE 1192 1192 1193.6 1193.6 1193.6 1193.6 1190.0 12 3 2 3 2 0 0 0 70 FECHIVIPR 130.7 130.7 130.7 130.8 1190.0 130.7 130.8 1190.0 130.0	P16070	CD44_HUMAN		CD44 antiger	n precursor	(Phagocyti	c glycoprotein I) (PGP-1) (HUTCH-I) (Ext	tracellular matrix recep	otor-III) (ECN	IR-III) (GP90 lymp	ohocyte homing,
1900 3.2 3.2 5.9 1.2 93.0 ALSIGETICAE 1152.6 1153.	346.0	3.3	3.3	4.0	1.3	95.0	ALSIGFETCR	1152.6	1153.6	1152.6	1153.6
1560	109.0	3.2	3.2	6.9	1.2	93.0	ALSIGFETCR	1152.6	1153.6	1152.6	1153.6
	156.0	4.6	4.6	7.5	1.3	95.0	ALSIGFETCR	1152.6	1153.6	1152.6	1153.6
1920 3.7 3.7 13.4 1.7 98.0 REVIGEDAL/ENMAGRIAN/AD 2224 1 2225 1 2226 1 2226 1 1930 4.0 4.0 13.4 2.0 98.0 GOAW/COLAPGE-SPR 2.0	P16152	CBR1_HUMAN		Carbonyl red	luctase [NAI	DPH] 1 (EC	1.1.1.184) (NADPH-dependent carbonyl	reductase 1) (Prostagl	andin-E(2) 9-1	reductase) (EC 1.1	.1.189) (Prosta
1930 40	329.0	3.7	3.7	13.4	1.7	98.0	KEYGGLDVLVNNAGIAFKVAD	2224.1	2225.1	2224.1	2225.1
	193.0	4.0	4.0	13.4	2.0	99.0	KEYGGLDVLVNNAGIAFKVAD	2210.1	2211.1	2210.1	2211.1
235.0 5.2 6.0 23.5 2.0 99.0 SETAPAETATRAVEKSPAKK 156.8 156.4 156.3 156.	P16401	H15_HUMAN		Histone H1.5	(Histone H	1a) - Homo	sapiens (Human)				
2460 23 23 226 20 990 SETAPAETATPAPUEKSPAK 1953 1954 1958 1954 1958 1954 1958 1954 1958 1954 1958 1954 1955	235.0	5.2	6.0	23.5	2.0	99.0	SETAPAETATPAPVEKSPAKK	2151.1	2152.1	2151.1	2152.1
451.0 2.0 6.0 23.5 2.0 99.0 SETAPLAPTIPAPAEXTPYKK 2315.3 2316.3 2315.3 2316.3 4510. 2.0 6.0 23.5 0.0 99.0 ALAAACYDVEKNINSR 1578.8 1579.8 1578.8 1579.8 4510. 2.0 6.0 23.5 0.0 99.0 ALAAACYDVEKNINSR 1578.8 1579.8 1578.8 1579.8 4510. 2.0 6.0 23.5 0.0 99.0 ALAAACYDVEKNINSR 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 4510. 2.0 6.0 23.5 0.0 99.0 ALAAACYDVEKNINSR 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 4510. 2.0 6.0 23.5 0.0 99.0 ALAAACYDVEKNINSR 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1578.8 1579.8 1578.8 1578.8 1578.8 1578.8 1578.8 1578.8 1578.8 1578.8 1579.8 1578.8 1579.8 1578.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8	246.0	2.3	2.3	22.6	2.0	99.0	SETAPAETATPAPVEKSPAK	2023.0	2024.0	2023.0	2024.0
4510 2.0 6.0 23.5 0.0 99.0 ALAMACYDVEKNINSR 1578.8 1579.8 1578.8 1579.8 4510.0 2.0 6.0 23.5 0.0 99.0 ALAMACYDVEKNINSR 1577.8 1578.8 1579.8 4510.0 2.0 6.0 23.5 0.0 99.0 ALAMACYDVEKNINSR 1578.8 1579.8 1578.8 1579.8 4510.0 2.0 6.0 23.5 0.0 99.0 ALAMACYDVEKNINSR 1578.8 1579.8 1578.8 1579.8 4510.0 2.0 6.0 23.5 0.0 99.0 ALAMACYDVEKNINSR 170.9 170.9 9 170			6.0					2315.3	2316.3	2315.3	2316.3
451.0 2.0 6.0 23.5 0.0 99.0 KALAAGYDVEKNINSR 1705.9 1706.9 1706.9 1706.9 1706.9 309.0 2.0 37 30.3 2.0 99.0 SETAPLAPITYEKK 2316.3 231	451.0	2.0		23.5			ALAAAGYDVEKNNSR		1579.8	1578.8	1579.8
3990 20 37 303 00 980 ALAAGYDVEKNINSR 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 15											
PIGEOR TILDE HISTORE											
227.0 5.4 11.4 22.1 2.0 99.0 SETAPAAPAAPPAEKAPVKK 2171.2 2172.2 2171.2 2172.2 2171.2 2172.2 2170.5 5.4 11.4 22.1 1.4 96.0 SETAPAAPAAPPAEKAPVKK 2171.2 2172.2 2171.2 2172.2 2171.2 2172.2 2170.5 5.4 11.4 22.1 1.4 96.0 SETAPAAPAAPPAEKAPVKK 1915.0 1916.0 191	P16403	H12_HUMAN	3.7			1d) - Homo	sapiens (Human)	1577.8			
227.0 5.4 11.4 22.1 0.0 99.0 ALAAAGYOVEKNISR 1578.8 1579.8 1578.8 1579.8 227.0 5.4 11.4 22.1 0.0 20.0 ALAAAGYOVEKNISR 1577.8 1578.8 1577.8 1578.8 227.0 5.4 11.4 22.1 0.0 20.0 ALAAAGYOVEKNISR 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1578.8 1579.8 1579.8 1578.8 1579.8 1578.8 1579.8 1520.8 1519.8 1520.8 1520.8 1520.5 1226.5 1226.5 1226.5 1226.5 1226.5 1226.5 1226.5 1226.5 1226.5 1226.5 1226.5 1226.5 1226.5	227.0 227.0	5.4 5.4	11.4	22.1 22.1	2.0 2.0	99.0 99.0	SETAPAAPAAAPPAEKAPVKK SETAPAAPAAAPPAEKAPVKKK	2171.2	2172.2	2171.2	2172.2
227 0 5 4 11.4 22.1 0.0 20.0 ALANACYOVEKNINSR 1578.8 1579.8 1578.8 1579.8 1579.8 2270 5 4 11.4 22.1 0.0 99.0 SETAPAAPAAPPAEKAPVK 1519.8 1520.8 1519.8 1520.8	227.0	5.4	11.4	22.1	0.0	99.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
102.0 5.4 11.4 22.1 0.0 99.0 SETAPARPARAPREK 1519.8 1520.8 1519.8 1520.8 102.0 7.7 7.5 7.7 7.7 7.7 7.7 7.5	227.0	5.4	11.4	22.1	0.0	20.0	ALAAAGYDVEKNNSR	1578.8	1579.8	1578.8	1579.8
102.0	227.0	5.4	11.4	22.1	0.0	99.0	SETAPAAPAAAPPAEK	1519.8	1520.8	1519.8	1520.8
102.0	102.0	7.7	7.7	23.5	2.0	99.0	SETAPAAPAAAPPAEKAPVKK	2043.1	2044.1	2043.1	2044.1
P16949 STMN1_HUMAN	102.0	7.7	7.7	23.5	1.7	98.0	ALAAAGYDVEKNNSR	1577.8	1578.8	1577.8	1578.8
243.0 4.9 4.9 27.5 2.0 99.0 LREKDKHIEEVRK 1679.0 1680.0 1678.9 1680.0 1478.9 149.0 243.0 4.9 4.9 27.5 0.9 88.0 RASGOAFELLISPR 1543.9 1544.9 1543.8 1544.9 149.0 2.0 2.0 12.8 2.0 99.0 ASGOAFELLISPR 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 297.0 2.0 20.0 21.5 2.0 99.0 ASGOAFELLISPR 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.7 1388.8 1387.0 1387.0 1387.0 1387.0 1387.0 1387.0 1387.0 1387.0 1387.0 1387.0 1387.0 1387.0 1387.0 1387.0 13.2 13.2 10.0 2.0 99.0 GNDVAFHFNPR 1272.6 1273.6 1272.6 1273.6 1272.6 1273.6 1272.6 1273.6 1272.0 1273.0 1272.0	P16949	STMN1_HUMAN		Stathmin - B	os taurus (B	Bovine); St	athmin (Phosphoprotein p19) (pp19) (Or	ncoprotein 18) (Op18)	(Leukemia-as	sociated phosphor	orotein p18) (pp
149	243.0	4.9	4.9	27.5	2.0	99.0	LREKDKHIEEVRK	1679.0	1680.0	1678.9	1680.0
P17931 LEG3 HUMAN Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (1gE-binding protein) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Lamini 357 0 3.2 3.2 10.0 2.0 99.0 GNDVAFHRPR 1272.6 1273.6 1272.6 1273.6 1273.6 1273.6 1273.6 1272.6 1273.6 1273.6 1272.6 1273.6 1273.6 1272.6 1273.6 1273.6 1272.6 1273.6 1273.6 1272.6 1273.6 1273.6 1272.6 1273.6 1273.6 1272.6 1273.6 1273.6 1272.6 1273.6 1273.6 1272.6 1273.6 1273.6 1272.6 1273.6 1273.6 1273.6 1272.6 1273.6 1	149.0	2.0	2.0	12.8	2.0	99.0	ASGQAFELILSPR	1387.7	1388.8	1387.7	1388.8
357.0 3.2 3.2 10.0 1.2 94.0 VANDAHLLOYNHR 1048.8 1649.8 1648.8 1649.9 124.0 2.3 2.3 14.4 2.0 99.0 GNDVAFHENPR 1272.6 1273.6 1272.6 1273.6 124.0 2.3 2.3 14.4 0.3 44.0 IQVLVEPDHFK 1323.7 1324.7 1323.7 1324.7 192.0 4.0 4.0 10.0 2.0 99.0 GNDVAFHENPR 1272.6 1273.6 1273.6 1273.6 1273.6 1273.0 4.0 4.0 10.0 2.0 99.0 GNDVAFHENPR 1272.6 1273.6 1273.6 1273.6 1273.6 1273.0 4.0 4.0 10.0 0.0 99.0 GNDVAFHENPR 1272.7 1273.7 1272.6 1273.6 1273.6 1273.6 1273.0 4.0 4.0 10.0 0.0 99.0 GNDVAFHENPR 1272.7 1273.7 1272.6 1273	P17931	LEG3_HUMAN		Galectin-3 (0	Galactose-sp	ecific lecti	n 3) (Mac-2 antigen) (IgE-binding proteir	n) (35 kDa lectin) (Carl	oohydrate-bin	ding protein 35) (CBP 35) (Lamini
124.0 2.3 2.3 14.4 0.3 44.0 IOUVEPDHFK 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.7 1323.7 1324.6 1323.6 13	357.0	3.2	3.2	10.0	1.2	94.0	VAVNDAHLLQYNHR	1648.8	1649.8	1648.8	1649.9
192.0 4.0 4.0 10.0 2.0 99.0 VANDAHLDYNIR 1648.8 1649.8 1648.8 1649.9 192.0 4.0 4.0 10.0 0.0 99.0 GNDVAFHENPR 1272.7 1273.6 1273.6 1273.6 192.0 4.0 4.0 10.0 0.0 99.0 GNDVAFHENPR 1273.6 1273.6 1274.6 1273.6 1274.6 192.0 4.0 4.0 10.0 0.0 99.0 VANDAHLDYNIR 1645.8 1646.8 1648.8 1649.9 1649.9 1645.8 1646.8 1649.9	124.0	2.3	2.3	14.4	0.3	44.0	IQVLVEPDHFK	1323.7	1324.7	1323.7	1324.7
192.0 4.0 4.0 10.0 0.0 99.0 SDVAFHFNPR 1273.6 1274.6 1273.6 1274.6 1273.6 1274.6 192.0 4.0 4.0 10.0 0.0 98.0 VAVNDAHLLQYNHR 164.8 1646.8	192.0	4.0	4.0	10.0	2.0	99.0	VAVNDAHLLQYNHR	1648.8	1649.8	1648.8	1649.9
P18465 1857_HUMAN	192.0	4.0	4.0	10.0	0.0	99.0	GNDVAFHFNPR	1273.6	1274.6	1273.6	1274.6
160.0 7.4 12.3 40.6 2.0 99.0 DGEDOTODTELVETRPAGDRTFQK 2735.3 2736.3 2735.3 2736.3 160.0 7.4 12.3 40.6 2.0 99.0 YTCHVOHEGLPKPLT 1778.9 1779.9 1779.9 1779.9 160.0 7.4 12.3 40.6 1.2 99.0 MYGCDVGPQ 1225.5 1226.5 1225.5 1226.5 160.0 7.4 12.3 40.6 0.2 38.0 AYLEGLCVEWLR 1507.8 1508.8 1507.7 1508.8	P18465	1B57_HUMAN		HLA class I h	nistocompati	ibility antiq	en, B-57 alpha chain precursor (MHC clas	ss I antigen B*57) (Bw	-57) - Homo s	sapiens (Human)	
160.0 7.4 12.3 40.6 1.2 99.0 MYGCDVGPDGR 1225.5 1226.5 1225.5 1226.5 160.0 7.4 12.3 40.6 0.2 38.0 AYLEGLCVEWLR 1507.8 1508.8 1507.7 1508.8	160.0	7.4	12.3	40.6	2.0	99.0	DGEDQTQDTELVETRPAGDRTFQK	2735.3	2736.3	2735.3	2736.3
	160.0	7.4	12.3	40.6	1.2	99.0	MYGCDVGPDGR	1225.5	1226.5	1225.5	1226.5

160.0	7.4	12.3	40.6	0.0	99.0	WAAVVVPSGEEQR	1426.7	1427.7	1426.7	1427.7
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	AAYKLVLIR ALPFWNEEIVPQIK	1087.7 1682.9	1088.7 1683.9	1087.7 1682.9	1088.7 1683.9
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	FSGWYDADLSPAGHEEAK FSGWYDADLSPAGHEEAKR	1978.9 2135.0	1979.9 2136.0	1978.9 2135.0	1979.9 2136.0
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	HGESAWNLENR HYGGLTGLNK	1311.6 1058.6	1312.6 1059.6	1311.6 1058.6	1312.6 1059.6
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	HYGGLTGLNKAETAAK SYDVPPPPMEPDHPFYSNISK	1629.8 2416.1	1630.8 2417.1	1629.8 2416.1	1630.9 2417.1
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	VLIAAHGNSLR YADLTEDQLPSCESLKDTIAR	1149.7 2424.1	1150.7 2425.2	1149.7 2424.1	1150.7 2425.2
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	0.5 0.1	68.0 20.0	ALPFWNEEIVPQIKEGKR TWRLNER	2153.2 973.5	2154.2 974.5	2153.2 973.5	2154.2 974.5
40.0 40.0	20.6	20.6 20.6	61.0 61.0	0.0	99.0 99.0	HGESAWNLENR HGESAWNLENR	1311.6 1323.6	1312.6 1324.6	1311.6 1323.6	1312.6 1324.6
40.0 36.0	20.6 8.6	20.6 8.6	61.0 38.6	0.0	99.0 99.0	HYGGLTGLNKAETAAK ALPFWNEEIVPOIK	1629.8 1682.9	1630.8 1683.9	1629.8 1682.9	1630.9 1683.9
36.0 36.0	8.6 8.6	8.6 8.6	38.6 38.6	2.0 2.0 2.0	99.0 99.0	FSGWYDADLSPAGHEEAK HGESAWNLENR	1978.9 1311.6	1979.9 1312.6	1978.9 1311.6	1979.9 1312.6
36.0 36.0	8.6 8.6	8.6 8.6	38.6 38.6	2.0 0.5	99.0 67.0	YADLTEDQLPSCESLKDTIAR FSGWYDADLSPAGHEEAKR	2424.2 2135.0	2425.2 2136.0	2424.1 2135.0	2425.2 2136.0
53.0	14.0	14.0	42.9	2.0	99.0	ALPFWNEEIVPQIK	1682.9	1683.9	1682.9	1683.9
53.0 53.0	14.0 14.0	14.0 14.0	42.9 42.9	2.0 2.0	99.0 99.0	FSGWYDADLSPAGHEEAK HGESAWNLENR	1978.9 1311.6	1979.9 1312.6	1978.9 1311.6	1979.9 1312.6
53.0 53.0	14.0 14.0	14.0 14.0	42.9 42.9	2.0 2.0	99.0 99.0	HYGGLTGLNK HYGGLTGLNKAETAAK	1058.6 1629.8	1059.6 1630.8	1058.6 1629.8	1059.6 1630.9
53.0 53.0	14.0 14.0	14.0 14.0	42.9 42.9	2.0 2.0	99.0 99.0	VLIAAHGNSLR YADLTEDQLPSCESLKDTIAR	1149.7 2424.1	1150.7 2425.2	1149.7 2424.1	1150.7 2425.2
53.0 53.0	14.0 14.0	14.0 14.0	42.9 42.9	0.0	99.0 99.0	HGESAWNLENR HGESAWNLENR	1311.6 1323.6	1312.6 1324.6	1311.6 1323.6	1312.6 1324.6
	14.0 PGAM1_HUMAN	14.0	42.9 Phosphoglyd			VLIAAHGNSLR .2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglyce		1151.7 ozyme B) (PGAN	1150.6 I-B) (BPG-depend	1151.7 dent PGAM 1) - H
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	AAYKLVLIR ALPFWNEEIVPQIK	1087.7 1682.9	1088.7 1683.9	1087.7 1682.9	1088.7 1683.9
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	FSGWYDADLSPAGHEEAK FSGWYDADLSPAGHEEAKR	1978.9 2135.0	1979.9 2136.0	1978.9 2135.0	1979.9 2136.0
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	HGESAWNLENR HYGGLTGLNK	1311.6 1058.6	1312.6 1059.6	1311.6 1058.6	1312.6 1059.6
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	HYGGLTGLNKAETAAK SYDVPPPPMEPDHPFYSNISK	1629.8 2416.1	1630.8 2417.1	1629.8 2416.1	1630.9 2417.1
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	2.0 2.0	99.0 99.0	VLIAAHGNSLR YADLTEDQLPSCESLKDTIAR	1149.7 2424.1	1150.7 2425.2	1149.7 2424.1	1150.7 2425.2
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	0.5 0.1	68.0 20.0	ALPFWNEEIVPQIKEGKR TWRLNER	2153.2 973.5	2154.2 974.5	2153.2 973.5	2154.2 974.5
40.0 40.0	20.6 20.6	20.6 20.6	61.0 61.0	0.0	99.0 99.0	HGESAWNLENR HGESAWNLENR	1311.6 1323.6	1312.6 1324.6	1311.6 1323.6	1312.6 1324.6
40.0 36.0	20.6 8.6	20.6 8.6	61.0 38.6	0.0	99.0 99.0	HYGGLTGLNKAETAAK ALPFWNEEIVPQIK	1629.8 1682.9	1630.8 1683.9	1629.8 1682.9	1630.9 1683.9
36.0 36.0	8.6 8.6	8.6 8.6	38.6 38.6	2.0	99.0 99.0	FSGWYDADLSPAGHEEAK HGESAWNLENR	1978.9 1311.6	1979.9 1312.6	1978.9 1311.6	1979.9 1312.6
36.0 36.0	8.6 8.6	8.6 8.6	38.6 38.6	2.0 0.5	99.0 67.0	YADLTEDOLPSCESLKDTIAR FSGWYDADLSPAGHEEAKR	2424.2 2135.0	2425.2 2136.0	2424.1 2135.0	2425.2 2136.0
53.0 53.0	14.0 14.0	14.0 14.0	42.9 42.9	2.0 2.0	99.0 99.0	ALPFWNEEIVPQIK FSGWYDADLSPAGHEEAK	1682.9 1978.9	1683.9 1979.9	1682.9 1978.9	1683.9 1979.9
53.0 53.0	14.0 14.0 14.0	14.0 14.0	42.9 42.9 42.9	2.0 2.0 2.0	99.0 99.0	HGESAWNLENR HYGGLTGLNK	1311.6 1058.6	1312.6 1059.6	1311.6	1312.6 1059.6
53.0 53.0	14.0 14.0 14.0	14.0 14.0 14.0	42.9 42.9 42.9	2.0 2.0 2.0	99.0 99.0	HYGGLTGLNKAETAAK VLIAAHGNSLR	1629.8 1149.7	1630.8 1150.7	1058.6 1629.8 1149.7	1630.9 1150.7
53.0	14.0	14.0	42.9	2.0	99.0	YADLTEDQLPSCESLKDTIAR	2424.1	2425.2	2424.1	2425.2
53.0 53.0	14.0 14.0	14.0 14.0	42.9 42.9	0.0	99.0 99.0	HGESAWNLENR HGESAWNLENR	1311.6 1323.6	1312.6 1324.6	1311.6 1323.6	1312.6 1324.6
53.0	14.0	14.0	42.9	0.0	64.0	VLIAAHGNSLR	1150.6	1151.7	1150.6	1151.7
	MLRM_HUMAN		Myosin regu			nsarcomeric (Myosin RLC) - Homo sapiens (Hur				
128.0 128.0	6.0 6.0	6.0 6.0	33.9 33.9	2.0 2.0	99.0 99.0	ELLTTMGDRFTDEEVDELYR GNFNYIEFTR	2431.2 1259.6	2432.2 1260.6	2431.1 1259.6	2432.1 1260.6
128.0 128.0 128.0 151.0	6.0 6.0 6.0 8.0	6.0 6.0 8.0	33.9 33.9 33.9 29.1	2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0	ELLTTMGDRFTDEEVDELYR GNFNYIEFTR NAFACFDEEATGTIQEDYLR ELLTTMGDRFTDEEVDELYR	2431.2 1259.6 2349.0 2431.1	1260.6 2350.0 2432.1	1259.6 2349.0 2431.1	1260.6 2350.0 2432.1
128.0 128.0 128.0 151.0 151.0 151.0	6.0 6.0 6.0 8.0 8.0	6.0 6.0 8.0 8.0	33.9 33.9 33.9 29.1 29.1 29.1	2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNYIEFTR NAFACFDEEATGTIQEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNYIEFTR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6	1260.6 2350.0 2432.1 1415.6 1260.6	1259.6 2349.0 2431.1 1414.6 1259.6	1260.6 2350.0 2432.1 1415.6 1260.6
128.0 128.0 128.0 151.0 151.0 151.0 151.0 146.0	6.0 6.0 6.0 8.0 8.0 8.0 8.0	6.0 6.0 8.0 8.0	33.9 33.9 33.9 29.1 29.1 29.1 29.1	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMODRETDEEVDELYR GNENVIEFTR NAFACFDEEATGTIQEDYLR ELLTIMODRETDEEVDELYR FTDEEVDELYR GNENVIEFTR NAFACFDEEATGTIQEDYLR GMENVIEFTR GMENVIEFTR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6
128.0 128.0 128.0 151.0 151.0 151.0 151.0 146.0 P19823 I	6.0 6.0 6.0 8.0 8.0 8.0 8.0 2.1 ITIH2_HUMAN 16.9	6.0 6.0 8.0 8.0 8.0 8.0 2.1	33.9 33.9 33.9 29.1 29.1 29.1 29.1 17.4 Inter-alpha- 13.4	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 trypsin inhill 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 bitor heavy 99.0	ELLTIMODRETDEEVDELYR GNENVIEFTR NAFACFDEEATGTIQEDYLR ELLTIMGDIREVDELYR FTDEEVDELYR GNENVIEFTR NAFACFDEEATGTIQEDYLR GNENVIEFTR Chain H2 precursor (1TI heavy chain H2) (Inter AHYSERPTVAQOR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 or-alpha-inhibit 1465.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6) (Inter-alpha-tr 1465.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 ypsin inhibitor cc 1466.8
128.0 128.0 128.0 151.0 151.0 151.0 146.0 P19823 55.0 55.0	6.0 6.0 6.0 8.0 8.0 8.0 2.1 ITIH2_HUMAN 16.9 16.9	6.0 6.0 8.0 8.0 8.0 2.1 16.9 16.9	33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 trypsin inhill 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMODRFIDEEVDELYR GNFNVIEFTR NAFACFDEEATCHIQEDYLR ELLTIMGDRFIDEEVDELYR FTDEEVDELYR GNFNVIEFTR GNFNVIEFTR CAID HILL PRECURSOR (ITI heavy chain H2) (Inte AHVSFKPTVAQOR FYNOVSTPLLR IOPSGGTNINEALLR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 tr-alpha-inhibit 1465.8 1336.7 1581.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6) (Inter-alpha-tr 1465.8 1336.7 1581.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 ypsin inhibitor cc 1466.8 1337.7 1582.9
128.0 128.0 128.0 151.0 151.0 151.0 151.0 146.0 P19823 55.0 55.0 55.0 55.0	6.0 6.0 6.0 8.0 8.0 8.0 2.1 ITIH2_HUMAN 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9	33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4	2.0 2.0 2.0 2.0 2.0 2.0 2.0 trypsin inhill 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMODRFIDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLITIMGDRFIDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR CABIN HZ FREVENTEFTR AFACFDEEATGTIGEDYLR GNFNVIEFTR FYNOVSTPLLR IOPSGGTNINFALLR IYGNODTSSOLKK KFYNOVSTPLLR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 tr-alpha-inhibit 1465.8 1336.7 1581.8 1492.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1465.8	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6) (Inter-alpha-tr 1465.8 1336.7 1581.8 1492.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 ypsin inhibitor cc 1466.8 1437.7 1582.9 1493.8 1465.8
128.0 128.0 128.0 151.0 151.0 151.0 151.0 155.0 55.0 55	6.0 6.0 6.0 8.0 8.0 8.0 2.1 1TIH2_HUMAN 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9	33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 trypsin inhill 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMODRFIDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLITIMGDRFIDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR CABIN HZ FYNOVSTPLLR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYGEVK VOFELHYGEVK	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 •-alpha-inhibit 1465.8 1336.7 1581.8 1492.8 1464.8 1418.7 1760.9	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6) (Inter-alpha-tr 1465.8 1336.7 1581.8 1492.8 1464.8 1418.7 1760.9	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 ypsin inhibitor cc 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9
128.0 128.0 128.0 151.0 151.0 151.0 146.0 P19823 55.0 55.0 55.0 55.0	6.0 6.0 8.0 8.0 8.0 8.0 2.1 1TIH2_HUMAN 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9	33.9 33.9 29.1 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GMFNVIEFTR CABIN 12 precursor (ITI heavy chain H2) (Intel AHVSFKPTVAOQR FYNOVSTPLLR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYGEVKWR VVNNSPOPONVVFDVQIPK VIEPOGLR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 17-alpha-inhibit 1465.8 1336.7 1581.8 1492.8 1464.8 1418.7 1760.9 2144.1 924.5	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1465.8	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6) (Inter-alpha-tr 1465.8 1336.7 1581.8 1492.8 1444.8 1418.7 1760.9 2144.1 924.5	1280.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 ypsin inhibitor cc 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7
128.0 128.0 151.0 151.0 151.0 151.0 151.0 55.0 55	6.0 6.0 8.0 8.0 8.0 8.0 8.0 10.1 11112_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9	33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 trypsin inhill 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR CHAIN HZ CHENVIEFTR CHAIN HZ CHENVIEFTR CHAIN HZ CHENVIEFTR CHAIN HZ CHENVIEFTR CHAIN HZ CHENVIEFT CHAIN CH	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 r-alpha-inhibit 1465.8 1336.7 1581.8 1492.8 1418.7 1760.9 2144.1	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1464.8 1437.7 1582.9 1493.8 1465.8 1419.7 1761.9 2145.1	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6) (Inter-alpha-tr 1465.8 1336.7 1581.8 1492.8 1464.8 1418.7 1760.9 2144.1	1280.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 ypsin inhibitor cc 1466.8 1465.8 1493.8 1465.8 1419.7 1761.9 2145.1
128.0 128.0 128.0 151.0 151.0 151.0 151.0 155.0 55.0 55	6.0 6.0 8.0 8.0 8.0 8.0 2.1 ITIH2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9 16.9 16.9	33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 13.4	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR CHAIN 12 precursor (ITI heavy chain H2) (Inte AHVSFKPTVAQQR FYNOVSTPLLR IOPSGGTNINEALLR IYGNQDTSSCLKK KFYNOVSTPLLR VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VIEFDGLR FYNOVSTPLLR VINNSPOPONVYFDVOIPK VIEPGGLR FYNOVSTPLLR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1465.8 1336.7 1581.8 1492.8 1441.8 1710.9 2144.1 924.5	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1464.8 1337.7 1552.9 1493.8 1465.8 1419.7 1761.9 2145.1 925.5 1336.7	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 (Inter-aipha-tr 1465.8 1336.7 1581.8 1492.8 1464.8 1418.7 1760.9 2144.1 924.5 1336.7	1280.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 2350.0 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 2245.1 925.5 1337.7
128.0 128.0 128.0 151.0 151.0 151.0 151.0 55.0 55.0 55.	6.0 6.0 6.0 8.0 8.0 8.0 2.1 1T1H2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16	33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 13.4	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 trypsin inhill 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMODRFIDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLITIMGDRFIDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR GAIN H2 precursor (LTL heavy chain H2) (Intel AHVSFKPTVAQQR FYNOVSTPLLR IOPSGGTNINEALLR IYGNQDTSSQLKK KFYNOVSTPLLR VOFELHYOEVK VVNNSPOPONVVFDVQIPK VIEPOGLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR IOPSGGTNINEALLR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1465.8 1336.7 1581.8 1492.8 1418.7 1760.9 2144.1 924.5 1335.7 1336.7	1260.6 2350.0 2432.1 1415.6 1260.6 2250.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1449.7 1761.9 2145.1 925.5 1336.7 1337.7 1582.8	1259.6 2349.0 2431.1 1414.6 1259.6 1259.6 1259.6 1336.7 1551.8 1445.8 1444.8 1448.7 1760.9 2144.1 924.5 1336.7 1336.7 1336.7	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 2145.1 925.5 1337.7 1337.7 1582.9
128.0 128.0 128.0 151.0 151.0 151.0 151.0 146.0 P198231 55.0 55.0 55.0 55.0 55.0 31.0 31.0 31.0	6.0 6.0 6.0 8.0 8.0 8.0 2.1 1T1H2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16	33.9 33.9 33.9 33.9 33.9 33.9 34.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 13.4	20 20 20 20 20 20 20 20 20 20 20 20 20 2	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMODRFIDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLITIMGDRFIDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR GNFNVIEFTR CABIN 12 precursor (LTL heavy chain H2) (Intel AHVSFKPTVAQOR FYNQVSTPLLR IOPSGGTNINEALLR IYGNQDTSSOLKK KFYNQVSTPLLR VOFELHYOEVK VVNNSPOPONVVFDVOIPK VIEPOGLR FYNQVSTPLLR IOPSGGTNINEALLR VOFELHYOEVK VVNNSPOPONVVFDVOIPK VIEPOGLR FYNQVSTPLLR IOPSGGTNINEALLR VOFELHYOEVK VVNNSPOPONVVFDVOIPK	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1-259.6 1-365.8 136.7 1581.8 1492.8 1464.8 1418.7 1760.9 2144.1 924.5 1335.7 1581.8 1418.7 2144.1 1760.9 1144.1 1760.9	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2250.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1449.7 1761.9 2145.1 1337.7 1582.8 1419.7 1337.7 1582.8 1419.7 1337.7 1582.8	1259.6 2349.0 2431.1 1414.6 1259.6 1259.6 1259.6 1326.7 1465.8 1336.7 1561.8 1492.8 1404.8 1418.7 1700.9 2144.1 924.5 1336.7 1581.8 1418.7 1214.1 1760.9 1814.8	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 2145.1 137.7 1337.7 1337.7 1337.7 1382.9 1419.7 1582.9 1419.7 1582.9
128.0 128.0 128.0 151.0 151.0 151.0 151.0 146.0 P198231 55.0 55.0 55.0 55.0 55.0 55.0 31.0 31.0 31.0 31.0	6.0 6.0 6.0 8.0 8.0 8.0 2.1 1TTH2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0	33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4	20 20 20 20 20 20 20 20 20 20 20 20 20 2	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR GAIN H2 precursor (ITI heavy chain H2) (Intel AHVSFKPTVAOOR FVNOVSTPLLR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYGEVKW VVNNSPOPONVVFDVOIPK VIEPOGLR FYNOVSTPLLR IOPSGGTNINEALLR IVPNOVSTPLLR VOFELHYGEVKWR VVNNSPOPONVVFDVOIPK VIEPOGLR FVNOVSTPLLR VOFELHYGEVKWR VOFELHYGEVKWR VOFELHYGEVKWR VOFELHYGEVKWR VOFELHYGEVKWR VOFELHYGEVKWR VOFELHYGEVKWR VOFELHYGEVKWR VOFELHYGEVKWR AEDHFSVIDFNONIR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 F-alpha-inhibit 1465.8 1336.7 1581.8 1464.8 1418.7 1760.9 2144.1 924.5 1336.7 1581.8 1418.7 1760.9	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1445.8 1449.7 1761.9 2145.1 925.5 1336.7 1337.7 1582.8 1419.7 1761.9	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1259.6 1336.7 1581.8 1492.8 1404.8 1418.7 1760.9 2144.1 924.5 1336.7 1336.7 1336.7 1581.8 1418.7 1760.9	1280.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 2350.0 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 225.5 1337.7 1337.7 1582.9 1419.7 1419.7 1419.7
128.0 128.0 128.0 151.0 151.0 151.0 151.0 151.0 155.0 55.0	6.0 6.0 6.0 8.0 8.0 8.0 2.1 1TTH2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 13.4	20 20 20 20 20 20 20 20 20 20 20 20 20 2	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR CABIN 12 precursor (ITI heavy chain H2) (Intel AHVSFKPTVAOOR FYNOVSTPLLR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYGEVKWR VVNNSPOPONVVFDVOIPK VIEPOGLR FYNOVSTPLLR IOPSGGTNINEALLR IOPSGGTNINEALLR VOFELHYGEVKWR VVNNSPOPONVVFDVOIPK VIEPOGLR FYNOVSTPLLR IOPSGGTNINEALLR VOFELHYGEVKWR VVNNSPOPONVVFDVOIPK VOFELHYGEVKWR VVNNSPOPONVVFDVOIPK VOFELHYGEVKWR AEDHFSVIDFINONIR KFYNOVSTPLLR VOFELHYGEVKWWR AEDHFSVIDFINONIR KFYNOVSTPLLR VOFELHYGEVKWWR KFYNOVSTPLLR VOFELHYGEVKWWR KFYNOVSTPLLR VOFELHYGEVKWWR KFYNOVSTPLLR VOFELHYGEVKWWR KFYNOVSTPLLR VOFELHYGEVKWWR KFYNOVSTPLLR VOFELHYGEVKWWR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1459.6 1365.7 1581.8 1336.7 1581.8 1464.8 1418.7 1760.9 2144.1 1760.9 1336.7 1581.8 1418.7 1244.1 1760.9 1814.8 1464.8 1419.7	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1445.8 1419.7 1761.9 2145.1 925.5 1336.7 1337.7 1582.8 1419.7 1582.8 1419.7 1761.9 2145.1 1761.9 1815.8 1445.1	1259.6 2349.0 2431.1 1414.6 1259.6 1259.6 1259.6 1356.7 1465.8 1336.7 1581.8 1464.8 1418.7 1700.9 2144.1 924.5 1336.7 1581.8 1441.7 1760.9 1814.8 1418.7	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 2145.1 1761.9 1419.7 1815.8 1465.8 1419.7
128.0 128.0 128.0 128.0 151.0 151.1 151.0 151.1 151.0 151.0 155.0 55.0	6.0 6.0 6.0 8.0 8.0 8.0 2.1 1TTH2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 13.4	20 20 20 20 20 20 20 20 20 20 20 20 20 2	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR CABIN 12 precursor (ITI heavy chain H2) (International Control of the Co	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1465.8 1336.7 1581.8 1492.8 1464.8 1418.7 1760.9 2144.1 924.5 1335.7 1581.8 1418.7 2144.1 1760.9 1814.8 1468.8 1468.7 1465.8 1468.7 1465.8 1465.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1365.7 1876.0 1581.8 1365.7 1876.0 1581.8 1365.7 1876.0 1581.8 1365.7 1876.0 1581.8 1365.7 1876.0 1581.8 1365.7 1876.0 1581.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1876.0 1581.8 1465.8 1365.7 1581.8 1465.8 146	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1446.8 1419.7 1761.9 2145.1 925.5 1336.7 1337.7 1582.8 1419.7 2145.1 1761.9 1815.8 1445.1 1761.9 1815.8 1465.8	1299.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6) (Inter-alpha-tr 1465.8 1336.7 1551.8 1492.8 1464.8 1418.7 1760.9 2144.1 1924.5 1336.7 1551.8 1418.7 1418.7 1418.7 1418.7 1418.7 1464.8 1418.7 148.7 148.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 2145.1 1761.9 2145.1 1761.9 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1468.8 1419.7 1468.8 1437.7 1486.8
128.0 128.0 128.0 128.0 151.0 151.1 151.1 151.0 151.0 151.0 155.0	6.0 6.0 6.0 8.0 8.0 8.0 2.1 1TIH2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 16.9 16.	33.9 33.9 33.9 32.9 1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 13.4	20 20 20 20 20 20 20 20 20 20 20 20 20 2	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR ELLTIMGDRFTDEEVDELYR FFDEEVDELYR GNFNYIEFTR NAFACFDEEATGTIQEDYLR GNFNYIEFTR NAFACFDEEATGTIQEDYLR GNFNYIEFTR NAFACFDEEATGTIQEDYLR GNFNYIEFTR NAFACFDEEATGTIQEDYLR GNFNYIEFTR NAFACFDEEATGTIQEDYLR GNFNYIEFTR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VONSTPLLR IOPSGGTNINEALLR IOPSGGTNINEALLR VOFELHYOEVK VVNNSPOPONVYFDVOIPK VIEPOGLR VOFELHYOEVK VNNNSPOPONVYFDVOIPK VOFELHYOEVK VNNNSPOPONVYFDVOIPK VOFELHYOEVK AFDFENTAGEN AFDFENTAGEN AFTAGENTAGEN GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2431.1 1414.6 1259.6 14	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1419.7 2145.1 1761.9 2145.1 1761.9 1419.7 1445.1 1761.9 1815.8 1440.7 1460.8 1337.7 1582.8 1440.7 1480.8 1480.8 1387.7 1877.1 1882.9	1299.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6) (Inter-alpha-tr 1465.8 1336.7 1551.8 1492.8 1464.8 1418.7 1760.9 2144.1 1924.5 1336.7 1551.8 1418.7 2144.1 1760.9 1814.8 1464.8 1418.7 1464.8 1418.7 1485.8 1464.8 1485.8 1464.8	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 2350.0 1260.6 1466.8 1337.7 1582.9 1493.8 1419.7 12145.1 125.5 1337.7 1582.9 1419.7 1337.7 1582.9 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 145.8 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1466.8 1419.7 1466.8 1419.7 1466.8 1419.7 1466.8
128.0 128.0 128.0 128.0 151.0 151.10 151.10 151.10 151.10 151.0 55.0 55	6.0 6.0 6.0 8.0 8.0 8.0 8.0 1.11H2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 23.9 23.9 23.9 23.9 23.9 23.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 16.9 23.9 23.	33.9 33.9 33.9 33.9 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	20 20 20 20 20 20 20 20 20 20 20 20 20 2	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNYIEFTR NAFACFDEEATGTIQEDYLR GNFNYIEFTR NAFACFDEEATGTIQEDYLR GNFNYIEFTR NAFACFDEEATGTIQEDYLR GNFNYIEFTR NAFACFDEEATGTIQEDYLR GNFNYIEFTR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VINNSPOPONLVFDVOIPK VIEPOGLR FYNOVSTPLLR IOPSGGTNINEALLR IOPSGGTNINEALLR VOFELHYOEVK VVNNSPOPONLVFDVOIPK VOFELHYOEVK VNNNSPOPONLVFDVOIPK VOFELHYOEVK VNNSPOPONLVFDVOIPK VOFELHYOEVK AEDHFSVIDFNONIR KFYNOVSTPLLR VOFELHYOEVK AAVSSFRYTVAQOR IQPSGGTNINEALLR IVGNQUTSSOLK IYGNQDTSSOLK KFYNOVSTPLLR IYGNQDTSSOLK KFYNOVSTPLLR IYGNQDTSSOLK KFYNOVSTPLLR IYGNQDTSSOLK KFYNOVSTPLLR IYGNQDTSSOLK KFYNOVSTPLLR IYGNQDTSSOLK KFYNOVSTPLLR IYGNODTSSOLK KFYNOVSTPLLR IYGNODTSSOLK KFYNOVSTPLLR IYGNODTSSOLK KFYNOVSTPLLR IYGNODTSSOLKK KFYNOVSTPLLR IYGNODTSSOLKK	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2349.0 1259.6 1581.8 1336.7 1581.8 1492.8 1464.8 1418.7 1760.9 1814.8 1419.7 1465.8 1336.7 1581.8 1418.7 1760.9 1814.8 1419.7 1465.8 1336.7 1876.0 9 1814.8 1419.7 1465.8 1336.7 1876.0 9 1814.8 1419.7 1465.8 1336.7 1876.0 1581.8 1419.7 1465.8 1464.8 1419.7 1465.8 1464.8 1419.7 1465.8 1464.8 1464.8 1464.8 1464.8 1464.8 1464.8 1464.8 1464.8 1464.8 1464.8 1464.8 1464.8 1468.8 1386.7	1260.6 2350.0 2432.1 1411.6 1260.6 1260.6 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 14419.7 2145.1 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1419.7 2145.1 1761.9 1815.8 140.7 1882.8 140.7 1882.9 1883.7 1882.9 1883.7 1882.9	1299.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6) (Inter-alpha-tr 1465.8 1336.7 1581.8 1492.8 1444.1 1760.9 2144.1 1924.5 1336.7 1581.8 1418.7 2144.1 1760.9 1814.8 1448.7 1465.8 1366.7 1871.8 1465.8 1465.8 1465.8 1465.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 2350.0 1260.6 1466.8 1337.7 1582.9 1493.8 1419.7 12145.1 1275.5 1337.7 1582.9 1419.7 2145.1 1761.9 1815.8 1465.8 1419.7 1466.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1466.8
128.0 128.0 128.0 128.0 151.0 151.10 151.10 151.10 151.10 151.10 151.10 155.0 55.0	6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 16.9 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 10.0 23.9 23.9 23.9 23.9 23.9 23.9 23.9 23.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10	33.9 33.9 33.9 33.9 29.1 29.1 17.4 Inter-alpha- 113.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NOWNIEFTR IOPSGGTNINEALLR IVGNODTSSOLKK KFYNOVSTPLLR VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VIEPGGLR FYNOVSTPLLR IOPSGGTNINEALLR IOPSGGTNINEALLR VOFELHYOEVK VNNNSPOPONVYEDVOIPK VOFELHYOEVK VNNNSPOPONVYEDVOIPK VOFELHYOEVK AEDHFSVIDFNONIR KFYNOVSTPLLR VOFELHYOEVK AHVSSFRFTVAQOR FYNOVSTPLLR GOGACHAVSKFRTVAQOR IOPSGGTNINEALLR IVGNODTSSOLK KFYNOVSTPLLR IVGNODTSSOLK KFYNOVSTPLLR TVGNODTSSOLK KFYNOVSTPLR TVGNODTSSOLK KFYNOVSTPLR TVGNODTSSOLK TVGNODTS	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 17-alpha-inhibit 1465.8 1336.7 1581.8 1492.8 1464.8 1418.7 1760.9 1814.8 1419.7 1465.8 1336.7 1581.8 1448.7 1760.9 1814.8 1419.7 1465.8 1336.7 1418.7 1418.7 1418.7	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 0r heavy chain 2 1466.8 1465.8 1419.7 1761.9 2145.1 925.5 1336.7 1337.7 1582.8 1419.7 2145.1 1761.9 1815.8 1449.7 1466.8 1337.7 1466.8 1337.7 1466.8 1337.7 1466.8 1337.7 1470.7	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1259.6 1361.8 1346.7 1551.8 1445.8 1446.8 1418.7 1760.9 1814.8 1418.7 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1386.7 1386.7 1386.7 1386.7 1488.7 1488.7 1488.7 1488.8 1488.8 1488.8 1488.8 1488.8 1488.8 1488.8 1488.8 1488.8 1488.8 1488.7 1488.7 1481.8 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7 1488.7	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 2350.0 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 1815.8 1466.8 1419.7 1761.9 1815.8 1466.8 1337.7 1382.9 1419.7 1466.8 1337.7 1382.9 1419.7 1466.8 1397.7 1466.8 1397.7 1466.8 1397.7 1466.8 1397.7 1493.8 1493.8 1495.8 1490.7 1493.8 1490.7 1419.7 1761.9
128.0 128.0 128.0 128.0 151.0 151.10	6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10	33.9 33.9 33.9 33.9 29.1 29.1 17.4 Inter-alpha- 113.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR OPFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VIEPOGLR FYNOVSTPLLR IOPSGGTNINEALLR IOPSGGTNINEALLR VOFELHYOEVK VNNNSPOPONVYFDVOIPK VOFELHYOEVK VNNNSPOPONVYFDVOIPK VOFELHYOEVK AEDHFSVIDFNONIR KFYNOVSTPLLR OOFELHYOEVK AHVSSFRFTVAQOR FYNOVSTPLLR GOGKAHVSFRFTVAQOR IOPSGGTNINEALLR IYGNODTSSOLK KFYNOVSTPLLR IYGNODTSSOLK KFYNOVSTPLLR TYRNOLISTSOLK VOFELHYOEVK VNNSPOPONVYFDUPK VOFELHYOEVK VNNSPOPONVYFDVIPK VOFELHYOEVKWR VNNSPOPONVYFDVIPK VOFELHYOEVKWR VNNSPOPONVYFDVIPK VOFELHYOEVKWR VNNSPOPONVYFDVIPK AEDHFSVIDFNONIR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1259.6 17-2159.6 1349.0 1259.6 17-2159.6 1365.7 1581.8 1492.8 1448.7 1760.9 1814.8 1419.7 1465.8 1336.7 1581.8 1418.7 1760.9 1814.8 1419.7 1465.8 1336.7 1419.7 1418.7 1419.7 1418.7 1419.7 1418.8 1418.7 1418.8 141	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 0r heavy chain 2 1464.8 1437.7 1582.9 1493.8 1449.7 1761.9 2145.1 925.5 1336.7 1337.7 1582.8 1419.7 2145.1 1761.9 1815.8 1466.8 1337.7 1466.8 1337.7 1466.8 1337.7 1466.8 1337.7 1466.8 1337.7 1470.7 1761.9 1815.8 1455.8	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 (Inter-alpha-tr 1465.8 1336.7 1581.8 1492.8 1404.8 1418.7 1760.9 2144.1 924.5 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1318.7 1465.8 1418.7 1465.8 1418.7 1465.8 1418.7 1465.8 1482.8 1484.8 1289.7 1418.7 1760.9 2144.1 1814.9	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1260.6 1360.6 1367.1 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 12145.1 1761.9 1815.8 1466.8 1337.7 1387.7 1582.9 1419.7 1761.9 1815.8 1465.8 1419.7 1761.9 1815.8 1465.8 149.7 1466.8 1337.7 1360.7 1466.8 1397.7 1466.8 1397.7 1466.8 1397.7 1466.8 1397.7 1466.8 1397.7 1466.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8
128.0 128.0 128.0 128.0 151.0 151.10 151.10 151.10 151.10 151.0 155.0 55.0	6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10	33.9 33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR IOPSGGTNINEALLR IVGNODTSSOLKK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VONSPOPONVYFDVQIPK VIEPGGLR FYNOVSTPLLR IOPSGGTNINEALLR VOFELHYGEVK VNNNSPOPONVYFDVQIPK VOFELHYGEVK VNNNSPOPONVFDVQIPK VOFELHYGEVK VNNSPOPONVFDVQIPK VOFELHYGEVK AFYNOVSTPLLR IOPSGGTNINEALLR VOFELHYGEVK KFYNOVSTPLLR IOPSGGTNINEALLR IVGNODTSSOLK KFYNOVSTPLLR IYGNODTSSOLK KFYNOVSTPLLR IYGNODTSSOLK IYGNODTSSOLK KFYNOVSTPLLR TWRNDLISATK VOFELHYGEVKWR VNNSPOPONVFDVQIPK VOFELHYGEVKWR VNNSPOPONVFDVQIPK VOFELHYGEVKWR VNNSPOPONVFDVQIPK AEDHFSVIDFNONIR KFYNOVSTPLLR TWRNDLISATK VOFELHYGEVKWR VNNSPOPONVFDVQIPK AEDHFSVIDFNONIR VIEPGGLR AHDSFERTVAQOR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 17-2159.6	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 07 heavy chain 2 1466.8 1337.7 1582.9 1493.8 1445.8 1419.7 1761.9 22145.1 925.5 1336.7 1337.7 1582.8 1419.7 2145.1 1761.9 1815.8 1465.8 1420.7 1466.8 1337.7 1466.8	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 (Inter-alpha-tr 1465.8 1336.7 1581.8 1492.8 1404.8 1418.7 1760.9 2144.1 1760.9 1814.8 1418.7 1760.9 1814.8 1418.7 1760.9 1814.8 1418.7 1760.9 1814.8 1418.7 1760.9 1814.8 1418.7 1760.9 1814.8 1418.7 1760.9 1814.8 148.7 1492.8 1484.8 148.8 1396.7 1485.8 1396.7 1485.8 1396.7 1485.8 1396.7 1482.8 1484.8 1482.8 1482.8 1484.8 1482.8 1484.8 1482.8 1484.8 1482.8 1484.8 1482.8 1484.8 1485.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1260.6 1367.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 221.5 1337.7 1337.7 1382.9 1419.7 1761.9 1815.8 1419.7 1761.9 1815.8 1419.7 1761.9 1815.8 1419.7 1761.9 1815.8 149.7 1466.8 1397.7 1487.7 1465.8 149.7 1466.8
128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.0 151.0 151.0 151.0 155.0 55.0	6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 16.9 23.9 23.	33.9 33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VONSPOPONVYFDVOIPK VIEPOGLR FYNOVSTPLLR VOFELHYOEVK VVNNSPOPONVYFDVOIPK VVNNSPOPONVYFDVOIPK VVNNSPOPONVYFDVOIPK VVNNSPOPONVYFDVOIPK VOFELHYOEVK AEDHFSVIDFNONIR KFYNOVSTPLLR VOFELHYOEVK AHVSFKPTVAQOR FYNOVSTPLLR IYGNODTSSOLKK KFYNOVSTPLLR IYGNOTSOLK VOFELHYOEVK VONSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2431.1 1414.6 1259.6 1259.6 17-alpha-inhibit 1465.8 1336.7 1581.8 1492.8 1448.7 1760.9 2144.1 924.5 1335.7 1581.8 1418.7 1760.9 1814.8 1419.7 1465.8 1336.7 1581.8 1418.7 1760.9 1814.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1492.8 1464.8 1492.8 1464.8 1492.8 1466.8 1492.8 1492.8 1466.8 1492.8 1466.8 1492.8 1466.8 1492.8 1466.8 1492.8 1466.8 1492.8 1466.8 1492.8 1466.8 1492.8 1492.8 1492.8 1492.8 1466.8 1492.8	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2452.1 1415.6 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1445.5 1346.8 1445.5 1336.7 1337.7 1582.8 1419.7 1761.9 2145.1 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 149.7 1493.8 149.7 1493.8 149.7 1493.8 149.7 1466.8 1337.7 1877.1 1582.9 145.1 1761.9 1815.8 1455.8 1290.7 1493.8 1455.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1491.8 1290.7 1493.8 1290.7 1290.8 1290	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 11259.6 1345.8 1336.7 1551.8 1492.8 1446.8 1446.8 1446.8 1441.7 1760.9 2144.1 1760.9 2144.1 1760.9 1814.8 148.7 148.7 148.8 148.7 148.8 148.8 148.7 148.8 148.7 148.8 148.7 148.8 148.7 148.8 1	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1260.6 1367.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 22145.1 1761.9 1815.8 1465.8 1419.7 1466.8 1337.7 1582.9 1419.7 1466.8 1317.7 1619.9 1815.8 1465.8 1419.7 1466.8 1317.7 1466.8 1317.7 1466.8 1317.7 1466.8 1317.7 1466.8 1317.7 1466.8 1317.7 1466.8 1317.7 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5 1466.8 1318.5
128.0 128.0 128.0 128.0 128.0 151.0	6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	6.0 6.0 8.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10	33.9 33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VVNNSPOPONVYFDVOIPK VIEPOGLR FYNOVSTPLLR VOFELHYOEVK VVNNSPOPONVYFDVOIPK VOFELHYOEVK VVNNSPOPONVYFDVOIPK VOFELHYOEVK AFYNOVSTPLLR VOFELHYOEVK AHVSFKPTVAQQR FYNOVSTPLLR VOFELHYOEVK VOFELHYOEVK KFYNOVSTPLLR VOFELHYOEVK V	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2431.1 1414.6 1259.6 12	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2432.1 1415.6 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1445.5 1345.1 925.5 1336.7 1351.7 1582.8 1419.7 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1465.8 1420.7 1466.8 1337.7 1877.1 1582.9 1465.8 1420.7 1466.8 1337.7 147.1 1582.9 1465.8 1420.7 1466.8 1337.7 147.1 1582.9 1465.8 1485.8 149.7 149.8 1465.8 1485	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1259.6 1336.7 1551.8 1346.7 1551.8 1404.8 1418.7 1760.9 2144.1 1760.9 2144.1 1760.9 1814.8 1464.8 1418.7 1465.8 1336.7 1876.0 1581.8 1418.7 1465.8 1386.7 1482.8 1484.1 1760.9 1814.8 1484.9 1814.9 1814.9 1814.9 1814.9 1814.9 1814.9 1814.9 1814.9 1814.9 1814.9 1814.9 1814.9 18	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 1260.6 1260.6 1337.7 1582.9 1493.8 1465.8 1465.8 1419.7 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1465.8 1419.7 1466.8 1337.7 1582.9 1419.7 1466.8 1337.7 1582.9 1419.7 1466.8 1337.7 1466.8 1419.7 1466.8 1337.7 1465.8 1419.7 1466.8 1337.7 1487.0 1582.9 1419.7 1466.8 1337.7 1486.8 1337.7 1487.0 1582.9 1485.1 1486.8 1337.7 1486.8 1337.7 1487.0 1582.9 1365.7 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8 1493.8 1465.8
128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.0 151.0 151.0 151.0 155.0 55.0	6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	6.0 6.0 8.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10	33.9 33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VIEFOGLR FYNOVSTPLLR VOFELHYOEVK VVNNSPOPONVYFDVOIPK VIEFOGLR VOFELHYOEVK VVNNSPOPONVYFDVOIPK VOFELHYOEVK VVNNSPOPONVYFDVOIPK VOFELHYOEVK AHVSFRFTVAQQR FYNOVSTPLLR VOFELHYOEVK VONNSPOPONVFDVOIPK AEDHFSVIDFNONIR VIEPOGLR AHVSFKFTVAQQR FYNOVSTPLLR FORGANYFPNOCOAR AREOGELLAPADGTVELVR FGGAAVFPNOCOAR AREOGELLAPADGTVELVR FGGAAVFPNOCOAR AREOGELLAPADGTVELVR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 12	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2452.1 1415.6 1260.6 2350.0 21260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1419.7 1761.9 2145.1 1925.5 1336.7 1337.7 1582.8 1419.7 1415.1 1761.9 1815.8 145.8 1420.7 1466.8 1337.7 1487.1 1582.9 1465.8 1290.7 1493.8 1465.8 1290.7 1491.7 1761.9 2145.1 1815.8 1465.8 1290.7 1493.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1493.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1493.8 1290.7 1493.8 1290.7 1493.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1290.6 11 growth factor) 1491.7 12906.1	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1359.7 1465.8 1336.7 1561.8 1492.8 1404.8 1418.7 1760.9 2144.1 1760.9 1814.8 1448.7 1465.8 1336.7 1356.7 1356.7 1356.7 1356.7 1356.7 1356.7 1356.7 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1485.8 1386.7 1485.8 1485.8 1386.7 1485.8 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7 1485.8 1386.7	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 1260.6 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1465.8 1419.7 1261.9 1215.1 1761.9 1215.1 1761.9 1815.8 1465.8 1419.7 1465.8 1419.7 1466.8 1337.7 1337.7 1582.9 1419.7 1465.8 1419.7 1466.8 1337.7 149.7
128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.0 151.0 155.0 55.0 55	6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	6.0 6.0 8.0 8.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 23.9 23.9 23.9 23.9 23.9 23.9 23.9 23.9	33.9 33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR MAFACFDEEATGTIGEDYLR GNFNVIEFTR CHAIN HZ PRECURSOR (ITI heavy chain H2) (Inter AHVSFKPTIVAQOR FYNOVSTPLLR IOPSGGTNINEALLR IYGNODTSSCLKK KFYNOVSTPLLR VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VIEPOGLR FYNOVSTPLLR IOPSGGTNINEALLR VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK VOFELHYGEVK AEDHFSVIDFNONIR KFYNOVSTPLLR IOPSGGTNINEALLR VOFELHYGEVK VOFELHYGEV VOFELHYGE VOFELHYGE VOFELHYGE VOFELHYGE VOFELHYGE VOFELHYGE VOFELHYGE VO	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 12	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 21260.6 Of heavy chain 2 1466.8 1337.7 1582.9 1493.8 1419.7 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1495.8 1419.7 1493.8 149.7 1493.8 149.7 1582.8 1419.7 1582.8 1419.7 1582.8 149.7 1493.8 1465.8 1420.7 1466.8 1337.7 1877.1 1582.9 1385.7 1493.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1493.8 1290.7 1493.8 1290.7 1493.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 13259.6 1336.7 1561.8 1492.8 1404.8 1418.7 1760.9 2144.1 1760.9 2144.1 1760.9 1814.8 1404.8 1418.7 1485.8 1494.8 1418.7 1485.8 1494.8 1494.8 1494.1 1760.9 1814.8 1494.8 1494.1 1760.9 1814.8 1494.8 1494.1 1760.9 1814.8 1494.8 1494.8 1495.8 1	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 1260.6 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1465.8 1419.7 1261.9 1215.1 1761.9 1215.1 1761.9 1815.8 1465.8 1419.7 1466.8 1337.7 1337.7 1387.7 1387.7 149.7 149.7 1465.8 1419.7 1466.8 1419.7 1466.8 1419.7 1466.8 1290.7 1419.7 1493.8 1465.8 1290.7 1419.7 1493.8 1465.8 1290.7 1419.7 1491.7 1295.5 1466.8 1338.7 1337.7 1337.7 1295.5 1466.8 1338.7 1397.0 1582.9 1491.7 12096.1 1491.7 12096.1 1491.7 1476.8 1529.9
128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.0 151.0 155.0 55.0 55	6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 10.0 23.9 23.9 23.9 23.9 23.9 23.9 23.9 23.9	33.9 33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR Chain H2 precursor (ITI heavy chain H2) (Inter AHVSFKPTIVAQOR FYNOVSTPLLR IOPSGGTNINEALIR IYGNQDTSSGLKK KFYNOVSTPLLR VOFELHYGEVK VOFELHYGEV VOFELHYGEV VOFELHYGEV VOFELHYGEV VOFELHYGEV VOFELHYGEV VOFELHYGEV VOFELHYGEV VOFELHYGEV VOFELHYGE VONDOTS VOFELHYGE VONDOTS VOFELHYGE VOFELHYGE VOFELHYGE VOFELHYGE VOFELHYGE VONDOTS VOFELHYGE VOFELHYGE VONDOTS VOFELHYGE VONDOTS VOFELHYGE VOND	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 12	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 21260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1419.7 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1492.7 1493.8 149.7 1493.8 149.7 1493.8 149.7 1493.8 149.7 1493.8 149.7 1493.8 149.7 1493.8 149.7 1493.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1493.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1290.1 1491.7 1290.1 1491.7 1491.7 1290.8 1529.9 885.5 1647.8	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1.259.6 1336.7 1551.8 1492.8 1404.8 1418.7 1760.9 2144.1 1760.9 2144.1 1760.9 1814.8 1418.7 1485.8 1492.8 1485.8 1492.8 1484.8 1289.7 1482.8 1482.8 1484.8 1289.7 1485.8 1336.7 1760.9 1814.8 1492.8 1484.8 1289.7 1418.7 1760.9 1814.8 1492.8 1484.8 1289.7 1418.7 1760.9 1418.7 1760.9 1814.8 1289.7 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1760.9 1418.7 1	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 1260.6 1260.6 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1465.8 1467.8 1487.0 1888.0 1898.0 18
128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.0 151.0 155.0 55.0 55	6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 16.9 16.9 16.9 16.9 16.9 16.9 10.0	33.9 33.9 33.9 33.9 29.1 29.1 29.1 129.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR Chain H2 precursor (ITI heavy chain H2) (Inter AHVSFKPTIVAQOR FYNOVSTPLLR IOPSGGTNINEALIR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW R VOFELHYGEVK VOFELHYGE VONDOTS VOFELHYGE VO	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 12	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2150.0 2160.6 21	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2349.0 2349.0 1259.6 1336.7 1551.8 1404.8 1418.7 1760.9 2144.1 1760.9 2144.1 1760.9 1814.8 1448.7 1485.8 1336.7 1876.0 18	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 1260.6 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1465.8 1419.7 1482.9 1491.7 1486.8 1290.7 1419.7 1466.8 1337.7 1387.7 1387.7 1387.7 1387.7 1387.7 1419.7 1465.8 1465.8 1419.7 1466.8 1419.7 1466.8 1290.7 1419.7 1419.7 1456.1 1815.9 1265.5 1466.8 1338.7 1337.7 1761.9 1245.1 1815.9 1265.5 1466.8 1290.7 1419.7 1476.9 1285.5 1466.8 1338.7 1337.7 1491.7 1476.8 1491.7 1476.8 1529.9 1855.5 1466.8 1338.7 1337.7 1491.7 1476.8 1529.9 1529.5 1466.8 1529.9 1529.5 1466.8 1529.9 1529.5 1466.8 1529.9 1529.5 1647.8 1529.9 1529.5 1647.8 1529.9 1529.5 1647.8 1529.9
128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.1 151.0 151.0 55.0 55	6.0 6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 2.1 ITIH2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	33.9 33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR Chain H2 precursor (ITI heavy chain H2) (Inter AHVSFKPTVAQQR FYNOVSTPLLR IOPSGGTNINEALLR IVSNOVSTPLLR VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVKW VOFELHYGEVK VOFELHYGEV VOFELHYGE VOFELHYGE VONDON ARDON VONDON ARDON VONDON ARDON ARDON	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 12	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2452.1 1466.8 1337.7 1582.9 1493.8 1449.7 1761.9 2145.1 1761.9 1815.8 1445.7 1337.7 1582.8 1419.7 1451.1 1761.9 1815.8 1465.8 1419.7 1466.8 1337.7 1877.1 192.9 1365.7 1491.7 1494.7 1830.4	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2431.1 1414.6 1259.6 1259.6 1336.7 1581.8 1492.8 1446.8 14418.7 1760.9 2144.1 1760.9 2144.1 1760.9 1814.8 1441.8 1464.8 1418.7 1465.8 1336.7 1876.0 1818.8 1485.8 1386.7 1876.0 1818.1 1384.7 1495.8 1384.7 1490.7 1495.8 1528.9 1844.5 1490.7 1490.7 1495.8 1528.9 1646.8 1788.4 1490.7 1688.4 1490.7 1688.4 1490.7 1688.4 1490.7 1688.4 1490.7 1688.4 1490.7 1688.4	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 1260.6 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1465.8 1419.7 1419.8 1465.8 1290.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1416.8 1338.7 1338.7 1338.7 1338.7 1338.7 1337.7 1419.7 1416.8 1529.9 885.5 1466.8 1338.7 1491.7
128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.1 151.0 151.0 55.0 55	6.0 6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 2.1 ITIH2_HUMAN 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	33.9 33.9 33.9 33.9 33.9 29.1 29.1 29.1 17.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR Chain H2 precursor (ITI heavy chain H2) (Inter AHVSFKPTVAQQR FYNOVSTPLLR IOPSGGTNINEALLR IVSNOVSTPLLR VOFELHYGEVKW R VOFSGGTNINEALLR VORNODTSSGLKK KEYNOVSTPLLR VOFSGGTNINEALLR VORNODTSSGLKK KEYNOVSTPLLR VORNODTSSGLKK KEYNOVSTPLLR VORNODTSSGLKK KEYNOVSTPLLR VORNDTSSGLKK KEYNOVSTPLLR VORNSTPLNE VONNSPOPONVFDVOIPK AEDHELSVIDFNONIR VIEPOGLR AHVSKFPTVAQQR VONNSPOPONVFDVOIPK AEDHELSVIDFNONIR VIEPOGLR VONNSPOPONVFDVOIPK AEDHELSVIDFNONIR VIEPOGLR AROSEELHAPAGGTVELVR FGGAAVFPNOEQAR VHRDGPALSGPGSR ALPLALVLHELGAGR RGTPWLR VAAALDDGSALGRFER VPMISGR FGGAAVFPNOEQAR RGTPWLR AGGPTTLSPTR COSLITEDLEFR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 2349.0 1259.6 12	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1260.6 1260.6 1260.6 1367.7 1582.9 1493.8 1445.8 1449.7 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1445.8 1419.7 1337.7 1337.7 1337.7 1337.7 13877.1 1761.9 1815.8 1465.8 1490.7 1491.7 1466.8 1290.7 1491.7 1476.8 1295.6 1466.8 1238.7 1491.7 1761.9 1365.7 1491.7 1761.9 1365.7 1491.7 1761.9 1365.7 1491.7 1761.9 1365.7 1491.7 1761.9 1365.7 1491.7 1761.9 1365.7 1491.7 1761.9 1365.6 1466.8 1280.7 1491.7 1761.9 1815.8 1465.8 1280.7 1491.7 1761.9 1815.8 1825.6 185.5 1847.8 185.5 1847.8 185.5 1847.8 1830.4	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2431.1 1414.6 1259.6 1259.6 1336.7 1581.8 1404.8 1418.7 1700.9 2144.1 1924.5 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1336.7 1340.9 2414.1 1760.9 2414.1 24	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1260.6 1360.8 1337.7 1582.9 1495.8 1465.8 1419.7 1261.9 145.1 1761.9 145.1 1761.9 1419.7 1445.1 1761.9 1815.8 1465.8 1419.7 1466.8 1337.7 1582.9 1419.7 1419.7 145.1 1761.9 1815.8 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1466.8 1337.7 1877.0 1888.0 1898.5 1898.5 1898.6 1898.6
128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.1 151.0 151.0 55.0 55	6.0 6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 16.9 16.9 16.9 16.9 16.9 16.9 16.9 16.9	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	33.9 33.9 33.9 33.9 33.9 29.1 29.1 17.4 Inter-alpha- 113.4 113.4 113.4 113.4 113.4 113.4 113.4 113.4 113.4 112.4 1	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHVOEVK VOFELHVOEVK VOFELHVOEVK VOFELHVOEVK VOFELHVOEVK VVNNSPOPONLVFDVOIPK VIEPOGLR FYNOVSTPLLR IOPSGGTNINEALLR VOFELHVOEVK VNNNSPOPONLVFDVOIPK VOFELHVOEVK VNNNSPOPONLVFDVOIPK VOFELHVOEVK VNNSPOPONLVFDVOIPK VOFELHVOEVK AATVSFRFTVAQQR FYNOVSTPLLR VOFELHVOEVK AHVSFRFTVAQQR IQPSGGTNINEALLR IYGNQDTSSOLK KFYNOVSTPLLR TVRNDLISATIK VOFELHVOEVK VNNSPOPONLVFDVOIPK VOFELHVOEVK VNNSPOPONLVFDVOIPK VOFELHVOEVK VNNSPOPONLVFDVOIPK VOFELHVOEVK AHVSFRFTVAQQR FYNQVSTPLLR TVRNDLISATIK VOFELHVOEVK VNNSPOPONLVFDVOIPK AEDHFSVIDFNONIR KFPNOVSTPLLR TVRNDLISATIK VOFELHVOEVK VNNSPOPONLVFDVOIPK AEDHFSVIDFNONIR VERGGGR AHVSFRFTVAQQR FYNQVSTPLLR FYNQVSTPLLR TVRNDLISATIK VOFELHVOEVK VNNSPOPONLVFDVOIPK AEDHFSVIDFNONIR VIEPGGLR AHVSFRFTVAQQR FYNQVSTPLLR FYNQVSTPLLR FYNQVSTPLLR FOGAAVFPNOEOAR AREOSELLAPADGTVELVR FGGAAVFPNOEOAR AREOSELLAPADGTVELVR FGGAAVFPNOEOAR RETPWLR AAGAPTTLSPTR COSLTEDLEFR COSLTEDLEFR LAOALHEMREOHDAOVR LOKEELENDR	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2349.0 2349.0 1359.6 17-3lpha-inhibit 1465.8 1336.7 1581.8 1492.8 1464.8 1418.7 1760.9 1814.8 1418.7 1760.9 1814.8 1419.7 1465.8 1336.7 1581.8 1418.7 1760.9 1814.8 1419.7 1418.7 1419.7 1418.7 1419.7	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1260.6 1260.6 1360.7 1582.9 1493.8 1445.1 1925.5 1336.7 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 149.7 1852.9 1865.8 1419.7 1865.8 1419.7 1865.8 1419.7 1865.8 1419.7 1865.8 1419.7 1865.8 1420.7 1466.8 1337.7 1877.1 1877.1 1877.1 1877.1 1877.1 1877.1 1815.8 1465.8 1490.7 1491.7 1761.9 2145.1 1815.8 1290.7 1419.7 1761.9 2145.1 1815.8 1290.7 1419.7 1761.9 2145.1 1815.8 1290.7 1419.7 1761.9 2145.1 1815.8 1290.7 1419.7 1761.9 2145.1 1815.8 1290.7 1419.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1815.8 1290.7 1491.7 1815.8 1386.7 2086.1 1816.8 1380.6 2032.0 1671.9	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1359.6 1359.6 1356.7 1551.8 1492.8 1404.8 1418.7 1700.9 2144.1 1700.9 2144.1 1700.9 1814.8 1404.8 1418.7 1405.8 1336.7 1551.8 1404.8 1418.7 1455.8 1464.8 1418.7 1465.8 1336.7 1876.0 18	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1260.6 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 12145.1 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1465.8 1419.7 1491.7 1805.5 1468.8 1529.9 1338.7 1337.7 1582.9 1385.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1491.7 1520.9 1885.5 1647.8 1529.9 1885.5 1647.8 1529.9 1885.5 1647.8 1529.9 1885.5 1647.8 1529.9 1885.5 1647.8 1529.9 1885.5 1647.8 1620.2 1154.6 1380.6 2032.0 1677.9
128.0 128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.1 151.0 151.0 151.0 151.0 155.0	6.0 6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	33.9 33.9 33.9 33.9 33.9 29.1 29.1 17.4 Inter-alpha- 113.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEEATGTIQEDYLR GNFNVIEFTR NAFACFDEATGTIQEDYLR GNFNVIEFTR IOPSGGTNINEALLR IYGNODTSSOLKK KFYNOVSTPLLR VOFELHVOEVK VOFELHVOEVK VOFELHVOEVK VOFELHVOEVK VOFELHVOEVK VONNSPOPONVYFDVOIPK VIEPOGLR FYNOVSTPLLR IOPSGGTNINEALLR IOPSGGTNINEALLR VOFELHVOEVK VNNNSPOPONVYFDVOIPK VOFELHVOEVK VNNNSPOPONVYFDVOIPK VOFELHVOEVK AFVSKFYTVAQQR FYNOVSTPLLR VOFELHVOEVK AHVSFKFYTVAQQR IOPSGGTNINEALLR IYGNQDTSSOLK KFYNOVSTPLLR VOFELHVOEVK VNNSPOPONVYFDVOIPK VOFELHVOEVK VNNSPOPONVYFDVOIPK VOFELHVOEVK VNNSPOPONVYFDVOIPK VOFELHVOEVK VNNSPOPONVYFDVOIPK VOFELHVOEVK VNNSPOPONVYFDVOIPK VOFELHVOEVK VNNSPOPONVYFDVOIPK ANDSFRANCK KFYNOVSTPLLR VOFELHVOEVKW VNNSPOPONVYFDVOIPK AEDHFSVIDFNONIR VIEPGGLR AHVSFKFTVAQQR FYNOVSTPLLR FYNOVSTPLLR COECHALDRAF VNNSPOPONVYFDVOIPK AEDHFSVIDFNONIR VIEPGGLR AHVSFKFTVAQQR FYNOVSTPLLR FYNOVSTPLLR FYNOVSTPLLR CEC 2.4.2.4) (TdRPase) (TP) (Platelet-derivec FGGAAVFPNOEQAR RAFORELBAPAGTVELVR FGGAAVFPNOEQAR RAFORELBAPAGTVELVR FGGAAVFPNOEQAR RAFORELBAPAGTVELVR GGGAAVFPNOEQAR RGTPWLR AGGPTTDLSPTR COSLTEDLEFR LAQALHEMREOHDAOVR LOKEKELERLINDR LYKEELEOTYHAK LKEYEAALINSK	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2431.1 1414.6 1259.6 1349.0 1-1259.6 1-1259.	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1449.7 1761.9 2145.1 1761.9 2145.1 1761.9 1815.8 1445.7 1337.7 1882.8 1419.7 1419.7 1415.8 145.8 145.8 1420.7 1466.8 1337.7 1877.1 192.5 1365.7 1491.7 1761.9 2145.1 1815.8 1290.7 1419.7 1761.9 2145.1 1815.8 1290.7 1419.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1296.1 1386.7 1396.7 1491.7 1396.7 1491.7 14	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 1259.6 1259.6 1359.6 1356.7 1551.8 1492.8 1404.8 1418.7 1700.9 2144.1 1700.9 2144.1 1700.9 1814.8 1418.7 1455.8 1336.7 1551.8 1464.8 1418.7 1455.8 1464.8 1418.7 1465.8 1336.7 1876.0 1551.8 1341.7 1495.8 1485.8 1336.7 1876.0 1561.8 1386.7 1876.0 1561.8 1386.7 1876.0 1561.8 1383.7 1475.8 1480.7 1485.8 1480.7 1485.8 1480.7 1485.8 1480.7 1485.8 1480.7 14	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 1260.6 1260.6 1466.8 1337.7 1582.9 1493.8 1465.8 1419.7 1761.9 2145.1 1761.9 2145.1 1761.9 1419.7 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1465.8 1419.7 1466.8 1337.7 1582.9 1381.6 1491.7 1476.9 1481.7 1491.7
128.0 128.0 128.0 128.0 128.0 128.0 151.0 151.0 151.0 151.0 151.0 151.0 151.0 151.0 151.0 151.0 155.0	6.0 6.0 6.0 6.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8.0 8	6.0 6.0 6.0 8.0 8.0 8.0 8.0 2.1 16.9 16.9 16.9 16.9 16.9 16.9 16.9 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10	33.9 33.9 33.9 33.9 29.1 29.1 29.1 1.9.1 11.4 Inter-alpha- 13.4 13.4 13.4 13.4 13.4 13.4 12.4 12.4 12.4 12.4 12.4 12.4 12.4 12	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	ELLTIMGDRFTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR ELLTIMGDRFTDEEVDELYR FTDEEVDELYR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR NAFACFDEEATGTIGEDYLR GNFNVIEFTR LOPSGGTNINEALLR IVGNODTSSOLKK KFYNOVSTPLLR OPSEGTNINEALLR IVGNODTSSOLKK KFYNOVSTPLLR VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VVNNSPOPONVYFDVOIPK VIEPOGLR FYNOVSTPLLR VOFELHYOEVK VVNNSPOPONVYFDVOIPK VOFELHYOEVK VVNNSPOPONVYFDVOIPK VOFELHYOEVK AHVSFRFTVAQQR FYNOVSTPLLR OOFSGGTNINEALLR VOFELHYOEVK AHVSFRFTVAQQR FYNOVSTPLLR VOFELHYOEVK VOFELHYOEVK AHVSFRFTVAQQR FYNOVSTPLLR TWRNDLISSOLK VSNODTSSOLK KFYNOVSTPLLR TWRNDLISATK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK RYNOVSTPLLR TWRNDLISATK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK RYNOVSTPLLR TWRNDLISATK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK VOFELHYOEVK RYNOVSTPLLR TWRNDLISATK VOFELHYOEVK	2431.2 1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2431.1 1414.6 1259.6 12	1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 2432.1 1415.6 1260.6 2350.0 1260.6 or heavy chain 2 1466.8 1337.7 1582.9 1493.8 1419.7 1761.9 2145.1 1761.9 1815.8 1452.8 1419.7 1451.1 1761.9 1815.8 1452.8 149.7 1456.8 149.7 1456.8 149.7 1466.8 1337.7 1877.1 1882.9 145.1 1877.1 1882.9 145.1 1877.1 1882.9 1466.8 1337.7 1493.8 1465.8 1290.7 1491.7 1761.9 2145.1 1815.8 1290.7 1491.7 1761.9 145.1 1815.8 1290.7 1491.7 1761.9 1493.8 1290.7 1491.7 1761.9 1493.8 1290.7 1491.7 1761.9 1815.8 1466.8 1290.7 1491.7 1761.9 1815.8 1466.8 1290.7 1491.7 1466.8 1338.7 1398.7 1398.7 1398.7 1398.7 1398.7 1398.7 1491.7 1476.8 1529.9 1494.7 1494.7 1494.7 1494.7 1830.4	1259.6 2349.0 2431.1 1414.6 1259.6 2349.0 2431.1 1414.6 1259.6 1359.6 1356.8 1336.7 1551.8 1492.8 1404.8 1418.7 1760.9 2144.1 1760.9 2144.1 1760.9 1814.8 1404.8 1418.7 1485.8 1336.7 1876.0 1581.8 1418.7 1485.8 1386.7 1876.0 1581.8 1418.7 1485.8 1386.7 1876.0 1581.8 1484.8 1289.7 1418.7 1760.9 2144.1 1814.9 244.5 1485.8 1386.7 1490.7 1490.7 2095.1 2011.0 2011.0 2011.0 2011.0 2011.0 2011.0 2011.0 2011.0 2011.0 2011.0 2011.0 2011.0 2011.0	1260.6 2350.0 2432.1 1415.6 1260.6 1260.6 1260.6 1260.6 137.7 1582.9 1493.8 1465.8 1465.8 1465.8 1419.7 1582.9 1419.7 1582.9 1419.7 1582.9 1419.7 1582.9 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.7 1419.8 1466.8 1337.7 1337.7 1337.7 1337.7 1497.8 1465.8 1419.7 1466.8 1337.7 1493.8 1465.8 1290.7 1419.7 1491.7 1476.8 1520.9 1651.8

100.0	7.8	7.8	27.6	2.0	99.0	CQSLTEDLEFR	1379.6	1380.6	1379.6	1380.6
100.0	7.8	7.8	27.6	2.0	99.0	CQSLTEDLEFRK	1507.7	1508.7	1507.8	1508.8
100.0	7.8	7.8	27.6	2.0	99.0	LQEKEELRELNDR	1670.9	1671.9	1670.9	1671.9
100.0	7.8	7.8	27.6	0.9	88.0	LYKEELEQTYHAK	1650.8	1651.8	1650.8	1651.8
100.0 P20742 PZ 358.0	7.8 P_HUMAN 3.1	7.8	27.6 Pregnancy zo	0.8 one proteir 2.0	84.0 precursor - 99.0	LREYEAALNSK Homo sapiens (Human) DLFHCVSFTLPR	1292.7	1293.7	1292.7	1293.7
358.0 358.0 358.0	3.1 3.1 3.1	7.7 7.7	8.4 8.4	1.0	99.0 99.0	QQNAQGGFSSTQDTVVALHALSR MVSGFIPLKPTVK	2503.2 1415.8	2504.2 1416.8	2503.2 1415.8	2504.2 1416.8
358.0	3.1	7.7	8.4	0.0	97.0	NQGNTWLTAFVLK	1635.7	1636.7	1635.7	1636.7
358.0	3.1	7.7	8.4		24.0	YGAATFTR	1013.5	1014.5	1013.5	1014.5
214.0	3.2	5.2	7.8	2.0	99.0	DLFHCVSFTLPR	1490.7	1491.7	1490.7	1491.7
214.0	3.2	5.2	7.8	1.0	91.0	FEIENCLANK	1275.6	1276.6	1275.6	1276.6
214.0 P21291 CS	3.2	5.2	7.8 Cysteine and	0.0	99.0	GRNQGNTWLTAFVLK (Cysteine-rich protein 1) (CRP1) - Bos tar	1635.8	1636.8	1635.8	1636.8
527.0	2.0	2.0	7.8	2.0	99.0	GFGFGQGAGALVHSE	1432.7	1433.7	1432.7	1433.7
360.0	2.0	2.0	7.8	2.0	99.0	GFGFGQGAGALVHSE	1432.7	1433.7	1432.7	1433.7
P21333 FLI 24.0	27.7	27.7	Filamin-A (A	2.0	99.0	(Endothelial actin-binding protein) (Ac AEAGVPAEFSIWTR	1532.8	1533.8	1532.8	1533.8
24.0	27.7	27.7	14.3	2.0	99.0	AFGPGLQGGSAGSPAR	1428.7	1429.7	1428.7	1429.7
24.0	27.7	27.7	14.3	2.0	99.0	ATCAPQHGAPGPGPADASK	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 24.0 24.0	27.7 27.7 27.7	27.7 27.7 27.7	14.3 14.3 14.3	2.0 2.0 2.0	99.0 99.0 99.0	EATTEFSVDAR LSPFMADIR	1423.7 1224.6 1048.5	1225.6 1049.6	1423.7 1224.6 1048.5	1225.6 1049.5
24.0	27.7 27.7	27.7	14.3 14.3	2.0	99.0 99.0	VANPSGNLTETYVQDR VHGPGIQSGTTNKPNKFTVETR	1762.9 2367.2	1763.9 2368.2	1762.8 2367.2	1763.9 2368.2
24.0	27.7	27.7	14.3	2.0	99.0	VHSPSGALEECYVTEIDQDKYAVR	2765.3	2766.3	2765.3	2766.3
24.0	27.7	27.7	14.3		99.0	WGDEHIPGSPYR	1412.6	1413.7	1412.6	1413.7
24.0	27.7	27.7	14.3	2.0	99.0	YGGQPVPNFPSK	1289.6	1290.6	1289.6	1290.6
24.0	27.7	27.7	14.3	2.0	99.0	YNEQHVPGSPFTAR	1601.8	1602.8	1601.8	1602.8
24.0	27.7	27.7	14.3	1.5	97.0	YGGDEIPFSPYRVR	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	AFGPGLQGGSAGSPAR	1428.7	1429.7	1428.7	1429.7
29.0	10.2	10.2	7.9	2.0	99.0	AGNNMLLVGVHGPR	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	WGDEHIPGSPYR	1412.6	1413.7	1412.6	1413.7
29.0	10.2	10.2	7.9	0.3	46.0	VANPSGNLTETYVQDR	1762.9	1763.9	1762.8	1763.9
29.0	10.2	10.2	7.9	0.1	27.0	LQVEPAVDTSGVQCYGPGIEGQGVFR	2763.3	2764.3	2762.3	2763.3
36.0 36.0 36.0	18.9 18.9 18.9	18.9 18.9 18.9	13.4 13.4 13.4	2.0 2.0 2.0	99.0 99.0 99.0	AEAGVPAEFSIWTR AFGPGLQGGSAGSPAR	1532.8 1428.7 1788.8	1533.8 1429.7 1789.8	1532.8 1428.7 1788.8	1533.8 1429.7 1789.8
36.0 36.0 36.0	18.9 18.9 18.9	18.9 18.9 18.9	13.4 13.4 13.4	2.0 2.0 2.0	99.0 99.0 99.0	ATCAPQHGAPGPGPADASK AWGPGLEGGVVGK WGDEHIPGSPYR	1788.8 1225.6 1412.7	1789.8 1226.6 1413.7	1225.6	1226.7
36.0 36.0	18.9 18.9	18.9 18.9	13.4 13.4 13.4	2.0 2.0 2.0	99.0 99.0 99.0	YGGPYHIGGSPFK YGGQPVPNFPSK	1378.7 1289.6	1379.7 1290.7	1412.6 1378.7 1289.6	1413.7 1379.7 1290.6
36.0 36.0	18.9 18.9	18.9 18.9	13.4 13.4 13.4	1.5 1.5	97.0 97.0	DAPQDFHPDRVK VANPSGNLTETYVQDR	1423.7 1762.9	1424.7 1763.9	1423.7 1762.8	1424.7 1763.9
36.0	18.9	18.9	13.4	1.2	93.0	LQVEPAVDTSGVQCYGPGIEGQGVFR	2762.3	2763.3	2762.3	2763.3
36.0	18.9	18.9	13.4		80.0	TGVAVNKPAEFTVDAK	1645.9	1646.9	1645.9	1646.9
36.0	18.9 BE1_HUMAN	18.9	13.4 Ubiquitin-act	0.0	56.0	AEAGVPAEFSIWTR S9 protein) - Homo sapiens (Human)	1528.8	1529.8	1532.8	1533.8
226.0	5.4	5.4	5.3	2.0	99.0	NEEDAAELVALAQAVNAR	1882.9	1883.9	1882.9	1883.9
226.0	5.4	5.4	5.3	2.0	99.0	QLYVLGHEAMKR	1426.7	1427.7	1426.7	1427.7
226.0	5.4	5.4	5.3	1.2	94.0	VGEFCHNR	1017.5	1018.5	1017.4	1018.5
226.0	5.4	5.4	5.3	0.2	30.0	QFLFRPWDVTK	1435.8	1436.8	1435.8	1436.8
261.0	2.2	2.2	9.4	2.0	99.0	NEEDAAELVALAQAVNAR	1882.9	1883.9	1882.9	1883.9
261.0	2.2	2.2	9.4	0.2	30.0	ALPAVQQNNLDEDLIR	1806.8	1807.8	1806.9	1807.9
P22392 NE 140.0 140.0	8.0 8.0	8.0 8.0	48.7 48.7	2.0 2.0 2.0	99.0 99.0	C 2.7.4.6) (NDK B) (NDP kinase B) (nm23 GDFCIQVGR	3-H2) (C-myc purine-l 1050.5 2310.2	1051.5	1050.5	1051.5
140.0 140.0 140.0	8.0 8.0 8.0	8.0 8.0 8.0	48.7 48.7 48.7	2.0	99.0 99.0 99.0	SAEKEISLWFKPEELVDYK TFIAIKPDGVQR VMLGETNPADSKPGTIR	1343.8 1784.9	2311.2 1344.8 1785.9	2310.2 1343.8 1784.9	2311.2 1344.8 1785.9
131.0 131.0	6.0 6.0	6.0 6.0	44.7 44.7 44.7	2.0	99.0 99.0	GDFCIQVGR TFIAIKPDGVQR	1050.5 1343.7	1051.5 1344.8	1050.5 1343.8	1051.5 1344.8
131.0 P27695 AP	6.0	6.0	44.7 DNA-(apurin	2.0	99.0 midinic site)	VMLGETNPADSKPGTIR lyase (EC 4.2.99.18) (AP endonuclease 1	1784.9	1785.9	1784.9	1785.9
158.0	7.6	7.6	24.8	2.0	99.0	GLDWVKEEAPDILCLQETK	2243.1	2244.1	2243.1	2244.1
158.0	7.6	7.6	24.8		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	NAGFTPQER	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	QGFGELLQAVPLADSFR	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
	2.0 PQ_HUMAN	2.0				ICSWNVDGLR ine-rich (Polypyrimidine tract-binding pro				
52.0 52.0	17.2 17.2	17.2 17.2	23.6 23.6	2.0	99.0 99.0	FAQHGTFEYEYSQR FGQGGAGPVGGQGPR GIVEFASKPAAR	1761.8 1340.7	1762.8 1341.7	1761.8 1340.7	1762.8 1341.7
52.0 52.0 52.0	17.2 17.2 17.2	17.2 17.2 17.2	23.6 23.6 23.6	2.0 2.0 2.0	99.0 99.0 99.0	LFVGNLPADITEDEFKR QHHPPYHQQHHQGPPPGGPGR	1244.7 1963.0 2385.1	1245.7 1964.0 2386.1	1244.7 1963.0 2385.1	1245.7 1964.0 2386.1
52.0	17.2	17.2	23.6	2.0	99.0	RMEELHNOEMOKR	1727.8	1728.8	1727.8	1728.8
52.0	17.2	17.2	23.6		99.0	TERFGQGGAGPVGGQGPR	1726.9	1727.9	1726.8	1727.9
52.0	17.2	17.2	23.6	1.2	94.0	GGRQHHPPYHQQHHQGPPPGGPGGR	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	FAQHGTFEYEYSQR	1761.8	1762.8	1761.8	1762.8
134.0	6.0	6.0	25.2	2.0	99.0	FAQHGTFEYEYSQR	1761.8	1762.8	1761.8	1762.8
134.0	6.0	6.0	25.2	2.0	99.0	YGEPGEVFINKGK	1436.7	1437.7	1436.7	1437.7
134.0	6.0	6.0	25.2	1.0	91.0	FGQGGAGPVGGQGPR	1340.7	1341.7	1340.7	1341.7
134.0	6.0	6.0	25.2	0.4	61.0	RPGEKTYTQRCR	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	RMEELHNQEMQKR	1727.8	1728.8	1727.8	1728.8
P23284 PP 142.0	2.1	2.1	Peptidyl-pro 6.7 10.1	2.0	99.0	B precursor (EC 5.2.1.8) (PPLase) (Rotan VIFGLFGK SIYGERFPDENFKLK	879.5	880.5	879.5 1841.9	880.5
248.0 248.0 248.0	2.3 2.3	2.3	10.1 10.1 10.1	2.0 0.3 0.0	47.0 34.0	VYFDLR VYFDLR VYFDLR	1841.9 859.4 811.4	1842.9 860.4 812.4	859.4 811.4	1842.9 860.4
248.0	2.3 2.3 WC_HUMAN	2.3 2.3	10.1	0.0	27.0	VYFDLR VYFDLR oplasmic (EC 6.1.1.2) (TryptophantRNA	843.4	844.4	811.4 843.4 Homo sapiens (Hur	812.4 844.4
43.0 43.0	19.9	19.9 19.9	32.9 32.9	2.0	99.0 99.0	ATGQRPHHFLR ATGQRPHHFLRR	1318.7 1474.8	1319.7 1475.8	1318.7 1474.8	1319.7 1475.8
43.0	19.9	19.9	32.9	2.0	99.0	EVTDEIVKEFMTPR	1692.8	1693.9	1692.8	1693.8
43.0	19.9	19.9	32.9		99.0	GIDYDKLIVR	1190.7	1191.7	1190.7	1191.7
43.0	19.9	19.9	32.9	2.0	99.0	HAFSGGRDTIEEHR	1610.8	1611.8	1610.8	1611.8
43.0	19.9	19.9	32.9	2.0	99.0	MSASDPNSSIFLTDTAK	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	TDIQCLIPCAIDQDPYFR	2224.0	2225.0	2224.0	2225.0
43.0	19.9	19.9	32.9	2.0	99.0	VNKHAFSGGRDTIEEHR	1952.0	1953.0	1952.0	1953.0
43.0	19.9	19.9	32.9	1.4	96.0	ALIEVLQPLIAEHQAR	1800.0	1801.0	1800.0	1801.0
43.0	19.9	19.9	32.9	0.5	68.0	GIFFSHR	862.4	863.5	862.4	863.5
43.0	19.9	19.9	32.9	0.0	11.0	ATGQRPHHFLR	1318.7	1319.7	1318.7	1319.7
110.0	3.1	3.1	24.8	2.0	99.0	GIDYDKLIVR	1190.7	1191.7	1190.7	1191.7
110.0	3.1	3.1	24.8	1.0	90.0	ATGQRPHHFLRR	1474.8	1475.8	1474.8	1475.8
110.0	3.1	3.1	24.8	0.1	20.0	MSASDPNSSIFLTDTAK	1783.8	1784.8	1783.8	1784.8
38.0	18.5	18.5	32.7	2.0	99.0	ALIEVLQPLIAEHQAR	1800.0	1801.0	1800.0	1801.0
38.0 38.0	18.5 18.5	18.5 18.5	32.7 32.7	2.0	99.0 99.0	EVTDEIVKEFMTPR FGSSKIDKELINR GIDVDKI IVR	1692.8 1505.8	1693.9 1506.8	1692.8 1505.8	1693.8 1506.8
38.0	18.5	18.5	32.7	2.0	99.0	GIDYDKLIVR	1190.7	1191.7	1190.7	1191.7
38.0	18.5	18.5	32.7	2.0	99.0	MSASDPNSSIFLTDTAK	1783.8	1784.8	1783.8	1784.8
38.0	18.5	18.5	32.7	2.0	99.0	RKEVTDEIVKEFMTPR	1977.0	1978.0	1977.0	1978.0
38.0 38.0 38.0	18.5 18.5 18.5	18.5 18.5 18.5	32.7 32.7 32.7	2.0 2.0 1.4	99.0 99.0 96.0	TKVNKHAFSGGRDTIEEHR GIFFSHR	2181.1 862.4	2182.1 863.5	2181.1 862.4	2182.1 863.5
38.0	18.5	18.5	32.7	1.0	90.0	KLSFDFQ	883.4	884.5	883.4	884.5

38.0 38.0	18.5 18.5	18.5 18.5	32.7 32.7	0.9 0.7	86.0 80.0	ATGQRPHHFLRR ATGQRPHHFLR	1474.8 1318.7	1475.8 1319.7	1474.8 1318.7	1475.8 1319.7
38.0 38.0	18.5 18.5 COF1_HUMAN	18.5 18.5	32.7 32.7 Cofilin-1 (Co	0.4 0.0	56.0 68.0 -muscle isofor	IDKELINR ATGQRPHHFLRR m) (18 kDa phosphoprotein) (p18) - Homo sa	999.6 1474.8	1000.6 1475.8	999.6 1474.8	1000.6 1475.8
42.0	7.2	7.2	29.5 29.5	2.0	99.0	ASGVAVSDGVIKVFNDMK	1877.9	1878.9	1878.0	1879.0
42.0 42.0	7.2 7.2	7.2 7.2	29.5	2.0	99.0 99.0	KLTGIKHELOANCYEEVKDR LTGIKHELOANCYEEVKDR	2430.2 2302.1	2431.2 2303.1	2430.2 2302.1	2431.2 2303.1
42.0 37.0	7.2 22.3	7.2 22.3	29.5 51.8	1.2 2.0	94.0 99.0	YALYDATYETK ASGVAVSDGVIK	1336.6 1143.6	1337.6 1144.6	1336.6 1143.6	1337.6 1144.6
37.0 37.0	22.3 22.3	22.3 22.3	51.8 51.8	2.0 2.0	99.0 99.0	ASGVAVSDGVIKVFNDMK ASGVAVSDGVIKVFNDMKVR	1877.9 2133.1	1879.0 2134.1	1878.0 2133.1	1879.0 2134.1
37.0 37.0	22.3 22.3	22.3 22.3	51.8 51.8	2.0 2.0	99.0 99.0	ESKKEDLVFIFWAPESAPLK ESKKEDLVFIFWAPESAPLKSK	2333.2 2548.4	2334.2 2549.4	2333.2 2548.4	2334.2 2549.4
37.0 37.0	22.3 22.3	22.3 22.3	51.8 51.8	2.0 2.0	99.0 99.0	HELQANCYEEVKDR KEDLVFIFWAPESAPLK	1789.8 1989.1	1790.8 1990.1	1789.8 1989.1	1790.8 1990.1
37.0 37.0	22.3 22.3	22.3 22.3	51.8 51.8	2.0 2.0	99.0 99.0	KLTGIKHELQANCYEEVKDR LTGIKHELQANCYEEVKDR	2430.3 2302.1	2431.4 2303.1	2430.2 2302.1	2431.2 2303.1
37.0 37.0	22.3	22.3 22.3	51.8 51.8	2.0 2.0	99.0 99.0	VFNDMKVR YALYDATYETK	1007.5 1336.6	1008.5 1337.6	1007.5 1336.6	1008.5 1337.6
37.0 54.0	22.3 13.7	22.3 13.7	51.8 60.2	0.3 2.0	50.0 99.0	MLPDKDCR ESKKEDLVFIFWAPESAPLK	1033.5 2333.2	1034.5 2334.2	1033.5 2333.2	1034.5 2334.2
54.0	13.7	13.7	60.2	2.0	99.0	HELQANCYEEVKDR	1789.8	1790.8	1789.8	1790.8
54.0 54.0	13.7 13.7	13.7 13.7	60.2 60.2	2.0 2.0	99.0 99.0	KLTGIKHELQANCYEEVKDR LTGIKHELQANCYEEVKDR	2431.2 2302.1	2432.2 2303.1	2431.2 2302.1	2432.2 2303.1
54.0 54.0	13.7 13.7	13.7 13.7	60.2 60.2	2.0 2.0	99.0 99.0	MIYASSKDAIKK YALYDATYETK	1353.7 1336.6	1354.7 1337.6	1353.7 1336.6	1354.7 1337.6
54.0 54.0	13.7 13.7	13.7 13.7	60.2 60.2	1.7 0.0	98.0 99.0	ASGVAVSDGVIKVFNDMKVR LTGIKHELQANCYEEVKDR	2133.1 2303.1	2134.1 2304.1	2133.1 2303.1	2134.1 2304.1
139.0	CATS_HUMAN 8.1	8.1	Cathepsin S 20.5	2.0	99.0	HPSFFLYR	1065.5	1066.5	1065.5	1066.5
139.0 139.0		8.1 8.1	20.5 20.5	2.0 2.0	99.0 99.0	NKGNHCGIASFPSYPEI NSWGHNFGEEGYIR	1889.9 1664.7	1890.9 1665.7	1889.9 1664.7	1890.9 1665.7
139.0 139.0		8.1 8.1	20.5 20.5	2.0 0.1	99.0 22.0	YTELPYGREDVLK YTELPYGR	1581.8 997.5	1582.8 998.5	1581.8 997.5	1582.8 998.5
139.0 39.0	8.1 8.0	8.1 8.0	20.5 30.2	0.0 2.0	99.0 99.0	NSWGHNFGEEGYIR HPSFFLYR	1665.7 1065.5	1666.7 1066.5	1665.7 1065.5	1666.7 1066.5
39.0 39.0	8.0 8.0	8.0 8.0	30.2 30.2	2.0 2.0	99.0 99.0	NKGNHCGIASFPSYPEI NSWGHNFGEEGYIR	1889.9 1664.7	1890.9 1665.7	1889.9 1664.7	1890.9 1665.7
39.0 58.0	8.0 13.0	8.0 13.0	30.2 23.3	2.0	99.0 99.0	YTELPYGREDVLK EAVANKGPVSVGVDAR	1581.8 1567.8	1582.8 1568.8	1581.8 1567.8	1582.8 1568.8
58.0 58.0	13.0 13.0	13.0 13.0	23.3 23.3	2.0 2.0	99.0 99.0	HPSFFLYR LPDSVDWR	1065.5	1066.5	1065.5 986.5	1066.5
58.0	13.0	13.0	23.3	2.0	99.0	LPDSVDWREK	986.5 1243.6	987.5 1244.6	1243.6	987.5 1244.6
58.0 58.0	13.0 13.0	13.0 13.0	23.3 23.3	2.0 2.0	99.0 99.0	NSWGHNFGEEGYIR YTELPYGREDVLK	1664.7 1581.8	1665.7 1582.8	1664.7 1581.8	1665.7 1582.8
58.0 58.0	13.0 13.0	13.0 13.0	23.3 23.3	0.9 0.1	87.0 25.0	GIDSDASYPYKAMDQK YTELPYGR	1803.8 997.5	1804.8 998.5	1803.8 997.5	1804.8 998.5
58.0 58.0	13.0 13.0	13.0 13.0	23.3 23.3	0.0 0.0	98.0 99.0	HPSFFLYR NSWGHNFGEEGYIR	1077.5 1665.7	1078.5 1666.7	1077.6 1665.7	1078.6 1666.7
58.0 P25786	13.0 PSA1_HUMAN	13.0	23.3 Proteasome	0.0 subunit a	99.0 Ipha type 1 (E	NSWGHNFGEEGYIR C 3.4.25.1) (Proteasome component C2) (Mac	1676.7 cropain subunit	1677.8 C2) (Multicataly)	1676.7 tic endopeptidas	1677.7 e complex subun
135.0 135.0	2.2 2.2	2.2 2.2	13.7 13.7	2.0 0.2	99.0 34.0	NQYDNDVTVWSPQGR FVFDRPLPVSR	1777.8 1331.7	1778.8 1332.7	1777.8 1331.7	1778.8 1332.7
118.0 118.0		9.7 9.7	26.2 26.2	2.0 2.0	99.0 99.0	AQPAQPADEPAEKADEPMEH HMSEFMECNLNELVK	2159.9 1879.8	2160.9 1880.8	2159.9 1879.8	2161.0 1880.8
118.0 118.0	9.7	9.7 9.7	26.2 26.2	2.0	99.0 99.0	LLCNFMR NQYDNDVTVWSPQGR	952.5 1777.8	953.5 1778.8	952.5 1777.8	953.5 1778.8
118.0	9.7	9.7	26.2	1.7	98.0	FVFDRPLPVSR	1331.7	1332.7	1331.7	1332.7
144.0 144.0	5.3 5.3	5.3 5.3	26.2 26.2	2.0	99.0 99.0	AQPAQPADEPAEKADEPMEH IHQIEYAMEAVK	2159.9 1430.7	2160.9 1431.7	2159.9 1430.7	2161.0 1431.7
144.0	5.3	5.3 5.3	26.2 26.2	0.8 0.5	84.0 65.0	NQYDNDVTVWSPQGR FVFDRPLPVSR	1778.8 1331.7	1779.8 1332.7	1778.8 1331.7	1779.8 1332.7
144.0	5.3	5.5								
P25787 435.0	PSA2_HUMAN 2.0	2.0	Proteasome 18.4	subunit a	lpha type 2 (E 99.0	C 3.4.25.1) (Proteasome component C3) (Mac HIGLVYSGMGPDYR	cropain subunit 1563.7	C3) (Multicataly) 1564.7	tic endopeptidas 1563.8	e complex subun 1564.8
P25787 435.0 187.0 273.0	PSA2_HUMAN 2.0 2.0 2.1		Proteasome 18.4 6.0 17.9	2.0 2.0 2.0 2.0 2.0	Ipha type 2 (E 99.0 99.0 99.0	CC 3.4.25.1) (Proteasome component C3) (Mar HIGLVYSGMGPDYR HIGLVYSGMGPDYR HIGLVYSGMGPDYR	1563.7 1563.8 1563.8 1563.8	C3) (Multicataly) 1564.7 1564.8 1564.8	tic endopeptidas 1563.8 1563.8 1563.8	e complex subun 1564.8 1564.8 1564.8
P25787 435.0 187.0 273.0 P25789 524.0	PSA2_HUMAN 2.0 2.0 2.1 PSA4_HUMAN	2.0 2.0 2.1	Proteasome 18.4 6.0	2.0 2.0 2.0 2.0 2.0	lpha type 2 (E 99.0 99.0 99.0 99.0 lpha type 4 (E 99.0	C. 3.4.25.1) (Proteasome component C3) (Mar HIGLVYSGMGPDYR HIGLVYSGMGPDYR HIGLVYSGMSPDYR C. 3.4.25.1) (Proteasome component C9) (Mar LLDEVFFSEK	cropain subunit 1563.7 1563.8 1563.8 cropain subunit 1225.6	C3) (Multicataly) 1564.7 1564.8 1564.8 C9) (Multicataly) 1226.6	tic endopeptidas 1563.8 1563.8 1563.8 tic endopeptidas 1225.6	e complex subun 1564.8 1564.8
P25787 435.0 187.0 273.0 P25789	PSA2_HUMAN 2.0 2.0 2.1 PSA4_HUMAN	2.0 2.0 2.1	18.4 6.0 17.9 Proteasome	subunit a 2.0 2.0 2.0 2.0 e subunit a	Ipha type 2 (E 99.0 99.0 99.0 Ipha type 4 (E	C. 3.4.25.1) (Proteasome component C3) (Mai HIGLVYSGMGPDYR HIGLVYSGMGPDYR HIGLVYSGMGPDYR IC 3.4.25.1) (Proteasome component C9) (Mai	cropain subunit 1563.7 1563.8 1563.8 cropain subunit	C3) (Multicataly) 1564.7 1564.8 1564.8 C9) (Multicataly)	tic endopeptidas 1563.8 1563.8 1563.8 tic endopeptidas	e complex subun 1564.8 1564.8 1564.8 e complex subun
P25787 435.0 187.0 273.0 P25789 524.0 147.0 359.0	PSA2_HUMAN 2.0 2.0 2.1 PSA4_HUMAN 2.0 2.0	2.0 2.0 2.1 2.0 2.0	Proteasome 18.4 6.0 17.9 Proteasome 3.8 12.6 3.8	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	Ipha type 2 (E 99.0 99.0 99.0 1pha type 4 (E 99.0 99.0 99.0	(C.3.4.25.1) (Proteasome component C3) (Mai HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR (C.3.4.25.1) (Proteasome component C9) (Mai LLDEVFFSEK	2000 1563.7 1563.8 1563.8 1563.8 2000 1563.8 2000 1563.8 2000 1563.8 2000 1563.8 2000 1563.8 2000 1563.8	C3) (Multicataly) 1564.7 1564.8 1564.8 C9) (Multicataly) 1226.6 1226.6	tic endopeptidas 1563.8 1563.8 1563.8 tic endopeptidas 1225.6 1225.6	e complex subun 1564.8 1564.8 1564.8 e complex subun 1226.6 1226.6
P25787 435.0 187.0 273.0 P25789 524.0 147.0 359.0 P26038	PSA2_HUMAN 2.0 2.0 2.1 PSA4_HUMAN 2.0 2.0 2.0 2.0 MOES_HUMAN	2.0 2.0 2.1 2.0 2.0 2.0 2.0 53.4 53.4	Proteasome 18.4 6.0 17.9 Proteasome 3.8 12.6 3.8 Moesin (Mer 55.3 55.3	e subunit a 2.0 2.0 2.0 2.0 e subunit a 2.0 2.0 2.0 2.0 mbrane-or	Ipha type 2 (E 99.0 99.0 99.0 1pha type 4 (E 99.0 99.0 99.0 ganizing exte 99.0 99.0	(C.3.4.25.1) (Proteasome component C3) (Mai HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR (C.3.4.25.1) (Proteasome component C9) (Mai LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK MISION Spike protein) - Homo sapiens (Human) AKFYPEDVSEELIODITOR APDFVFYAPD	ropain subunit 1563.7 1563.8 1563.8 1563.8 cropain subunit 1225.6 1225.6 1225.6	C3) (Multicataly) 1564.7 1564.8 1564.8 C9) (Multicataly) 1226.6 1226.6 1226.6	tic endopeptidas 1563.8 1563.8 1563.8 1563.8 tic endopeptidas 1225.6 1225.6 1225.6	e complex subun 1564.8 1564.8 1564.8 e complex subun 1226.6 1226.6 1226.6
P25787 435.0 187.0 273.0 P25789 524.0 147.0 359.0 P26038 5.0 5.0 5.0	PSA2_HUMAN	2.0 2.0 2.1 2.0 2.0 2.0 2.0 53.4 53.4 53.4	Proteasome 18.4 6.0 17.9 Proteasome 3.8 12.6 3.8 Moesin (Mer 55.3 55.3 55.3 55.3	e subunit a 2.0 2.0 2.0 e subunit a 2.0 2.0 2.0 mbrane-or 2.0 2.0 2.0	Ipha type 2 (E 99.0 99.0 99.0 1pha type 4 (E 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	(C.3.4.25.1) (Proteasome component C3) (Mai HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR (C.3.4.25.1) (Proteasome component C9) (Mai LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK HIGHER (HUMAN) - Homo sapiens (Human) AKFYPEDVSEELIGDITOR APDFVFYAPR AOMVGEDLEKTRAELK	cropain subunit 1563.7 1563.8 1563.8 1563.8 cropain subunit 1225.6 1225.6 1225.6 2280.1 1181.6 1446.7 1888.0	C3) (Multicataly/ 1564.8 1564.8 1564.8 1564.8 1226.6 1226.6 1226.6 2281.1 1182.6 1447.7 1889.0	tic endopeptidas 1563.8 1563.8 1563.8 1563.8 tic endopeptidas 1225.6 1225.6 1225.6 2280.1 1181.6 1446.7 1888.0	e complex subun 1564.8 1564.8 1564.8 1564.8 1564.8 e complex subun 1226.6 1226.6 1226.6 1447.7 1889.0
P25787 435.0 187.0 273.0 P25789 524.0 359.0 P26038 5.0 5.0 5.0 5.0 5.0	PSA2_HUMAN	2.0 2.0 2.1 2.0 2.0 2.0 2.0 53.4 53.4 53.4 53.4 53.4	Proteasome 18.4 6.0 17.9 Proteasome 3.8 12.6 3.8 Moesin (Mer 55.3 55.3 55.3 55.3 55.3 55.3	e subunit a 2.0 2.0 2.0 2.0 2 subunit a 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	Ipha type 2 (E 99.0 99.0 99.0 99.0 1pha type 4 (E 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	(C.3.4.25.1) (Proteasome component C3) (Mai HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR (C.3.4.25.1) (Proteasome component C9) (Mai LIDEVFFSEK LIDEVFFSEK LIDEVFFSEK LIDEVFFSEK HOPEVFSEK INDEVFENT (HOPEVFSEK) AGNOVEDLEKTRAELK ROMOVEDLEKTRAELK ESEAVEWOOK ESPLIFKER	cropain subunit 1563.7 1563.8 1563.8 1563.8 225.6 1225.6 1225.6 1225.6 2280.1 1181.6 1446.7 1888.0 1232.6	C3) (Multicataly: 1564.8 1564.8 1564.8 1564.8 1564.8 1226.6 1226.6 1226.6 1226.6 1447.7 1889.0 1233.6 1136.7	tic endopeptidas 1563.8 1563.8 1563.8 1563.8 tic endopeptidas 1225.6 1225.6 1225.6 2280.1 1181.6 1446.7 1888.0 1232.6 1135.6	e complex subun 1564.8 1564.8 1564.8 1564.8 1226.6 1226.6 1226.6 1226.6 1447.7 1889.0 1233.6 1136.6
P25787 435.0 187.0 273.0 P25789 524.0 147.0 359.0 P26038 5.0 5.0 5.0 5.0 5.0 5.0 5.0	PSA2_HUMAN	2.0 2.0 2.1 2.0 2.0 2.0 2.0 53.4 53.4 53.4 53.4 53.4 53.4	Proteasome 18.4 6.0 17.9 Proteasome 3.8 12.6 3.8 Moesin (Mer 55.3 55.3 55.3 55.3 55.3 55.3 55.3	e subunit a 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	Ipha type 2 (E 990 990 990 990 990 990 990 990 990 99	IC. 3.4.25.1) (Proteasome component C3) (Mai HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR IC. 3.4.25.1) (Proteasome component C9) (Mai LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK HORDEVFSEK	cropain subunit 1563.7 1563.8 1563.8 1563.8 1225.6 1225.6 1225.6 1225.6 1225.6 1232.6 1181.6 1446.7 1888.0 1232.6 1135.6 1659.8 2081.0	C3) (Multicataly: 1564 8 1564 8 1564 8 1564 8 1226 6 1226 6 1226 6 1447.7 1889.0 1233.6 1136.7 1660.8 2082.0	tic endopeptidas 1563.8 1563.8 1563.8 1255.6 1225.6 1225.6 2280.1 1181.6 1446.7 1888.0 1232.6 1135.6 1659.8 2081.0	e complex subun 1564.8 1564.8 1564.8 1564.8 e complex subun 1226.6 1226.6 1226.6 1447.7 1889.0 1233.6 1136.6 1660.8 2082.0
P25787 435.0 187.0 273.0 P25789 524.0 147.0 359.0 P26038 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0	PSA2_HUMAN	2.0 2.0 2.1 2.0 2.0 2.0 53.4 53.4 53.4 53.4 53.4 53.4 53.4 53.4	Proteasome 18.4 4.6.0 17.9 Proteasome 3.8 12.6 3.8 Moesin (Mer 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	subunit a 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	Ipha type 2 (IC. 3.4.25.1) (Proteasome component C3) (Mai HIGLVYSGMGPDYR HIGLVYSGMGPDYR HIGLVYSGMGPDYR HIGLVYSGMGPDYR HIGLYYSGMGPDYR HIGLYYSGMGPDYR HIGLOVFFSEK LDEVFFSEK AUMOGEDLEKTR ADMYGEDLEKTR A	cropain subunit 1563.7 1563.8 1563.8 1225.6 1225.6 1225.6 1225.6 1225.6 1225.6 1232.6 135.6 135.6 135.6 135.6 135.6 135.6 135.6 135.6 135.6 135.6 135.6 135.6 135.6 135.8 135.8	C3) (Multicataly: 1564.7 1564.8 1564.8 1564.8 1564.8 C9) (Multicataly: 1226.6 1226.6 1226.6 1226.6 1447.7 1889.0 1233.6 1136.7 1660.8 2082.0 1104.6 1720.8	tic endopeptidas 1563.8 1563.8 1563.8 1563.8 1256.6 1225.6 1225.6 1225.6 1225.6 1232.6 1181.6 1446.7 1888.0 1232.6 1135.6 1659.8 2081.0 1103.6 1719.8	e complex subun 1564.8 1564.8 e complex subun 1226.6 1226.6 1226.6 1447.7 1889.0 1233.6 1136.6 1660.8 2082.0 1104.6 1720.8
P25787 435.0 187.0 273.0 P25789 524.0 147.0 359.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5	PSA2_HUMAN	2.0 2.0 2.1 2.0 2.0 2.0 53.4 53.4 53.4 53.4 53.4 53.4 53.4 53.4	Proteasome 18.4 4.6.0 17.9 Proteasome 3.8 12.6 3.8 Moesin (Mer 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	20 2.0 2.0 2.0 mbrane-or 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	Ipha type 2 (E 990 990 990 990 990 990 990 990 990 99	(C.3.4.25.1) (Proteasome component C3) (Mai HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR G.3.4.25.1) (Proteasome component C9) (Mai LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK ADMYCEDLEKTRALK ESEAVEWOOK ESPLIEKER EVWFFGLOYODTK FYPEDVSEELIODITOR IGFWSEIR ILALOMGHELKTRALK ESEAVEWOOK ESPLIEKER EVWFFGLOYODTK FYPEDVSEELIODITOR IGFWSEIR ILALOMGHHELYMR IOWHEEHR ISOLEMAR	cropain subunit 1563.8 1563.8 1563.8 1563.8 1225.6 1225.6 1225.6 1225.6 1225.6 1232.6 133.6 133.6 133.6 1659.8 2081.0 1103.6 1719.8 1232.6 946.5	C3) (Multicataly/ 1564 8 1564.8 1564.8 1564.8 1564.8 1226.6 1226.6 1226.6 1233.6 1447.7 1889.0 1233.6 1136.7 1660.8 2082.0 1104.6 1720.8 1233.6 947.5	tic endopeptidas 1563.8 1563.8 1563.8 1563.8 1225.6 1225.6 1225.6 1225.6 1232.6 1313.6	e complex subun 1564.8 1564.8 1564.8 1564.8 e complex subun 1226.6 1226.6 1226.6 1231.1 1182.6 1447.7 1889.0 1233.6 1136.6 160.8 2082.0 1104.6 1720.8 1233.6 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8 1720.8
P25787 4350.0 273.0 P25789] 524.0 3759.0 P26038] 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0	PSA2_HUMAN	2.0 2.0 2.1 2.0 2.0 2.0 2.0 53.4 53.4 53.4 53.4 53.4 53.4 53.4 53.4	Proteasome 18.4 4.6.0 17.9 Proteasome 3.8 12.6 3.8 Moesin (Mei 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	e subunit a 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	Ipha type 2 (E 990 990 990 990 990 990 990 990 990 99	IC. 3.4.25.1) (Proteasome component C3) (Mai HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR HIGLIVYSGMGPDYR C. 3.4.25.1) (Proteasome component C9) (Mai LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK LLDEVFFSEK AUDEVFFSEK LLOPIFFSEK AUDEVFFSEK AUDEVFFSEK AUDEVFFSEK AUDEVFFSEK AUDEVFFSEK AUDEVFSEK AUDEVF	cropain subunit 1563.7 1563.8 1563.8 1563.8 1563.8 1225.6 1225.6 1225.6 1225.6 1225.6 1225.6 1232.6 1335.6 1446.7 1888.0 1232.6 1335.6 1659.8 2081.0 1103.6 1719.8 1232.6 1309.7 1514.8	C3) (Multicataly/ 1564 7 1564 8 1564.8 1564.8 1564.8 1226.6 1226.6 1226.6 1233.6 1447.7 1889.0 1233.6 1136.7 1660.8 2082.0 1104.6 1720.8 1233.6 947.5 1310.7 1515.8	tic endopeptidas 1563.8 1563.8 1563.8 1563.8 1225.6 1225.6 1225.6 1225.6 1225.6 1232.6 1332.6 1332.6 1332.6 1332.6 1332.6 1335.6 1719.8 1232.6 1309.7 1514.8	e complex subun 1564.8 1564.8 1564.8 1564.8 1664.8 1226.6 1226.6 1226.6 1226.6 1231.1 1182.6 1447.7 1889.0 1233.6 1136.6 1660.8 2082.0 1104.6 1720.8 1233.6 1310.7 1515.8
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7.0	44.9	44.9	56.7	2.0	99.0	KAPDFVFYAPR	1309.7	1310.7	1309.7	1310.7
7.0	44.9 44.9	44.9 44.9	56.7 56.7	2.0	99.0 99.0	KTANDMIHAENMR RKPDTIEVQQMK	1529.7	1530.7 1530.7 1472.8	1529.7 1471.8	1530.7 1530.7 1472.8
7.0 7.0 7.0	44.9 44.9	44.9 44.9	56.7 56.7	2.0 2.0 2.0	99.0 99.0	RRKPDTIEVQQMK SGYLAGDKLLPQR	1471.8 1627.9 1416.8	1628.9 1417.8	1627.9 1416.8	1628.9 1417.8
7.0	44.9 44.9	44.9 44.9 44.9	56.7	2.0 2.0 2.0	99.0	TANDMIHAENMR TOEOLALEMAELTAR	1401.6	1402.6 1703.9	1401.6	1402.6
7.0 7.0	44.9	44.9	56.7 56.7	2.0	99.0 99.0	VLEQHKLNKDQWEER	1702.8 1951.0	1952.0	1702.9 1951.0	1703.9 1952.0
7.0	44.9	44.9	56.7	2.0	99.0	YGDFNKEVHK	1235.6	1236.6	1235.6	1236.6
7.0	44.9	44.9	56.7	1.7	98.0	LFFLQVK	893.5	894.5	893.5	894.5
7.0	44.9	44.9	56.7	1.5	97.0	QRIDEFESM	1136.5	1137.5	1136.5	1137.5
7.0	44.9	44.9	56.7	1.4	96.0	FYPEDVSEELIQDITQR	2081.0	2082.0	2081.0	2082.0
7.0	44.9	44.9	56.7	1.2	94.0	ESPLLFKFR	1135.6	1136.6	1135.6	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	1988.9	1989.9	1988.9	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	RALELEQER	1142.6	1143.6	1142.6	1143.6
7.0	44.9	44.9	56.7	0.2	30.0	KAQQELEEQTRR	1514.8	1515.8	1514.8	1515.8
7.0	44.9	44.9	56.7	0.1	27.0	EVWFFGLQYQDTK	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		33.0	IQVWHEEHR	1286.5	1287.5	1286.5	1287.5
7.0	44.9	44.9	56.7	0.0	78.0	RRKPDTIEVQQMK	1627.9	1628.9	1627.9	1628.9
7.0 P26447 S1			56.7 Protein S1		99.0 calcium-bine	VLEQHKLNKDQWEER ding protein A4) (Metastasin) (Protein Mts1) (1952.0 - 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 HN	MGB2_HUMAN	16.0	High mobi	lity group pro	otein B2 (Hig	h mobility group protein 2) (HMG-2) - Bos tau	rus (Bovine) ; I	High mobility gro	up protein B2 (H	ligh mobility grou
288.0	4.0		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	LGEMWSEQSAKDKQPYEQK	2281.1	2282.1	2281.1	2282.1
288.0	4.0	16.0	50.7	0.0	99.0	GKMSSYAFFVQTCR	1680.8	1681.8	1680.8	1681.8
288.0	4.0	16.0	50.7	0.0	99.0	GKMSSYAFFVOTCREEHKK	2332.1	2333.1	2332.1	2333.1
288.0	4.0	16.0	50.7		99.0	LKEKYEKDIAAYR	1625.9	1626.9	1625.9	1626.9
288.0	4.0	16.0	50.7	0.0	99.0	MSSYAFFVQTCR	1498.7	1499.7	1495.7 1495.7	1496.7
288.0	4.0	16.0	50.7	0.0	99.0	MSSYAFFVQTCR	1495.7	1496.7	2147.0	1496.7
288.0	4.0	16.0	50.7	0.0	99.0	MSSYAFFVQTCREEHKK	2147.0	2148.0		2148.0
288.0	4.0	16.0	50.7	0.0	99.00	YEKDIAAYR	1127.6	1128.6	1127.6	1128.6
264.0	2.1	8.2	39.7	2.0	99.00	KLGEMWSEQSAKDKQPYEQK	2409.1	2410.1	2409.1	2410.1
264.0	2.1	8.2	39.7	0.1	25.00	IKSEHPGLSIGDTAK	1551.8	1552.8	1551.8	1552.8
264.0	2.1	8.2	39.7	0.0	99.00	GKMSSYAFFVQTCR	1680.8	1681.8	1680.8	1681.8
264.0	2.1	8.2	39.7	0.0	99.00	LKEKYEKDIAAYR	1625.9	1626.9	1625.9	1626.9
264.0	2.1	8.2	39.7		35.00	LKEKYEKDIAAYR	1622.8	1623.8	1622.8	1623.8
264.0	2.1	8.2	39.7	0.0	99.00	YEKDIAAYR	1127.6	1128.6	1127.6	1128.6
P27695 AF 158.0	7.6	7.6	24.8	2.0	midinic site) 99.0	Iyase (EC 4.2.99.18) (AP endonuclease 1) (AP GLDWVKEEAPDILCLOETK	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	NAGFTPQER	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		21.0	QGFGELLQAVPLADSFR	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
	2.0 ALR_HUMAN				99.0 (CRP55) (Cali	ICSWNVDGLR regulin) (HACBP) (ERp60) (grp60) - Homo sap		1219.6	1218.6	1219.6
86.0	12.2	12.2	25.4	2.0	99.0	EPAVYFKEQFLDGDGWTSR	2244.0	2245.1	2244.0	2245.1
86.0	12.2	12.2	25.4	2.0	99.0	EQFLDGDGWTSR	1409.6	1410.6	1409.6	1410.6
86.0	12.2	12.2	25.4	2.0	99.0	FVLSSGKFYGDEEKDKGLQTSQDAR	2804.3	2805.4	2804.4	2805.4
86.0	12.2	12.2	25.4	2.0	99.0	FYGDEEKDKGLQTSQDAR	2086.0	2087.0	2086.0	2087.0
86.0	12.2	12.2	25.4	2.0	99.0	HEONIDCGGGYVK	1475.7	1476.7	1475.6	1476.7
86.0	12.2	12.2	25.4		99.0	IKDPDASKPEDWDER	1799.8	1800.8	1799.8	1800.8
86.0	12.2	12.2	25.4	0.2	38.1	AVYFKEQFLDGDGWTSR	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	FYGDEEKDKGLQTSQDAR	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	EQFLDGDGWTSR	1409.6	1410.6	1409.6	1410.6
123.0	6.0	6.0	13.9	0.3	54.0	HEQNIDCGGGYVK	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
	SB8_HUMAN 8.0			ne subunit be		cursor (EC 3.4.25.1) (Proteasome component FQHGVIAAVDSR				
149.0	8.0	8.0	21.7	2.0	99.0	GMGLSMGSMICGWDK	1628.7	1629.7	1628.7	1629.7
149.0	8.0	8.0	21.7	2.0	99.0	KGPGLYYVDEHGTR	1590.8	1591.8	1590.8	1591.8
149.0	8.0	8.0	21.7	2.0	99.0	LLSNMMCQYR	1314.6	1315.6	1314.6	1315.6
149.0	8.0	8.0	21.7	0.0	99.0	KGPGLYYVDEHGTR	1590.8	1591.8	1590.8	1591.8
131.0	2.2	2.2	13.0	2.0	99.0	FQHGVIAAVDSR	1298.7	1299.7	1298.7	1299.7
131.0	2.2	2.2	13.0	0.2	35.0	LLSNMMCQYR	1314.6	1315.6	1314.6	1315.6
120.0	6.2	6.2	21.4	2.0	99.0	FQHGVIAAVDSR	1298.7	1299.7	1298.7	1299.7
120.0	6.2	6.2	21.4	2.0	99.0	GMGLSMGSMICGWDK	1628.7	1629.7	1628.7	1629.7
120.0	6.2	6.2	21.4		99.0	LLSNMMCQYR	1314.6	1315.6	1314.6	1315.6
120.0	6.2	6.2	21.4	0.1	26.0	KGPGLYYVDEHGTR	1590.8	1591.8	1590.8	1591.8
	6.2 SA5_HUMAN					ECRLYYLR C 3.4.25.1) (Proteasome zeta chain) (Macropa				
169.0	6.7	6.7	26.6	2.0	99.0	AIGSASEGAQSSLQEVYHK	1960.9	1961.9	1960.9	1962.0
169.0	6.7	6.7	26.6	2.0	99.0	GVNTFSPEGR	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	LFQVEYAIEAIK	1422.8	1423.8	1422.8	1423.8
169.0	6.7	6.7	26.6	0.0	99.0	AIGSASEGAQSSLQEVYHK	1958.9	1959.9	1960.9	1962.0
169.0	6.7	6.7	26.6		99.0	SEYDRGVNTFSPEGR	1712.8	1713.8	1712.8	1713.8
190.0	4.0	4.0	14.1	2.0	99.0	AIGSASEGAQSSLQEVYHK	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 PS	B4_HUMAN		Proteasom	ne subunit be	ta type 4 pre	cursor (EC 3.4.25.1) (Proteasome beta chain)	(Macropain be	ta chain) (Multic	atalytic endopep	tidase 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	EVLEKQPVLSQTEAR	1725.9	1726.9	1725.9	1726.9
	IK01_HUMAN 2.0			ctivated prot 2.0		(EC 2.7.11.24) (Extracellular signal-regulated LKELIFEETAR				
175.0	4.0	4.0	11.9	2.0	99.0	GQVFDVGPR	973.5	974.5	973.5	974.5
175.0	4.0	4.0	11.9		99.0	LKELIFEETAR	1347.7	1348.7	1347.7	1348.7
P28799 GF 368.0			Granulins	precursor (P 2.0		(PEPI) [Contains: Acrogranin; Paragranulin; Gr QHCCPAGYTCNVK				
368.0	2.9	2.9	10.1	0.9	86.0	QGWACCPYR	1179.5	1180.5	1179.5	1180.5
229.0	2.8	2.8	13.2	1.5	97.0	QHCCPAGYTCNVK	1576.6	1577.6	1576.6	1577.6
229.0	2.8	2.8	13.2	0.6	73.0	CDMEVSCPDGYTCCR	1907.6	1908.6	1908.7	1909.7
229.0	2.8	2.8	13.2	0.4	60.0	QGWACCPYR	1179.5	1180.5	1179.5	1180.5
229.0	2.8	2.8	13.2	0.3	51.0	DVECGEGHFCHDNQTCCR	2279.8	2280.8	2279.8	2280.8
229.0 P28838 AN	2.8	2.8	13.2	0.0 ninopeptidas	21.0	QGWACCPYR 1) (Leucine aminopeptidase) (LAP) (Leucyl am	1196.5	1197.5	1196.5	1197.5
44.0	MPI HUMAN			2.0	99.0	AAGIDEQENWHEGKENIR EKEDDVPQFTSAGENFDKLLAGK	2095.0 2537.2	2096.0	2095.0	2096.0
	19.5	19.5	30.1						2527.2	2520.2
44.0 44.0	19.5 19.5 19.5	19.5 19.5	30.1 30.1	2.0 2.0	99.0 99.0	GVLFASGQNLAR	1231.7	2538.2 1232.7	2537.2 1231.7	2538.2 1232.7
44.0 44.0 44.0 44.0	19.5 19.5 19.5 19.5 19.5	19.5 19.5 19.5 19.5	30.1 30.1 30.1 30.1	2.0 2.0 2.0 2.0	99.0 99.0 99.0	GVLFASGONLAR KAAGIDEQENWHEGKENIR LYGSGDQEAWQK	1231.7 2223.1 1380.6	1232.7 2224.1 1381.6	1231.7 2223.1 1380.6	1232.7 2224.1 1381.6
44.0 44.0 44.0	19.5 19.5 19.5 19.5	19.5 19.5 19.5 19.5 19.5 19.5	30.1 30.1 30.1	2.0 2.0 2.0	99.0 99.0	GVLFASGONLAR KAAGIDEQENWHEGKENIR	1231.7 2223.1	1232.7 2224.1	1231.7 2223.1	1232.7 2224.1
44.0 44.0 44.0 44.0 44.0 44.0	19.5 19.5 19.5 19.5 19.5 19.5 19.5	19.5 19.5 19.5 19.5 19.5 19.5 19.5	30.1 30.1 30.1 30.1 30.1 30.1 30.1	2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0	GVLFASGONLAR KAAGIDEOENWHEGKENIR LYGSGDOEAWOK MPLEEHYTR OLMETPANEMTPTR SWIEEOAMGSFLSVAK	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9
44.0 44.0 44.0 44.0 44.0 44.0 44.0 44.0	19.5 19.5 19.5 19.5 19.5 19.5 19.5 19.5	19.5 19.5 19.5 19.5 19.5 19.5 19.5 19.5	30.1 30.1 30.1 30.1 30.1 30.1 30.1 30.1	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 1.4	99.0 99.0 99.0 99.0 99.0 99.0 99.0	GVLFASGONLAR KAAGIDEOENWHEGKENIR LYGSGDOEAWOK MPLFEHYTR OLMETPANEMTPTR SWIEEOAMGSFLSVAK TLIEFLIR FAEILEK	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9 1003.6 848.5	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9 1004.6 849.5	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9 1003.6 848.5	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9 1004.6 849.5
44.0 44.0 44.0 44.0 44.0 44.0 44.0 44.0	19.5 19.5 19.5 19.5 19.5 19.5 19.5 19.5	19.5 19.5 19.5 19.5 19.5 19.5 19.5 19.5	30.1 30.1 30.1 30.1 30.1 30.1 30.1 30.1	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 1.4 0.0	99.0 99.0 99.0 99.0 99.0 99.0 96.0 72.0 81.0	GVIFASGONLAR KAAGIDEOENWHEGKENIR LYGSGODEAWOK MPLFEHYTR OLMETPANEMTPTR SWIEEOAMGSFLSVAK TLIEFLIR FAEIIEK AAGIDEOENWHEGKENIR OLMETPANEMTPTR	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9 1003.6 848.5 2095.0 1617.8	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9 1004.6 849.5 2096.0 1618.8	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9 1003.6 848.5 2095.0 1617.7	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9 1004.6 849.5 2096.0 1618.8
44.0 44.0 44.0 44.0 44.0 44.0 44.0 44.0	19.5 19.5 19.5 19.5 19.5 19.5 19.5 19.5	19.5 19.5 19.5 19.5 19.5 19.5 19.5 19.5	30.1 30.1 30.1 30.1 30.1 30.1 30.1 30.1	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 0.0 0.0	99.0 99.0 99.0 99.0 99.0 99.0 96.0 72.0 81.0 99.0	GYLFASGONLAR KAAGIDEOENWHEGKENIR LYGSGDQEAWOK MPLEHYTR OLMETPANEMTPTR SWIEEOAMGSFLSVAK TLIEFLIR FAEILEK AAGIDEOENWHEGKENIR QLMETPANEMTPTR MPLEFHYTR MPLEFHYTR SWIEEOAMGSFLSVAK	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9 1003.6 848.5 2095.0 1617.8 1192.6 1781.9	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9 1004.6 849.5 2096.0 1618.8 1193.6 1782.9	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9 1003.6 848.5 2095.0 1617.7 1192.6 1781.9	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9 1004.6 849.5 2096.0 1618.8 1193.6 1782.9
44.0 44.0 44.0 44.0 44.0 44.0 44.0 44.0	19.5 19.5 19.5 19.5 19.5 19.5 19.5 19.5	19.5 19.5 19.5 19.5 19.5 19.5 19.5 19.5	30.1 30.1 30.1 30.1 30.1 30.1 30.1 30.1	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 1.4 0.0 0.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 96.0 72.0 81.0 99.0	GYLFASGONLAR KAAGIDFOENWHEGKENIR LYGSGDOEAWOK MPLEFHYTR OLMETPANEMTPTR SWIEEGAMGSFLSVAK TLIEFLIR FAEILEK AAGIDEOENWHEGKENIR OLMETPANEMTPTR MPLEFHYTR	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9 1003.6 848.5 2095.0 1617.8 1192.6	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9 1004.6 849.5 2096.0 1618.8 1193.6	1231.7 2223.1 1380.6 1192.6 1600.7 1781.9 1003.6 848.5 2095.0 1617.7 1192.6	1232.7 2224.1 1381.6 1193.6 1601.7 1782.9 1004.6 849.5 2096.0 1618.8 1193.6

32.0 32.0 32.0	20.0 20.0 20.0	20.0 20.0 20.0	37.2 37.2 37.2	2.0 2.0 2.0	99.0 99.0 99.0	LYGSGDQEAWQK LYGSGDQEAWQKGVLFASGQNLAR MPLFEHYTR	1380.6 2594.3 1192.6	1381.6 2595.3 1193.6	1380.6 2594.3 1192.6	1381.6 2595.3 1193.6
32.0 32.0	20.0 20.0	20.0 20.0	37.2 37.2	2.0 2.0	99.0 99.0	QLMETPANEMTPTR QVVDCQLADVNNIGKYR	1600.7 1991.0	1601.7 1992.0	1600.7 1991.0	1601.7 1992.0
32.0 32.0	20.0	20.0 20.0	37.2 37.2	2.0 1.3	99.0 95.0	SWIEEQAMGSFLSVAK FAEIIEK	1781.9 848.5	1782.9 849.5	1781.9 848.5	1782.9 849.5
32.0 32.0 32.0	20.0 20.0 20.0	20.0 20.0 20.0	37.2 37.2 37.2	0.6 0.0 0.0	72.0 99.0 99.0	TLIEFLLR AAGIDEQENWHEGKENIR KAAGIDEQENWHEGKENIR	1003.6 2095.0 2223.1	1004.6 2096.0 2224.1	1003.6 2095.0 2223.1	1004.6 2096.0 2224.1
P29350 128.0	PTN6_HUMAN	9.2	Tyrosine-pro	otein phosp	hatase non-	receptor type 6 (EC 3.1.3.48) (Protein-tyr AGFWEEFESLQK			lematopoietic cell 1469.7	protein-tyrosine 1470.7
128.0 128.0	9.2	9.2 9.2	25.0 25.0	2.0	99.0 99.0	AGFWEEFESLQKQEVK YKNILPFDHSR	1953.9 1388.7	1955.0 1389.7	1953.9 1388.7	1955.0 1389.7
128.0 128.0	9.2	9.2 9.2	25.0 25.0	1.3 1.0	95.0 89.0	AYGPYSVTNCGEHDTTEYKLR DLSGLDAETLLK	2460.1 1303.7	2461.1 1304.7	2460.1 1303.7	2461.1 1304.7
128.0 128.0	9.2	9.2 9.2	25.0 25.0	0.7 0.1	82.0 26.0	VGDQVTHIR NKCVPYWPEVGMQR	1023.5 1762.8	1024.6 1763.9	1023.5 1762.8	1024.6 1763.8
287.0 P29401	TKT_HUMAN	2.0	7.4 Transketolas			YKNILPFDHSR omo sapiens (Human)	1388.7	1389.7	1388.7	1389.7
53.0 53.0 53.0	17.1 17.1 17.1	17.1 17.1 17.1	30.0 30.0 30.0	2.0 2.0 2.0	99.0 99.0 99.0	GITGVEDKESWHGKPLPK ILATPPQEDAPSVDIANIR LGQSDPAPLQHQMDIYQK	1977.0 2019.1 2068.0	1978.0 2020.1 2069.0	1977.0 2019.1 2068.0	1978.0 2020.1 2069.0
53.0 53.0 53.0	17.1 17.1 17.1	17.1 17.1 17.1	30.0 30.0 30.0	2.0 2.0 2.0	99.0 99.0 99.0	MESYHKPDQQK MFGIDRDAIAQAVR	1431.6 1561.8	1432.7 1562.8	1431.6 1561.8	1432.7 1562.8
53.0 53.0	17.1 17.1	17.1 17.1	30.0 30.0	2.0	99.0 99.0	SVPTSTVFYPSDGVATEK TSRPENAIIYNNNEDFQVGQAK	1883.9 2507.2	1884.9 2508.2	1883.9 2507.2	1884.9 2508.2
53.0 53.0	17.1 17.1	17.1 17.1	30.0 30.0	2.0 0.4	99.0 64.0	VLDPFTIKPLDR YFDKASYR	1412.8 1048.5	1413.8 1049.5	1412.8 1048.5	1413.8 1049.5
53.0 53.0	17.1 17.1	17.1 17.1	30.0 30.0	0.4 0.1	61.0 29.0	GICFIR VLDPFTIKPLDRK	764.4 1540.9	765.4 1541.9	764.4 1540.9	765.4 1541.9
62.0 62.0	5.6 5.6	5.6 5.6	23.4 23.4	2.0 2.0	99.0 99.0	ILATPPQEDAPSVDIANIR VLDPFTIKPLDR	2019.1 1412.8	2020.1 1413.8	2019.1 1412.8	2020.1 1413.8
62.0 62.0	5.6 5.6	5.6 5.6	23.4 23.4	1.2 0.2	94.0 34.0	TSRPENAIIYNNNEDFQVGQAK GICFIR MFGIDRDAIAQAVR	2507.2 764.4	2508.2 765.4	2507.2 764.4	2508.2 765.4
62.0 66.0	5.6 11.8	5.6 11.8	23.4 22.8 22.8	0.1 2.0	28.0 99.0	GITGVEDKESWHGKPLPK ILATPPQEDAPSVDIANIR	1561.8 1977.0	1562.8 1978.0	1561.8 1977.0	1562.8 1978.0
66.0 66.0 66.0	11.8 11.8 11.8	11.8 11.8 11.8	22.8 22.8 22.8	2.0 2.0 2.0	99.0 99.0 99.0	KKILATPPQEDAPSVDIANIR TSRPENAIIYNNNEDFQVGQAK	2019.1 2275.2 2507.2	2020.1 2276.3 2508.2	2019.1 2275.3 2507.2	2020.1 2276.3 2508.2
66.0 66.0	11.8	11.8 11.8	22.8 22.8	2.0	99.0 98.0	VLDPFTIKPLDR MFGIDRDAIAQAVR	1412.8 1561.8	1413.8 1562.8	1412.8 1561.8	1413.8 1562.8
P30041 561.0	PRDX6_HUMAN	1.7	Peroxiredoxi		1.1.15) (An 98.0					
215.0 215.0	3.2	3.2 3.2	18.3 18.3	2.0 1.2	99.0 93.0	PGGLLLGDVAPNFEANTTVGR DFTPVCTTELGR	2097.1 1394.7	2098.1 1395.7	2097.1 1394.7	2098.1 1395.7
542.0		2.0	D-dopachron 9.3	2.0	99.0	FFPLESWQIGK	1350.7	1351.7	omo sapiens (Hum 1350.7	1351.7
	RL12_HUMAN	2.0	9.3 60S ribosom			FFPLESWQIGK sapiens (Human)	1350.7	1351.7	1350.7	1351.7
411.0 411.0	2.2	2.2	19.4 19.4	2.0 0.2	99.0 43.0	HSGNITFDEIVNIAR ELSGTIK	1684.9 803.4	1685.9 804.4	1684.9 803.4	1685.9 804.4
331.0 P30086 102.0		10.6	17.0 Phosphatidy 55.1	2.0 lethanolam 2.0	99.0 ine-binding 99.0	HSGNITFDEIVNIAR protein 1 (PEBP-1) (Prostatic-binding pro APVAGTCYOAEWDDYVPK	1684.9 otein) (HCNPpp) (Neu 2068.9	1685.9 ropolypeptide 2069.9	1684.9 h3) (Raf kinase in 2068.9	1685.9 hibitor protein) 2069.9
102.0 102.0 102.0	10.6	10.6 10.6	55.1 55.1	2.0 2.0 2.0	99.0 99.0	GNDISSGTVLSDYVGSGPPKGTGLHR LYEQLSGK	2570.2 936.5	2571.2 937.5	2570.3 936.5	2571.3 937.5
102.0 102.0	10.6	10.6 10.6	55.1 55.1	2.0	99.0 96.0	YVWLVYEQDRPLK NRPTSISWDGLDSGK	1707.9 1631.8	1708.9 1632.8	1707.9 1631.8	1708.9 1632.8
102.0 184.0		10.6 4.0	55.1 31.0	1.2	94.0 99.0	YVWLVYEQDRPLKCDEPILSNR APVAGTCYQAEWDDYVPK	2792.4 2068.9	2793.4 2069.9	2792.4 2068.9	2793.4 2069.9
184.0 P30101		4.0	31.0 Protein disul	2.0 Ifide-isome	99.0 rase A3 pred	GNDISSGTVLSDYVGSGPPKGTGLHR cursor (EC 5.3.4.1) (Disulfide isomerase E	2571.3 R-60) (ERp60) (58 kI	2572.3 Da microsomal	2570.3 protein) (p58) (El	2571.3 Rp57) (58 kDa g
63.0 63.0	15.7 15.7	15.7 15.7	23.6 23.6	2.0 2.0	99.0 99.0	AASNLRDNYR ELSDFISYLQR	1178.6 1369.7	1179.6 1370.7	1178.6 1369.7	1179.6 1370.7
63.0 63.0	15.7 15.7	15.7 15.7	23.6 23.6	2.0 2.0	99.0 99.0	FVMQEEFSR GFPTIYFSPANK	1171.5 1340.7	1172.5 1341.7	1171.5 1340.7	1172.5 1341.7
63.0 63.0	15.7 15.7	15.7 15.7	23.6 23.6	2.0 2.0	99.0 99.0	IFRDGEEAGAYDGPR LAPEYEAAATR	1651.8 1190.6	1652.8 1191.6	1651.8 1190.6	1652.8 1191.6
63.0 63.0	15.7 15.7	15.7 15.7	23.6 23.6	2.0 1.7	99.0 98.0	MDATANDVPSPYEVR FVMQEEFSRDGK	1663.7 1471.7	1664.8 1472.7	1663.8 1471.7	1664.8 1472.7
63.0 61.0	15.7 5.8	15.7 5.8	23.6 17.8	0.0 1.7	78.0 98.0	IFRDGEEAGAYDGPR ELSDFISYLQR	1651.8 1369.7	1652.8 1370.7	1651.8 1369.7	1652.8 1370.7
61.0 61.0	5.8 5.8	5.8 5.8 5.8	17.8 17.8 17.8	1.7 1.7 0.7	98.0 98.0 78.0	FLQDYFDGNLKR FVMQEEFSR MDATANDVPSPYEVR	1514.8 1171.5	1515.8 1172.5	1514.8 1171.5	1515.8 1172.5
61.0 97.0 97.0	5.8 8.0 8.0	8.0 8.0	16.4 16.4	2.0	99.0 99.0	ELSDFISYLQR FLQDYFDGNLKR	1663.8 1369.7 1514.7	1664.8 1370.7 1515.8	1663.8 1369.7 1514.8	1664.8 1370.7 1515.8
97.0 97.0	8.0 8.0	8.0 8.0	16.4 16.4	2.0	99.0 99.0	FVMQEEFSR IFRDGEEAGAYDGPR	1171.5 1651.8	1172.5 1652.8	1171.5 1651.8	1172.5 1652.8
	1C12_HUMAN 16.6	16.6				en, Cw-12 alpha chain precursor (MHC cla AEHPKTHVTHHPVSDHEATLR				2399.2
59.0 59.0	16.6 16.6	16.6 16.6	48.9 48.9	2.0 2.0	99.0 99.0	APWVEQEGPEYWDRETQK AYLEGTCVEWLR	2247.0 1495.7	2248.0 1496.7	2247.0 1495.7	2248.0 1496.7
59.0 59.0	16.6	16.6 16.6	48.9 48.9	2.0	99.0 99.0	DGEDQTQDTELVETRPAGDGTFQK FIAVGYVDDTQFVR	2636.2 1628.8	2637.2 1629.8	2636.2 1628.8	2637.2 1629.8
59.0 59.0	16.6	16.6 16.6	48.9 48.9	2.0 2.0	99.0 99.0	THVTHHPVSDHEATLR WAAVVVPSGEEQR	1835.9 1426.7	1836.9 1427.7	1835.9 1426.7	1836.9 1427.7
59.0 59.0	16.6	16.6 16.6	48.9 48.9	2.0 0.3	99.0 46.0	YFYTAVSRPGRGEPR MYGCDLGPDGR	1754.9 1239.5	1755.9 1240.5	1754.9 1239.5	1755.9 1240.5
59.0 59.0 270.0	16.6	16.6 16.6 7.4	48.9 48.9 30.9	0.1 0.1 2.0	26.0 23.0 99.0	RQAQADR APWVEQEGPEYWDR APWVEQEGPEYWDRETQK	844.4 1760.8 2247.0	845.4 1761.8 2248.0	844.4 1760.8 2247.0	845.4 1761.8 2248.0
270.0 270.0 270.0	2.1	7.4 7.4 7.4	30.9 30.9 30.9	0.0 0.0	99.0 99.0 99.0	FIAVGYVDDTQFVR WAAVVVPSGEEQR	1628.8 1426.7	1629.8 1427.7	1628.8 1426.7	1629.8 1427.7
270.0		7.4	30.9	0.0	94.0	YLENGKETLQR Serpin B1) (Monocyte/neutrophil elastas	1350.7	1351.7	1350.7	1351.7
155.0 155.0	7.7	7.7 7.7	14.0 14.0	2.0 2.0	99.0 99.0	FKLEESYTLNSDLAR TFHFNTVEEVHSR	1784.9 1601.8	1785.9 1602.8	1784.9 1601.8	1785.9 1602.8
155.0 155.0	7.7	7.7	14.0 14.0	2.0	99.0 98.0	TYNFLPEFLVSTQK FQSLNADINKR	1685.9 1304.7	1686.9 1305.7	1685.9 1304.7	1686.9 1305.7
272.0		2.1	11.3	2.0	99.0	TFHFNTVEEVHSR 7) (Coronin-like protein A) (Clipin-A) (Tr	1601.8 yptophan aspartate-c	1602.8 ontaining coat	1601.8 protein) (TACO) -	1602.8
26.0 26.0	25.9 25.9	25.9 25.9	41.2 41.2	2.0 2.0	99.0 99.0	CEPIAMTVPR FRHVFGQPAK	1155.5 1185.6	1156.6 1186.6	1155.6 1185.6	1156.6 1186.6
26.0 26.0		25.9 25.9	41.2 41.2	2.0 2.0	99.0 99.0	FRHVFGQPAKADQCYEDVR FYKLHER	2322.1 991.5	2323.1 992.5	2322.1 991.5	2323.1 992.5
26.0 26.0	25.9 25.9	25.9 25.9	41.2 41.2	2.0	99.0 99.0	HVFGQPAKADQCYEDVR ILTTGFSR	2018.9 893.5	2019.9 894.5	2018.9 893.5	2019.9 894.5
26.0 26.0	25.9	25.9 25.9	41.2 41.2	2.0	99.0 99.0	LORLEETVOAK LOATVOELOKR	1300.7 1312.7	1301.7 1313.8	1300.7 1312.7	1301.7 1313.8
26.0 26.0 26.0	25.9	25.9 25.9 25.9	41.2 41.2 41.2	2.0 2.0 2.0	99.0 99.0 99.0	RCEPIAMTVPR RGLEVNKCEIAR RLDRLEETVOAK	1328.7 1443.8	1329.7 1444.8	1328.7 1443.8	1329.7 1444.8 1457.8
26.0 26.0 26.0	25.9	25.9 25.9 25.9	41.2 41.2 41.2	2.0 2.0 1.2	99.0 99.0 94.0	VSQTTWDSGFCAVNPK AAPEASGTPSSDAVSRLEEEMR	1456.8 1795.8 2289.0	1457.8 1796.8 2290.1	1456.8 1795.8 2289.1	1457.8 1796.8 2290.1
26.0 26.0 26.0	25.9	25.9 25.9 25.9	41.2 41.2 41.2	0.3 0.1	53.0 27.0	KGTVVAEKDRPHEGTRPVR AAPEASGTPSSDAVSR	2131.2 1501.7	2132.2 1502.7	2131.2 1501.7	2132.2 1502.7
26.0 26.0 26.0		25.9 25.9 25.9	41.2 41.2 41.2	0.1 0.0	26.0 99.0	ADQCYEDVRVSQTTWDSGFCAVNPK FRHVFGQPAK	2933.3 1185.6	2934.3 1186.6	2932.3 1185.6	2933.3 1186.6
26.0 20.0	25.9	25.9 13.9	41.2 41.2 28.2	0.0 2.0	76.0 99.0	ILTTGFSR HVFGQPAKADQCYEDVR	893.5 2018.9	894.5 2019.9	893.5 2018.9	894.5 2019.9
20.0 20.0	13.9	13.9 13.9	28.2 28.2	2.0	99.0 99.0	ILTTGFSR RCEPIAMTVPR	893.5 1328.7	894.5 1329.7	893.5 1328.7	894.5 1329.7
20.0 20.0		13.9 13.9	28.2 28.2	2.0 1.7	99.0 98.0	VSQTTWDSGFCAVNPK FYKLHER	1795.8 991.5	1796.8 992.5	1795.8 991.5	1796.8 992.5

20.0 20.0 20.0 20.0	13.9 13.9 13.9 13.9	13.9 13.9 13.9 13.9	28.2 28.2 28.2 28.2	1.5 1.4 1.2 0.1	97.0 96.0 93.0 23.0	FRHVFGOPAK KLOATVOELOKR CEPIAMTVPR GTVVAEKORPHEGTRPVR	1185.6 1440.8 1155.5 2089.1	1186.6 1441.9 1156.6 2090.1	1185.6 1440.8 1155.6 2089.1	1186.6 1441.8 1156.6 2090.1
20.0 25.0 25.0	13.9 21.5 21.5	13.9 21.5 21.5	28.2 32.8 32.8	0.0 2.0 2.0	44.0 99.0 99.0	FRHVFGQPAK FRHVFGQPAK FYKLHER	1187.7 1185.6	1188.7 1186.7 992.5	1185.6 1185.6 991.5	1186.6 1186.6 992.5
25.0 25.0 25.0	21.5 21.5 21.5	21.5 21.5 21.5	32.8 32.8	2.0 2.0 2.0	99.0 99.0	HVFGQPAKADQCYEDVR KGTVVAEKDRPHEGTRPVR	991.5 2018.9 2131.2	2019.9 2132.2	2018.9 2131.2	2019.9 2132.2
25.0 25.0 25.0	21.5 21.5 21.5	21.5 21.5 21.5	32.8 32.8 32.8	2.0 2.0 2.0	99.0 99.0 99.0	KLQATVQELQKR RCEPIAMTVPR RGLEVNKCEIAR	1440.8 1328.7 1443.8	1441.9 1329.7 1444.8	1440.8 1328.7 1443.8	1441.8 1329.7 1444.8
25.0 25.0 25.0	21.5 21.5 21.5	21.5 21.5 21.5	32.8 32.8	1.7 1.5	98.0 97.0	LQATVQELQKR CEPIAMTVPR	1312.8 1155.5	1313.8 1156.6	1312.7 1155.6	1313.8 1156.6
25.0 25.0 25.0	21.5 21.5 21.5	21.5 21.5 21.5	32.8 32.8 32.8	1.4 0.9 0.6	96.0 88.0 75.0	QVALWDTK DGGLICTSCR II TTGESR	942.5 1137.5 891.5	943.5 1138.5 892.5	942.5 1137.5 893.5	943.5 1138.5 894.5
25.0 25.0	21.5 21.5	21.5 21.5	32.8 32.8	0.6 0.6	75.0 73.0	VSQTTWDSGFCAVNPK RLDRLEETVQAK	1795.8 1456.8	1796.8 1457.8	1795.8 1456.8	1796.8 1457.8
25.0 25.0 25.0	21.5 21.5 21.5	21.5 21.5 21.5	32.8 32.8 32.8	0.1 0.0 0.0	20.0 95.0 95.0	FYKLHERR FRHVFGQPAK FYKLHER	1147.6 1185.6 991.5	1148.6 1186.7 992.5	1147.6 1185.6 991.5	1148.6 1186.6 992.5
25.0 P31153	21.5 METK2_HUMAN	21.5	32.8 S-adenosyln	0.0 nethionine s	42.0 ynthetase is	RCEPIAMTVPR soform type-2 (EC 2.5.1.6) (Methionine adeno	1344.7 syltransferase 2	1345.7) (AdoMet synth	1344.7 etase 2) (Methic	1345.7 onine adenosyltra
239.0 239.0 239.0	5.0	5.0 5.0 5.0	18.7 18.7 18.7	2.0 2.0 0.9	99.0 99.0 87.0	DLDLKKPIYQR YLDEDTIYHLQPSGR TQVTVQYMQDR	1387.8 1805.9 1367.7	1388.8 1806.9 1368.7	1387.8 1805.9 1367.7	1388.8 1806.9 1368.7
239.0 177.0	5.0 4.0	5.0 4.0	18.7 12.2	0.1 2.0	25.0 99.0	FVIGGPQGDAGLTGR FVIGGPQGDAGLTGR	1443.7 1443.7	1444.8 1444.8	1443.7 1443.7	1444.8 1444.8
177.0 P31949 210.0	S10AB_HUMAN	6.0	12.2 Protein S100 46.7	2.0 D-A11 (S100 2.0	99.0 calcium-bir 99.0	TQVTVQYMQDR nding protein A11) (Protein S100C) (Calgizzar CIESLIAVFQK	1367.7 rin) (MLN 70) - H 1306.7	1368.7 lomo sapiens (H 1307.7	1367.7 uman) 1306.7	1368.7
210.0 210.0	6.0	6.0 6.0	46.7 46.7	2.0 2.0	99.0 99.0	TEFLSFMNTELAAFTK YAGKDGYNYTLSK	1848.9 1478.7	1849.9 1479.7	1848.9 1478.7	1849.9 1479.7
189.0 310.0 310.0	2.0	2.0 2.4 2.4	10.5 37.1 37.1	2.0 2.0 0.0	99.0 99.0 59.0	CIESLIAVFQK YAGKDGYNYTLSK TEFLSFMNTELAAFTK	1306.7 1478.7 1848.9	1307.7 1479.7 1849.9	1306.7 1478.7 1848.9	1307.7 1479.7 1849.9
P32455 54.0	GBP1_HUMAN 17.0	17.0	Interferon-in	nduced guar 2.0	99.0	ng protein 1 (GTP-binding protein 1) (Guanine AIAHYEQQMGQK	e nucleotide-bino 1402.7	1403.7	GBP-1) (HuGBP- 1402.7	-1) - Homo sapier 1403.7
54.0 54.0 54.0	17.0 17.0 17.0	17.0 17.0 17.0	27.2 27.2 27.2	2.0 2.0 2.0	99.0 99.0 99.0	ASEIHMTGPMCLIENTNGR GIQAEEILQTYLK IMKNEIQDLQTK	2173.0 1504.8 1459.8	2174.0 1505.8 1460.8	2173.0 1504.8 1459.8	2174.0 1505.8 1460.8
54.0 54.0		17.0 17.0	27.2 27.2	2.0	99.0 99.0	KGIQAEEILQTYLK SKESMTDAILQTDQTLTEKEKEIEVER	1632.9 3150.5	1633.9 3151.5	1632.9 3150.6	1633.9 3151.6
54.0 54.0 54.0	17.0	17.0 17.0 17.0	27.2 27.2 27.2	2.0 1.7 0.8	99.0 98.0 85.0	TLSGGIQVNGPR AGIYSKPGGYR CFVFDRPVHR	1197.7 1167.6 1331.7	1198.7 1168.6 1332.7	1197.6 1167.6 1331.7	1198.7 1168.6 1332.7
54.0 42.0	17.0 17.7	17.0 17.7	27.2 37.7	0.4 2.0	62.0 99.0	MLQEMQR AGIYSKPGGYR	934.4 1167.6	935.4 1168.6	934.4 1167.6	935.4 1168.6
42.0 42.0 42.0	17.7 17.7 17.7	17.7 17.7 17.7	37.7 37.7 37.7	2.0 2.0 2.0	99.0 99.0 99.0	AIAHYEQQMGQK ASEIHMTGPMCLIENTNGR EAIEVFIR	1402.7 2173.0 975.5	1403.7 2174.0 976.5	1402.7 2173.0 975.5	1403.7 2174.0 976.5
42.0 42.0	17.7 17.7	17.7 17.7	37.7 37.7	2.0	99.0 99.0	GTSQKDETFNLPR KGIQAEEILQTYLK	1491.7 1632.9	1492.7 1633.9	1491.7 1632.9	1492.7 1633.9
42.0 42.0 42.0	17.7 17.7 17.7	17.7 17.7 17.7	37.7 37.7 37.7	2.0 2.0 1.7	99.0 99.0 98.0	KGTSQKDETFNLPR MENDRVQLLKEQER SYQEHLKQLTEK	1619.8 1786.9 1502.8	1620.8 1787.9 1503.8	1619.8 1786.9 1502.8	1620.8 1787.9 1503.8
P32456 234.0 234.0		7.3 7.3	9.6 9.6	nduced guar 2.0 2.0	nylate-bindii 99.0 99.0	ng protein 2 (GTP-binding protein 2) (Guanine DIWDIQMR NSFKDVDQMFQR	e nucleotide-bind 1075.5 1513.7	ding protein 2) (1076.5 1514.7	GBP-2) (HuGBP- 1075.5 1513.7	-2) - Homo sapier 1076.5 1514.7
234.0 234.0 234.0	5.3	7.3 7.3	9.6 9.6	1.2 0.0	94.0 99.0	CFVFDWPAPK AIAHYEQQMGQK	1248.6 1402.7	1249.6 1403.7	1248.6 1402.7	1249.6 1403.7
222.0 222.0 222.0	3.0	5.0 5.0 5.0	14.9 14.9 14.9	2.0 1.0 0.0	99.0 90.0 99.0	DIWDIQMR LLKEGFENESKR AIAHYEQQMGQK	1075.5 1448.8 1402.7	1076.5 1449.8 1403.7	1075.5 1448.8 1402.7	1076.5 1449.8 1403.7
P33241										
84.0	12.3	12.3	Lymphocyte 35.7	2.0	99.0	ein pp52) (52 kDa phosphoprotein) (Lymphod IDQWLEQYTQAIETAGR	2021.0	2022.0	kDa actin-bindir 2021.0	2022.0
84.0 84.0 84.0 84.0	12.3 12.3	12.3 12.3 12.3 12.3			99.0 99.0 99.0	IDQWLEQYTQAIETAGR QQHEGAQGALDSGEPPQCR WETGEVQAQSAAK	2021.0 2063.9 1403.7	2022.0 2064.9 1404.7	2021.0 2063.9 1403.7	2022.0 2064.9 1404.7
84.0 84.0 84.0 84.0 84.0	12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3	35.7 35.7 35.7 35.7 35.7 35.7	2.0 2.0 2.0 2.0 1.7 1.4	99.0 99.0 99.0 99.0 98.0 96.0	IDOWLEOYTOAIETAGR QOHEGAQGALDSGEPPQCR WETGEVOAQSAAK YKFVATGHGK LIDRTESLNR QLOAQDEEGGGHVPERPK	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0
84.0 84.0 84.0 84.0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 4.2	12.3 12.3 12.3 12.3	35.7 35.7 35.7 35.7 35.7	2.0 2.0 2.0 2.0 1.7	99.0 99.0 99.0 99.0 98.0	IDOWLEOYTOAIETAGR OOHEGAOGALDSGEPPQCR WETGEVQAQSAAK YKFVATGHGK LIDRTESLNR	2021.0 2063.9 1403.7 1106.6 1215.7	2022.0 2064.9 1404.7 1107.6 1216.7	2021.0 2063.9 1403.7 1106.6 1215.7	2022.0 2064.9 1404.7 1107.6 1216.7
84.0 84.0 84.0 84.0 84.0 168.0 168.0 168.0 P35579	12.3 12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2 4.2 MYH9_HUMAN	12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 21.5 21.5 Myosin-9 (M	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 0.2	99.0 99.0 99.0 98.0 96.0 94.0 99.0 99.0 36.0 9 (chain 9) (N	IDOWLEOYTOAIETAGR OOHEGAGCALDSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSQRPEQR WETGEVOAQSAAK YKFVATGHGKYEK LIDRTESLINR UDSTEELNR WETGHGKYEK LIDRTESLINR (Nonmuscle II a) (Nonmuscle	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1215.7 cle myosin heavy	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1216.7 chain II.a) (NMI	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1215.7 MHC II-a) (NMM	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1216.7
84.0 84.0 84.0 84.0 84.0 168.0 168.0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2 4.2 MYH9_HUMAN 36.9 36.9	12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0	99.0 99.0 99.0 98.0 96.0 94.0 99.0 36.0	IDOWLEOYTOAIETAGR OOHEGAGCAL DSGEPPQCR WETGEVQAQSAAK YKFVATGHGK LIDRTESLINR OLQAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSQRPEQR WETGEVQAQSAAK YKFVATGHGKYEK LIDRTESLINR	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1215.7	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1216.7	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1215.7 MHC II-a) (NMM 1645.8 1869.0 2492.2	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1216.7
84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2 4.2 MYH9_HUMAN 36.9 36.9 36.9 36.9	12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2 4.2 36.9 36.9 36.9 36.9	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 21.5 Myosin-9 (M 25.6 25.6 25.6 25.6 25.6	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 0.2 lyosin heavy 2.0 2.0 2.0 2.0	99.0 99.0 99.0 98.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEGYTOAIETAGR ODHEGAGCAI DSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLNR OLOAODEEGGHVPERPK LKPSEAPELDEDEGFGDWSQRPEQR WETGEVOAQSAAK YKFVATGHGKYEK LIDRTESLNR ALEEAMEOKAELER ANLOIDOINTDLNLER DFSALESOLOTTOELLOEENR IAEFTTNLTEEEEKSK IAGLEEELEEGGMTEUIDR	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1215.7 Cle myosin heavy 1645.8 1869.0 2492.2 1867.9 2471.1	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 2 chain II a) (NMI 1646.8 1870.0 2493.2 1868.9 2472.1	2021.0 2063 9 1403 7 1106 6 1215 7 1974.0 2914.3 1403.7 1526.8 1215.7 MHC II-a) (NMM 1645.8 1869.0 2492.2 1867.9 2471.2	2022.0 2064 9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1HC-11A) (Cellular 1646.8 1870.0 2493.2 1868.9 2472.2
84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2 4.2 36.9 36.9 36.9 36.9 36.9 36.9 36.9 36.9	35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 21.5 25.6 25.6 25.6 25.6 25.6 25.6 25.6 25	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 0.2 dyosin heavy 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 98.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEOYTOAIETAGR ODHEGAGCALDSGEPPOCR WETGEVOAOSAAK KYEVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAOSAAK YKFVATGHGKYEK LIDRTESLINR YGSVATGHGKYEK LIDRTESLINR JOSAILESOLODTOELLOEENR JALESOLODTOELLOEENR JAEFTINLTEEEKSK JAOLEELEELEOGRITELINDR JAOLEECLEELEOGRITELINDR JA	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1215.7 2e myosin heavy 1645.8 1869.0 2492.2 1867.9 2471.1 1814.9	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1216.7 • chain II a) (NMI 1646.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1156.7 MHC II-a) (NMM 1645.8 1869.0 2492.2 1867.9 2471.2 1814.9 1614.8 2170.1	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1216.7 1HC-IIA) (Cellular 1646.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2171.1
84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2 4.2 4.2 36.9 36.9 36.9 36.9 36.9 36.9 36.9 36.9	35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 21.5 25.6 25.6 25.6 25.6 25.6 25.6 25.6 25	2.0 2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 0.2 lyosin heavy 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 98.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEGYTOAIETAGR ODHEGAGCAI DSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESUNR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGEGGWSORPEOR WETGEVOAOSAAK YKFVATGHGKYEK LIDRTESUNR MYSOSIN heavy chain, nonmuscle II a) (Nonmuscle Moster Aleean Moster Aleean Moster Aleean Moster Aleean Moster Moster Aleean Moster Moste	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1215.7 20 myosin heavy 1645.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1216.7 chain II.a) (NMI 1646.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1751.9	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1215.7 MHC II-a) (NMM 1645.8 1869.0 2492.2 1867.9 2471.2 1814.9 1614.8 2170.1 1949.0	2022.0 2064 9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1216.7 1HC-IIA) (Cellular 1646.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2171.1 1950.0 1751.9
84.0 84.0 84.0 84.0 84.0 188.0 188.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 Myosin-9 (M 25.6 25.6 25.6 25.6 25.6 25.6 25.6 25.6	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 98.0 96.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLECYTOAIETAGR OCHECAGCALDSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSQRPEQR WETGEVOAQSAAK YKFVATGHGKYEK LIDRTESLINR YKFVATGHGKYEK LIDRTESLINR HOSSIN HEAVY CHAIL OF THE STANDARD AND AND AND AND AND AND AND AND AND AN	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 7750.8 2332.0 1723.8	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1527.8 1540.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2170.9 2333.0 1724.8	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1125.7 MHC II-a) (NMM 1645.8 1869.0 2492.2 1867.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1HC-ITA) (Cellular 1646.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2177.1 1950.0 1751.9 2333.1 1724.8 1709.9
84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 Myosin-9 (M 25.6 25.6 25.6 25.6 25.6 25.6 25.6 25.6	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 98.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLECYTOAIETAGR OCHECAGCALDSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSQRPEQR WETGEVOAOSAAK YKFVATGHGK LKPSEAPELDEDEGFGDWSQRPEQR WETGEVOAQSAAK YKFVATGHGKYEK LIDRTESLINR YKFVATGHGKYEK LIDRTESLINR POSIN HEAVY Chain, nonmuscle II a) (Nonmuscle II a) (Nonmu	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1527.8 1546.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1751.9 2333.0 1724.8 1700.9 1729.9 1155.7	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1645.8 1645.8 1649.0 2492.2 1667.9 2471.2 1814.9 1614.8 1949.0 1750.8 1723.8 1708.9 1728.9 1154.7	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1HC-11A) (Cellular 1646.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2171.1 1950.0 1751.9 2333.1 1724.8 1709.9 1155.7
84.0 84.0 84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2 4.2 36.9 36.9 36.9 36.9 36.9 36.9 36.9 36.9	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 21.5 25.6 25.6 25.6 25.6 25.6 25.6 25.6 25	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 98.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLECYTOAIETAGR OOHEGAGCAL DSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLNR OLOAODEEGGHVPERPK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAOSAAK YKFVATGHGKYEK LIDRTESLNR YKFVATGHGKYEK LIDRTESLNR ALLEDAMENTESLNR ANLOIDOINTOLILLER FSALESOLODTOELLOENR IAEFTINLTEEEKK IAOLEEELEECGNTELINDR IAOLEECLIDNETKER IMGIPEEECMGLIR KTLEEEAKTHEAOIOEMR LOGELDDLUVDLDHOR LTEMETLOSOLMAEK NOONIOELEOLEEESAR NAEOYKOOAOKASTR OLLOANPILEAFGNAK CITLENERGELANEVK RGDLPFVVPR SMEAEMIOLOEELAAAER VSHLLGINVTOFTR	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1215.7 216 myosin heavy 1645.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1154.7 2047.9 1570.8	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1216.7 chain II a) (NMI 1646.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1751.9 2333.0 1724.8 1709.9 1155.7 2048.9 1571.8	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2974.3 1403.7 1526.8 1215.7 1526.8 1249.2 1867.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 1728.9 1154.7 2048.0 1570.8	2022.0 2064 9 1404 7 1107 6 1216.7 1975.0 2915.3 1404.7 1527.8 1216.7 1HC-11A) (Cellular 1646.8 1870.0 2493.2 1868.9 2472.2 1815.9 2472.2 1815.8 2171.1 1950.0 1751.9 2333.1 1724.8 1709.9 1729.9 1155.7 2049.0 1571.9 1280.6
84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2 4.2 36.9 36.9 36.9 36.9 36.9 36.9 36.9 36.9	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 21.5 25.6 25.6 25.6 25.6 25.6 25.6 25.6 25	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 98.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLECYTOAIETAGR OCHECAGCAL DSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLNR QLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAQSAAK YKFVATGHGKYEK LIDRTESLNR YKFVATGHGKYEK LIDRTESLNR ANLOIDOINTDLINLER DFSALESOLODTOELLOEENR IAFTINLIFEEEKSK IAQLEEELEEOGNTELINDR IAGLEELEEDONTELINDR IAGLEELEELEOGNTELINDR IAGLEELEELEOGNTELINDR IAGLEELEELEOGNTELINDR IAGLEELEELEOGNTELINDR IAGLEELEELONTERR WIGHPEECOMGLIR KTLEEAKTHEAOIOMR LOGELDDLUDLDHOR LTEMETLOSOLMAEK MOONIOELEEOLEEESSAR NAEGYKDOADKASTR OLLOANPILEFOEMAK OTLENERGELANEVK RODIPFVVPR SMEAEMIOLOEELAAAER VSHLLGINVTDFTR LOAOMKOCMR ASREILAOAKENEK NWOWWR	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1526.8 1645.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9 1570.8 1279.6 1714.9 1947.9	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1404.7 1527.8 1816.9 1868.9 2472.1 1815.9 1615.8 21771.1 1950.0 1751.9 2333.0 1724.8 1709.9 1729.9 1155.7 2048.9 1571.8 1280.6 1715.9 975.5	2021.0 2063.9 1403.7 1106.6 1215.7 1174.0 2914.3 1403.7 1526.8 1215.7 MHC II-a) (NMM 1849.0 2492.2 1867.9 2471.2 1814.9 1614.8 21770.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9 1154.7 2048.0 1570.8	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1216.7 1HC-11A) (Cellular 1646.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2171.1 1950.0 1751.9 2333.1 1724.8 1709.9 1729.9 1155.7 2049.0 1571.9 1280.6 1715.9 975.5
84.0 84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 Myosin-9 (M 25.6 25.6 25.6 25.6 25.6 25.6 25.6 25.6	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 98.0 94.0 94.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEOYTOAIETAGR OOHEGAGCALDSGEPPOCR WETGEVOAOSAAK KYEVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAOSAAK YKFVATGHGKYEK LIDRTESLINR YGSAIN ON	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1528.8 1215.7 1528.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1708.9 1728.9 1728.9 1571.8 1279.6 1714.9 974.4 1203.6 1407.7	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1527.8 1527.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1724.8 1709.9 1155.7 2048.9 1571.8 1280.6 1715.9 975.5 1204.6 1408.7	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1403.7 1526.8 1869.0 2492.2 1867.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9 1154.7 2048.0 1570.6	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2177.1 1950.0 1751.9 2333.1 1724.8 1709.9 1729.9 1155.7 2049.0 1571.9 1280.6 1715.9 975.5 1204.6 1408.7 1261.7
84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 4.2 4.2 4.2 36.9 36.9 36.9 36.9 36.9 36.9 36.9 36.9	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 Myosin-9 (M 25.6 25.6 25.6 25.6 25.6 25.6 25.6 25.6	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 98.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLECYTOAIETAGR OCHECAGCAL DSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLNR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAQSAAK YKFVATGHGKYEK LIDRTESLNR YKFVATGHGKYEK LIDRTESLNR MYSOSIN DEAVY Chain, nonmuscle II a) (Nonmuscle II a) (Nonmu	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1755.8 2332.0 1723.8 1708.9 1728.9 1571.8 1279.6 1714.9 1570.8 1279.6 1714.9 1570.8	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1216.7 1527.8 1816.9 1868.9 2472.1 1815.9 1615.8 21771.1 1950.0 1751.9 2333.0 1724.8 1709.9 1729.9 1155.7 2048.9 1571.8 1280.6 1715.9 975.5	2021.0 2063.9 1403.7 1106.6 1215.7 1170.6 1215.7 1274.0 2914.3 1403.7 1526.8 1215.7 MHC II-a) (NMM 1645.8 1869.0 2492.2 1867.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9 1728.9 1728.9 1728.9 1728.9 1728.9 1728.9 1728.9 1728.9 1729.6 17714.9 174.5 1203.6 17714.9 174.5 1203.6	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1216.7 1HC-11A) (Cellular 1646.8 1870.0 2493.2 1868.9 2472.2 21815.9 1615.8 2171.1 1950.0 1751.9 1280.6 1719.9 1155.7 2049.0 1571.9 1280.6 1715.9 975.5 1204.6
84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35.7 35.7 35.7 35.7 35.7 35.7 35.7 35.7	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 98.0 96.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLECYTOAIETAGR OCHECAGCALDSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSORPEOR WETGSEVOAOSAAK YKFVATGHGK KLYSEAPELDEDEGFGDWSORPEOR WETGSEVOAOSAAK YKFVATGHGKYEK LIDRTESLINR YKFVATGHGKYEK LIDRTESLINR POSIN HEAVY CHAIN, NONMUSCIE II a) (NONMUSCIE ALEEAMEOKAELER ANLOIDOINTOLLLOERN DEFELEREOGNTELINDR IAGLEFELLEECOGNTELINDR IAGLEFELLEECOGNTELINDR IAGLEFELLEECOGNTELINDR IAGLEFELLEECOGNTELINDR LOLOEDLUVDLDHOR LTEMETLOSOLIMAEK MOONIOELEECLEEESAR NAEOYKODAOKASTR OLLOANPILEFOLHARK OTLENERGELANAEK YSHLLGINVTOFTR LOAOMKDCMR ASREHIAOAKENK NWOWWR ALEOAVERM KLOAOMKDCMR KLOAOMKDCMR VKLOEMEGTWK VEEEEERCOHLOAK KLOAOMKDCMR VKLOEMEGTWK VEEEEERCOHLOAK IAGLEELLEEEGGNTELINDR ANLOIDOINTOLINER ELESQUSELOEDLESER IMGIPEEEROMGLIR	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9 1154.7 2047.9 1570.8 1279.6 1714.9 974.4 1203.6 1407.7 1260.7 1912.8 2472.1 1869.0 2033.0 1614.8	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1527.8 1527.8 1646.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2177.1 1950.0 1751.9 2333.0 1724.8 1709.9 1729.9 1155.7 2048.9 1571.8 1280.6 1715.9 975.5 1204.6 1408.7 1261.7 1913.9 2473.1 1870.0 2034.0 1615.8	2021.0 2063.9 1403.7 1106.6 1215.7 1107.0 2914.3 1403.7 1526.8 1869.0 2492.2 1864.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 1272.8 1708.9 1728.9 1728.9 1728.9 1728.9 174.7 2048.0 1570.8 1279.6 1714.9 974.5 1200.7 1912.9 2471.2 1869.0 2032.9 1614.8	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2171.1 1950.0 1751.9 1724.8 1709.9 1729.9 1155.7 2049.0 1571.9 1280.6 1715.9 175.9 175.9 175.7 2049.0 1571.9 1280.6 1715.9 1715.9 1729.9 175.7 2049.0 1571.9 1280.6 1715.9 1715.9 1715.9 1720.4 1715.9 1715.9 1715.9 1720.4 1715.9
84.0 84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 21. 5 21. 5 Myosin-9 (M 25. 6 25. 6	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 98.0 94.0 94.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEOYTOAIETAGR OOHEGAGCALDSGEPPOCR WETGEVOAOSAAK KYEVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSQRPEOR WETGEVOAOSAAK YKFVATGHGK LKPSEAPELDEDEGFGDWSQRPEOR WETGEVOAOSAAK YKFVATGHGKYEK LIDRTESLINR YKSPATGHGKYEK LIDRTESLINR TYPOSIT AND TO THE TENT OF THE TE	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9 1154.7 2047.9 1570.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 174.9 1750.8 2170.1 1750.8 2170.1 1750.8 217	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1404.7 1527.8 1816.9 1868.9 2472.1 1815.9 1615.8 21771.1 1950.0 1751.9 2333.0 1724.8 1709.9 1155.7 2048.9 1571.8 1280.6 1717.9 975.5 1204.6 1408.7 1261.7 1913.9 2473.1 1870.0 2034.0 1615.8 1709.9 1729.9 1155.7 2048.9 1571.8 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1280.6 1717.9 1724.8 1709.9 1155.7	2021.0 2063.9 1403.7 1106.6 1215.7 1174.0 2914.3 1403.7 1526.8 1215.7 1526.8 1215.7 1645.8 1869.0 2492.2 1867.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1714.9 1714.9 1750.8 1279.6 1714.9 1750.8 1279.6 1714.9 1714.9 1750.8 1279.6 1714.9 17	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 1770.9 2333.1 1724.8 1709.9 1759.9 18
84.0 84.0 84.0 84.0 84.0 84.0 84.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35.7 35.7 35.7 35.7 35.7 35.7 35.7 35.7	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 98.0 96.0 96.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLECYTOAIETAGR OCHECAGCAL DSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAQSAAK YKFVATGHGKYEK LIDRTESLINR YKFVATGHGKYEK LIDRTESLINR MYSOSIN DEAVY CHAIN, NONMUSCE II a) (Nonmusce ALEEAMEOKAELER ANLOIDOINTDLILLER DFSALESOLODTOELLOEENR IAFFITHLTEEEKSK IAOLEEELEEOGNTELINDR IAOLEEOLDNETKER IMGIPEEEOMGLIR KTLEEEAKTHEAOIOEMR LTEMETLOSOLMAEK MOONIOELEEOLEEESSAR NAEGYKDOADKASTR OLLOANPILEFOEMSK OTLENERGELANEVK RODIPFVVPR SMEAEMIOLOEELAAAER VSHLLGINVTDFTR LOAOMKDCMR ASREEILAOAKENEK NWOWWR ALEOOVEEMK KLOAOMKDCMR VKLOEMEGTVK VEEEERECOHLOAEK IAOLEEELEEEOGNTELINDR ANLOIDOINTOLNIER ELESOISELOEDLESER IMGIPEEEOMGLIR NKOWOWR ALEOOVEEMK KLOAOMKDCMR VKLOEMEGTVK VEEEERECOHLOAEK IAOLEEELEEEOGNTELINDR ANLOIDOINTOLNIER ELESOISELOEDLESER IMGIPEEEOMGLIR NAEGYKODAOKASTR OLLOANPILEAFGNAK GALAOMNDCMR VKLOEMEGTVK VEEEERECOHLOAEK IAOLEEELEEEOGNTELINDR ANLOIDOINTOLNIER ELESOISELOEDLESER IMGIPEEEOMGLIR NAEGYKODAOKASTR OLLOANPILEAFGNAK GRUPEVVPR SMEAEMIOLOEELAAAER KAGULPOVORD	2021.0 2063.9 1403.7 1106.6 1215.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1755.8 2332.0 1723.8 1708.9 1728.9 1547.7 2047.9 1570.8 1279.6 1407.7 1260.7 1912.8 2472.1 1869.0 1723.8 1708.9 1728.9 1154.7 2047.9 1570.8 1279.6 17714.9 1949.0 1750.8 17718.9 1154.7 2047.9 1570.8 1279.6 17714.9 1869.0 1789.9	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1216.7 1527.8 1816.9 1868.9 2472.1 1815.9 1615.8 21771.1 1950.0 1751.9 2333.0 1724.8 1709.9 1729.9 1155.7 2048.9 1571.8 1280.6 1715.9 975.5 1204.6 1408.7 1261.7 1913.9 2473.1 1870.0 2034.0 1615.8 1724.8 1709.9 1729.9 1155.7 2048.9 1729.9 1155.7 2048.9 1729.9 1155.7 2048.9 1729.9 1720.9	2021.0 2063.9 1403.7 1106.6 1215.7 1106.6 1215.7 1174.0 2914.3 1403.7 1526.8 1215.7 1526.8 1215.7 1526.8 1247.1 1645.8 1869.0 2492.2 1867.9 2471.2 1814.9 1614.8 2170.1 1750.8 2332.0 1723.8 1708.9 1728.9 1728.9 1728.9 1738.9 1728.9 1738.9 1728.9 1738.9 1738.9 1738.9 1749.0 1503.6 17714.9 2048.0 1570.8 1279.6 17714.9 2471.2 1868.9 1279.6 17714.9 2471.2 1868.9 1279.6 17714.9 2471.2 1868.9 1279.6 1407.7 1260.7 1260.7 1260.7 12912.9 2471.2 1868.9 1293.9 1614.8 1723.8 1708.9 1154.7 2048.0 15708.9 1154.7 2048.0 1407.7	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1216.7 1527.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2171.1 1950.0 1751.9 1280.6 1719.9 1724.8 1709.9 1755.7 2049.0 1571.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 1280.6 1715.9 175.5 1204.6 1715.9 175.5 1204.6 1715.9 175.5 1204.6 1715.9 175.5 1204.6 1715.9 175.5 1204.6 1715.9 175.5 1204.6 1715.9 175.5 1204.6 1715.9 175.5 1204.6 175.5 1204.6 175.5 1204.6 175.5 1204.6 175.5 1204.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 1704.6 175.5 175.6 175
84.0 84.0 84.0 84.0 84.0 84.0 84.0 84.0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35.7 35.7 35.7 35.7 35.7 35.7 35.7 21.5 21.5 Myosin-9 (M 25.6 25.6 25.6 25.6 25.6 25.6 25.6 25.6	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 98.0 94.0 98.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEOYTOAIETAGR OOHEGAGCALDSGEPPOCR WETGEVOAOSAAK KYEVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAOSAAK YKFVATGHGKYEK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAOSAAK YKFVATGHGKYEK LIDRTESLINR VYEVATGHGKYEK LIDRTESLINR JOSSIN HEAVY	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 15268.8 11525.7 15268.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9 1728.9 1728.9 1728.9 1728.9 174.1 1814.9 1614.8 1729.6 1714.9 174.1 1860.0 1771.8 1771.9 178.	2022.0 2024.9 1404.7 1107.6 1216.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1724.8 1709.9 1729.9 1155.7 2048.9 1715.9 233.0 1724.8 1709.9 1755.7	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 29914.3 1403.7 1526.8 1526.8 1869.0 2492.2 1864.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1728.9 1728.9 1728.9 1728.9 1749.9 1749.0 1879.6 1407.7 1912.9 2471.2 1889.0 232.9 1614.8 1708.9 1614.8 1708.9 1714.9	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1527.8 1870.0 2493.2 1868.9 2472.2 1816.9 1751.9 2333.1 1724.8 1709.9 1755.7 2049.0 1571.9 1280.6 1408.7 1261.7 1913.9 2472.2 1870.0 2034.0 1615.8 1724.8
84.0 84.0 84.0 84.0 84.0 84.0 168.0 168.0 17.0 17.0 17.0 17.0 17.0 17.0 17.0 17	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 31. 7 21. 5 21. 5 21. 5 21. 6 25. 6	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 98.0 94.0 98.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEOYTOAIETAGR OOHEGAGCALDSGEPPOCR WETGEVOAOSAAK KYEVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAOSAAK YKFUATGHGKYEK LKPSEAPELDEDEGFGDWSORPEOR WETGEVOAOSAAK YKFUATGHGKYEK LIDRTESLINR YOSIN heavy chain, nonmuscle II a) (Nonmuscle I	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1728.9 1728.9 1728.9 1728.9 1728.9 1728.9 1728.9 1728.9 174.1 1814.9 1614.8 1729.6 1714.9 174.1 1814.9 1614.8 1728.9 178.9	2022.0 2024.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1216.7 1527.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1724.8 1709.9 1729.9 1155.7 2048.9 1715.9 1751.8 1280.6 1715.9 1751.8 1280.6 1715.9 1751.8 1280.6 1715.9 1751.8 17	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1526.8 1645.8 1645.8 1645.9 2492.2 1667.9 2471.2 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1724.7 2048.0 1874.9 1614.8 1279.6 1407.7 1912.9 2471.2 1889.0 1773.8 1279.6 1407.7 1912.9 1614.8 1779.6 1407.7 1912.9 1614.8 1789.9 1614.8 1798.9 1644.9 1794.5 1949.0 1664.7	2022.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 1770.9 1751.9 2333.1 1724.8 1709.9 1755.7 2049.0 1751.9 1866.7
84.0 84.0 84.0 84.0 84.0 84.0 84.0 84.0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35.7 35.7 35.7 35.7 35.7 35.7 35.7 35.7	2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 98.0 99.0 98.0 96.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEOYTOAIETAGR OOHEGAGCALDSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEGGGHVPERPK LKPSEAPELDEDEGGGDWSQRPEQR WETGSEVOAQSAAK YKFVATGHGK KLKPSEAPELDEDEGFGDWSQRPEQR WETGSEVOAQSAAK YKFVATGHGKYEK LIDRTESLINR YKSVATGHGKYEK LIDRTESLINR FLYSONITHESELNR FOSALESOLODTOELLOEENR ANLOIDOINTDLILLER DFSALESOLODTOELLOEENR IAGETINLITEEEKSK IAOLEFELEFEOGNTELINDR IAOLEFELDHETEKSK IAOLEFELGEFOGNTELINDR IAOLEFELDHOTHER MOGNIFOELGEFUR LOGELDDLLVDLDHOR LTEMETLOSOLMAEK NOONIOELEFOLEFESAR NAEOYKODAOKASTR OLLOANPILEFOLATAR OTLLOANPILEFOLATAR WEDLEFOLATAR SMELAGOAKENK NOOWWR ALEOOVEEMK KLOAOMKDCMR VKLOEMGTVK VEETEERCOHLOAEK IAOLGELAADER VKLOEMGTVK VEETEERCOHLOAEK IAOLGELAADER VKLOEMGTVK VEETEERCOHLOAEK IAOLGELAADER VKLOEMGTVK VEETEERCOHLOAEK IAOLGELAADER KLOAOMKDCMR ASREHLAOAKENK NOOWWR ALEOOVEEMK KLOAOMKDCMR NAEOGUSTUR VKLOEMGTVK VEETEERCOHLOAEK IAOLGELASER IMGIPEEGEMGLLR NAEOYKOOAOKASTR OLLOANPILEAFGNAK GRUPFVVPR SMEAEMIOLOELAAAER KLOAOMKDCMR NAEOGUSTUR NAEOGUSTUR SMEAEMIOLOELAAAER KLOAOMKDCMR RANCILENERGELANEVK IAOLEGELDEEFER MIGIPEEGEMGLLR NAEOYKOOAOKASTR OLLOANPILEAFGNAK RGDLPFVVPR SMEAEMIOLOELAAAER KLOAOMKDCMR RACTILENERGELANEVK IAOLEGOLDNETKER NWOWWR LLOANPILEAFGNAK RGDLPFVVPR SMEAEMIOLOELAAAER KLOAOMKDCMR RACTILENERGELANEVK IAOLEGOLDNETKER NWOWWR LOADHUNDLUNDHOR YAEEROREAREAR KLOAOMKDCMR AKOTLENERGELANEVK IAOLEGOLDNETKER NWOWWR LOALPHUR LOGELDDLUVDLOHOR YAEEROREARAER KLOAOMKOCMR NAEGROFFORD STONAWGWAR LOGELDDLUVDLOHOR YAEEROREARAER KLOAOMKOCMR SMEAEMIOLOEELAAAER KLOAOMKOCMR RACTILENERGELANEVK IAOLEGOLDNETKER NWOWWR LOACHORD ROADROCH ORDORD ROADROCH O	2021.0 2063.9 1403.7 1106.6 1215.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 17550.8 2332.0 1723.8 1708.9 1728.9 1154.7 2047.9 1570.8 1279.6 1714.9 974.4 1203.6 1407.7 1260.7 1912.8 1472.8 1472.8 1708.9 1154.7 2047.9 154.7 2047.9 154.7 2047.9 1550.8 1279.6 1714.9 154.7 2047.9 154.7 2047.9 154.7 2047.9 154.7 2047.9 154.7 2045.9 1407.7 1928.9 1154.7 2045.9 1407.7 1928.9 1154.7 2045.9 1407.7 1928.9 1154.7 2045.9 1407.7 1928.0 1814.9 974.4 1949.0 2033.0 1614.8 1728.9 1154.7 2045.9 1407.7 1928.0	2022.0 2024.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1616.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1751.9 2333.0 1724.8 1709.9 1729.9 1155.7 2048.9 1536.7 1248.7 1261.7 1274.8 1280.6 1715.9 1571.8 1280.6 1715.9 1571.8 1280.6 1715.9 1571.8 1280.6 1715.9 1571.8 1280.6 1715.9 1571.8 1280.6 1715.9 1571.8 1280.6 1715.9 1575.7 1261.7 1272.8 1729.9 1155.7 1204.6 1408.7 1215.7 1215.7 1221.7 1221.8 1222.8 1759.9 1155.7 1248.7 1251.7 1261.7 1272.8 1724.8 1729.9 1155.7 1261.7 1913.9 1755.7 1261.7 1870.0 1615.8 1724.8 1729.9 1155.7 1615.8 1724.8 1759.9 1155.7 1616.8 1724.8 1759.9 1155.7 1920.0 1155.7 1920.0 1155.7 1920.0 1155.7 1920.0 1155.7 1920.0 1155.7 1920.0 1155.7 1920.0 1155.7 1920.0 1155.7 1920.0 1155.7 1920.0 1155.7	2021.0 2063.9 1403.7 1106.6 1215.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1869.0 2492.2 1867.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 1279.6 1714.9 974.5 1206.7 1814.9 1614.8 1708.9 1729.6 1749.9 1741.2 1869.0 2032.9 1614.8 1723.8 1708.9 1614.8 1723.8 1708.9 1614.8 1723.8 1749.9 1614.8 1723.8 1749.9 1614.8 1723.8 1749.9 1614.8 1723.8 1749.9 174.5 1869.0 1874.9	2022.0 2064.9 1404.7 1107.6 1216.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1527.8 1527.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2171.1 1950.0 1751.9 1752.9 1752.9 1752.9 1752.9 1752.9 1752.9 1753.9 1753.9 1753.9 1753.9 1753.9 1753.9 1753.9 1754.8 1709.9 1755.7 1754.8 1770.9 1755.7 1755.7 1755.7 17
84 0 84 0 84 0 84 0 84 0 84 0 84 0 84 0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 21. 5 21. 5 Myosin-9 (M 25. 6	2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 99.0 98.0 96.0 98.0 96.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEOYTOAIETAGR OOHEGAGCALDSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEGGGHVPERPK LKPSEAPELDEDEGGGBWSQRPEQR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEGGGHVPERPK LKPSEAPELDEDEGGGBWSQRPEQR WETGEVOAOSAAK YKFVATGHGKYEK LIDRTESLINR YKFVATGHGKYEK LIDRTESLINR FLOSTINGTESLING ANLOIDOINTOLILLE DESALESOLODTOELLOEENR ANLOIDOINTOLILLE DESALESOLODTOELLOEENR IAGEFTINLTEEEKSK IAOLEEELEEOGNTELINDR IAOLEEOLDOINTKER IMGIPEEFOMGLLR KTLEEEAKTHEAOIOEMR LOGELDDLLVDLDHOR LTEMETLOSOLMAEK MOONIOELEEOLEEESSAR NAEOYKODAOKASTR OLLOANPILEAFGMAK OTLENERGELANEVK RODLPEVVPR SMEAEMIOLOEELAAAER VSHLLGINVTOFTR LOAOMKDCMR VKLOEMEGTVK VEEEEERCOHLOAEK INOWWR ALEOOVEEMK KLOAOMKDCMR VKLOEMEGTVK VEEEERCOHLOAEK IAOLGELAAAER VKLOEMEGTVK VEEEERCOHLOAEK IAOLGEELSESR IMGIPEEEOMGLLR NAEOYKOOAOKASTR OLLOANPILEAFGMAK GLIDLYDLDHOR VKLOEMEGTVK VEEEERCOHLOAEK IAOLGEELSESR IMGIPEEEOMGLLR NAEOYKOOAOKASTR OLLOANPILEAFGMAK GRUPFVVPR SMEAEMIOLOEELAAAER KLOAOMKDCMR KACHENERGELANEVK KOLOEMEGTK NAEOYKOOAOKASTR OLLOANPILEAFGMAK RGDLPFVVPR SMEAEMIOLOEELAAAER KLOAOMKDCMR RACTLENERGELANEVK IAOLEEOLDNETKER NYOWWR LOGELDDLLVDLDHOR YAEERRREAEARAR LOGELDDLLVDLDHOR VAEERRREAEARAR ROMUNCYDDDESVKSK	2021.0 2063.9 1403.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9 1154.7 2047.9 1570.8 1279.6 1407.7 1260.7 1912.8 1407.7 1260.7 1912.8 1728.9 1154.7 2047.9 154.7 2045.9 1407.7 1260.7 1912.8 1407.7 1928.9 1154.7 2045.9 1407.7 1928.0 1814.9 1752.8 1778.9 1154.7 2045.9 1407.7 1928.0 1814.9 1754.7 2045.9 1407.7 1928.0 1814.9 1754.7 2045.9 1407.7 1928.0 1814.9 1754.7 2045.9 1407.7 1928.0 1814.9 1754.7 2045.9 1407.7 1928.0 1814.9 1754.7 2045.9 1407.7 1928.0 1814.9 1755.7 1928.0 1814.9 1754.7 2045.9 1407.7 2045.9 1407.7 2045.9 1407.7 2045.9 15535.7 1623.7 25ynovial protein 1819.8 1535.7 1623.7 1838.9	2022.0 2024.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1646.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1751.9 2333.0 1724.8 1709.9 1729.9 1155.7 2048.9 1536.7 1261.7 1913.9 2473.1 1870.0 2034.0 1615.8 1724.8 1729.9 1155.7 2048.9 1155.7 2047.0 1408.7 1261.7 1913.9 1155.7 2047.0 1408.7 1299.0 1815.9 1724.8 1729.9 1155.7 2047.0 1408.7 1261.7 1913.9 1155.7 2047.0 1408.7 1261.7 1929.0 1815.9 1755.1 1820.0 1815.9 1755.1 1820.0 1815.9 1755.1 1820.0 1815.9 1755.1 1820.0 1815.9 1755.1 1820.0 1815.9 1755.1 1820.0 1815.9 1755.1 1820.0 1815.9 1755.1 1820.0 1815.9 1755.1 1820.0 1815.9 1755.1 1820.0 1815.9	2021.0 2063.9 1403.7 1106.6 1215.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1869.0 2492.2 1862.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 1279.6 1714.9 974.5 1203.6 1407.7 1208.9 1614.8 1723.8 1708.9 1714.9 1614.8 1729.6 1714.9 171	2022.0 2064.9 1404.7 1107.6 1216.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1527.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 2171.1 1950.0 1751.9 2333.1 1724.8 1709.9 1755.7 2049.0 1571.9 1280.6 1715.9 1715.9 1715.9 1715.9 1715.9 1715.9 1729.9 175.7 2049.0 1615.8 1709.9 1715.7 2049.0 1615.8 1709.9 1715.7 2049.0 1615.8 1724.8 1709.9 175.7 2049.0 1615.8 1724.8 1709.9 1815.9 1755.7 2049.0 1615.8 1724.8 1709.9 1815.9 1950.0 1815.9 1950.0 1815.9 1955.7 2049.0 1815.9 1955.7 2049.0 1815.9 1955.7 2049.0 1815.9 1955.7 2049.0 1815.9 1955.7 2049.0 1815.9 1955.7 2049.0 1815.9 1955.7 2049.0 1815.9 1955.7 1929.0 1815.9 1950.0 1815.9 1950.0 1815.9 1950.0 1815.9 1950.0 1815.9
84.0 84.0 84.0 84.0 84.0 84.0 84.0 84.0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 32. 5 7 32. 5 21. 5 Myosin-9 (M 25. 6 25.	2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 98.0 94.0 99.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEOYTOAIETAGR OOHEGAGCALDSGEPPOCR WETGEVOAOSAAK KYEVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGGGHVPERPK LIDRTESLINR JUSSIA IN INDICATE JOHN JOHN JOHN JOHN JOHN JOHN JOHN JOHN	2021.0 2063.9 1403.7 1106.6 1215.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1215.7 126.8 1215.7 126.8 1215.7 126.9 1869.0 1492.2 1867.9 1471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1708.9 1154.7 2047.9 1570.8 1279.6 1714.9 1714.	2022.0 2024.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1216.7 1646.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1751.9 2333.0 1724.8 1709.9 1155.7 2048.9 1715.9 1729.9 1155.7 2048.9 1715.9 1729.9 1155.7 2048.9 1715.9 1729.9 1155.7 2048.9 1715.9 1729.9	2021.0 2063.9 1403.7 1106.6 1215.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1215.7 MHC II-a) (NMM 1645.8 1869.0 2492.2 1867.9 2471.2 1867.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 2332.0 1723.8 1708.9 1728.9 1154.7 2048.0 1407.7 1912.9 2471.2 1869.0 2492.2 1614.8 1774.9 1	2022.0 2064.9 1404.7 1107.6 1216.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1870.0 2493.2 1868.9 2472.2 1815.9 1615.8 1770.9 1751.9 2333.1 1724.8 1709.9 1759.9 1850.6 1408.7 1961.7 1971.9 1280.6 1408.7 1961.7 1971.9 1280.6 1408.7 1261.7 1971.9 1280.6 1408.7 1261.7 1971.9 1280.6 1408.7 1261.7 1971.9 1972.9 1155.7 2049.0 1615.8 1724.8 1729.9 1155.7 2049.0 1615.9 175.9 175.9 1870.0 2034.0 1615.8 1724.8 1729.9 1155.7 2049.0 1615.8 1729.9 1155.7 2049.0 1615.8 1729.9 1155.7 2049.0 1615.8 1724.8 1729.9 1155.7 2049.0 1615.8 1724.8 1729.9 1155.7 2049.0 1615.8 1724.8 1729.9 1155.7 2049.0 1615.8 1724.8 1729.9 1155.7 2049.0 1615.8 1724.8 1729.9 1155.7 2049.0 1615.8 1724.8 1724.8 1729.9 1155.7 2049.0 1615.8 1724.8 1724.8 1724.8 1729.9 1155.7 2049.0 1815.9 175.5 2049.0 1815.9 175.6 204.7 1839.9 1209.6 1217.7 1839.9 1209.6 1217.7 1090.6
84.0 84.0 84.0 84.0 84.0 84.0 84.0 84.0	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	12.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3	35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 35. 7 21. 5 21. 5 Myosin-9 (M 25. 6	2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 1.7 1.4 1.2 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2	99.0 99.0 99.0 99.0 98.0 96.0 96.0 99.0 99.0 99.0 99.0 99.0 99	IDOWLEOYTOAIETAGR OOHEGAGCALDSGEPPOCR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGGGDWSORPEOR WETGEVOAOSAAK YKFVATGHGK LIDRTESLINR OLOAODEEGGGHVPERPK LKPSEAPELDEDEGGGDWSORPEOR WETGEVOAOSAAK YKFVATGHGKYEK LIDRTESLINR YKFVATGHGKYEK LIDRTESLINR JOSIN BEAVY Chain, nonmuscle II a) (Nonmuscle ALEEAMEOKAELER ANLOIDOINTOLILLER DFSALESOLODTOELLOEENR IAGETTINLTEEEKSK IAOLEEELEEGGRTELINDR IAOLEEOLDOINTKER IMGIPEEFOMGLIR KTLEEEAKTHEAOIOEMR LOGELDOILVOLDHOR LTEMETLOSOLMAEK MOONIOELEOLEEESAR NAEOYKOOAOKASTR OLLOANPILEAFGMAK OTLENERGELANEVK RODLPEVVPR SMEAEMIOLOEELAAAER VSHLLGINVTOFTR LOAOMKDCMR ASREEILAOAKENEK NWOWWR ALEOOVEEMK KLOAOMKDCMR XSREEILAOAKENEK NWOWWR ALEOOVEEMK KLOAOMKDCMR VKLOEMEGTVK VEEEERCOHLOAEK IAOLEECLEEGERINDR NAEOGWEEMK KLOAOMKDCMR RASREEILAOAKENEK NWOWWR ALEOOVEEMK KLOAOMKDCMR RASREEILAOAKENEK NOOWWR ALEOOVEEMK KLOAOMKDCMR RASREEILAOAKENEK NOOWWR ALEOOVEEMK KLOAOMKDCMR RASREEILAOAKENEK NOOWWR ROLLOANPILEAFGNAK GRUPFVVPR SMEAEMIOLOEELAAAER KLOAOMKDCMR RACHLEBEGGNTELINDR NALOIGHGTWKER NAEOGYKOOAOKASTR OLLOANPILEAFGNAK ROLLPFVVPR SMEAEMIOLOEELAAAER KLOAOMKDCMR RACHLERGEGLANEVK KAOLEEOLDNETKER NOOWWYDDDESVKS GTTCHHSPLFR LIGOOVPATK CHICHOPATK	2021.0 2063.9 1403.7 1106.6 1215.7 1106.6 1215.7 1974.0 2914.4 1403.7 1526.8 1869.0 2492.2 1867.9 2471.1 1814.9 1614.8 2170.1 1949.0 1750.8 2322.0 1723.8 1708.9 1728.9 1154.7 2047.9 1570.8 1279.6 1407.7 1260.7 1912.8 2472.1 1889.0 1614.8 1723.8 1708.9 1714.9 1714.9 1714.9 1715.8 1714.9 1715.9 17	2022.0 2024.0 2064.9 1404.7 1107.6 1216.7 1975.0 2915.4 1404.7 1527.8 1527.8 1527.8 1870.0 2493.2 1868.9 2472.1 1815.9 1615.8 2171.1 1950.0 1751.9 2333.0 1724.8 1709.9 1729.9 1155.7 2048.9 1571.8 1280.6 1715.9 975.5 1204.6 1408.7 1261.7 1913.9 2473.1 1870.0 2034.0 1615.8 1724.8 1729.9 1155.7 2047.0 1408.7 1261.7 1929.0 1815.9 1155.7 2047.0 1408.7 1262.0 1815.9 1755.1 1850.0 18565.7 1928.0 1815.9 1755.1 1950.0 18565.7 1928.0 1815.9 1755.1 1950.0 18565.7 1928.0 1815.9 1755.1 1950.0 18565.7 1928.0 1815.9 1755.1 1950.0 18565.7 1928.0 1815.9 1755.1 1950.0 18565.7 1928.0 1815.9 1755.1 1950.0 18565.7 1928.0 1815.9 1955.0 1950.0 18565.7	2021.0 2063.9 1403.7 1106.6 1215.7 1106.6 1215.7 1974.0 2914.3 1403.7 1526.8 1215.8 1215.7 MHC II-a) (NMM 1645.8 1869.0 2492.2 1867.9 2471.2 1814.9 1614.8 2170.1 1949.0 1750.8 1279.6 1714.9 974.5 1203.6 1407.7 1208.0 17123.8 1708.9 1714.9 1	2022.0 2064.9 1404.7 1107.6 1216.7 1107.6 1216.7 1975.0 2915.3 1404.7 1527.8 1527.8 1870.0 2493.2 1868.9 2472.2 1816.9 1615.8 2171.1 1950.0 1751.9 2333.1 1724.8 1709.9 1755.7 2049.0 1571.9 1280.6 1408.7 1261.7 1913.9 2472.2 1870.0 2034.0 1615.8 1724.8 1709.9 1155.7 2049.0 1515.7 2049.0 1515.7 2049.0 1515.7 2049.0 1516.8 1729.9 1155.7 2049.0 1615.8 1724.8 1709.9 1155.7 2049.0 1615.8 1724.8 1729.9 1850.0 1656.7 1829.0 1856.7 1829.0 1856.7 1820.9 1856.7 1820.9 1850.7 1624.7 1839.9 1850.9 1850.7 1820.9 1850.7 1820.9 1850.7 1820.9 1839.9 1850.7 1624.7 1839.9 1850.7 1624.7 1839.9 1820.9 1839.9 1820.9 1839.9 1820.9 1839.9 1820.9 1839.9 1209.6

38.0	22.0	22.0	43.9	1.5	97.0	ILGQQVPYATKGNQWVGYDDQESVK	2822.4	2823.4	2822.4	2823.4
38.0 38.0	22.0 22.0	22.0 22.0	43.9 43.9	0.4	63.0 99.0	GQEDASPDRFSNTDYAVGYMLR EAGTLAYYEICDFLR	2491.1 1801.8	2492.1 1802.9	2491.1 1801.8	2492.1 1802.8
38.0 38.0	22.0 22.0	22.0 22.0	43.9 43.9	0.0 0.0	99.0 99.0	GTTGHHSPLFR ILGQQVPYATK	1208.6 1216.7	1209.6 1217.7	1208.6 1216.7	1209.6 1217.7
38.0 168.0	22.0 2.0	22.0 2.0	43.9 15.7	0.0 2.0	76.0 99.0	LVMGIPTFGR LVMGIPTFGR	1091.6 1089.6	1092.6 1090.6	1089.6 1089.6	1090.6 1090.6
104.0 104.0	7.7 7.7	7.7 7.7	18.3 18.3	2.0 2.0	99.0 99.0	EAGTLAYYEICDFLR GTTGHHSPLFR	1819.8 1208.6	1820.8 1209.6	1819.8 1208.6	1820.9 1209.6
104.0 104.0	7.7 7.7	7.7 7.7	18.3 18.3	2.0 1.7	99.0 98.0	TLLSVGGWNFGSQR GNQWVGYDDQESVKSK	1520.8 1838.9	1521.8 1839.9	1520.8 1838.8	1521.8 1839.9
104.0 104.0	7.7 7.7	7.7 7.7	18.3 18.3	0.0 0.0	70.0 99.0	EAGTLAYYEICDFLR GTTGHHSPLFR	1801.8 1208.6	1802.8 1209.6	1801.8 1208.6	1802.8 1209.6
P37802 T 66.0	AGL2_HUMAN 14.8	14.8	Transgelin-2 61.3	2.0	ha homolog) - Homo sapiens (Human) ANRGPAYGLSR	1202.6	1203.6	1202.6	1203.6
66.0 66.0	14.8 14.8	14.8 14.8	61.3 61.3	2.0	99.0 99.0	DDGLFSGDPNWFPK GASQAGMTGYGMPR	1593.8 1382.6	1594.8 1383.6	1593.7 1382.6	1594.7 1383.6
66.0 66.0	14.8 14.8	14.8 14.8	61.3 61.3	2.0	99.0 99.0	NFSDNQLQEGKNVIGLQMGTNR QMEQISQFLQAAER	2462.2 1660.8	2463.2 1661.8	2462.2 1660.8	2463.2 1661.8
66.0 66.0	14.8 14.8	14.8 14.8	61.3 61.3	2.0	99.0 99.0	TLMNLGGLAVAR YGINTTDIFOTVDLWEGK	1214.7 2099.0	1215.7 2100.0	1214.7 2099.0	1215.7 2100.0
66.0 66.0	14.8 14.8	14.8 14.8	61.3 61.3	0.8	85.0 99.0	DDGLFSGDPNWFPKK QMEQISQFLQAAER	1721.8 1677.8	1722.8 1678.8	1721.8 1677.8	1722.8 1678.8
97.0 97.0	3.8 3.8	3.8 3.8	32.7 32.7	2.0 1.4	99.0 96.0	GASQAGMTGYGMPR DDGLFSGDPNWFPKK	1384.6 1721.8	1385.6 1722.8	1382.6 1721.8	1383.6 1722.8
97.0 143.0	3.8 5.4	3.8 5.4	32.7 51.8	0.4 2.0	61.0 99.0	OMEQISOFLOAAER GASQAGMTGYGMPR	1660.8 1382.6	1661.8 1383.6	1660.8 1382.6	1661.8 1383.6
143.0 143.0 143.0	5.4 5.4 5.4	5.4 5.4 5.4	51.8 51.8 51.8	2.0 1.4 0.0	99.0 96.0 99.0	QMEQISQFLQAAER ANRGPAYGLSR	1660.8 1202.6 1677.8	1661.8 1203.6 1678.8	1660.8 1202.6	1661.8 1203.6 1678.8
P37837 T	ALDO_HUMAN		Transaldolas	se (EC 2.2.1	.2) - Homo	QMEQISQFLQAAER sapiens (Human)			1677.8	
219.0 219.0 219.0	5.9 5.9 5.9	5.9 5.9 5.9	11.9 11.9 11.9	2.0	99.0 99.0 95.0	LSFDKDAMVAR WLHNEDOMAVEK IYNYYKK	1251.6 1498.7 990.5	1252.6 1499.7 991.5	1251.6 1498.7 990.5	1252.6 1499.7 991.5
219.0 219.0 209.0	5.9 5.9 1.4	5.9 5.9 1.4	11.9	1.3 0.6 1.4	75.0 96.0	FAADAVKLER WLHNEDOMAVEK	1118.6 1498.7	1119.6 1499.7	1118.6 1498.7	1119.6 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 P38159 H 107.0	3.1 HNRPG_HUMAN 10.1	10.1	18.4 Heterogeneo	1.0 ous nuclear 2.0	90.0 ribonucleop	LVPVLSAK protein G (hnRNP G) (RNA-binding motif protein AIKVEQATKPSFESGR	825.5 , X chromosor 1746.9	826.5 me) (Glycoproteil 1747.9	825.5 n p43) - Homo sa 1746.9	826.5 piens (Human) 1747.9
107.0 107.0 107.0	10.1	10.1	32.5 32.5	2.0	99.0 99.0	ALEAVFGKYGR DSYGGPPRREPLPSRR	1209.6 1839.0	1210.7 1840.0	1209.7 1838.9	1210.7 1840.0
107.0 107.0 107.0	10.1 10.1 10.1	10.1 10.1 10.1	32.5 32.5 32.5	2.0 2.0 2.0	99.0 99.0 99.0	GFAFVTFESPADAK GFAFVTFESPADAKDAAR	1485.7 1898.9	1486.7 1899.9	1485.7 1898.9	1486.7 1899.9
151.0 294.0	2.0 2.0	2.0 2.0	33.2 39.4	2.0 2.0 2.0	99.0 99.0	AIKVEQATKPSFESGR GFAFVTFESPADAKDAAR	1746.9 1898.9	1747.9 1899.9	1746.9 1898.9	1747.9 1899.9
	F4A1_HUMAN	2.1	Eukaryotic ir							
231.0	2.7	2.7	12.3	2.0	99.0 81.0	GIYAYGFEKPSAIQQR DFTVSAMHGDMDQKER	1826.9 1865.8	1827.9 1866.8	1826.9 1865.8	1827.9 1866.8
231.0 P40121 C	CAPG_HUMAN 6.4	6.4	12.3 Macrophage 19.3		otein (Actir	-regulatory protein CAP-G) - Homo sapiens (Hu EVOGNESDLFMSYFPR		1918.9	1917.9	1918.9
181.0 181.0 181.0	6.4 6.4 6.4	6.4 6.4	19.3 19.3 19.3	2.0 2.0 2.0	99.0 99.0 99.0	MQYAPNTQVEILPQGR QAALQVAEGFISR	1843.9 1371.7	1844.9 1372.7	1843.9 1371.7	1844.9 1372.7
181.0 181.0	6.4	6.4	19.3 19.3	0.3 0.0	54.0 98.0	QFFKDWK	980.5 1388.7	981.5 1389.8	980.5 1388.7	981.5 1389.7
30.0 30.0	10.0 10.0	10.0 10.0	23.0 23.0	2.0 2.0	99.0 99.0	QAALQVAEGFISR EVQGNESDLFMSYFPR MQYAPNTQVEILPQGR	1917.9 1843.9	1918.9 1844.9	1917.9 1843.9	1918.9 1844.9
30.0	10.0	10.0	23.0	2.0	99.0	QAALQVAEGFISR	1371.7	1372.7	1371.7	1372.7
30.0 30.0 30.0	10.0 10.0 10.0	10.0 10.0 10.0	23.0 23.0 23.0	2.0 2.0 0.0	99.0 99.0 94.0	OFFKDWK YOEGGVESAFHK EVOGNESDLFMSYFPR	997.5 1350.6 1916.9	998.5 1351.6 1918.0	997.5 1350.6 1916.9	998.5 1351.6 1917.9
30.0 30.0	10.0 10.0 10.0	10.0	23.0 23.0 23.0	0.0	99.0 55.0	QAALQVAEGFISR OFFKDWK	1388.7	1389.7 981.5	1388.7	1389.7 981.5
30.0										981.5 1258.7
72.0	10.1	10.1	30.2	2.0	99.0	DLALAIRDSER EVOCNESDI EMEYERR	1257.7	1258.7	1257.7	
72.0 72.0	10.1 10.1	10.1 10.1	30.2 30.2	2.0 2.0	99.0 99.0	EVQGNESDLFMSYFPR MQYAPNTQVEILPQGR	1917.9 1843.9	1918.9 1844.9	1917.9 1843.9	1918.9 1844.9
72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1	30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0	EVQGNESDLFMSYFPR MQYAPNTOVEILPQGR QAALQVAEGFISR YQEGGVESAFHK	1917.9 1843.9 1371.7 1350.6	1918.9 1844.9 1372.7 1351.6	1917.9 1843.9 1371.7 1350.6	1918.9 1844.9 1372.7 1351.6
72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1	30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 0.0 0.0	99.0 99.0 99.0 99.0 56.0 99.0	EVQGNESDLFMSYFPR MQYAPNTQVEILPQGR QAALQVAEGFISR YQEGGYESAFHK EVQGNESDLFMSYFPR QAALQVAEGFISR	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7	1917.9 1843.9 1371.7	1918.9 1844.9 1372.7
72.0 72.0 72.0 72.0 72.0 72.0 72.0 P40925 N 90.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 MDHC_HUMAN 12.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehye	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0	99.0 99.0 99.0 99.0 56.0 99.0 cytoplasmi 99.0	EVOGNESDLFMSYFPR MQYAPNTQVEILPQGR QAALQVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALQVAEGFISR C (EC 1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 siens (Human) 1751.9	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7
72.0 72.0 72.0 72.0 72.0 72.0 72.0 P40925 N 90.0 90.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 31.4 31.4 31.4	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0	99.0 99.0 99.0 99.0 56.0 99.0 cytoplasmi 99.0 99.0	EVOGNESDLFMSYFPR MQYAPHOVELIPOGR QAALQVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALQVAEGFISR CEC 1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVQOR	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 e) - Homo sap 1750.9 1392.7 1163.6	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 biens (Human) 1751.9 1393.7 1164.6	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6
72.0 72.0 72.0 72.0 72.0 72.0 72.0 90.0 90.0 90.0 90.0 90.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehy 31.4 31.4 31.4 31.4	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 cytoplasmi 99.0 99.0 99.0	EVOGNESDLEMSYFPR MOYAPHOVELPOGR QAALQVAEGFISR YOEGGVESAFHK EVOGNESDLEMSYFPR QAALQVAEGFISR C(EC 1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKODSWLK FVEGUPINDFSR GEFVTTVQOR NVIIWGNHSSTQYPDVNHAK SAPSIFKEMFSCLTR	1917.9 1843.9 1371.7 1350.6 1933.9 1750.9 1750.9 1392.7 1163.6 2279.1 1705.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9
72.0 72.0 72.0 72.0 72.0 72.0 72.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 9	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehy! 31.4 31.4 31.4 31.4 31.4	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 56.0 99.0 cytoplasmi 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLEMSYFPR MOYAPHOVELIPOGR OAALQVAEGFISR YOEGGVESAFHK EVOGNESDLEMSYFPR QAALQVAEGFISR (CEC 1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKODSWLK FYEGLPINDFSR GEFYTTVOOR NVIIWGNHSSTQYPDVNHAK SAPSIFKEMFSCLTR VIVVGNPANTNCLTASK FYEGLPINDFSR	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 2) - Homo sap 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 (Human) 1751.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7
72.0 72.0 72.0 72.0 72.0 72.0 72.0 90.0 90.0 90.0 90.0 90.0 90.0 58.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehyr 31.4 31.4 31.4 31.4 31.4 31.4 21.2 9	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 56.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 9	EVOGNESDLFMSYFPR MOYAPHOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR (CEC 1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKODSWLK FVEGLPINDFSR GEFVTTVOOR NVIIWGMINSTGVYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEEKESAFEFLSSA FVEGLPINDFSR ELTEEKESAFEFLSSA FVEGLPINDFSR	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 2) - Homo sap 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7 1816.8	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7 1816.8 1393.7
72.0 72.0 72.0 72.0 72.0 72.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 9	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehyr 31.4 31.4 31.4 31.4 31.4 21.9 12.9 12.9 26.3	2.0 2.0 2.0 2.0 0.0 0.0 0.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYFPR MOYAPHOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR (ECE 1.1.3.7) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOGR MVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR VIVVORPAATNICLTASK FVEGLPINDFSR ELTEEKESAFEFLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEEKESAFEFLSSA ELTEEKESAFEFLSSA ELTEEKESAFEFLSSA	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 2) - Homo sap 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7 1705.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7 1816.8 1393.7 1706.8 1816.9	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7 1705.8 1395.7	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1706.9 1816.8
72.0 72.0 72.0 72.0 72.0 72.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 9	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	10.1 10.1 10.1 10.1 10.1 10.1 11.0 12.0 12	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehy! 31.4 31.4 31.4 31.4 31.4 12.9 12.9 12.9 26.3 26.3	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYFPR MOYAPHOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR (EC 1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGMINSSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKESAFELSSA FVEGLPINDFSR SAPSIPKEMFSCLTR ELTEKESAFELSSA EVGVYEALKDDSWLK FVEGLPINDFSR SAPSIPKEMFSCLTR ELTEKESAFELSSA EVGVYEALKDDSWLK FVEGLPINDFSR	1917.9 1843.9 1371.7 1350.6 1933.9 1398.7 1398.7 1398.7 1398.7 1163.6 2279.1 1705.8 1756.9 1393.7 1163.6 2279.1 1705.8 1756.9 1393.7 1705.8 1392.7 1705.8 1392.7 1705.8	1918.9 1844.9 1372.7 13551.6 1934.9 1389.7 13551.6 1934.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1706.8 1816.9 1751.9 1393.7	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1705.8 1815.8 1750.9	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1706.9 1816.8 1751.9
72.0 72.0 72.0 72.0 72.0 72.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 9	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 Malate dehyi 31.4 31.4 31.4 31.4 31.4 21.2 9 12.9 26.3 26.3	2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 56.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 9	EVOGNESDLEMSYFPR MOYAPHOVELPOGR QAALQVAEGFISR YOEGGVESAFHK EVOGNESDLEMSYFPR QAALQVAEGFISR QAALQVAEGFISR GCE 1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKODSWLK FYEGLPINDFSR GEFYTTVQOR NVIIWGNHSSTOYPDVNHAK SAPSIPKEMFSCLTR VIVVGNPANTNCLTASK FYEGLPINDFSR ELTEEKESAFFFLSSA FYEGLPINDFSR SAPSIPKEMFSCLTR ELTEEKESAFFELSSA EVEGLPINDFSR SAPSIPKEMFSCLTR ELTEEKESAFFELSSA EVGVYEALKDDSWLK	1917.9 1843.9 1371.7 1350.6 1933.9 1938.7 19 - Homo sap 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7 1705.8 1815.8 1815.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1389.7 1164.6 2280.1 1706.9 1757.9 1394.7 1816.8 1816.9 1751.9	1917.9 1843.9 1371.7 1550.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7 1705.8 1815.8 1815.8 1815.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7 1816.8 1393.7 1706.9 1816.8
72.0 72.0 72.0 72.0 72.0 72.0 72.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 9	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehy! 31.4 31.4 31.4 31.4 31.4 21.2 9 12.9 26.3 26.3 26.3 26.3 26.3	2.0 2.0 2.0 2.0 0.0 0.0 0.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 56.0 56.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYFPR MOYAPHOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC 1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FYEGLPINDFSR GEFVTTVOOR MINIMGHISSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTINCLTASK FVEGLPINDFSR ELTEKESAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFFELSSA EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVOQR GIFTONFSR GEFVTTVOQR MINIMGNHSSTOYPDVNHAK	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.7 19.86.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1392.7 1705.8 1756.9 1392.7 1705.8 1815.8 1750.9 1392.7 1705.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1351.6 1934.9 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1706.8 1816.9 1751.9 1393.7 1164.6 2280.1	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1705.8 1392.7 1750.9 1392.7 1765.9 1393.7 1750.9 1392.7 1163.6 1750.9 1392.7 1163.6 2279.1	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1751.9 1816.8 1751.9 1816.8 1751.9 1816.8 1751.9 1816.8 1751.9 1816.8 1751.9 1816.8 1751.9 1816.8 1751.9 1816.8
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehyi 31.4 31.4 31.4 31.4 31.4 31.4 31.4 32.9 12.9 12.9 26.3 26.3 26.3 26.3 26.3 26.3 26.3	2.0 2.0 2.0 2.0 0.0 0.0 0.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 56.0 99.0 Cytoplasmi 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	EVOGNESDLEMSYFPR MOYAPHOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLEMSYFPR QAALOVAEGFISR (ECE 1.1.3.7) (Cytosolic malate dehydrogenas EVGVYEALKODSWIK FYEGLPINDFSR GEFYTTVOGR MILWIGHISSTOYPDVNHAK SAPSIPKENFSCLTR VIVVONPANTINCLTASK FVEGLPINDFSR ELTEKESAFERLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFERLSSA EVGVYEALKODSWIK FVEGLPINDFSR GEFYTTVOGR SAPSIPKENFSCLTR ELTEKESAFERLSSA EVGVYEALKODSWIK FVEGLPINDFSR GEFYTTVOGR GITTER GETTTVOGR MILWIGHISTOYPDVNHAK SAPSIPKENFSCLTR Tali precursor (EC 1.1.1.37) - Homo sapiens (Hui ACAGSSTLSMYAGAR GYLGPEOLPDCLK IFGYTTLDUVR	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.7 19.86.7 19.87 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1392.7 1705.8 1750.9 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7 1816.8 1393.7 1706.8 1816.9 1751.9 1790.9 1751.9 1393.7 1164.6 2280.1 1706.9	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1453.7 1488.7 1488.7 1423.7	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 1280.1 1706.9 1394.7 1816.8 1751.9 1393.7 1164.6 1280.1 1706.9 1816.8 1751.9 1393.7 1164.6 1751.9 1393.7 1164.6 1751.9 1393.7 1164.6 1751.9 1393.7 1164.6 1751.9 1393.7 1164.6 1791.9 1454.7 1489.7 1233.7
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehyi 31.4 31.4 31.4 31.4 31.4 31.4 32.9 12.9 12.9 26.3 26.3 26.3 26.3 26.3 26.3 26.3 26.3	2.0 2.0 2.0 2.0 2.0 0.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 Cytoplasmi 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	EVOGNESDLFMSYFPR MOYAPHOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR GEG.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWIK FYEGLPINDFSR GEFYTTVOGR MILWIGHISSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKESAFEFLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFEFLSSA EVGVYEALKDDSWIK FVEGLPINDFSR GEFYTTVOGR SAPSIPKENFSCLTR ELTEKESAFEFLSSA EVGVYEALKDDSWIK FVEGLPINDFSR GEFYTTVOGR MINIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR Iai precursor (EC 1.1.1.37) - Homo sapiens (Hui ACAGSATLSMAYAGAR GYLGFEOLPDCLK IFGYTTLDUR LTLYDIAHTPGVAADLSHIETK SOFTECTYSTPILLLGKK	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1383.7 139.8 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1392.7 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1453.7 1468.7 1488.7 1488.7 1232.7 12364.2 2101.0	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1391.7 1151.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7 1816.8 1393.7 1706.8 1816.9 1751.9 17	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7 1705.8 1453.7 1683.6 2279.1 1705.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7 1816.8 1751.9 1393.7 1164.6 1751.9 1394.7 1766.9 1454.7 1490.7 1490.7 1490.7 1233.7 12365.2 1202.0
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 30.2 31.4 31.4 31.4 31.4 31.4 31.4 31.2 9 12.9 26.3 26.3 26.3 26.3 26.3 26.3 26.3 26.3	2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 cytoplasmi 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	EVOGNESDLFMSYFPR MOYAPNTOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVOQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKEKSAFFELSSA FVEGLPINDFSR ELTEKEKSAFFELSSA FVEGLPINDFSR ELTEKEKSAFFELSSA FVEGLPINDFSR ELTEKESAFFELSSA FVEGLPINDFSR ELTEKESAFFELSSA FVEGLPINDFSR GEFVTTVQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR LITE LITEMESAFFELSSA FVEGLPINDFSR GEFVTTVQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR LITE LITEMESAFFELSSA FVEGLPINDFSR GEFVTTVQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR LITE LITEMESAFFELSSA FVEGLPHOFSR GEFVTTVQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR LITEMESAFFELSSA FVEGLPHOFSR GEFVTTQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR LITEMESAFFELSSAFF	1917.9 1843.9 1371.7 1350.6 1933.9 1382.7 1383.9 1388.7 2) - Homo sap 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1392.7 1705.8 1815.8 1392.7 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1183.6 2279.1 1705.8	1918.9 1844.9 1372.7 1351.6 1334.9 1389.7 10lens (Human) 1751.9 1393.7 1164.6 2280.1 1706.9 1393.7 1816.8 1393.7 1816.8 1393.7 1164.6 2280.1 1706.9 1454.7 1489.7 1233.7 1245.7	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1166.8 1393.7 1166.9 1816.8 1751.9 1394.7 1706.9 1816.8 1751.9 1393.7 1164.6 2280.1 1706.9
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 11.0 12.0 12	30.2 30.2 30.2 30.2 30.2 30.2 Malate dehyi 31.4 31.4 31.4 31.4 31.4 31.2 9 12.9 12.9 26.3 26.3 26.3 26.3 26.3 26.3 26.3 26.3	2.0 2.0 2.0 2.0 0.0 0.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 cytoplasmi 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	EVOGNESDLFMSYFPR MOYAPNTOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC 1.1.3.7) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGMINSSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKESAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFFELSSA EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR RVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR TEIL PECURSOF (EC 1.1.3.7) - Homo sapiens (Hu AGAGSATLSMAYAGAR GVLGPEOLPDCLK IFGYTTLDIVR LTLYDIAHTPGVAADLSHIETK SOETECTYFSTPLLLGKK TIIPLISOCTPK VOFPODOLTALTGR HGVYNPNKIFGYTTLDIVR ETANSCRIPTION 1 - Jalpha/beta (Transcription factor	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1382.7 1163.6 2279.1 1705.8 1756.9 1392.7 1705.8 1756.9 1392.7 1705.8 1755.9 1392.7 1705.8 1750.9 1392.7 1705.8 1750.9 1392.7 1705.8 1750.9 1392.7 1163.6 2279.1 1705.8 1750.9 1392.7 1163.6 2279.1 1705.8 1750.9 1392.7 1163.6 2279.1 1705.8 1750.9 1392.7 1163.6 1750.9 1392.7 1163.6 1750.8 1750.9 1392.7 1163.6 1750.8 1750.8 1750.9 1392.7 1163.6 1750.8 17	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1351.6 1934.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1706.8 1816.9 1751.9 1393.7 1164.6 2280.1 1706.9 1751.9 1393.7 1164.6 2280.1 1706.9	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7 1705.8 1392.7 1705.8 1392.7 1705.8 1488.7 1232.7 163.6 2279.1 1705.8 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1498.8 1559.8 1459.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1393.7 1816.8 1393.7 1761.9 1816.8 1751.9 1393.7 1164.6 2280.1 1706.9 1454.7 1489.7 1233.7 1233.7 1245.2 11706.9
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	30.2 30.2 30.2 30.2 30.2 30.2 30.2 Malate dehyi 31.4 31.4 31.4 31.4 31.4 21.2 9 12.9 26.3 26.3 26.3 26.3 26.3 26.3 26.3 26.3	2.0 2.0 2.0 2.0 0.0 0.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 cytoplasmi 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	EVOGNESDLFMSYFPR MOYAPNTOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC 1.1.3.7) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVOOR NVIIWGMINSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTINCLTASK FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFFELSSA FVEGLPINDFSR GEFVTTVOQR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVQQR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR Tail precursor (EC 1.1.1.37) - Homo sapiens (Hui AGAGSATLSMAYAGAR GYLGFEOLPDCLK LIFGVTTLDIVR LITXDILAHTPGWAADLSHIETK SOETECTYFSTPLLLGKK TIIPLISOCTPK VOFPODOLITALTGR HGVYNPNKIFGVTTLDIVR TEANSCIPTION 1-alpha/beta (Transcription factor EGALTFTWWER ELSANTFPDIIR	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1382.7 1163.6 2279.1 1163.6 2279.1 1705.8 1392.7 1705.8 1392.7 1705.8 1392.7 1705.8 1392.7 1705.8 1392.7 1705.8 1392.7 1163.6 2279.1 1705.8 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1163.6 2279.1 1705.8 1392.7 1163.6 2279.1 1705.8 1392.7 1163.6 2279.1 1705.8 1300.9 1300.8 1300.8 1300.8 1300.8 1300.8 1300.8 1300.8 1300.7	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1361.6 1934.9 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1706.8 1816.9 1751.9 17	1917.9 1843.9 1371.7 1380.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7 1750.9 1392.7 1705.8 1392.7 1705.8 1488.7 1232.7 168.6 2279.1 1705.8 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1488.7 1232.7 1489.8	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1393.7 1161.8 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1280.1 1706.9 1454.7 1233.7 1245.2 120.0 1370.8 1500.8 2143.2 (Human) 1308.7 1308.7
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 30.2 Malate dehyi 31.4 31.4 31.4 31.4 31.4 31.2 9 12.9 12.9 26.3 26.3 26.3 26.3 26.3 26.3 26.3 26.3	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 Cytoplasmi 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	EVOGNESDLFMSYFPR MOYAPNTOVELIPOGR OAALOVAEGFISR YOEGGVESAFIK EVOGNESDLFMSYFPR OAALOVAEGFISR C (EC.1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVOOR NVIIWGHISSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKESAFERLSSA FVEGLPINDFSR ELTEKESAFERLSSA FVEGLPINDFSR ELTEKESAFERLSSA EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFERLSSA EVGLPHOFSR GEFVTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR TIAI precursor (EC.1.1.1.37) - Homo sapiens (Hui AGAGSATLSMAYAGAR GYLGPEOLPDCLK IFGVTLDIVR LITLYDIAHTPGVAADLSHIETK SOETECTYFSTPLLIGKK TIIPLISGCTPK VOFPODOLTALTGR HGVYNPNKIFGVTTLDIVR TEANSCRIPTOR	1917.9 1843.9 1371.7 1350.6 1933.9 1382.7 1383.7 2) - Homo sap 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 1750.9 1392.7 1163.6 1750.9 1392.7 1163.6 1750.9 1392.7 1163.6 1750.9 1392.7 1163.6 1750.9 1750.9 17	1918.9 1844.9 1372.7 1351.6 1934.9 1398.7 10lens (Human) 1751.9 1393.7 1164.6 2280.1 1706.9 1393.7 1164.6 2280.1 1706.8 1816.9 1393.7 1164.6 2280.1 1706.9 1454.7 1489.7 1233.7 1236.5 1370.8 12102.1 1370.8 12102.2 11370.8 12102.2 11370.8 12103.7	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1683.6 2279.1 1705.8 1815.8 1750.9 1392.7 1683.6 2279.1 1705.8 1815.8 1750.9 1392.7 1683.6 2279.1 1705.8 185.8 1750.9 1392.7 1683.6 2279.1 1705.8 185.8 1700.9 1850.9	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1757.9 1394.7 1816.8 1751.9 1393.7 1164.6 2280.1 1706.9 1816.8 1751.9 1393.7 1164.6 2280.1 1706.9 1454.7 1489.7 1233.7 2365.2 2102.0 1370.8 1560.8 2143.2 (Human) 1308.7
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 11.0 12.0 12	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 0.0 0.0 0.0 0.0 2.0 2.0	99.0 99.0 99.0 99.0 cytoplasmi 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	EVOGNESDLFMSYFPR MOYAPNTOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC 1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOQR NVIIWGMINSTGYVPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKESAFERLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFERLSSA FVEGLPINDFSR ELTEKESAFERLSSA FVEGLPINDFSR GEFYTTVOQR NVIIWGNHSSTGYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFERLSSA FVEGLPINDFSR GEFYTTVOQR NVIIWGNHSSTGYPDVNHAK SAPSIPKENFSCLTR TEIL PECURSOF (EC 1.1.37) - Homo sapiens (Hui AGAGSATLSMAYAGAR GYLGPECIPDCLK IFGYTTLDIVR LTLYDIAHTPGWAADLSHIETK SOETECTYFSTPLILGKK TIPLISGCTPK VOFPODOLTALTGR HGYYPNNKIFGYTTLDIVR LTANTAMTHONALONICATION LTANTAMTHONALO	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1392.7 1163.6 2279.1 1705.8 1756.9 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1705.8 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1393.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 1279.1 1705.8 1815.8 1750.9 1392.7 1153.6 1279.1 1755.8 1815.8 1559.8 2142.1 1SGF-3 comp 1307.7 1359.7 1735.8 1841.8 1160.6	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1351.6 1934.9 1399.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1816.8 1393.7 1164.6 2280.1 1706.9 1454.7 126.8 1816.9 1751.9 1393.7 1164.6 1280.1 1706.9 1454.7 1233.7 1236.5 1243.2 0102.1 1370.8 1540.8 1540.8 1540.8 1550.8 1842.9 1161.6 1550.1 1716.8	1917.9 1843.9 1371.7 1350.6 1933.9 1398.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 13750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1163.6 2279.1 1705.8 1483.7 1232.7 2364.2 2101.0 1369.8 1559.8 2142.2 - Homo sapiens 1307.7 1358.7 1359.7 1358.9 1841.8 1160.6 1500.7	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1164.6 280.1 1706.9 1816.8 1751.9 1393.7 1164.6 2280.1 1706.9 1849.7 1233.7 1249.7 1234.7 1249.7 1235.5 1240.0 1370.8 1560.8 2143.2 (Human) 1308.7 1366.7 1376.8 1842.8 1161.6 1501.7
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 11.0 12.0 12	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYFPR MOYAPNTOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVOQR NVIIWGMINSTGVYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKEKSAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFFELSSA FVEGLPINDFSR GEFVTTVQQR NVIIWGNHSSTGYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA FVGTPINDFSR GEFVTTVQQR RVIIWGNHSSTGYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA FVGTPITVQQR RVIIWGNHSSTGYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA FVGTPITVTQQR RVIIWGNHSSTGYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA FVGTPITVQR RVIIWGNHSSTGYPDVNHAK SAPSIPKENFSCLTR ELTEKTSTPLLCKK TILTIJLATPGVAADLSHIETK SOETECTYFSTPLLLGKK TILTIJLATPGVAADLSHIETK SOETECTYFSTPLLLGKK TILTIJLATPGVAADLSHIETK SOETECTYFSTPLLLGKK TILTIJLATPGVAADLSHIETK SOETECTYFSTPLLCKK TILTIJLATPGVAADLSHIETK SOETECTYFSTPLLTCH TILTIJLATPGVAADLSHIETK SOETECTYFSTPLLTCH TILTIJLATPGVAADLSHIETK SOETECTYFSTPLTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1388.7 2) - Homo Sap 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1392.7 1815.8 1392.7 1705.8 1815.8 1392.7 1705.8 1815.8 1750.9 1392.7 1105.8 1815.8 1750.9 1392.7 1105.8 1855.7 1105.8 1855.7 1105.8 1850.7 1392.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1350.7 1350.7 1555.7 1565.7 1565.7	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1391.7 1164.6 2280.1 1706.9 1393.7 1164.6 1393.7 1816.8 1393.7 1816.8 1393.7 1164.6 2280.1 1706.9 1751.9 1393.7 1164.6 1280.1 1706.9 1454.7 1249.7 1233.7 1233.7 1233.7 1233.7 1300.8 1500.8 1500.8 144.7 1300.7 1300.7 1300.7 1300.7 1300.7 1300.7 1300.7 1300.7 1300.7 1300.7 1306.8 1842.9 1161.6 1501.7 1566.7 1566.7 1560.8	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 1279.1 1705.8 1850.7 1389.7 13	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1164.6 2380.1 1706.9 1816.8 1751.9 1394.7 164.6 2280.1 1706.9 1845.7 1706.9 1846.8 1751.9 1393.7 1164.6 2280.1 1706.9 1454.7 1230.7 1230.7 1230.7 1230.7 1230.7 1230.7 1230.7 1230.7 1230.7 1360.7 1360.7 1360.7 1360.7 1360.8
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYFPR MOYAPNTOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVOQR NVIIWGMHSSTQYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKEKSAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKEKSAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKEKSAFFELSSA FVEGLPINDFSR GEFVTTVQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFELSSA FVGTPINDFSR GEFVTTVQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR ELTEKTSTPLLCKK TIIPLISGCTECTF VFFPDQDCLTALTGR HOYLPNFWGF ELSAVTFPDIIR FHDLLSOLDDGYSR GOVMEHANDVSFATIR OYLAGWLEK SUMPLINDRINGFKTTIDNR TEANSTPIDIOR FHOLLSOLDDGYSR GOVMEHANDVSFATIR OYLAGWLEK SUMPLINDRINGFK SUMVELQOLDSK YLYPNINDROHAPGK GUNVPOLNMLGEK GUNVELQOLDSK YLYPNINDROHAPGK GUNVPOLNMLGEK	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1388.7 2) - Homo sap 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1392.7 1815.8 1392.7 1705.8 1815.8 1392.7 1105.8 1815.8 1750.9 1392.7 1105.8 1815.8 1750.9 1392.7 1105.8 1815.8 1750.9 1392.7 1105.8 1855.7 1105.8 1855.7 1392.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1399.7 1300.7 1565.7 1679.8 1429.7 1858.9	1918.9 1844.9 1372.7 1351.6 1394.9 1398.7 10iens (Human) 1751.9 1393.7 1164.6 2280.1 1706.9 1393.7 1816.8 1393.7 1816.8 1393.7 1164.6 2280.1 1706.9 1751.9 1393.7 1164.6 2280.1 1706.9 1454.7 1489.7 1233.7 1233.7 1233.7 1340.7 1340.7 1340.7 1340.7 1340.7 1340.7 1340.7 1340.7 1340.7 1350.7 1360.8 1842.9 1161.6 1501.7 1566.7 1680.8 1430.7 1859.9	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 1279.1 1705.8 1850.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1375.8 1841.8 1160.6 1500.7 1565.7 1679.8 1429.7 1858.9	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1849.7 1233.7 1164.6 2280.1 1706.9 1454.7 1489.7 1233.7 1236.5 22102.0 1370.8 1560.8 1430.7 1300.7 1300.7 1360.8 1642.8 1161.6 1501.7 1566.7 1680.8 1430.7 1859.9
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYFPR MOYAPNTOVELIPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGHISSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKEKSAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKEKSAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKEKSAFFELSSA FVEGLPINDFSR GEFYTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR LITA LITA LITA LITA LITA LITA LITA LITA	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1382.7 1163.6 2279.1 1705.8 1756.9 1392.7 1163.6 2279.1 1705.8 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 11705.8 1815.8 1750.9 1392.7 1183.6 1279.1 1183.6 1279.1 1183.7 1232.7 1236.4 12 110.0 1369.8 1559.8 1242.1 1SGF-3 comp 1307.7 1359.7 1359.7 1359.7 1359.7 1359.7 1355.8 1841.8 1160.6 1500.7 1555.7 1679.8 1429.7 1858.9 1735.8	1918.9 1844.9 1372.7 1351.6 1334.9 1389.7 10iens (Human) 1751.9 1393.7 1164.6 2280.1 1706.9 1393.7 1816.8 1393.7 1816.8 1393.7 1816.8 1393.7 1164.6 2280.1 1706.9 1751.9 1393.7 1164.6 2280.1 1706.9 1454.7 1489.7 1233.7 1233.7 1245.3 12102.1 1370.8 1500.8 144.2 1300.7 134.2 1360.7 1360.7 1360.7 1360.7 1360.7 1360.7 1368 1842.9 1161.6 1501.7 1566.7 1859.9 1336.7	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1550.9 1392.7 1163.6 2279.1 1705.8 1815.8 1550.9 1392.7 1353.7 1488.7 1232.7 2364.2 2101.0 1369.8 1559.8 2142.2 - Homo sapiens 1307.7 1359.7 1359.7 1359.7 1359.7 1359.7 1359.7 1359.7 1359.7 1359.7 1359.7 1359.7 1359.7 1358.9 1429.7 1358.9 1358.9 1358.9 1358.9 1358.9 1358.9 1358.9 1358.9	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1751.9 1393.7 1164.6 2280.1 1706.9 1816.8 1751.9 1393.7 1164.6 2280.1 1706.9 1816.8 1751.9 1393.7 1164.6 2280.1 1706.9 1846.8 1751.9 1393.7 1164.6 1280.1 1706.9 1454.7 1489.7 1233.7 1236.8 1482.8 1161.6 1501.7 1566.7 1680.8 1430.7 1859.9 1736.8 1842.8 1161.6 1501.7 1566.7
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYPER MOYAPNTOVELIPOGR OAALOVAEGFISR YOEGGVESAFIK EVOGNESDLFMSYPER OAALOVAEGFISR C (EC 1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGHNESTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKESAFERLSSA FVEGLPINDFSR ELTEKESAFERLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFERLSSA FVEGLPINDFSR GEFYTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR LITEMESAFERLSSA FVEGLPINDFSR GEFYTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR LIAID FROM THE STANDAY GEFYTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR LIAID FROM THE STANDAY FOR THE STANDAYAGAR GFLYTTLDIVR LITYDIAHTPGVAADLSHIETK SOETECTYFSTPLLLGKK TIIPLISCTPK VOFPODOLTALTGR HOVLYDNKIFGVTTLDIVR TLANDAYAGRA GVLGPGLDDCK SLAVTFPDIIR HOLLSOLDDOYSR ODWEHAANDVSFATIR HOLLSOLDDOYSR SOWYELOOLDSK VLYPNIDKOHAFGK GLNWEHAANDVSFATIR HIDLLSOLDDOYSR SOWYELOOLDSK ODWEHAANDVSFATIR HIDLLSOLDDOYSR SOWYELOOLDSK OWEHAANDVSFATIR HIDLLSOLDDOYSR OWEHAANDVSFATIR HIDLLSOLDDOYSR	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1382.7 1163.6 2279.1 1705.8 1756.9 1392.7 1163.6 2279.1 1705.8 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1841.8 1705.8 1841.8 1850.7 1232.7 12364.2 1210.0 1369.8 1242.1 1SGF-3 comp 1307.7 1359.7 1735.8 1841.8 1160.6 1500.7 1735.8 1842.7 1735.8 1842.7 1735.8 1842.7 1735.8 1843.8 1150.6 1500.7 1735.8 1844.8 1150.6 1500.7 1735.8	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1151.9 1399.7 1164.6 2280.1 1706.9 1393.7 1816.8 1393.7 1816.8 1393.7 1816.8 1393.7 1816.8 1393.7 1816.9 1393.7 1164.6 2280.1 1706.9 1499.7 1233.7 1236.5 1202.1 1370.8 186.9 1501.8 1500.8 144.9 1300.7 1330.7 136.8 1842.9 1161.6 1501.7 1566.7 1680.8 1430.7 1889.9 1736.8	1917.9 1843.9 1371.7 1350.6 1393.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 150.9 1392.7 1355.8 1841.8 110.6 1500.7 1355.8 1841.8 1429.7 1355.7 1679.8 1429.7 1556.7 1679.8 1429.7 1556.7 1658.9 1735.8	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 124.7 1236.7 124.7 1256.7 1250.8 144.9 1308.7 1308.
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 12.0 12.0	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYPER MOYAPNTOVELIPOGR OAALOVAEGFISR YOEGGVESAFIK EVOGNESDLFMSYPER OAALOVAEGFISR C (EC.1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGHNESTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKEKSAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEEKESAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEEKESAFFELSSA FVEGLPINDFSR GEFYTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFLSSA FVGTPINDFSR GEFYTTVOOR INTERPROVED TO THE STANDARD TO THE STAN	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1382.7 1350.9 1392.7 1163.6 2279.1 1705.8 1392.7 1163.6 2279.1 1705.8 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1841.8 1705.8 1841.8 1500.7 1395.8 1841.8 1160.6 1500.7 1555.7 1679.8 1429.7 1858.9 1735.8 1842.7 1735.8 1841.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1391.7 1164.6 1280.1 1706.9 1393.7 1164.6 1393.7 1816.8 1393.7 1816.8 1393.7 1816.8 1393.7 1164.6 1280.1 1706.9 1751.9 1393.7 1164.6 1280.1 1706.9 1454.7 1233.7 1233.7 1233.7 1233.7 1233.7 1233.7 1249.9 1300.7 1330.8 1842.9 1410.6 1501.7 1368.8 1842.9 1161.6 1501.7 1566.7 1859.9 1736.8 1859.9 1736.8 1859.9 1736.8 1859.9 1736.8 1859.9 1736.8	1917.9 1843.9 1371.7 1350.6 1393.9 1372.7 1163.6 1393.7 11705.8 1392.7 1392.7 1392.7 1392.7 1392.7 1392.7 1392.7 1392.7 1483.6 2279.1 1705.8 1815.8 1392.7 1232.7 1232.7 1232.7 1235.8 185.9 1345.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1453.7 1355.8 1455.7 1355.8 1455.7 1555.7 1556.7 1556.7 1556.7 1556.7 1556.7 1556.7 1556.7	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1303.7 1304.7 1235.7 1236.7 1489.7 1233.7 1236.8 1849.7 1233.7 1360.7 1373.6 1842.8 1161.6 1501.7 1360.7 1373.8 1842.8 1161.6 1501.7 1368.7 1859.9 1736.8 1859.9 1736.8 1556.7 1859.9 1736.8 1556.7 1859.9 1736.8
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 2.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYPER MOYAPNTOVELIPOGR OAALOVAEGFISR YOEGGVESAFIK EVOGNESDLFMSYPER OAALOVAEGFISR C (EC.1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGHISSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTINCLTASK FVEGLPINDFSR ELTEKESAFEFLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEEKESAFEFLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEEKESAFEFLSSA FVEGLPINDFSR GEFVTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR LITAID FROM THE STANDERS (CONTROLL THE STANDERS CONTROLL THE STANDE	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1382.7 130.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1841.8 1709.8 1850.9 1392.7 1236.7 1236.7 1236.7 1399.8 142.1 1SGG-3 comp 1307.7 1359.7 1735.8 1841.8 1160.6 1500.7 1555.7 1679.8 1429.7 1858.9 1735.8 1850.7 1735.8 1500.7 1679.8 1555.7 1679.8 1556.7 1858.9 1735.8 1500.7 1735.8 1500.7 1679.8	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1351.6 1398.7 1164.6 1280.1 1706.9 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1280.1 1706.9 1489.7 1233.7 1233.7 1236.5 13170.8 124.2 1230.7 136.6 1280.1 1370.8 124.2 1360.7 136.7 136.8 136.9 149.7 130.7 136.8 136.9 149.7 130.7 136.8 186.9 1736.8 186.9 1736.8 186.7 1886.8 1850.9 1736.8 1856.7 1856.7 1866.7 1866.7 1866.7 1866.7 1866.7 1866.7 1866.7 1866.7 1866.7 1866.7 1866.7	1917.9 1843.9 1371.7 1350.6 1333.9 1372.7 1163.6 1393.7 11750.9 1392.7 1163.6 1393.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1392.7 1232.7 1232.7 1232.7 1235.8 185.8 1550.9 1392.7 1355.8 1453.7 1488.7 1232.7 1355.8 1453.7 1355.8 1453.7 1355.8 1550.9 1359.8 14	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1393.7 1816.8 1393.7 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1233.7 1249.7 1233.7 1236.7 1300.7 1300.7 1300.7 1300.7 1300.7 136.8 1842.8 1161.6 1501.7 1566.7 1680.8 1430.7 1859.9 1736.8 1459.9 1736.8 1501.7 1859.9 1736.8 1506.7 1886.8 1501.7 1886.8 1501.7 1889.9 1736.8 1506.7 1886.8 1500.7 1886.8 1500.7 1886.8 1500.7 1886.8
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYPER MOYAPNTOVELIPOGR OAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYPER OAALOVAEGFISR C (EC.1.1.3.3) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGHISSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKEKSAFERLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFERLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFERLSSA FVEGLPINDFSR GEFYTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFERLSSA FVEGLPINDFSR GEFYTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR ITAL FOR THE STANDAR SAPSIPKENFSCLTR TICAL FOR THE STANDAR SAPSIPKENFSCLTR THE SAPSIPKENFSCLTR THE SAPSIPKENFSCLTR THE SAPSIPKENFSCLTR THE SAPSIPKE	1917.9 1843.9 1371.7 1350.6 1933.9 1382.7 1383.9 1388.7 2) - Homo sap 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1841.8 1709.8 1841.8 1559.8 2142.1 1SGG-3 comp 1307.7 1359.7 1735.8 1841.8 1160.6 1500.7 1679.8 1429.7 1858.9 1735.8 1841.8 1500.7 1656.7 1679.8 1500.7 1656.7 1679.8 1598.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8	1918.9 1844.9 1372.7 1351.6 1934.9 1398.7 1351.6 1934.9 1399.7 1164.6 12280.1 1706.9 1751.9 1393.7 1164.6 1280.1 1706.9 1454.7 1286.7 1286.3 1290.1 1303.7 1484.7 1303.8 1803.8 1809.9 1736.8 1809.8 1809.9 1736.8 1800.8 1899.9 1736.8 1800.8 1899.9 1736.8 1880.8 1899.9 1736.8	1917.9 1843.9 1371.7 1350.6 1333.9 1382.7 11750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1683.6 2279.1 1705.8 1815.8 1750.9 1382.7 1683.6 2279.1 1705.8 1815.8 1750.9 1382.7 1683.6 2279.1 1755.8 1841.8 165.8 165.9 165.7 165	1918.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1751.9 1394.7 1816.8 1751.9 1394.7 1816.8 1751.9 1394.7 1706.9 1454.7 1489.7 1233.7 1236.5 1210.0 1370.8 1500.8 1410.7 1308.7 1308.7 1308.7 1308.7 1308.7 1308.7 1308.7 1308.7 1308.7 1308.7 1308.7 136.8 1842.8 1161.6 1501.7 1566.7 1889.9 1736.8 1430.7 1859.9 1736.8 1560.7 1889.9 1736.8 1560.7 1889.9 1736.8 1599.9 1736.8 1599.9 1736.8 1599.9 1736.8 1599.9 1736.8 1599.9 11596.7
72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 11.0 12.0 12	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 0.0 0.0 drogenase, 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYPER MOYAPNTOVELIPOGR OAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYPER OAALOVAEGFISR C (EC.1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVOOR NVIIWGHISSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKEKSAFERLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEEKESAFERLSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEEKESAFERLSSA FVEGLPINDFSR GEFVTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFERLSSA FVGTPINDFSR GEFVTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR ITAID FOR THE STANDARD STANDARD GEFVTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR ITAID THE STANDARD GEFVTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR THE CLITTOR GEFVTTVOOR NVIIWGNHSSTOYPDVNHAK SAPSIPKENFSCLTR THE CLITTOR GEFVTTLOUR TO THE STANDARD GEFVTTLOUR TO THE STANDARD GEFVTLOUR VOORTHANDVSFATIR FHOLLSOLDDOYSR OWEHAANDVSFATIR FHOLLSOLDDOYSR SOWYELOOLDSK VLYNDINGNHAEK CONVEHAANDVSFATIR FHOLLSOLDDOYSR SCOWYELOOLDSK VLYNDINGNHAEK SOWYELOOLDSK VLYNDINGNHAEN SOWYELOOLDSK VLYNDINGNHAEN SOWYELOOLDSK VLYNDINGNHAEN SOWYELOOLDSK VLYNDINGNHAEN SOWYELOOLDSK VLYNDINGNHAEN	1917.9 1843.9 1371.7 1350.6 1933.9 1382.7 1383.9 1388.7 2) - Homo sap 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1815.8 1392.7 1815.8 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1709.8 1841.8 1709.8 1841.8 1559.8 2142.1 1SGG-3 comp 1307.7 1359.7 1735.8 1841.8 160.6 1500.7 1679.8 1429.7 1858.9 1735.8 1850.7 1755.7 1679.8 1556.7 1679.8 1559.9 1735.8 1565.7 1679.8 1500.7 1755.8 1500.7 1755.8 1500.7 1755.8 1868.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8 1500.7 1858.9 1735.8	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1351.6 1398.7 1164.6 1280.1 1706.9 1751.9 1393.7 1164.6 1393.7 1164.6 1280.1 1706.9 1751.9 1393.7 1164.6 1280.1 1706.9 1489.7 1233.7 1236.5 1370.8 1243.2 1202.1 1370.8 1243.2 1243.2 1250.1 1370.8 1244.7 1360.7 136.8 143.9 136.7 136.8 143.9 136.7 136.8 143.9 146.8 146.9 146.8 146.9 146.8 146.9 146.8 146.9 146.8 146.9 146.8 146.8 146.9 146.8	1917.9 1843.9 1371.7 1350.6 1333.9 1382.7 1390.9 1392.7 1163.6 1393.7 1390.7 13	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 184.7 1164.6 1501.7 1680.8 1430.7 1300.7 1300.7 136.8 1842.8 1401.7 1566.7 1680.8 1430.7 1859.9 1736.8 1501.7 1859.9 1736.8 1501.7 1859.9 1736.8 1500.7 1889.9 1736.8 1500.7 1889.9 1736.8 1500.7
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYFPR MOYAPNTOVEILPOGR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC 1.1.3.7) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGMINSTOYPDVNHAK SAPSIPKENFSCLTR VIVVGNPANTINCLTASK FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFFELSSA FVEGLPINDFSR SAPSIPKENFSCLTR ELTEKESAFFELSSA EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGNISTSTOYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA EVGVYEALKDDSWLK FVEGLPINDFSR GEFYTTVOOR NVIIWGNISSTOYPDVNHAK SAPSIPKENFSCLTR EIGI PTECUTSOT (EC 1.1.3.7) - Homo sapiens (Hui AGAGSATLSMAYAGAR GYLGPEOLPOLK IFGVTTLDIVR LITLYDIAHTPGWAADLSHIETK SOETECTYFSTPLLLGKK TIIPLISOCTPK VOFPODDLTALTGR HGVYNPNKIFGVTTLDIVR TEANSCIPTION EGALTFTWWER ELSAVTFPDIIR FHOLLSOLDDOYSR OWEHAANDVSFATIR OVLAOWLEK SLEDLODEVPFK SOWYELOOLDSK VLYPNIDKDHAFGK GUNYBLOLDDOYSR SOWWELOOLDSK VMMELGSTINSSLAGER VLYPNIDKDHAFGK GUNYBLOLDDOYSR SOWWELOOLDSK VMMELGSTINSSLAGER VLYPNIDKDHAFGK SOWYELOOLDSK VMMELGSTINSSLAGER VLYPNIDKDHAFGK SOWYELOOLDSK VMMELGSTINSSLAGER VLYPNIDKDHAFGK SOWYELOOLDSK VMMELGSTINSSLAGER VLYPNIDKDHAFGK GUNYBLOOLDSK SOWYELOOLDSK SOWYELOOLDSK VMMELGSTINSSLAGER VLYPNIDKDHAFGK GULTUMER ELSAVTFPOIIR FHOLLSOLDDOYSR SOWYELOOLDSK SOWYELOOLDSK VMMELGESTINSSLAGER VLYPNIDKDHAFGK GLLKOPTFLLR OVLADMLEK EGAITTIWER ELSAVTFPOIIR FERSE (EC 2.4.2.12) (NAMPRTase) (Nampt) (Pro	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1382.7 1163.6 2279.1 1163.6 2279.1 1705.8 1756.9 1393.7 1815.8 1392.7 1705.8 1392.7 1705.8 1392.7 1163.6 2279.1 1705.8 1750.9 1392.7 1163.6 2279.1 1705.8 1750.9 1392.7 1163.6 2279.1 1163.6 2279.1 1363.6 2279.1 1363.6 1363.7 1232.7 2364.2 22101.0 1369.8 1360.8 1359.8 1160.6 1500.7 1555.7 1679.8 1429.7 1858.9 1735.8 1565.7 1858.9 1735.8 1565.7 1858.9 1735.8 1500.7 1565.7 1858.9 1735.8 1500.7 1565.7 1858.9 1735.8 1500.7 1565.7 1858.9 1735.8 1500.7 1858.9 1735.8	1918.9 1844.9 1372.7 1381.6 1934.9 1393.7 1381.6 1934.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1816.9 1751.9 1393.7 1164.6 2280.1 1706.9 1454.7 1233.7 2365.3 2102.1 1370.8 1360.7 1370.8 1384.2 0nents p91/p84) 1308.7 1308.7 1308.7 1308.7 1308.7 1308.7 1308.8 1560.8 1591.9 1308.7 136.8 1842.9 1161.6 1501.7 1566.7 1889.9 1736.8 1560.7 1889.9 1736.8 1560.7 1889.9 1736.8 1560.7 1889.9 1736.8 1560.7 1889.9 1736.8 1560.7 1889.9 1736.8 1560.7 1889.9 1736.8 1560.7 1889.9 1736.8 1680.8 1591.7 1566.7 1889.9 1736.8 1680.8 1591.7 1566.7 1889.9 1736.8 1680.8 1591.7 1566.7 1889.9 1736.8 1680.8 1591.7 1566.7 1889.9 1736.8 1680.8 1591.7 1566.7 1889.9 1736.8 1680.8 1591.7 1666.7	1917.9 1843.9 1371.7 1380.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1393.7 1705.8 1392.7 1705.8 1392.7 1705.8 1392.7 1705.8 1392.7 163.6 2279.1 1705.8 1488.7 1232.7 1648.8 1559.8 22101.0 1369.8 1459.7 1359.7 1359.7 1358.8 1429.7 1358.9 1429.7 1358.9 1429.7 1565.7 1679.8 1429.7 1858.9 1735.8 1650.7 1656.7 1679.8	1918.9 1844.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1375.7 1816.8 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1164.6 1393.7 1489.7 1233.7 1236.2 1370.8 1560.8 1430.7 1330.7 1336.8 1560.7 1336.8 1560.7 1336.8 1560.7 1356.8 1430.7 1368.8 159.9 1736.8 159.9 1736.8 1599.9 1736.8 1599.9 1736.8 1599.9 1736.8 1599.9 1736.8 1599.9 1736.8 1680.8 1599.9 1736.8 1736.7 1736.7 1736.8 1736.7 1736.8 1736.7 1736.8
72.0 72.0 72.0 72.0 72.0 72.0 72.0 72.0	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	10.1 10.1 10.1 10.1 10.1 10.1 10.1 10.1	30.2 30.2 30.2 30.2 30.2 30.2 30.2 30.2	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	EVOGNESDLFMSYFPR MOYAPNTOVELPOQR QAALOVAEGFISR YOEGGVESAFHK EVOGNESDLFMSYFPR QAALOVAEGFISR C (EC1.1.1.37) (Cytosolic malate dehydrogenas EVGVYEALKDDSWLK FVEGLPINDFSR GEFVTTVOQR NVIIWGMINSTGYPDVNHAK SAPSIPKEMFSCLTR VIVVGNPANTNCLTASK FVEGLPINDFSR ELTEKEKSAFFELSSA FVEGLPINDFSR SAPSIPKEMFSCLTR ELTEKESAFFELSSA FVEGLPINDFSR SAPSIPKEMFSCLTR ELTEKESAFFELSSA FVEGLPINDFSR GEFVTTVQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA FVGTPINDFSR GEFVTTVQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA FVGTPITVQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR ELTEKESAFFELSSA FVGTPITVTQQR NVIIWGNHSSTQYPDVNHAK SAPSIPKENFSCLTR ELTEYDLFTVTQR LITYDLATTPOWADLSHIETK SOFTECTYFSTPLLLGKK TIIPLISGCTPK VOFPODQLTALTGR HGYYNPNIKIFGVTTLDINR TLANDIATHTPWARP ELSAVTFPDIIR FHDLLSGLDDOYSR ODWEHAANDVSFATIR FHDLLSGLDDOYSR SUMPLICOLDSK VYNPNIDKDHAFGK KLIKDQDOYSR SUMPLICOLDSK VMMMEESTNGSLAEFR VLYPNIDKDHAFGK KLIKDQPGFFLLR QVLAQWLEK EGAITFTWER ELSAVTFPDIR FHDLLSGLDDOYSR SUMPLICOLDSK VMMMEESTNGSLAEFR VLYPNIDKDHAFGK KLIKDQPGFFLLR QVLAQWLEK EGAITFTWER ELSAVTFPDIR FHDLLSGLDDOYSR SUMPLICOLDSK VMMMEESTNGSLAAEFR VLYPNIDKDHAFGK KLIKDQPGFFLLR QVLAQWLEK EGAITFTWER ELSAVTFPDIR FHOLLSGLDDOYSR SUMPLICOLDSK VMMMEESTNGSLAAEFR VLYPNIDKDHAFGK KLIKDQPGFFLLR QVLAQWLEK EGAITFTWER ELSAVTFPDIR FFRENCER ELSAVTFPDIR FFRENCER FFREN	1917.9 1843.9 1371.7 1350.6 1933.9 1371.7 1350.6 1933.9 1388.7 2) - Homo Sap 1750.9 1392.7 1163.6 2279.1 1705.8 1756.9 1392.7 1815.8 1392.7 1705.8 1815.8 1392.7 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1163.6 2279.1 1705.8 1815.8 1750.9 1392.7 1185.7 1185.7 1232.7 2364.2 2101.0 1369.8 1559.8 2142.1 1SGF-3 comp 1307.7 1735.8 1810.6 1500.7 1555.7 1858.9 1735.8 1500.7 1555.7 1858.9 1735.8 1500.7 1555.7 1858.9 1735.8 1500.7 1555.7 1858.9 1735.8 1500.7 1555.7 1858.9 1735.8 1500.7 1555.7	1918.9 1844.9 1372.7 1351.6 1934.9 1399.7 1391.7 1164.6 2280.1 1706.9 1393.7 1164.6 1393.7 1816.8 1393.7 1816.8 1393.7 1816.8 1393.7 186.6 1393.7 186.6 1393.7 186.6 1393.7 186.6 1393.7 186.6 1393.7 186.6 1393.7 186.7 1393.7 186.7 1393.7 186.7 1393.7 186.7 1393.7 186.7 1393.7 189.7 136.7	1917.9 1843.9 1371.7 1350.6 1933.9 1388.7 1750.9 1392.7 1163.6 2279.1 1705.8 1392.7 1163.6 1393.7 1815.8 1392.7 1163.6 1393.7 1815.8 1392.7 1163.6 1392.7 1163.6 1392.7 1163.6 1392.7 1163.6 1392.7 1163.6 1392.7 1163.6 1392.7 1163.6 1392.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1389.7 1388.9 1390.7 1565.7 1858.9 1391.7 1858.9 1395.7 1858.9	1918.9 1844.9 1844.9 1372.7 1351.6 1934.9 1389.7 1751.9 1393.7 1164.6 2280.1 1706.9 1394.7 1816.8 1393.7 1164.6 2380.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1816.8 1393.7 1164.6 2280.1 1706.9 1845.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 123.7 1360.7 1373.8 1566.7 1859.9 1736.8 1501.7 1566.7 1889.9 1736.8 1501.7 1566.7 1889.9 1736.8 1501.7 1566.7 1889.9 1736.8 1501.7 1566.7 1889.9 1736.8 1501.7 1566.7 1889.9 1736.8 1501.7 1566.7 1889.9 1736.8 1501.7 1566.7 1889.9 1736.8 1501.7 1566.7 1889.9 1736.8 1500.7 1736.8

55.0 55.0 55.0 55.0	13.4 13.4 13.4 13.4	13.4 13.4 13.4 13.4	20.2 20.2 20.2 20.2 20.2	2.0 2.0 2.0 2.0 1.4	99.0 99.0 99.0 99.0 96.0	LLPPYLR MNPAAEAEFNILLATDSYK SYSFDEIRK VYSYFECR IWGEDLR	870.5 2139.0 1143.6 1122.5 887.5	871.5 2140.0 1144.6 1123.5 888.5	870.5 2139.0 1143.6 1122.5 887.5	871.5 2140.0 1144.6 1123.5 888.5
55.0 P46777 1	13.4 RL5_HUMAN 13.3	13.4	20.2 60S riboson 35.0	0.0 nal protein L! 2.0	97.0 5 - Homo si 99.0	LHDFGYR ppiens (Human) DIICQIAYAR	906.5	907.5	906.4	907.4
79.0 79.0	13.3 13.3	13.3	35.0 35.0	2.0	99.0 99.0	HIMGONVADYMR KAHAAIRENPVYEKKPK	1433.6 1978.1	1434.7 1979.1	1433.7 1978.1	1434.7 1979.1
79.0 79.0	13.3 13.3	13.3 13.3	35.0 35.0	2.0	99.0 99.0	NSVTPDMMEEMYKK RFPGYDSESKEFNAEVHRK	17701.7 2295.1	1702.8 2296.1	17701.7 1701.7 2295.1	1702.7 2296.1
79.0 79.0	13.3 13.3 13.3	13.3 13.3	35.0 35.0	1.7 1.5	98.0 97.0	YLMEEDEDAYKKQFSQYIK AHAAIRENPVYEK	2427.1 1496.8	2428.1 1497.8	2427.1 1496.8	2428.1 1497.8
79.0	13.3	13.3	35.0	0.1	20.0	AHAAIRENPVYEKKPK	1850.0	1851.0	1850.0	1851.0
244.0 244.0	2.3 2.3	2.3 2.3	24.9 24.9 40S ribosom	2.0 0.2	99.0 39.0	HIMGQNVADYMR AHAAIRENPVYEK	1433.6 1496.8	1434.7 1497.8	1433.7 1496.8	1434.7 1497.8
P46781 220.0	5.8	5.8	28.4	2.0	99.0 98.0	piens (Human) RLQTQVFK	1018.6	1019.6	1018.6	1019.6
220.0 220.0	5.8 5.8	5.8 5.8	28.4 28.4	1.7	95.0	QVVNIPSFIVR LIGEYGLR	1253.7 919.5	1254.7 920.5	1253.7 919.5	1254.7 920.5
220.0 220.0	5.8 5.8	5.8 5.8	28.4 28.4	0.7	81.0 98.0	KNAKKGQGGAGAGDDEE QVVNIPSFIVR	1613.8 1270.7	1614.8 1271.7	1613.7 1270.7	1614.7 1271.7
210.0 210.0	3.3 3.3	3.3 3.3	47.9 47.9	1.2 1.0	93.0 89.0	KQVVNIPSFIVR HIDFSLR	1398.8 886.5	1399.8 887.5	1398.8 886.5	1399.8 887.5
210.0 210.0	3.3 3.3	3.3	47.9 47.9	0.6 0.3	77.0 46.0	LIGEYGLR QVVNIPSFIVR	919.5 1270.7	920.5 1271.7	919.5 1270.7	920.5 1271.7
210.0 P46940		3.3	47.9 Ras GTPase-		35.0 ke protein	CGAP1 (p195) - Homo sapiens (Human)	1483.8	1484.8	1483.8	1484.8
180.0 180.0	6.4	6.4	6.8 6.8	2.0	99.0 99.0	ATFYGEQVDYYK IFYPETTDIYDRK	1482.7 1659.8	1483.7 1660.8	1482.7 1659.8	1483.7 1660.8
180.0 180.0	6.4 6.4	6.4 6.4	6.8 6.8	2.0 0.4	99.0 59.0	QNVAYEYLCHLEEAKR MREEVITLIR	2022.0 1258.7	2023.0 1259.7	2022.0 1258.7	2023.0 1259.7
162.0 162.0	4.4 4.4	4.4 4.4	11.2 11.2	2.0 1.7	99.0 98.0	ATFYGEQVDYYK IFYPETTDIYDRK	1482.7 1659.8	1483.7 1660.8	1482.7 1659.8	1483.7 1660.8
162.0 162.0	4.4 4.4	4.4 4.4	11.2 11.2	0.5 0.1	66.0 27.0	YKATGLHFR QLLSDKQQKR	1091.6 1275.6	1092.6 1276.6	1091.6 1275.7	1092.6 1276.7
473.0 329.0	PI PNB_HUMAN 2.0 2.0	2.0 2.0	14.4 10.3	2.0 2.0 2.0	99.0 99.0	n beta isoform (PtdIns transfer protein beta) FKWWGLQSK AWNAYPYCR	1178.6 1199.5	TP-beta) - Homo 1179.6 1200.5	1178.6 1199.5	1179.6 1200.5
P49368 87.0	TCPG_HUMAN	12.2	T-complex p				omo sapiens (Hu		1336.6	1337.6
87.0 87.0 87.0	12.2 12.2 12.2	12.2 12.2 12.2	23.9 23.9 23.9	2.0 2.0 2.0	99.0 99.0 99.0	GISDLAQHYLMR GVMINKDVTHPR	1336.6 1402.7 1365.7	1337.6 1403.7 1366.7	1336.6 1402.7 1365.7	1337.6 1403.7 1366.7
87.0 87.0	12.2 12.2 12.2	12.2	23.9 23.9 23.9	2.0	99.0 99.0	KIGDEYFTFITDCKDPK NLQDAMQVCR	2076.0 1233.6	2077.0 1234.6	2076.0 1233.6	2077.0 1234.6
87.0 87.0 87.0	12.2 12.2 12.2	12.2 12.2 12.2	23.9 23.9 23.9	0.9 0.8	86.0 84.0	MLLDPMGGIVMTNDGNAILR TLIQNCGASTIR	2130.0 1332.7	2131.0 1333.7	2130.1 1332.7	2131.1 1333.7
87.0 285.0	12.2	12.2	23.9	0.5 2.0	69.0 99.0	TAVETAVLLLR GVMINKDVTHPR	1332.7 1184.7 1365.7	1333.7 1185.7 1366.7	1332.7 1184.7 1365.7	1185.7
	2.0 GDIB_HUMAN 13.8	13.8	14.7 Rab GDP dis	sociation inh 2.0		(Rab GDI beta) (Guanosine diphosphate diss	ociation inhibito	r 2) (GDI-2) - Ho	mo sapiens (Hur 1364.7	1366.7 man) 1365.7
75.0 75.0	13.8 13.8	13.8 13.8	25.4 25.4 25.4	2.0 2.0 2.0	99.0 99.0	GRDWNVDLIPK MTGSEFDFEEMKR	1311.7 1605.7	1303.7 1312.7 1606.7	1311.7 1605.7	1312.7 1606.7
75.0 75.0	13.8 13.8	13.8 13.8	25.4 25.4 25.4	2.0	99.0 99.0	NPYYGGESASITPLEDLYKR TDDYLDQPCYETINR	2272.1 1901.8	2273.1 1902.8	2272.1 1901.8	2273.1 1902.8
75.0 75.0 75.0	13.8 13.8	13.8 13.8	25.4 25.4 25.4	2.0 1.2	99.0 93.0	TYDATTHFETTCDDIKNIYKR LYSESLAR	2591.2 937.5	2592.2 938.5	2591.2 937.5	2592.2 938.5
75.0	13.8	13.8	25.4	0.7	79.0 99.0	FKIPGSPPESMGR	1401.7	1402.7	1401.7	1402.7
54.0 54.0 54.0	6.1 6.1 6.1	6.1 6.1 6.1	16.0 16.0 16.0	2.0 2.0 2.0	99.0 99.0	DLGTESQIFISR MTGSEFDFEEMKR TDDYLDQPCYETINR	1364.7 1605.7 1901.8	1365.7 1606.7 1902.8	1364.7 1605.7 1901.8	1365.7 1606.7 1902.8
54.0 91.0	6.1 8.1	6.1 8.1	16.0 20.4	0.1 2.0	24.0 99.0	GRDWNVDLIPK DLGTESQIFISR	1311.7 1364.7	1312.7 1365.7	1311.7 1364.7	1312.7 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 91.0 91.0	8.1 8.1 8.1	8.1 8.1 8.1	20.4 20.4 20.4	2.0 1.5 0.6	99.0 97.0 75.0	TYDATTHFETTCDDIK MTGSEFDFEEMKR LYSESLAR	1916.8 1605.7 937.5	1917.8 1606.7 938.5	1916.8 1605.7 937.5	1917.8 1606.7 938.5
	SPB9_HUMAN 6.0	6.0				ise 3) (CAP-3) (CAP3) (Protease inhibitor 9) ANSILFCGR			1036.5	1037.5
209.0 209.0	6.0 6.0	6.0 6.0	14.9 14.9	2.0 2.0	99.0 99.0	AQLLELPYAR GKWNEPFDETYTR	1172.7 1641.7	1173.7 1642.8	1172.7 1641.7	1173.7 1642.7
379.0	1.7 VASP_HUMAN	1.7	12.2	1.7 stimulated p	98.0	AQLLELPYAR tein (VASP) - Homo sapiens (Human)	1172.7	1173.7	1172.7	1173.7
83.0 83.0	12.7 12.7	12.7 12.7	31.8 31.8	2.0 2.0	99.0 99.0	GVKYNQATPNFHQWR SGGGGLMEEMNAMLAR	1844.9 1622.7	1845.9 1623.7	1844.9 1622.7	1845.9 1623.7
83.0 83.0	12.7 12.7	12.7 12.7	31.8 31.8	2.0 2.0	99.0 99.0	SSSSVTTSETQPCTPSSSDYSDLQR YNQATPNFHQWR	2706.2 1560.7	2707.2 1561.7	2706.2 1560.7	2707.2 1561.7
83.0 83.0	12.7 12.7	12.7 12.7	31.8 31.8	0.8 0.7	83.0 80.0	WLPAGTGPQAFSR VQIYHNPTANSFR	1386.7 1545.8	1387.7 1546.8	1386.7 1545.8	1387.7 1546.8
83.0 83.0	12.7 12.7	12.7 12.7	31.8 31.8	0.7 0.4	78.0 56.0	VPAQSESVRRPWEK MKSSSSVTTSETQPCTPSSSDYSDLQR	1667.9 2965.3	1668.9 2966.3	1667.9 2965.3	1668.9 2966.3
83.0 138.0	12.7 5.8	12.7 5.8	31.8 21.1	0.2 2.0	41.0 99.0	QQPGPSEHIER ATVMLYDDGNKR	1259.6 1381.7	1260.6 1382.7	1259.6 1381.7	1260.6 1382.7
138.0 138.0	5.8 5.8	5.8 5.8	21.1 21.1	2.0 1.7	99.0 98.0	YNQATPNFHQWR VQIYHNPTANSFR	1560.7 1545.8	1561.7 1546.8	1560.7 1545.8	1561.7 1546.8
208.0	TCPQ_HUMAN 6.0	6.0	6.4	2.0	99.0	TCP-1-theta) (CCT-theta) (Renal carcinoma a FAEAFEAIPR	1149.6	1150.6	1149.6	1150.6
208.0 208.0	6.0 6.0	6.0	6.4 6.4	2.0 2.0	99.0 99.0	HFSGLEEAVYR KFAEAFEAIPR	1306.6 1277.7	1307.6 1278.7	1306.6 1277.7	1307.6 1278.7
208.0 113.0	6.0 2.9	6.0 2.9	6.4 7.3	0.0 2.0	87.0 99.0	FAEAFEAIPR FAEAFEAIPR	1147.6 1149.6	1148.6 1150.6	1149.6 1149.6	1150.6 1150.6
	2.9 RAB7A_HUMAN	2.9		0.9 protein Rab-		HFSGLEEAVYR sapiens (Human)	1306.6	1307.6	1306.6	1307.6
362.0 362.0	3.0 3.0	3.0 3.0	20.3 20.3	2.0 1.0	99.0 90.0	EAINVEQAFQTIAR FQSLGVAFYR	1588.8 1186.6	1589.8 1187.6	1588.8 1186.6	1589.8 1187.6
209.0 209.0	3.4 3.4	3.4 3.4	11.6 11.6	2.0 1.4	99.0 96.0	FQSLGVAFYR EAINVEQAFQTIAR	1186.6 1588.8	1187.6 1589.8	1186.6 1588.8	1187.6 1589.8
162.0	ROA3_HUMAN 7.3	7.4	39.7	ous nuclear r 2.0	99.0	rotein A3 (hnRNP A3) - Homo sapiens (Huma MEVKPPPGRPQPDSGR	1788.9	1789.9	1788.9	1789.9
162.0 162.0	7.3 7.3	7.4 7.4	39.7 39.7	2.0	99.0 99.0	YGKIETIEVMEDR YHTINGHNCEVKK SSGSPYGGGYGSGGGSGGYGSR	1581.8 1599.7	1582.8 1600.7	1581.8 1599.7	1582.8 1600.8
162.0 162.0	7.3 7.3	7.4 7.4	39.7 39.7	1.3 0.0	95.0 94.0	YHTINGHNCEVKK	1909.8 1537.8	1910.8 1538.8	1909.8 1537.8	1910.8 1538.8
208.0 208.0	3.4 3.4 3.4	3.7 3.7	29.6 29.6 29.6	2.0 0.9	99.0 88.0 67.0	YGKIETIEVMEDR SSGSPYGGGYGSGGSGGYGSR YHTINGHNCEVKK	1581.8 1909.8	1582.8 1910.8	1581.8 1909.8	1582.8 1910.8
208.0 208.0	3.4 3.4 6PGD_HUMAN	3.7 3.7	29.6	0.5 0.0	39.0	YHTINGHNCEVKK DYFEKYGK e, decarboxylating (EC 1.1.1.44) - Homo sapi	1599.7 1048.5	1600.8 1049.5	1599.7 1048.5	1600.8 1049.5
414.0 414.0	2.2 2.2	2.2 2.2	13.5 13.5	2.0 0.1	99.0 27.0	VGTGEPCCDWVGDEGAGHFVK GILFVGSGVSGGEEGAR	2276.0 1590.8	2277.0 1591.8	2276.0 1590.8	2277.0 1591.8
121.0 121.0	2.4 2.4 2.4	2.4	10.8 10.8	2.0 0.4	99.0 58.0	GILFVGSGVSGGEEGAR VGTGEPCCDWVGDEGAGHFVK	1590.8 2276.0	1591.8 2277.0	1590.8 2276.0	1591.8 2277.0
50.0 50.0	15.5 15.5	15.5 15.5	26.3 26.3	2.0	99.0 99.0	FQDTDGKHLLPK GILFVGSGVSGGEEGAR	1397.7 1590.8	1398.7 1591.8	1397.7 1590.8	1398.7 1591.8
50.0 50.0	15.5 15.5 15.5	15.5 15.5 15.5	26.3 26.3 26.3	2.0 2.0 2.0	99.0 99.0	HEMLPASLIQAQR LVPLLDTGDIIIDGGNSEYR	1492.8 2159.1	1493.8 2160.1	1492.8 2159.1	1493.8 2160.1
50.0 50.0	15.5 15.5	15.5 15.5	26.3 26.3	2.0	99.0 99.0	SAVENCQDSWRR VGTGEPCCDWVGDEGAGHFVK	1506.7 2276.0	1507.7 2277.0	1506.7 2276.0	1507.7 2277.0
50.0 50.0	15.5 15.5	15.5 15.5	26.3 26.3	2.0 1.5	99.0 97.0	YGPSLMPGGNKEAWPHIK LKGPQKFQFDGDKK	1981.0 1634.9	1982.0 1635.9	1981.0 1634.9	1982.0 1635.9
P52565 1 28.0	GDIR_HUMAN 24.6	24.6	Rho GDP-dis	sociation inh	nibitor 1 (R 99.0	no GDI 1) (Rho-GDI alpha) - Homo sapiens (I AEEYEFLTPVEEAPK	Human) 1750.8	1751.8	1750.8	1751.8
28.0	24.6	24.6	49.0	2.0	99.0	GVKIDKTDYMVGSYGPR	1884.9			1885.9
28.0 28.0	24.6	24.6	49.0	2.0	99.0 99.0	IDKTDYMVGSYGPR KGVKIDKTDYMVGSYGPR	1600.8 2013.0	1885.9 1601.8	1884.9 1600.8	1601.8 2014.0

28.0	24.6	24.6	49.0	2.0	99.0	KYKEALLGR	1076.6	1077.6	1076.6	1077.6
28.0	24.6	24.6	49.0	2.0	99.0	QSFVLKEGVEYR	1453.8	1454.8	1453.8	1454.8
28.0	24.6	24.6	49.0		99.0	SIQEIQELDKDDESLR	1914.9	1915.9	1916.9	1917.9
28.0	24.6	24.6	49.0	2.0	99.0	SIQEIQELDKDDESLRK	2045.0	2046.0	2045.0	2046.0
28.0	24.6	24.6	49.0		99.0	YIQHTYR	979.5	980.5	979.5	980.5
28.0 28.0 28.0	24.6 24.6	24.6 24.6	49.0 49.0	2.0	99.0 99.0	YIOHTYRK YKEALLGR	1107.6	1108.6 949.5	1107.6 948.5	1108.6 949.5
28.0	24.6	24.6	49.0	1.7	98.0	AEEYEFLTPVEEAPKGMLAR	948.5 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	AEEYEFLTPVEEAPKGMLAR	2279.1	2280.1	2279.1	2280.1
28.0	24.6	24.6	49.0	0.0	99.0	SIQEIQELDKDDESLR	1916.9	1917.9	1916.9	1917.9
82.0	4.1	4.1	26.0	2.0	99.0	AEEYEFLTPVEEAPKGMLAR	2280.1	2281.1	2279.1	2280.1
82.0	4.1	4.1	26.0	2.0	99.0	GVKIDKTDYMVGSYGPR	1884.9	1885.9	1884.9	1885.9
86.0	8.8	8.8	51.0	2.0	99.0	AEEYEFLTPVEEAPKGMLAR	2279.1	2280.1	2279.1	2280.1
86.0	8.8	8.8	51.0	2.0	99.0	IDKTDYMVGSYGPR	1600.8	1601.8	1600.8	1601.8
86.0	8.8	8.8	51.0	2.0	99.0	SIQEIQELDKDDESLR	1916.9	1917.9	1916.9	1917.9
86.0	8.8	8.8	51.0	2.0	99.0	YKEALLGR	948.5	949.6	948.5	949.5
86.0	8.8	8.8	51.0	0.5	69.0	KYKEALLGR	1076.6	1077.7	1076.6	1077.6
86.0 P52566	8.8 GDIS_HUMAN	8.8	51.0 Rho GDP-dis	0.2 sociation in	34.0 nhibitor 2 (Ri	KQSFVLKEGVEYR no GDI 2) (Rho-GDI beta) (Ly-GDI) - Hom	1630.8 no sapiens (Human)	1631.9	1630.8	1631.8
101.0		12.0	49.8	2.0	99.0	ATFMVGSYGPRPEEYEFLTPVEEAPK	2943.4	2944.4	2943.4	2944.4
101.0		12.0	49.8	2.0	99.0	ETIVLKEGSEYR	1422.7	1423.8	1422.7	1423.7
101.0 101.0	11.1	12.0 12.0	49.8 49.8	2.0	99.0 99.0	IHFKVNR SLKELQEMDKDDESLIK	912.5 2020.0	913.5 2021.0	912.5 2020.0	913.5 2021.0
101.0		12.0	49.8	1.5	97.0	APNVVVTR	854.5	855.5	854.5	855.5
101.0		12.0	49.8	1.0	99.0	YVQHTYR	965.5	966.5	965.5	966.5
101.0	11.1	12.0	49.8	0.5	66.0	TLLGDGPVVTDPKAPNVVVTR	2147.2	2148.2	2147.2	2148.2
269.0	2.1	2.1	49.3	2.0	99.0	IHFKVNR	912.5	913.5	912.5	913.5
269.0	2.1	2.1	49.3	0.0	98.0	IHFKVNR	912.5	913.5	912.5	913.5
334.0	HNRPF_HUMAN 3.6	6.0	20.7	2.0	ribonucleop 99.0	rotein F (hnRNP F) (Nucleolin-like protein HSGPNSADSANDGFVR	1629.7	1630.7	1629.7	1630.7
334.0	3.6	6.0	20.7	1.5	99.0	ITGEAFVQFASQELAEK	1866.9	1867.9	1866.9	1867.9
334.0		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	ITGEAFVQFASQELAEK	1866.9	1867.9	1866.9	1867.9
230.0	2.7	2.7	12.3	1.2	94.0	HSGPNSADSANDGFVR	1629.7	1630.7	1629.7	1630.7
P52907 233.0	CAZA1_HUMAN 5.3	5.3	F-actin capp 19.9	ing protein 2.0	subunit alph 99.0	a-1 (CapZ alpha-1) - Homo sapiens (Hum FITHAPPGEFNEVFNDVR	nan) 2088.0	2089.0	2088.0	2089.0
233.0		5.3	19.9	2.0	99.0	TIDGQQTIIACIESHQFQPK	2313.2	2314.2	2313.1	2314.1
233.0		5.3	19.9	1.3	95.0	LLLNNDNLLR	1196.7	1197.7	1196.7	1197.7
166.0	2.0	2.0	19.2	2.0	99.0	FITHAPPGEFNEVFNDVR	2088.0	2089.0	2088.0	2089.0
282.0	2.1	2.1	15.4	2.0	99.0	TIDGQQTIIACIESHQFQPK	2313.2	2314.2	2313.1	2314.1
	CATC_HUMAN 3.5		Dipeptidyl-p			C 3.4.14.1) (Dipeptidyl-peptidase I) (DPP NVHGINFVSPVR				ansferase) [Con 1338.7
101.0		3.5 3.5	11.9 11.9	1.4	96.0 22.0	WFAFFK NWACFTGKK	844.4 1110.5	845.4 1111.6	844.4 1110.5	845.4 1111.5
311.0	2.0	2.0	3.7	2.0	99.0	NVHGINFVSPVR	1337.7	1338.7	1337.7	1338.7
189.0	KAD2_HUMAN 6.1	6.1	34.7	2.0	99.0	chondrial (EC 2.7.4.3) (ATP-AMP transpho LAENFCVCHLATGDMLR	2005.9	2006.9	2005.9	2006.9
189.0	6.1	6.1	34.7	2.0	99.0	LQAYHTQTTPLIEYYR	1996.0	1997.0	1996.0	1997.0
189.0	6.1	6.1	34.7	2.0	99.0	NGFLLDGFPR	1135.6	1136.6	1135.6	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	LQAYHTQTTPLIEYYR	1996.0	1997.0	1996.0	1997.0
126.0	6.0	6.0	28.9	2.0	99.0	LAENFCVCHLATGDMLR	2005.9	2006.9	2005.9	2006.9
126.0	6.0	6.0	28.9	2.0	99.0	LQAYHTQTTPLIEYYR	1996.0	1997.0	1996.0	1997.0
126.0	6.0	6.0	28.9	2.0	99.0	NGFLLDGFPR	1135.6	1136.6	1135.6	1136.6
126.0	6.0 TERA_HUMAN	6.0	28.9 Transitional	0.0	99.0	LQAYHTQTTPLIEYYR ATPase (TER ATPase) (15S Mg(2+)-ATPase	1997.0	1998.0	1997.0	1998.0
45.0	19.1	19.1	25.3	2.0	99.0	ELQELVQYPVEHPDKFLK	2211.1	2212.1	2211.1	2212.1
45.0	19.1	19.1	25.3	2.0	99.0	GILLYGPPGTGK	1171.7	1172.7	1171.7	1172.7
45.0	19.1	19.1	25.3		99.0	GPELLTMWFGESEANVR	1950.9	1951.9	1950.9	1951.9
45.0	19.1	19.1	25.3	2.0	99.0	KYEMFAQTLQQSR	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	1922.9	1924.0
45.0	19.1	19.1	25.3	2.0	99.0	YEMFAQTLQQSR	1500.7	1501.7	1500.7	1501.7
45.0	19.1	19.1	25.3	1.7	98.0	WALSQSNPSALR	1328.7	1329.7	1328.7	1329.7
45.0	19.1	19.1	25.3	1.2	94.0	RDHFEEAMR	1189.5	1190.5	1189.5	1190.5
61.0	12.8	12.8	18.7	2.0	99.0	KYEMFAQTLQQSR	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		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	RDHFEEAMR	1189.5	1190.5	1189.5	1190.5
61.0	12.8	12.8	18.7	0.5	71.0	NAPAIIFIDELDAIAPKR	1966.1	1967.1	1966.1	1967.1
61.0	12.8	12.8	18.7	0.2	36.0	WALSQSNPSALR	1328.7	1329.7	1328.7	1329.7
	12.8 NP1L1_HUMAN	12.8				RDHFEEAMR 2 1 (NAP-1-related protein) (hNRP) - Hom		1190.6	1189.5	1190.5
198.0		6.0	10.5	2.0	99.0	FYEEVHDLER	1335.6	1336.6	1335.6	1336.6
198.0		6.0	10.5	2.0	99.0	KYAVLYQPLFDKR	1639.9	1640.9	1639.9	1640.9
198.0	6.0	6.0	10.5	2.0	99.0	NVDLLSDMVQEHDEPILK	2094.0	2095.1	2094.0	2095.0
98.0	3.8	3.8	10.2	2.0	99.0	KYAVLYQPLFDKR	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	YAVLYQPLFDKR	1511.8	1512.8	1511.8	1512.8
187.0	4.0	4.0	10.0	2.0	99.0	FYEEVHDLER	1335.6	1336.6	1335.6	1336.6
187.0	4.0	4.0	10.0	2.0	99.0	LDGLVETPTGYIESLPR	1859.0	1860.0	1859.0	1860.0
P55786 I	PSA_HUMAN	2.3				e (EC 3.4.11) (PSA) - Homo sapiens (Hu AFFESHPAPSAER		1445.7	1444.7	1445.7
407.0 407.0 152.0	2.3	2.3 2.3 2.0	3.8 7.5	0.2 2.0	36.0 99.0	YAAVTQFEATDAR DAESIHQYLLQR	1444.7 1441.7 1471.7	1445.7 1442.7 1472.7	1444.7 1441.7 1471.7	1445.7 1442.7 1472.7
181.0	4.0 4.0	4.0	6.7	2.0 2.0 2.0	99.0	AFFESHPAPSAER	1444.7	1445.7	1444.7	1445.7
181.0 P59998	ARPC4_HUMAN	4.0	6.7 Actin-related	d protein 2		DAESIHQYLLQR ubunit 4 (ARP2/3 complex 20 kDa subuni				1472.7
197.0 197.0	6.0	6.0	29.8 29.8	2.0	99.0 99.0	AENFFILR IVAEEFLK	1008.5 947.5	1009.5 948.5	1008.5 947.5	1009.5 948.5
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	29.8	0.0	21.0	AENFFILR	1010.5	1011.5	1010.5	1011.5
123.0		2.3	23.8	2.0	99.0	AENFFILR	1008.5	1009.6	1008.5	1009.5
123.0		2.3	23.8	0.3	53.0	TATLRPYLSAVR	1388.8	1389.8	1388.8	1389.8
327.0 P601741	2.0 TPIS_HUMAN	2.0	19.0 Triosephosp	2.0 hate isome	99.0 rase (EC 5.3.	AENFFILR 1.1) (TIM) (Triose-phosphate isomerase)	1008.5 - Homo sapiens (Hu	1009.5 iman)	1008.5	1009.5
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	HVFGESDELIGQK	1457.7	1458.7	1457.7	1458.7
23.0	28.0	28.0	61.0		99.0	IAVAAQNCYK	1136.6	1137.6	1136.6	1137.6
23.0 23.0 23.0	28.0	28.0 28.0 28.0	61.0	2.0 2.0 2.0	99.0 99.0	IIYGGSVTGATCK KFFVGGNWK	1325.7	1326.7 1082.6	1325.7	1326.7
23.0	28.0 28.0	28.0	61.0 61.0	2.0	99.0	QSLGELIGTLNAAK	1081.6 1396.8	1397.8	1081.6 1396.8	1082.6 1397.8
23.0	28.0	28.0	61.0	2.0	99.0	RHVFGESDELIGQK	1613.8	1614.8	1613.8	1614.8
23.0	28.0	28.0	61.0		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	VPADTEVVCAPPTAYIDFAR	2191.1	2192.1	2191.1	2192.1
23.0	28.0	28.0	61.0	2.0	99.0	VTNGAFTGEISPGMIK	1621.8	1622.8	1621.8	1622.8
23.0	28.0	28.0	61.0	2.0	99.0	VVLAYEPVWAIGTGK	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	28.0	28.0	61.0		82.0	LRGWLK	771.5	772.5	771.5	772.5
23.0	28.0	28.0	61.0	0.0	99.0	FFVGGNWK	954.5	955.5	954.5	955.5
23.0	28.0	28.0	61.0		99.0	FFVGGNWK	954.5	955.5	954.5	955.5
23.0	28.0	28.0	61.0	0.0	40.0	HYGGSVTGATCK	1477.7	1478.7	1477.7	1478.7
23.0	28.0	28.0	61.0	0.0	68.0	KFFVGGNWK	1084.6	1085.6	1081.6	1082.6
13.0	18.3	18.3	66.7	2.0	99.0	DCGATWVVLGHSER	1585.7	1586.7	1585.7	1586.7
13.0	18.3	18.3	66.7	2.0	99.0	FFVGGNWK	953.5	954.5	953.5	954.5
13.0	18.3	18.3	66.7	2.0	99.0	HVFGESDELIGQK	1457.7	1458.7	1457.7	1458.7
13.0	18.3	18.3	66.7	2.0	99.0	IIYGGSVTGATCK	1325.7	1326.7	1325.7	1326.7
13.0	18.3	18.3	66.7	2.0	99.0	KFFVGGNWK	1081.6	1082.6	1081.6	1082.6
13.0	18.3	18.3	66.7	2.0	99.0	TATPQQAQEVHEK	1465.7	1466.7	1465.7	1466.7

40.0	10.0	10.0		2.0	99.0	MADANAKDIAKK	1070 (1074.7	4070.7	1074.7
13.0 13.0	18.3 18.3	18.3 18.3	66.7 66.7	2.0	99.0	VIADNVKDWSK VPADTEVVCAPPTAYIDFAR	1273.6 2191.1	1274.7 2192.1	1273.7 2191.1	1274.7 2192.1
13.0	18.3	18.3	66.7	2.0	99.0	VVLAYEPVWAIGTGK	1601.9	1602.9	1601.9	1602.9
13.0	18.3	18.3	66.7	0.3	48.0	IAVAAQNCYK	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	65.0	VPADTEVVCAPPTAYIDFAR	2192.1	2193.1	2191.1	2192.1
40.0	18.1	18.1	57.0	2.0	99.0	DCGATWVVLGHSER	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	IIYGGSVTGATCK	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	VAHALAEGLGVIACIGEK	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	VVLAYEPVWAIGTGK	1601.9	1602.9	1601.9	1602.9
40.0	18.1	18.1	57.0	1.5	97.0	DCGATWVVLGHSERR	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
	YL6_HUMAN 10.0	10.0	Myosin light 50.3		e 6 (Smooth 99.0	muscle and nonmuscle myosin light cha ALGONPTNAEVLK			3) (Myosin light of 1353.7	
112.0	10.0	10.0	50.3	2.0	99.0	EAFQLFDR	1024.5	1025.5	1024.5	1025.5
112.0	10.0	10.0	50.3		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	NKDQGTYEDYVEGLR	1785.8	1786.8	1785.8	1786.8
65.0	5.2	5.2	31.1	2.0	99.0	EAFQLFDR	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	NKDQGTYEDYVEGLR	1785.8	1786.8	1785.8	1786.8
65.0	5.2	5.2	31.1		48.0	ALGQNPTNAEVLK	1353.7	1354.7	1353.7	1354.7
122.0	6.1	6.1	50.3	2 2	99.00	ILYSQCGDVMR	1340.6	1341.6	1340.6	1341.6
122.0	6.1	6.1	50.3		99.00	NKDQGTYEDYVEGLR	1785.8	1786.8	1785.8	1786.8
122.0	6.1 CTB_HUMAN	6.1	50.3 Actin, cytop	2	99.00	VFDKEGNGTVMGAEIR	1722.8	1723.8	1722.8	1723.8
449.0	2.0	54.1	69.9	2.0	99.0	Homo sapiens (Human) DDDIAALVVDNGSGMCK	1821.8	1822.8	1821.8	1822.8
449.0 449.0	2.0	54.1 54.1	69.9 69.9	0.0	99.0 96.0	AGFAGDDAPR AGFAGDDAPR	975.4 978.5	976.4 979.5	975.4 975.4	976.4 976.4
449.0	2.0	54.1	69.9	0.0	99.0	AVFPSIVGRP	1041.6	1042.6	1041.6	1042.6
449.0	2.0	54.1	69.9		99.0	AVFPSIVGRPR	1197.7	1198.7	1197.7	1198.7
449.0	2.0	54.1	69.9	0.0	99.0	CYVALDFEQEMATAASSSSLEK	2549.0	2550.0	2549.0	2550.0
449.0	2.0	54.1	69.9		99.0	DDDIAALVVDNGSGMCK	1973.8	1974.8	1973.8	1974.8
449.0	2.0	54.1	69.9	0.0	99.0	DDDIAALVVDNGSGMCK	1821.8	1822.8	1821.8	1822.8
449.0	2.0	54.1	69.9		99.0	DDDIAALVVDNGSGMCK	1821.8	1822.8	1821.8	1822.8
449.0	2.0	54.1	69.9	0.0	99.0	DDDIAALVVDNGSGMCK	1973.8	1974.8	1973.8	1974.8
449.0	2.0	54.1	69.9	0.0	99.0	DLYANTVLSGGTTMYPGIADR	2214.0	2215.1	2214.1	2215.1
449.0	2.0	54.1	69.9	0.0	99.0	EITALAPSTMK	1160.6	1161.6	1160.6	1161.6
449.0	2.0	54.1	69.9		99.0	GYSFTTTAER	1131.5	1132.5	1131.5	1132.5
449.0	2.0	54.1	69.9	0.0	98.0	GYSFTTTAEREIVR	1628.8	1629.8	1628.8	1629.8
449.0	2.0	54.1	69.9	0.0	99.0	GYSFTTTAEREIVRDIK	1985.1	1986.1	1985.0	1986.0
449.0	2.0	54.1	69.9	0.0	95.0	GYSFTTTAEREIVRDIKEK	2242.2	2243.2	2242.2	2243.2
449.0	2.0	54.1	69.9		86.0	GYSFTTTAEREIVRDIKEK	2243.2	2244.2	2242.2	2243.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGVMVGMGQK	1170.6	1171.6	1170.6	1171.6
449.0	2.0	54.1	69.9		99.0	HQGVMVGMGQK	1186.6	1187.6	1186.6	1187.6
449.0	2.0	54.1	69.9	0.0	99.0	HQGVMVGMGQK	1182.6	1183.6	1182.6	1183.6
449.0	2.0	54.1	69.9		99.0	HQGVMVGMGQK	1172.6	1173.6	1170.6	1171.6
449.0	2.0	54.1	69.9	0.0	29.0	HQGVMVGMGQK	1186.6	1187.6	1186.6	1187.6
449.0	2.0	54.1	69.9		99.0	HQGVMVGMGQKDSYVGDEAQSK	2366.1	2367.1	2366.1	2367.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSK	2350.1	2351.1	2350.1	2351.1
449.0	2.0	54.1	69.9		99.0	HQGVMVGMGQKDSYVGDEAQSK	2394.1	2395.1	2394.1	2395.1
449.0	2.0	54.1	69.9	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSK	2366.1	2367.1	2366.1	2367.1
449.0	2.0	54.1	69.9		99.0	HQGVMVGMGQKDSYVGDEAQSK	2378.1	2379.1	2378.1	2379.1
449.0 449.0	2.0	54.1 54.1	69.9 69.9	0.0	99.0 99.0	HQGVMVGMGQKDSYVGDEAQSKR HQGVMVGMGQKDSYVGDEAQSKR	2522.2 2522.2	2523.2 2523.2	2522.2 2522.2	2523.2 2523.2
449.0 449.0	2.0	54.1 54.1	69.9 69.9	0.0	99.0 99.0	HQGVMVGMGQKDSYVGDEAQSKR HQGVMVGMGQKDSYVGDEAQSKR	2506.2 2534.2	2507.2 2535.2	2506.2 2534.2	2507.2 2535.2
449.0	2.0	54.1	69.9	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSKR	2518.2	2519.2	2518.2	2519.2
449.0	2.0	54.1	69.9		95.0	HQGVMVGMGQKDSYVGDEAQSKR	2538.2	2539.2	2538.2	2539.2
449.0	2.0	54.1	69.9	0.0	23.0	IIAPPER	794.5	795.5	794.5	795.5
449.0	2.0	54.1	69.9		83.0	IIAPPERK	922.6	923.6	922.6	923.6
449.0 449.0	2.0	54.1 54.1	69.9 69.9	0.0	99.0 99.0	IKIIAPPER IKIIAPPER	1035.6 1035.6	1036.7 1036.7	1035.6 1035.6	1036.7 1036.7
449.0 449.0	2.0 2.0 2.0	54.1 54.1	69.9 69.9	0.0	86.0 41.4	IKIIAPPERK ISKQEYDESGPSIVHR	1163.7 1843.9	1164.8 1844.9	1163.7 1843.9	1164.7 1844.9
449.0 449.0	2.0 2.0 2.0	54.1 54.1	69.9 69.9	0.0	89.0 26.8	IWHHTFYNE IWHHTFYNEL	1245.5 1359.7	1246.6 1360.7	1245.6 1358.6	1246.6 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		99.0	IWHHTFYNELR	1516.7	1517.7	1514.7	1515.7
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		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		56.0	IWHHTFYNELR	1499.7	1500.7	1499.7	1500.7
449.0	2.0	54.1	69.9	0.0	44.0	IWHHTFYNELR	1470.7	1471.7	1470.7	1471.7
449.0	2.0	54.1	69.9		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		99.0	MQKEITALAPSTMK	1547.8	1548.8	1547.8	1548.8
449.0	2.0	54.1	69.9	0.0	99.0	QEYDESGPSIVHR	1515.7	1516.7	1515.7	1516.7
449.0	2.0	54.1	69.9	0.0	99.0	QEYDESGPSIVHR	1498.7	1499.7	1498.7	1499.7
449.0	2.0	54.1	69.9	0.0	99.0	QEYDESGPSIVHRK	1643.8	1644.8	1643.8	1644.8
449.0	2.0	54.1	69.9	0.0	99.0	QEYDESGPSIVHRK	1626.8	1627.8	1626.8	1627.8
449.0	2.0	54.1	69.9	0.0	92.0	RGILTLK	799.5	800.5	799.5	800.5
449.0	2.0	54.1	69.9	0.0	28.4	SLSTFQQMWISK	1454.7	1455.7	1454.7	1455.7
449.0	2.0	54.1	69.9	0.0	99.0	SYELPDGQVITIGNER	1789.9	1790.9	1789.9	1790.9
449.0	2.0	54.1	69.9	0.0	99.0	SYELPDGQVITIGNER	1789.9	1790.9	1789.9	1790.9
449.0	2.0	54.1	69.9	0.0	99.0	SYELPDGQVITIGNER	1790.9	1791.9	1790.9	1791.9
449.0	2.0	54.1	69.9		95.0	SYELPDGQVITIGNER	1786.0	1787.0	1785.9	1786.9
449.0	2.0	54.1	69.9	0.0	96.0	SYELPDGQVITIGNERFR	2093.1	2094.1	2093.1	2094.1
449.0	2.0	54.1	69.9		99.0	VAPEEHPVLLTEAPLNPK	1953.0	1954.0	1953.1	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	YPIEHGIVTNWDDMEK	1959.9	1960.9	1959.9	1960.9
449.0	2.0	54.1	69.9		99.0	YPIEHGIVTNWDDMEK	1945.9	1946.9	1945.9	1946.9
5.0	31.5	31.5	66.4	2.0	99.0	AVFPSIVGRPR	1197.7	1198.7	1197.7	1198.7
5.0	31.5	31.5	66.4	2.0	99.0	DDDIAALVVDNGSGMCK	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	2214.1	2215.1	2214.1	2215.1
5.0	31.5	31.5	66.4	2.0	99.0	HQGVMVGMGQK	1170.6	1171.6	1170.6	1171.6
5.0	31.5	31.5	66.4	2.0	99.0	HQGVMVGMGQKDSYVGDEAQSK	2350.1	2351.1	2350.1	2351.1
5.0	31.5	31.5	66.4	2.0	99.0	HQGVMVGMGQKDSYVGDEAQSKR	2506.2	2507.2	2506.1	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	LCYVALDFEQEMATAASSSSLEK	2549.0	2550.0	2549.1	2550.1
5.0	31.5	31.5	66.4	2.0	99.0	QEYDESGPSIVHRK	1643.8	1644.8	1643.8	1644.8
5.0	31.5	31.5	66.4	2.0	99.0	SYELPDGQVITIGNER	1789.9	1790.9	1789.9	1790.9
5.0	31.5	31.5	66.4		99.0	VAPEEHPVLLTEAPLNPK	1953.1	1954.1	1953.1	1954.1
5.0	31.5	31.5	66.4	2.0	99.0	VAPEEHPVLLTEAPLNPKANREK	2551.4	2552.4	2551.4	2552.4
5.0	31.5	31.5	66.4		99.0	YPIEHGIVTNWDDMEK	1959.9	1960.9	1959.9	1960.9
5.0	31.5	31.5	66.4	1.7	98.0	GYSFTTTAEREIVR	1628.8	1629.8	1628.8	1629.8
5.0	31.5	31.5	66.4		89.0	IKIIAPPER	1035.7	1036.7	1035.6	1036.7
5.0	31.5	31.5	66.4	0.4	64.0	VAPEEHPVLLTEAPLNPKANR	2294.2	2295.3	2294.2	2295.2
5.0	31.5	31.5	66.4		36.0	QEYDESGPSIVHR	1496.7	1497.7	1496.7	1497.7
5.0	31.5	31.5	66.4	0.1	28.1	DDDIAALVVDNGSGMCKA	1972.8	1973.8	1972.8	1973.8
5.0	31.5	31.5	66.4		99.0	DDDIAALVVDNGSGMCK	1821.8	1822.8	1821.8	1822.8
5.0 5.0	31.5 31.5	31.5 31.5 31.5	66.4 66.4	0.0	99.0 99.0	DDDIAALVVDNGSGMCK DDDIAALVVDNGSGMCK DDDIAALVVDNGSGMCK	1820.8 1816.7	1821.8 1817.7	1820.8 1816.7	1821.8 1817.7
5.0 5.0	31.5 31.5	31.5 31.5 31.5	66.4 66.4	0.0	99.0 94.0	DDDIAALVVDNGSGMCK HQGVMVGMGQK	1973.8 1171.6	1974.8 1172.6	1973.8 1170.6	1974.8 1171.6
5.0 5.0	31.5 31.5	31.5 31.5 31.5	66.4 66.4	0.0	22.0 96.0	HQGVMVGMGQK HQGVMVGMGQKDSYVGDEAQSKR	1186.6 2506.2	1187.6 2507.2	1186.6 2506.2	1187.6 2507.2
5.0 5.0	31.5 31.5 31.5	31.5 31.5 31.5	66.4 66.4	0.0 0.0 0.0	99.0 98.0	IWHHTFYNELR IWHHTFYNELR	1515.8 1546.7	1516.8 1547.7	1515.7 1546.7	1516.7 1547.7
5.0	31.3	31.3	00.4	0.0	70.U		1340.7	1347.7	1540.7	1047.7

5.0	31.5 IRAC2 HUMAN	31.5	66.4	0.0	74.0	QEYDESGPSIVHRK	1626.8	1627.8	1626.8	1627.8
304.0 304.0	0 4.0	4.0 4.0	9.4 9.4	2.0 2.0	99.0 99.0	strate 2 precursor (p21-Rac2) (Small G protein AKWFPEVR YLECSALTOR	1031.55481 1239.592773	1032.562 1240.6	1031.55525 1239.591772	1032.562527 1240.599048
356.0		2.0	5.2 Eukaryotic ir	2.0 nitiation fact	99.0	YLECSALTQR 3.6.1) (ATP-dependent RNA helicase el F4A-	1239.595703	1240.603	1239.591772	1240.599048
231.0 231.0	2.7	2.7 2.7	12.3 12.3	2.0 0.7	99.0 81.0	GIYAYGFEKPSAIQQR DFTVSAMHGDMDQKER	1826.9 1865.8	1827.9 1866.8	1826.9 1865.8	1827.9 1866.8
	RS20_HUMAN		10.8 40S ribosom			GIYAYGFEKPSAIQQR apiens (Human)	1826.9	1827.9	1826.9	1827.9
354.0 354.0	0 3.2	3.2 3.2	29.4 29.4	2.0 1.2	99.0 93.0	AFKDTGKTPVEPEVAIHR TWDRFQMR	2036.1 1138.5	2037.1 1139.5	2036.1 1138.5	2037.1 1139.5
165.0 165.0	0 4.4	4.4 4.4	21.8 21.8	2.0 1.4	99.0 96.0	AFKDTGKTPVEPEVAIHR TWDRFQMR	2036.1 1138.5	2037.1 1139.5	2036.1 1138.5	2037.1 1139.5
165.0 P60900	PSA6_HUMAN		21.8 Proteasome			DTGKTPVEPEVAIHR C 3.4.25.1) (Proteasome iota chain) (Macropa				
69.0 69.0	14.4	14.4 14.4	40.2 40.2	2.0 2.0	99.0 99.0 99.0	AINOGGLTSVAVR CDPAGYYCGFK	1284.7 1319.5	1285.7 1320.5	1284.7 1319.5	1285.7 1320.6
69.0 69.0 69.0	14.4	14.4 14.4 14.4	40.2 40.2 40.2	2.0 2.0 2.0	99.0 99.0	HITIFSPEGR ILTEAEIDAHLVALAERD ITENIGCVMTGMTADSR	1155.6 1978.0 1854.8	1156.6 1979.0 1855.8	1155.6 1978.0 1854.8	1156.6 1979.0 1855.8
69.0 69.0	14.4	14.4 14.4	40.2 40.2 40.2	2.0 2.0 2.0	99.0 99.0	LYOVEYAFK YGYEIPVDMLCKR	1159.6 1642.8	1160.6 1643.8	1159.6 1642.8	1160.6 1643.8
69.0 180.0	14.4	14.4	40.2 8.5	0.4	64.0 99.0	GSSAGFDRHITIFSPEGR HITIFSPEGR	1932.9 1155.6	1934.0 1156.6	1932.9 1155.6	1934.0 1156.6
94.0 94.0	8.1	8.1 8.1	24.8 24.8	2 2	99.00 99.00	AINQGGLTSVAVR HITIFSPEGR	1284.7 1155.6	1285.7 1156.6	1284.7 1155.6	1285.7 1156.6
94.0 94.0	8.1	8.1 8.1	24.8 24.8	2 2	99.00 99.00	ILTEAEIDAHLVALAERD LYQVEYAFK	1978.0 1159.6	1979.0 1160.6	1978.0 1159.6	1979.0 1160.6
P61158		Actin-like pro	otein 3 (Action 14.4	n-related pro 2.0	otein 3) - Ho 99.0	omo sapiens (Human) AGRLPACVVDCGTGYTK	1865.9	1866.9	1865.9	1866.9
111.0 111.0	0 10.0	10.0 10.0	14.4 14.4	2.0 2.0	99.0 99.0	EFSIDVGYER KDYEEIGPSICR	1213.6 1465.7	1214.6 1466.7	1213.6 1465.7	1214.6 1466.7
111.0 111.0	0 10.0	10.0 10.0	14.4 14.4	2.0 2.0	99.0 99.0	KEFSIDVGYER NIVLSGGSTMFR	1341.7 1280.7	1342.7 1281.7	1341.7 1280.7	1342.7 1281.7
111.0 79.0	9.5	10.0 9.5	14.4 18.2	0.0 2.0	99.0 99.0	KDYEEIGPSICR AGRLPACVVDCGTGYTK	1465.7 1865.9	1466.7 1866.9	1465.7 1865.9	1466.7 1866.9
79.0 79.0	9.5	9.5 9.5	18.2 18.2	2.0 2.0	99.0 99.0	EFSIDVGYER KDYEEIGPSICR	1213.6 1465.7	1214.6 1466.7	1213.6 1465.7	1214.6 1466.7
79.0 79.0	9.5	9.5 9.5	18.2 18.2	2.0	99.0 96.0	LKPKPIDVQVITHHMQR DYEEIGPSICR	2039.1 1337.6	2040.1 1338.6	2039.1 1337.6	2040.2 1338.6
141.0		8.0	Actin-like pro 24.6	2.0 2.0 2.0	99.0 99.0 99.0	rotein 2) - Homo sapiens (Human) GYAFNHSADFETVR HIVESCOSTMARCERSP	1612.7 1770.9	1613.7	1612.7	1613.7
141.0 141.0 141.0	0 8.0	8.0 8.0 8.0	24.6 24.6 24.6	2.0 2.0 2.0	99.0 99.0 99.0	HIVLSGGSTMYPGLPSR HLWDYTFGPEK SMLEVNYPMENGIVR	1770.9 1391.7 1751.8	1771.9 1392.7 1752.8	1770.9 1391.7 1751.8	1771.9 1392.7 1752.8
141.0	0 8.0	8.0	24.6 15.5	0.0	99.0 96.0	SMLEVNYPMENGIVR VGNIEIKDLMVGDEASELR	1751.8 1751.8 2087.1	1752.8 1752.8 2088.1	1751.8 2087.1	1752.8 1752.8 2088.1
112.0 112.0	0 2.9	2.9	15.5 15.5	1.0	89.0 74.0	HLWDYTFGPEK SMLEVNYPMENGIVR	1391.7 1750.8	1392.7 1751.8	1391.7 1750.8	1392.7 1751.8
364.0		2.0	4.8 40S ribosom	2.0	99.0	VGNIEIKDLMVGDEASELR apiens (Human)	2088.0	2089.0	2088.0	2089.0
73.0 73.0	14.0	14.0 14.0	30.7 30.7	2.0 2.0	99.0 99.0	ACQSIYPLHDVFVR APAMFNIR	1703.8 918.5	1704.9 919.5	1703.8 918.5	1704.9 919.5
73.0 73.0		14.0 14.0	30.7 30.7	2.0 2.0	99.0 99.0	KTSYAQHQQVR LFCVGFTK	1344.7 970.5	1345.7 971.5	1344.7 970.5	1345.7 971.5
73.0 73.0		14.0 14.0	30.7 30.7	2.0 2.0	99.0 99.0	NCLTNFHGMDLTR TSYAQHQQVR	1577.7 1216.6	1578.7 1217.6	1577.7 1216.6	1578.7 1217.6
73.0 63.0	5.5	14.0 5.5	30.7 16.3	2.0 2.0	99.0 99.0	VVDPFSKKDWYDVK APAMFNIR	1724.9 918.5	1725.9 919.5	1724.9 918.5	1725.9 919.5
63.0 63.0	5.5	5.5 5.5	16.3 16.3	2.0 1.5	99.0 97.0	NCLTNFHGMDLTR ACQSIYPLHDVFVR	1577.7 1703.8	1578.7 1704.9	1577.7 1703.8	1578.7 1704.9
136.0 136.0	5.8	5.8 5.8	18.2 18.2	2.0 2.0	99.0 99.0	ACQSIYPLHDVFVR APAMFNIR	1703.8 918.5	1704.8 919.5	1703.8 918.5	1704.9 919.5
136.0	5.8	5.8 5.8	18.2 18.2	1.7 0.1	98.0 20.0	NCLTNFHGMDLTR KTSYAQHQQVR	1577.7 1361.7	1578.7 1362.7	1577.7 1361.7	1578.7 1362.7
P61254		2.0	60S ribosom 15.2	2.0	99.0	sapiens (Human) MKFNPFVTSDR	1340.7	1341.7	1340.7	1341.7
									1240.7	
	2.1 CH10_HUMAN	2.1	29.7 10 kDa heat			MKFNPFVTSDR ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLFDR				
	0 2.1 - CH10_HUMAN 0 5.7 0 5.7	2.1	29.7				Early-pregnanc 1034.6 1528.8			
P61604 221.0 221.0	0 2.1 - CH10_HUMAN 0 5.7 0 5.7 0 5.7 0 1.9	2.1 5.7 5.7	29.7 10 kDa heat 26.5 26.5	shock prote 2.0 2.0	in, mitochor 99.0 99.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLFDR VVLDDKDYFLFR	(Early-pregnanc 1034.6	y factor) (EPF) - Hi 1035.6 1529.8	omo sapiens (H 1034.6 1528.8	uman) 1035.6 1529.8
P61604 221.0 221.0 221.0 374.0 374.0 P61626 41.0	2.1 CH10_HUMAN 0 5.7 0 5.7 0 5.7 0 1.9 0 1.9 LYSC_HUMAN 0 20.4	2.1 5.7 5.7 5.7 1.9 1.9	29.7 10 kDa heat 26.5 26.5 26.5 26.5	2.0 2.0 1.7 1.7 0.2 precursor (E	in, mitochor 99.0 99.0 98.0 98.0 34.0 CC 3.2.1.17) 99.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLFDR VVLDDKDYFLFR FLPLFDR FLPLFDR VVLDDKDYFLFR (VLDDKDYFLFR VVLDDKDYFLFR ATNYNAGDRSTDYGIFGINSR	(Early-pregnanc 1034.6 1528.8 906.5 906.5 1528.8 biens (Human) 2362.1	y factor) (EPF) - He 1035.6 1529.8 907.5 907.5 1529.8 2363.1	omo sapiens (H 1034.6 1528.8 906.5 906.5 1528.8 2362.1	uman) 1035.6 1529.8 907.5 907.5 1529.8 2363.1
P61604 221.0 221.0 221.0 374.0 961626 41.0 41.0	2.1 CH10_HUMAN 0 5.7 0 5.7 0 5.7 0 1.9 0 1.9	2.1 5.7 5.7 5.7 1.9 1.9 20.4 20.4 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 Lysozyme C 81.8 81.8 81.8	2.0 2.0 1.7 1.7 0.2 precursor (E 2.0 2.0 2.0	in, mitochor 99.0 99.0 98.0 98.0 34.0 CC 3.2.1.17) 99.0 99.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLERB VVLDDKDYFLFR FLPLEDR FLPLERB VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo sap ATNYNAGDRSTDYGIFQINSR GISLANWMCLAK QVVQGCGV	(Early-pregnanc 1034.6 1528.8 906.5 906.5 1528.8 biens (Human) 2362.1 1378.7 909.4	y factor) (EPF) - Hi 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4	omo sapiens (H 1034.6 1528.8 906.5 906.5 1528.8 2362.1 1378.7 909.4	uman) 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4
P61604 221.0 221.0 221.0 374.0 374.0 P61626 41.0 41.0 41.0 41.0 41.0	2.1 (2H10_HUMAN) 0 5.7 0 5.7 0 1.9 1.9 1_LYSC_HUMAN 0 20.4 0 20.4 0 20.4 0 20.4	2.1 5.7 5.7 5.7 1.9 1.9 20.4 20.4 20.4 20.4 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 Lysozyme C 81.8 81.8 81.8 81.8 81.8	2.0 2.0 1.7 1.7 0.2 precursor (E 2.0 2.0 2.0 2.0 2.0	in, mitochol 99.0 99.0 98.0 98.0 34.0 CC 3.2.1.17) 99.0 99.0 99.0 99.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDYFLFR VVLDDKDYFLFR VVLDDKDYFLFR G14-beta-N-acetylmuramidase C) - Homo sag ATNYNAGDRSTDYGIFQINSR G1SLANWMCLAK QYVQGCGV RVRDPQGIR STDYGIFQINSR	(Early-pregnanc 1034.6 1528.8 906.5 906.5 1528.8 piens (Human) 2362.1 1378.7 909.4 1194.7 1400.7	y factor) (EPF) - Hi 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7	omo sapiens (H 1034.6 1528.8 906.5 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7	uman) 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7
P61604 221.0 221.0 221.0 374.0 374.0 P61626 41.0 41.0 41.0 41.0 41.0 41.0	2.1 (2H10_HUMAN) 0 5.7 0 5.7 0 5.7 0 1.9 0 1.9 1 (2U.4) 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4 0 20.4	2.1 5.7 5.7 5.7 1.9 1.9 20.4 20.4 20.4 20.4 20.4 20.4 20.4 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 281.8 81.8 81.8 81.8 81.8 81.8 81.8 81.	2.0 2.0 1.7 1.7 0.2 precursor (E 2.0 2.0 2.0 2.0 2.0 2.0 2.0	in, mitochoi 99.0 98.0 98.0 34.0 6C 3.2.1.17) 99.0 99.0 99.0 99.0 99.0 99.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDYFLFR VVLDDKDYFLFR VVLDDKDYFLFR GISLANWACLAK OYVOGCGV RVVRDPOGIR STDVGIFGINSR STDVGIFGINSR STDVGIFGINSR WESGYNTR	(Early-pregnanc 1034.6 1528.8 906.5 1528.8 906.5 1528.8 plens (Human) 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4	y factor) (EPF) - Hi 1035 6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4	omo sapiens (H 1034.6 1528.8 906.5 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1503.7	uman) 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4
P61604 221.0 221.0 221.0 374.0 961626 41.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0	2.1 (CH10_HVMAN) 0 5.7 0 5.7 0 5.7 0 5.7 0 1.9 0 1.9 0 20.4 0 20.	2.1 5.7 5.7 5.7 1.9 1.9 20.4 20.4 20.4 20.4 20.4 20.4 20.4 20.4 20.4 20.4 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 Lysozyme C 81.8 81.8 81.8 81.8 81.8 81.8 81.8	2.0 2.0 1.7 1.7 0.2 precursor (E 2.0 2.0 2.0 2.0 2.0 2.0 2.0 1.7 1.2	in, mitochoi 99.0 99.0 98.0 34.0 6. 3.2.1.17) 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo say ATNYNAGDRSTDYGIFQINSR GISLANWMCLAK OYVGGCGV RVWRDPGGIR STDYGIFQINSR STDYGIFQINSR STDYGIFQINSRY WESGYNTR YWCNDGK LGMDGYR	(Early-pregnanc 1034.6 1528.8 906.5 906.5 1528.8 90e.5 1528.8 10ens (Human) 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4	omo sapiens (H 1034.6 1528.8 906.5 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4	uman) 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4
P61604 221.0 221.0 221.0 374.0 P61626 41.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0	2.1 (CH10_HMAN) 0 5.7 0 5.7 0 5.7 0 5.7 0 1.9 0 1.9 0 20.4	2.1 5.7 5.7 5.7 1.9 1.9 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 26.5 Lysozyme C 81.8 81.8 81.8 81.8 81.8 81.8 81.8 81.8 81.8 81.8 81.8 81.8	shock prote 2.0 2.0 1.7 1.7 0.2 precursor (E 2.0 2.0 2.0 2.0 2.0 2.0 2.0 1.7 1.2 1.0 1.0	in, mitochoi 99.0 99.0 98.0 34.0 34.0 36.3.2.1.17) 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLFDR FLPLFDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo sag ATNYNAGDRSTDYGIFGINSR GISLANWMCLAK QYVGGCGV RVWRDPGGIR STDYGIFGINSR STDYGIFGINSR STDYGIFGINSR WESGYNTR YWCNDGK LGMDGYR DVRQYVGGCGV AWYAWR	(Early-pregnance 1034 6 1528 8 906.5 1528 8 906.5 1528 8 1658 1658 1438 7 909.4 11378.7 909.4 1104.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.4	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4	omo sapiens (H 1034 6 1528 8 906.5 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.4	uman) 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4
P61604 221.0 221.1 221.1 374.0 374.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0 4	2.1 (CH10_HUMAN) 0 5.7 0 5.7 0 5.7 0 1.9 0 1.9 0 1.9 0 20.4 0 20.	2.1 5.7 5.7 5.7 1.9 1.9 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 81.8 81.8 81.8 81.8 81.8 81.8 81.8 81	shock prote 2.0 2.0 1.7 1.7 0.2 precursor (E 2.0 2.0 2.0 2.0 2.0 2.0 2.0 1.7 1.2 1.0 0.8 0.4	in, mitochoi 99.0 98.0 98.0 34.0 63.2.1.17) 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo sag ATNYNAGDRSTDYGIFGINSR GISLANWMCLAK QYVQSCGV KVVKDPOGIR STDYGIFGINSR STDYGIFGINSR STDYGIFGINSR WESGYNTR YWCNDGK LGMBCYR DVRQYVQGCGV AWYAWR RAWAWR RAWAWR RLGMDGYR	(Early-pregnance) 1034-6 1528-8 906.5 1528-8 1628-8 1628-8 1628-7 1378-7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4 1279-6 787.4 959.4 966.5	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.4 967.5	omo sapiens (H 1034 6 1528 8 906.5 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.4 995.5 966.5	uman) 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1012.4 942.4 811.4 1280.6 788.4 960.5
P61604 221.0 221.0 221.0 221.0 374.4 374.4 41.0 41.0 41.0 41.0 41.0 41.0 41.0 4	2.1 (CH10_HUMAN) 0 5.7 0 5.7 0 5.7 0 5.7 0 1.9 0 1.9 0 1.9 1 (LYSC_HUMAN) 0 20.4 0 20.	2.1 5.7 5.7 5.7 1.9 1.9 20.4 20.4 20.4 20.4 20.4 20.4 20.4 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 81.8 81.8 81.8 81.8 81.8 81.8 81.8 81	shock prote 2 0 2 0 2 0 1.7 1.7 0.2 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2 0 2	in, mitocho 99.0 98.0 98.0 98.0 38.0 33.2.1.17) 99.0 99.0 99.0 99.0 99.0 94.0 94.0 90.0 83.0 94.0 90.0 84.0 90.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo sag ATNYNAGDRSTDYGIFGINSR GISLANWMCLAK QYVQGCGV VVKDPOGIR STDYGIFGINSR STDYGIFGINSR STDYGIFGINSR STDYGIFGINSR WESGYNTR VWCNDGK LGMDGYR DVRCYVOGCGV AWVAWR RAWVAWR RLGMDGYR VVRDPOGIR GISLANWMCLAK GISLANWMCLAK GROUP (10 kD	(Early-pregnance 1034.6 1528.8 906.5 1528.8 1628.8 1628.8 1628.7 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 810.4 1279.6 787.4 959.4 966.5 1038.6 1305.7	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 11012.4 942.4 811.4 1280.6 788.4 960.4 967.5 1039.6 1306.7	omo sapiens (H 1034 6 1528 8 906.5 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.6 996.5 1038.6 1305.7	uman) 1035.6 1529.8 107.5 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1012.4 942.4 811.4 1280.6 788.4 960.5 967.5 1039.6 1306.7
P61604 221.0 221.0 221.0 221.0 374.4 374.2 41.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0	2.1 (CH10_HUMAN) 0 5.7 0 5.7 0 5.7 0 5.7 0 1.9 0 1.9 1 [LYSC_HUMAN] 0 20.4	2.1 5.7 5.7 5.7 1.9 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 28.5 28.5 81.8 81.8 81.8 81.8 81.8 81.8 81.8 8	shock prote 20 20 1.7 1.7 1.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	in, mitocho 99.0 98.0 98.0 38.0 32.1.17) 99.0 99.0 99.0 99.0 99.0 99.0 99.0 91.0 91	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR FLPLEDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo say ATNYNAGDRSTDYGIFQINSR GISLANWMCLAK OYVOGCGV RVWRDPGGIR STDYGIFQINSR STDYGIFQINSR STDYGIFQINSR WESGYNTR YWCNDGK LGMDCYR DVROYVOGCGV AWVAWR RAWVAWR RAWVAWR RAWVAWR RAWWAWR RAWWAWR RAWWAWR GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK	(Early-pregnance 1034.6 1528.8 906.5 1528.8 906.5 906.5 1528.8 10 12362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.4 959.4 966.5 1038.6	y factor) (EPF) - Hi 1035 6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.4 967.5 1039.6	pmo sapiens (H 1034 6 1034 6 906.5 906.5 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.4 959.5 966.5	uman) 1035 6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.5 967.5
P61604 211. 221.0 221.0 221.0 374.4 374.4 41.0 41.0 41.0 41.0 41.0 41.0 41.0 4	2.1 (CH10_HUMAN) 0 5.7 0 5.7 0 5.7 0 5.7 1.9 1 1.9 1 [LYSC_HUMAN] 0 20.4	2.1 5.7 5.7 5.7 1.9 20.4 20.4 20.4 20.4 20.4 20.4 20.4 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 81.8 81.8 81.8 81.8 81.8 81.8 81.8 81	shock prote 2 0 1.7 1.7 1.7 1.7 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	in, mitochoi 99.0 98.0 98.0 98.0 98.0 98.0 99.0 99.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo sag ATNYNAGDRSTDYGIFGINSR GISLANWMCLAK QYVGGCGV VVKDPGGIR STDYGIFGINSR STDYGIFGINSR STDYGIFGINSR WESGYNTR VWCNDGK LGMDGYR DVRQYVGCCGV AWVAWR RAWVAWR RAWVAWR RLGMDGYR VKDPDGIR GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK	(Early-pregnance 1034.6 1528.8 906.5 1908.5 1908.5 1908.5 1908.5 1908.7 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 810.4 1279.6 787.4 966.5 1038.6 1305.7 1362.7 1362.7 1362.7 1362.7 1363.7	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.4 967.5 1039.6 1306.7 1363.7 1363.7	pmo sapiens (H 1034 6 1528 8 906 5 906.5 1528.8 2362.1 1378.7 909.4 11194.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.4 956.5 1038.6 1305.7 1362.7	uman) 1035.6 1529.8 907.5 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.5 967.5 1039.6 1306.7 1363.7
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P61604 211. 221.1	2.1 (CH10_HUMAN) 0	2.1 5.7 5.7 5.7 1.9 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 26.5 26.5	shock prote 20	in, mitochoi 99.0 98.0 98.0 98.0 98.0 98.0 98.0 98.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLFDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo sag ATNYNAGDRSTDYGIFGINSR GISLANWMCLAK QYVQGCGV RVWRDPDGIR STDYGIFGINSR STDYGIFGINSR STDYGIFGINSR WESGYNTR VWCNDGK LGMBCYR DVRQYVQGCGV AWVAWR RAWVAWR RAWVAWR RAWWAWR RLGMDGYR VVRDPDGIR GISLANWMCLAK GISLANGROUND STDYGIFGINSR WESGYNTR WESGYNTR	(Early-pregnance) 1034.6 1528.8 906.5 1528.8 10ens (Human) 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.4 959.4 966.5 1038.6 1305.7 1362.7 1361.7 911.4 1399.7 1362.7 1361.7 911.4 1399.7 1362.7 1023.4 1012.4	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.4 967.5 1039.6 1306.7 1363.7 1362.7 912.4 911.4 1400.7 1383.7 1024.4 1410.7	omo sapiens (H 1034 6 1528 8 906.5 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.4 959.5 966.5 1038.6 1305.7 1362.7 1363.7 1361.7 911.4 999.4 1399.7 1363.7 1012.4	uman) 1035,6 1529,8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1012.4 942.4 811.4 1280.6 788.4 960.5 967.5 1039.6 1306.7 1363.7 1364.7 1362.7 912.4 1400.7 1363.7
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P61604 211. 221.1	2.1 (CH10_HUMAN) 0	2.1 5.7 5.7 5.7 5.7 1.9 20.4	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 26.5 26.5	shock prote 20	in, mitochoi 99.0 98.0 98.0 98.0 98.0 98.0 98.0 99.0 99	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo sag ATNYNAGDRSTDYGIFOINSR GISLANWMCLAK QYVGCGV VVXPDPGIR STDYGIFOINSR STDYGIFOINSR STDYGIFOINSR WESGYNTR WCNDGK LGMDCYR DVRQYVQCGCV AWVAWR RAWVAWR RAWVAWR RLGMDGYR VVRDPQGIR GISLANWMCLAK GISLANWCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWCLAK GISLANWMCLAK GISLANWMCLAK	(Early-pregnance) 1034-6 1528-8 1528-8 1528-8 1528-8 1528-8 1528-8 1528-8 1528-8 1528-8 1528-8 1528-8 1528-8 1528-8 1528-1528-1528-1528-1528-1528-1528-1528-	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.4 967.5 1039.6 1306.7 1363.7 1363.7 1364.7 1362.7 912.4 911.4 1400.7 1383.7 1024.4 1013.4 1016.5 2363.1 1363.7 1101.4	pmo sapiens (H 1034 6 1528 8 906.5 1528.8 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 810.4 1279.6 787.4 1279.6 787.4 1279.6 787.4 1279.6 1305.7 1362.7 1362.7 1362.7 1362.7 1362.7 1362.7 1362.7 1011.4 909.4 1399.7 1362.7 1021.4 1011.4 2362.1 1362.7 909.4	uman) 1035,6 1529,8 907.5 907.5 1529.8 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1012.4 942.4 811.4 1280.6 788.4 960.5 967.5 1039.6 1306.7 1363.7 1364.7 1362.7 910.4 1400.7 1383.7 1024.4 1012.4 910.4 1400.7 1383.7 1024.4 1012.4 1012.4 1012.4 1013.4 1012.4 1013.4 1012.4 1013.4 1012.4 1013.4 1014.5
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P61604 2211. 2211. 374.4 374.4 P61626 41.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0	20 2.1 (CH10_HUMAN) 0 5.7 0 5.7 0 5.7 0 5.7 1.9 1.9 1.9 1.9 1.9 20.4 0 2	2.1 5.7 5.7 5.7 1.9 20.4 20.5 20.6	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 26.5 26.5	shock prote 20	in, mitochoi 99.0 98.0 98.0 98.0 98.0 34.0 34.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 9	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo saj ATNYNAGDRSTDYGIFOINSR GISLANWMCLAK QYVOGCGY STDYGIFOINSR STDYGIFOINSR STDYGIFOINSR WESGYNTR YWCNDGK LGMDGYR DVRQYVOGCGV AWVAWR RLGMDGYR VWRDPOGIR GISLANWMCLAK GYVOGCGV YVYOGCGV STDYGIFOINSR WESGYNTR W	(Early-pregnance 1034.6 1528.8 1065.2 18.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5 1528.8 106.5	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.4 967.5 1039.6 1306.7 1363.7 1364.7 1362.7 912.4 911.4 1010.5 1039.6 1013.4 1016.5 2363.1 1103.4 1016.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 2363.7 910.4 1010.5 1039.6 1039.6 1039.6 1039.7 1040.7 1040.7 1050.	omo sapiens (H 1034,6 1528,8 906,5 906,5 1528,8 2362,1 1378,7 909,4 1194,7 1400,7 1503,7 1011,4 810,4	uman) 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.5 967.5 1039.6 1306.7 1363.7 1364.7 1362.7 910.4 4 1013.4 1014.7 104.4 105.7 104.4 105.7 106.7 10
P61604 211. 221.1 221.1 221.1 221.1 374.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0 4	2.1 (CH10_HUMAN) 0 5.7 0 5.7 0 5.7 0 5.7 1.9 1.9 1.9 1.9 1.9 1.9 1.9 20.4 0 20.	2.1 5.7 5.7 5.7 5.7 1.9 20.4 20.5 20.6	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 26.5 26.5	shock prote 20 20 20 1.7 1.2 20 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.	in, mitochoi 99.0 98.0 98.0 98.0 98.0 98.0 98.0 98.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo sag ATNYNAGDRSTDYGIFQINSR GISLANWMCLAK QYVQGCGV KYWRDPOGIR STDYGIFQINSR STDYGIFQINSR STDYGIFQINSR WESGYNTR WCNDGK LGMDGYR DVRCYVQGCGV AWWAWR RAWWAWR RAWWAWR RIGISLANWMCLAK GISLANWMCLAK GISLANWCLAK GISLANWMCLAK GISLANWCLAK GISLANWCLAK GISLANWMCLAK GISLANWCLAK GISLANWCLAK GISLANWCLAK GISLANWCLAK G	(Early-pregnance) 1034-6 1034-6 1034-6 1034-6 1034-6 1034-6 1034-6 1034-6 1034-6 1034-6 1034-7 1034-	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 10112.4 942.4 811.4 1280.6 788.4 960.4 967.5 1039.6 1306.7 1363.7 1364.7 1362.7 912.4 911.4 1400.7 1383.7 1024.4 1013.4 1016.5 2363.1 1363.7 1024.4 1010.5 1039.6 788.4 1013.4 1010.5 1039.6 788.4 1504.7 1504.7 1504.7 1504.7 1504.7 1507.8 1039.6	pmo sapiens (H 1034 6 1528 8 906.5 1528.8 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 941.4 810.4 1279.6 787.4 1050.5 7 1362.7 1363.7 1011.4 909.4 1399.7 1309.7 1023.4 1011.4 909.4 1399.7 1023.4 1011.4 1038.6 790.9 4 1399.7 1023.4 1011.4 1038.6 7 1050.7 1050	uman) 1035,6 1036,6 1036,6 1036,6 1036,6 1036,6 107,5 107,5 107,5 107,5 107,5 107,7 107,4 1195,7 1401,7 107,4 1195,7 1401,7 107,4 1280,6 1306,7 1363,7 1364,7 1364,7 1362,7 1364,7 1363,7 1364,7 1363,7 1364,7 1363,7 1364,7 1363,7 1024,4 1012,4 1012,4 1012,4 1012,4 1012,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,4 1012,4 1013,
P61604 2211. 2211. 2211. 374.4 P61626 41.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0	2.1 (CH10_HUMAN) 0 5.7 0 5.7 0 5.7 0 5.7 1.9 1.9 1.9 1.9 1.9 1.9 1.9 20.4 0 20.	2.1 5.7 5.7 5.7 1.9 20.4 20.5 20.6	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 26.5 26.5	shock prote 20	in, mitochoi 99.0 98.0 98.0 98.0 34.0 34.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0 9	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDYFLFR (1,4-beta-N-acetylmuramidase C) - Homo saj ATNYNAGDRSTDYGIFOINSR GISLANWMCLAK QYVOGCGY STDYGIFOINSR STDYGIFOINSR STDYGIFOINSR WESGYNTR YWCNDGK LGMDGYR DVRQYVOGCGV AWVAWR RLGMDGYR VWRDPOGIR GISLANWMCLAK GYVOGCGY OYVOGCGY STDYGIFOINSR WESGYNTR STDYGIFOINSR WESGYNTR WYRDPOGIR WWAWWR STDYGIFOINSR GISLANWMCLAK GISLANW	(Early-pregnance 1034.6 1528.8 106.5 1528.8	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 10112.4 942.4 811.4 1280.6 788.4 960.4 967.5 1039.6 1306.7 1363.7 1364.7 1362.7 1364.7 1362.7 1362.7 1363.7 101.4 1010.5 2363.1 1300.7 1383.7 1024.4 1010.5 2363.1 1300.7 1383.7 1024.4 1010.5 2363.1 1300.7 1383.7 910.4 1400.7 1010.5 2363.1 1364.7 910.4 1504.7 967.5 2364.1 1379.7 1364.7 1367.7 1368.7 910.4 1504.7 967.5 2364.1 1379.7 1364.7 1369.7 1361.7	pmo sapiens (H 1034,6 1528,8 906,5 1528,8 906,5 1528,8 2362,1 1378,7 909,4 1194,7 1400,7 1503,7 1011,4 910,4 1279,6 787,4 959,5 966,5 1038,6 1036,7 1361,7 1361,7 1362,7 1382,7 1011,4 1011,4 1038,6 1339,7 1382,7 1011,4 1011,4 1038,6 1339,7 1382,7 1011,4 1038,6 1339,7 1382,7 1023,4 1011,4 1038,6 1339,7 1382,7 1023,4 1011,4 1038,6 1339,7 1382,7 1023,4 1011,4 1038,6 1339,7 1382,7 1023,4 1011,4 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1038,6 1339,7 1382,7 1	uman) 1035.6 1529.8 907.5 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.5 967.5 1039.6 1309.7 1364.7 1362.7 1364.7 1362.7 1364.7 1362.7 1364.7 1362.7 1364.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1024.4 1013.
P61604 211. 221.1 221.1 374.0 21.1 374.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0 4	2.1 CICH10_HUMAN 0	2.1 5.7 5.7 5.7 5.7 1.9 20.4 20.6 12.6 13.6 16.3	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 26.5 26.5	shock prote 20	in, mitocho 99 0 98 0 98 0 98 0 98 0 98 0 99 0 99 0 99 0 99 0 99 0 99 0 90 0 83 0 94 0 91 0 92 0 93 0 94 0 95 0 97 0 99 0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDYFLFR FLPLEDR STDVGIFOINSR STDVGIFOINSR STDVGIFOINSR STDVGIFOINSR WESGYNTR VWCNDGK LGMDGYR DVROVVGCGV AWVAWR RAWVAWR RLGMDGYR VVRDPOGIR GISLANWMCLAK GIS	(Early-pregnance) 1034.6 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.8 1006.5 1528.6 1528.	y factor) (EPF) - Hi 1035 6 1035 6 1035 7 1035 7 1037 7 1037 7 1037 7 1037 7 1037 7 1040 7 1050 7 1060 7 1060 7 1060 7 107 107 107 107 107 107 107 107 107 107	pmo sapiens (H 1034 6 1528 8 906.5 1528.8 906.5 1528.8 2362.1 1378.7 909.4 11194.7 1400.7 1503.7 1011.4 810.4 1279.6 787.4 956.5 1038.6 7 1362.7 1362.7 1362.7 1363.7 1361.7 111.4 1038.6 787.4 1011.4 1038.6 787.4 1011.4	uman) 1035.6 1035.6 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1012.4 942.4 811.4 1280.6 788.4 942.4 811.4 1280.6 788.4 1280.6 788.4 1280.6 790.5 1306.7 1363.7 1364.7 1363.7 1364.7 1012.4 1013.7 104.7 105.7 105.7 105.7 105.7 105.7 105.7 105.7 105.7 105.7 105.7 105.7 105.7 105.7 105.7 1195.7
P61604 211. 221.1 221.1 374.0 211.1 374.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0 4	2.1 CICH10_HUMAN 0	2.1 5.7 5.7 5.7 5.7 5.7 1.9 20.4 20.6 12.6 13.6 16.3 1	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 26.5 26.5	shock prote 20	in, mitochoi 99.0 98.0 98.0 98.0 98.0 99.0 99.0 99.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR FLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDYFLFR FLPLEDR FLPLEDR VVLDDKDF FLPLEDR FLETT FL	(Early-pregnance) 1034.6 1528.8 1066.5 1528.8 1066.5 1528.8 1066.5 1528.8 1066.5 1528.8 1066.5 1528.8 1066.5 1528.8 1066.5 1528.8 1066.5 1528.8 1066.5 1528.8 1066.5 1528.6 1528.	y factor) (EPF) - Hi 1035 6 1035 6 1035 7 1035 7 1037 7 1037 7 1037 7 1037 7 1037 7 1040 7 1050 7 1060 7 10	pmo sapiens (H 1034 6 1528 8 906.5 1528 8 906.5 1528.8 2362.1 1378.7 909.4 1194.7 1400.7 1503.7 1011.4 810.4 1279.6 6.5 1038.6 7 1362.7 1362.7 1362.7 1362.7 1363.7 1011.4 1038.6 7 1362.7 1363.7 1361.7 911.4 1038.6 7 1362.7 1362.7 1362.7 1362.7 1362.7 1363.7 1361.7 911.4 1038.6 7 1362.7 1362.7 1363.7 1364.7 1378.7 1363.7 1364.7 1378.7 1382.7 1023.4 1012.4 1013.6 1023.4 1023.4 10	uman) 1035.6 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 960.5 967.5 1039.6 1306.7 1363.7 1364.7 1363.7 1012.4 1400.7 1383.7 1012.4 1013
P61604 211.0 221.1 221.1 374.4 P61626 41.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0	2.1 (CH10_HUMAN) 0 5.7 0 5.7 0 5.7 0 5.7 0 5.7 1.9 1.9 1.9 1.19 20.4 0 20.6 0 12.6 0 1	2.1 5.7 5.7 5.7 1.9 20.4 20.5 12.6	29.7 10 kDa heat 26.5 26.5 26.5 26.5 26.5 26.5 26.5 26.5	shock prote 20	in, mitochoi 99.0 98.0 98.0 98.0 98.0 98.0 99.0 99.0	ndrial (Hsp10) (10 kDa chaperonin) (CPN10) KFLPLEDR VVLDDKDYFLER FLPLEDR FLPLEDR VLDDKDYFLER (1,4-beta-N-acetylmuramidase C) - Homo saj ATMYNACDRSTDYGIFQINSR GISLANWMCLAK QYVQGCGV RVWRDPQGIR STDYGIFQINSR STDYGIFQINSR WESGYNTR WCNDGK LGMDCYR DVRQYVQGCGV AWVAWR RAWWAWR RLGMDGYR VVRDPQGIR GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GISLANWMCLAK GYVQGCGV GYVQGCGV STDYGIFQINSR WESGYNTR WRDPQGIR WINDPQGIR WESGYNTR	(Early-pregnance) 1034.6 1528.8 1065.5 1528.8 1065.5 1528.8 1065.1 1528.8 1065.1 1528.8 1065.1 1528.8 1065.1 1528.8 1065.1 1528.8 1065.1 1528.8 1065.1 1528.8 1065.1 1528.8 1065.1 1528.8 1065.1 1528.8 1065.1 1528.	y factor) (EPF) - Hi 1035 6 1529 8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1012.4 811.4 1280.6 788.4 960.4 967.5 1039.6 1306.7 1364.7 1362.7 912.4 911.4 101.6 1383.7 1364.7 1362.7 912.4 911.4 101.5 2363.1 137.7 1383.7 1364.7 1362.7 912.4 917.4 1017.7 1383.7 1364.7 1362.7 917.4 1017.7 1383.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1365.7 1365.7 1365.7 1365.7 1365.7 1400.7 1010.5 1039.6 788.4 11379.7 1364.7 1401.7 1583.7 910.4 1504.7 967.5 1384.7 1401.7 1583.7 910.4 1597.7 1401.7 1583.7 910.4 1597.7 1401.7 1583.7 910.4 1597.7 1364.7 1401.7 1583.7 1400.7 1012.5 1024.5 102	pmo sapiens (H 1034,6 1528,8 906,5 1528,8 906,5 1528,8 152	uman) 1035.6 1529.8 907.5 907.5 1529.8 2363.1 1379.7 910.4 1195.7 1401.7 1504.7 1012.4 942.4 811.4 1280.6 788.4 900.5 967.5 1039.6 1306.7 1364.7 1362.7 912.4 910.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1012.4 1013.7 1363.7 1364.7 1364.7 1363.7 1364.7 1363.7 1364.7 1364.7 1363.7 1364.7 1364.7 1364.7 1365.7 1364.7 1364.7 1365.7 1364.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7 1364.7 1365.7

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	STDYGIFQINSR	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 B3	2MG_HUMAN 11.7	11.7	Beta-2-micro	oglobulin p	recursor [Co	ntains: Beta-2-microglobulin variant pl 5 IEKVEHSDLSFSK	5.3] - Homo sapiens (F 1517.8	Human) 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	VNHVTLSQPK	1121.6	1122.6	1121.6	1122.6
94.0	11.7	11.7	49.6	2.0	99.0	YTEFTPTEKDEYACR	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		99.0	VNHVTLSQPK	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	VNHVTLSQPK	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	99.00	IEKVEHSDLSFSK	1517.8	1518.8	1517.8	1518.8
69.0	10.4	10.4	37.8	2.0	99.00	IQVYSR	764.4	765.4	764.4	765.4
69.0	10.4	10.4	37.8		99.00	IQVYSRHPAENGK	1498.8	1499.8	1498.8	1499.8
69.0	10.4	10.4	37.8	2.0	99.00	IVKWDRDM	1061.5	1062.5	1061.5	1062.5
69.0	10.4	10.4	37.8	2.0	99.00	VNHVTLSQPK	1121.6	1122.6	1121.6	1122.6
69.0	10.4	10.4	37.8	0.4	60.00	IVKWDR	815.5	816.5	815.5	816.5
69.0	10.4	10.4	37.8	0.0	97.00	IQVYSRHPAENGK	1497.8	1498.8	1497.8	1498.8
69.0	10.4	10.4	37.8	0.0	99.00	VNHVTLSQPK	1122.6	1123.6	1121.6	1122.6
69.0	10.4	10.4	37.8	0.0	99.00	VNHVTLSQPK	1104.6	1105.6	1104.6	1105.6
P61916 N 536.0	NPC2_HUMAN 2.0	2.0	Epididymal s 10.6	secretory p 2.0	orotein E1 pre	ecursor (Niemann-Pick disease type C2 p EVNVSPCPTQPCQLSK	rotein) (hE1) - Homo 1842.9	sapiens (Humai 1843.9	n) 1842.9	1843.9
386.0	1.7	1.7	10.6	1.7	98.0	EVNVSPCPTQPCQLSK	1842.9	1843.9	1842.9	1843.9
237.0	ALM_HUMAN 5.2	5.2	Calmodulin (36.9	CaM) - Hoi 2.0	mo sapiens (99.0	Human) ADQLTEEQIAEFK	1562.7	1563.7	1562.7	1563.8
237.0	5.2	5.2	36.9	2.0	99.0	EADIDGDGQVNYEEFVQMMTAK	2489.1	2490.1	2489.1	2490.1
237.0	5.2	5.2	36.9	1.2	94.0	HVMTNLGEKLTDEEVDEMIR	2400.2	2401.2	2400.2	2401.2
254.0	2.2	2.2	19.5	2.0	99.0	ADQLTEEQIAEFK	1562.7	1563.8	1562.7	1563.8
254.0 P62241 R	S8_HUMAN	2.2	19.5 40S ribosom	0.2 al protein :	38.0 S8 - Homo sa	VFDKDGNGYISAAELR piens (Human)	1754.9	1755.9	1754.8	1755.9
106.0	10.1	10.1	52.4	2.0	99.0	ADGYVLEGKELEFYLR	1901.0 968.5	1902.0	1901.0 968.5	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	IIDVVYNASNNELVR	1717.9	1718.9	1717.9	1718.9
106.0	10.1	10.1	52.4	2.0	99.0	ISSLLEEQFQQGK	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	OWYESHYALPLGR	1618.8	1619.8	1618.8	1619.8
169.0	4.1	4.1	52.9	2.0	99.0	ADGYVLEGKELEFYLR	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 R	S15A_HUMAN		40S ribosom	al protein :	S15a - Homo	sapiens (Human)				
296.0	4.0	4.0	21.5	2.0	99.0	HGYIGEFEIIDDHR	1699.8	1700.8	1699.8	1700.8
296.0	4.0	4.0	21.5	2.0	99.0	IVVNLTGR	870.5	871.5	870.5	871.5
387.0	1.7	1.7	16.9	0.9	87.0	HGYIGEFEIIDDHR	1699.8	1700.8	1699.8	1700.8
387.0	1.7	1.7	16.9		84.0	IVVNLTGR	870.5	871.5	870.5	871.5
P62249 R	S16_HUMAN		40S ribosom	al protein :	S16 - Homo 9	apiens (Human)				
159.0	7.4	7.4	47.3	2.0	99.0	GGGHVAQIYAIR	1240.7	1241.7	1240.7	1241.7
159.0	7.4	7.4	47.3	2.0	99.0	LLEPVLLLGK	1093.7	1094.7	1093.7	1094.7
159.0	7.4	7.4	47.3	2.0	99.0	PSKGPLQSVQVFGR	1498.8	1499.8	1498.8	1499.8
159.0	7.4	7.4	47.3	0.8	85.0	EIKDILIQYDR	1404.8	1405.8	1404.8	1405.8
159.0	7.4	7.4	47.3	0.6	75.0	VKGGGHVAQIYAIR	1467.8	1468.8	1467.8	1468.8
106.0	3.3	3.3	35.6	2.0	99.0	PSKGPLQSVQVFGR	1498.8	1499.8	1498.8	1499.8
106.0	3.3	3.3	35.6	1.2	94.0	EIKDILIQYDR	1404.8	1405.8	1404.8	1405.8
68.0	10.9	10.9	52.1	2.0	99.0	EIKDILIQYDR	1404.8	1405.8	1404.8	1405.8
68.0	10.9	10.9	52.1	2.0	99.0	GGGHVAQIYAIR	1240.7	1241.7	1240.7	1241.7
68.0	10.9	10.9	52.1	2.0	99.0	PSKGPLQSVQVFGR	1498.8	1499.8	1498.8	1499.8
68.0	10.9	10.9	52.1	2.0	99.0	VKGGGHVAQIYAIR	1467.8	1468.8	1467.8	1468.8
68.0	10.9	10.9	52.1	1.5	97.0	FAGVDIR	776.4	777.4	776.4	777.4
68.0	10.9	10.9	52.1	1.3	95.0	ALVAYYQK	954.5	955.5	954.5	955.5
P62258 14 109.0	433E_HUMAN 10.0	12.0	14-3-3 prote 37.3	in epsilon 2.0	(14-3-3E) - F 99.0	Homo sapiens (Human) IISSIEQKEENKGGEDKLK	2144.1	2145.1	2144.1	2145.1
109.0	10.0	12.0	37.3	2.0	99.0	LAEQAERYDEMVESMKK	2056.0	2057.0	2056.0	2057.0
109.0	10.0	12.0	37.3	2.0	99.0	MDDREDLVYQAK	1523.7	1524.7	1523.7	1524.7
109.0	10.0	12.0	37.3	2.0	99.0	YLAEFATGNDRK	1383.7	1384.7	1383.7	1384.7
109.0	10.0	12.0	37.3	2.0	99.0	YLAEFATGNDRKEAAENSLVAYK	2559.2	2560.3	2559.3	2560.3
109.0	10.0	12.0	37.3	0.0	99.0	DSTLIMOLLR	1188.7	1189.7	1188.7	1189.7
256.0	2.2	3.5	18.8	2.0	99.0	MDDREDLVYQAK	1523.7	1524.7	1523.7	1524.7
256.0	2.2	3.5	18.8	0.2	36.0	YLAEFATGNDRK	1383.7	1384.7	1383.7	1384.7
256.0	2.2	3.5	18.8	0.0	94.0	DSTLIMQLLR	1188.7	1189.7	1188.7	1189.7
P62269 R9	S18_HUMAN 7.2	7.2	40S ribosom 34.9	al protein : 2.0	S18 (Ke-3) (I 99.0	(e3) - Homo sapiens (Human) IPDWFLNR	1059.5	1060.5	1059.6	1060.6
164.0	7.2	7.2	34.9	2.0	99.0	SLVIPEKFQHILR	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	YAHVVLRK	984.6	985.6	984.6	985.6
164.0	7.2	7.2	34.9	0.4	59.0	YAHVVLR	856.5	857.5	856.5	857.5
164.0	7.2	7.2	34.9		46.0	HFWGLR	814.4	815.4	814.4	815.4
164.0	7.2	7.2	34.9	0.0	70.0	VITIMONPR	1070.6	1071.6	1070.6	1071.6
164.0	7.2	7.2	34.9	0.0	45.0	VITIMONPR	1232.6	1233.6	1232.6	1233.7
135.0	5.9	5.9	37.5	2.0	99.0	IPDWFLNR	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	SLVIPEKFQHILR	1620.9	1621.9	1620.9	1621.9
135.0	5.9	5.9	37.5	0.3	50.0	HFWGLR	814.4	815.4	814.4	815.4
135.0 P622731R	5.9 S29_HUMAN	5.9	37.5 40S ribosom	0.2 al protein :	37.0 S29 - Homo s	YAHVVLR sapiens (Human)	856.5	857.5	856.5	857.5
379.0	2.6	2.6	33.9	2.0	99.0	GHQQLYWSHPR	1407.7	1408.7	1407.7	1408.7
379.0	2.6	2.6	33.9	0.6	73.0	YGLNMCR	912.4	913.4	912.4	913.4
379.0	2.6	2.6	33.9	0.0	99.0	GHQQLYWSHPR	1407.7	1408.7	1407.7	1408.7
240.0	2.4	2.4	33.9	2.0	99.0	GHQQLYWSHPR	1407.7	1408.7	1407.7	1408.7
240.0		2.4	33.9	0.3	49.0	YGLNMCR	912.4	913.4	912.4	913.4
240.0	2.4	2.4	33.9	0.0	99.0	GHQQLYWSHPR	1407.7	1408.7	1407.7	1408.7
P62280 R:	S11_HUMAN	12.8	40S ribosom	al protein :	S11 - Bos tau	Irus (Bovine); 40S ribosomal protein S1°	1 - Rattus norvegicus	(Rat) ; 40S ribo	somal protein S1	1 - Mus musculu
82.0	12.8		39.2	2.0	99.0	AYQKQPTIFQNK	1464.8	1465.8	1464.8	1465.8
82.0	12.8	12.8	39.2	2.0	99.0	AYOKOPTIFONKKR	1749.0	1750.0	1749.0	1750.0
82.0	12.8	12.8	39.2	2.0		DYLHYIR	978.5	979.5	978.5	979.5
82.0	12.8	12.8	39.2	2.0	99.0 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	VLLGETGKEKLPR	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	CPFTGNVSIR	1132.5	1133.5	1132.5	1133.5
116.0	6.6	6.6	34.2	2.0	99.0	CPFTGNVSIR	1132.5	1133.5	1132.6	1133.6
116.0	6.6	6.6	34.2	2.0	99.0	DYLHYIR	978.5	979.5	978.5	979.5
116.0	6.6	6.6	34.2		99.0	NMSVHLSPCFR	1346.6	1347.6	1346.6	1347.6
116.0	6.6	6.6	34.2	0.6	74.0	AYQKQPTIFQNK	1464.8	1465.8	1464.8	1465.8
72.0	4.9	4.9	25.3	2.0	99.0	DYLHYIR	978.5	979.5	978.5	979.5
72.0	4.9	4.9	25.3	1.7	98.0	AYQKQPTIFQNK	1464.8	1465.8	1464.8	1465.8
72.0	4.9	4.9	25.3	1.2	93.0	CPFTGNVSIR	1132.5	1133.6	1132.5	1133.5
311.0	SM3_HUMAN 4.0	4.0	28.4	2.0	99.0	in LSm3 - Homo sapiens (Human) ADDVDQQQTTNTVEEPLDLIR	2441.2	2442.2	2441.2	2442.2
311.0	4.0	4.0	28.4	2.0	99.00	NIPMLFVR	988.6	989.6	988.6	989.6
361.0	2.0	2.0	7.8		99.00	NIPMLFVR	988.5	989.6	988.6	989.6
P62318 SI	MD3_HUMAN		Small nuclea	r ribonucle	eoprotein Sm	D3 (snRNP core protein D3) (Sm-D3) - H	Homo sapiens (Human	1)		
207.0	6.0	6.0	38.9	2.0	99.0	FLILPDMLK	1088.6	1089.6	1088.6	1089.6
207.0	6.0	6.0	38.9		99.0	LIEAEDNMNCQMSNITVTYR	2401.1	2402.1	2401.1	2402.1
207.0	6.0	6.0	38.9	2.0	99.0	VAQLEQVYIR	1217.7	1218.7	1217.7	1218.7
333.0	2.0	2.0	19.8	2.0	99.0	VAQLEQVYIR	1217.7	1218.7	1217.7	1218.7
	YB4_HUMAN 24.5	24.5	Thymosin be			ontains: Hematopoietic system regulator KTETQEKNPLPSKETIEQEK			ens (Human) 2356.2	2357.2
27.0	24.0	24.0	71.1	2.0	77.U	KILIGERINI EI GRETTEGER	2350.2	2001.2	2330.2	2337.2

						V				
29.0	24.5	24.5	97.7	2.0	99.0	KTETQEKNPLPSKETIEQEKQAGES	2828.4	2829.4	2828.4	2829.4
29.0	24.5	24.5	97.7		99.0	LKKTETQEKNPLPSKETIEQEK	2597.4	2598.4	2597.4	2598.4
29.0	24.5	24.5	97.7	2.0	99.0	LKKTETQEKNPLPSKETIEQEKQAGES	3069.6	3070.6	3069.6	3070.6
29.0	24.5	24.5	97.7	2.0	99.0	NPLPSKETIEQEK	1511.8	1512.8	1511.8	1512.8
29.0	24.5	24.5	97.7	2.0	99.0	NPLPSKETIEQEKQAGES	1984.0	1985.0	1984.0	1985.0
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAEIEKFDK	1693.8	1694.8	1693.8	1694.8
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAEIEKFDKSK	1908.9	1909.9	1908.9	1909.9
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAEIEKFDKSKLK	2150.1	2151.1	2150.1	2151.1
29.0	24.5	24.5	97.7	2.0	99.0	SDKPDMAEIEKFDKSKLKK	2278.2	2279.2	2278.2	2279.2
29.0	24.5	24.5	97.7	2.0	99.0	TETQEKNPLPSKETIEQEK	2228.1	2229.1	2228.1	2229.1
29.0	24.5	24.5	97.7	2.0	99.0	TETQEKNPLPSKETIEQEKQAGES	2700.3	2701.3	2700.3	2701.3
29.0	24.5	24.5	97.7	0.5	67.0	SDKPDMAEIEK	1303.6	1304.6	1303.6	1304.6
29.0	24.5	24.5	97.7	0.0	91.0	LKKTETQEKNPLPSKETIEQEKQAGES	3069.6	3070.6	3069.6	3070.6
28.0	21.1	21.1	97.7	2.0	99.0	KTETQEKNPLPSKETIEQEK	2356.3	2357.3	2356.2	2357.2
28.0	21.1	21.1	97.7	2.0	99.0	KTETQEKNPLPSKETIEQEKQAGES	2828.4	2829.4	2828.4	2829.4
28.0	21.1	21.1	97.7	2.0	99.0	LKKTETQEKNPLPSKETIEQEK	2597.4	2598.4	2597.4	2598.4
28.0	21.1	21.1	97.7	2.0	99.0	NPLPSKETIEQEKQAGES	1984.0	1985.0	1984.0	1985.0
28.0	21.1	21.1	97.7	2.0	99.0	SDKPDMAEIEK	1303.6	1304.6	1303.6	1304.6
28.0	21.1	21.1	97.7 97.7	2.0	99.0 99.0	SDKPDMAEIEKFDK SDKPDMAEIEKFDKSK	1693.8 1908.9	1694.8 1909.9	1693.8 1908.9	1694.8 1909.9
28.0	21.1	21.1	97.7	2.0	99.0	SDKPDMAEIEKFDKSKLK	2150.1	2151.1	2150.1	2151.1
28.0	21.1	21.1	97.7		99.0	TETQEKNPLPSKETIEQEK	2228.1	2229.1	2228.1	2229.1
28.0 28.0	21.1	21.1 21.1	97.7 97.7	2.0	99.0 92.0	TETQEKNPLPSKETIEQEKQAGES LKKTETQEKNPLPSKETIEQEKQAGES	2700.3 3070.6	2701.3 3071.6	2700.3 3070.6	2701.3 3071.6
28.0	21.1 21.1 CNBP_HUMAN	21.1	97.7 97.7 Cellular nuc	0.0	40.0	TETQEKNPLPSKETIEQEK	2228.1	2229.1	2228.1	2229.1
353.0	3.2	3.2	43.5	2.0	99.0	EQCCYNCGKPGHLAR	1848.8	1849.8	1848.8	1849.8
353.0	3.2	3.2	43.5	1.2	94.0	CGESGHLAKDCDLQEDACYNCGR	2697.0	2698.0	2697.0	2698.0
179.0	2.0	2.0	16.5	2.0	99.0	EQCCYNCGKPGHLAR	1848.8	1849.8	1848.8	1849.8
93.0	RS4X_HUMAN 8.1	8.1	40S ribosom 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	FDTGNLCMVTGGANLGR	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 P627531	6.0 RS6_HUMAN	6.0	21.7 40S ribosom	2.0 nal protein S	99.0 6 (Phospho	GNKPWISLPR protein NP33) - Homo sapiens (Human)	1166.7	1167.7	1166.7	1167.7
192.0	6.0	6.0	27.3	2.0	99.0	ISGGNDKQGFPMKQGVLTHGR	2226.1	2227.1	2226.1	2227.1
192.0		6.0	27.3	2.0	99.0	MATEVAADALGEEWKGYVVR	2194.1	2195.1	2194.1	2195.1
192.0		6.0	27.3	2.0	99.0	MKLNISFPATGCOK	1593.8	1594.8	1593.8	1594.8
140.0		2.1	37.8	2.0	99.0	MATEVAADALGEEWKGYVVR	2194.1	2195.1	2194.1	2195.1
140.0 291.0		2.1 2.0	37.8 24.9	0.1	25.0 99.0	MKLNISFPATGCQK MATEVAADALGEEWKGYVVR	1593.8 2194.1	1594.8 2195.1	1593.8 2194.1	1594.8 2195.1
	H4_HUMAN 15.6	15.6	Histone H4 - 82.5				1324.7	1325.8	1324.7	1325.8
64.0	15.6	15.6	82.5	2.0	99.0	DNIQGITKPAIR DNIQGITKPAIRR ISGLIYEETR	1480.8	1481.9	1480.8	1481.9
64.0 64.0	15.6 15.6	15.6 15.6	82.5 82.5	2.0 2.0	99.0 99.0 99.0	ISGLIYEETRGVLK	1179.6 1576.9	1180.6 1577.9	1179.6 1576.9	1180.6 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		TVTAMDVVYALKR	1465.8	1466.8	1465.8	1466.8
64.0	15.6	15.6	82.5	2.0	99.0	VFLENVIR	988.6	989.6	988.6	989.6
64.0	15.6	15.6	82.5	1.3	95.0	TLYGFGG	713.3	714.3	713.3	714.3
64.0	15.6	15.6	82.5	0.2	37.0	DAVTYTEHAKR	1289.6	1290.6	1289.6	1290.6
64.0	15.6	15.6	82.5	0.1	28.0	RISGLIYEETR	1335.7	1336.7	1335.7	1336.7
64.0	15.6	15.6	82.5	0.0	80.0	DNIQGITKPAIRR	1480.9	1481.9	1480.8	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	1465.8	1466.8	1465.8	1466.8
46.0	6.6	6.6	70.9	0.6	73.0	KVLRDNIQGITKPAIRR	2005.2	2006.2	2005.2	2006.2
46.0	6.6	6.6	70.9	0.2	39.0	RISGLIYEETR	1335.7	1336.7	1335.7	1336.7
46.0	6.6	6.6	70.9	0.1	20.0	DNIQGITKPAIR	1324.8	1325.8	1324.7	1325.8
31.0		20.7	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 31.0	20.7 20.7	20.7	88.3 88.3	2.0	99.0 99.0	ISGLIYEETR KVLRDNIQGITKPAIR	1179.6 1849.1	1180.6 1850.1	1179.6 1849.1	1180.6 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	714.4	713.3	714.3
31.0	20.7	20.7	88.3	2.0	99.0	TVTAMDVVYALKR	1465.8	1466.8	1465.8	1466.8
31.0	20.7	20.7	88.3	2.0	99.0	VFLENVIR	988.6	989.6	988.6	989.6
31.0	20.7	20.7	88.3	1.5	97.0	DAVTYTEHAK	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 pro	Itein Ran (G	TPase Ran) - Bos taurus (Bovine) ; GTP-bii	nding nuclear prote	in Ran (GTPase	Ran) (Ras-like pr	otein TC4) (Andı
397.0	2.3	2.3	28.7	1.3	95.0	VCENIPIVLCGNKVDIKDRK	2369.3	2370.3	2369.3	2370.3
397.0	2.3	2.3	28.7	0.7	78.0	AAQGEPQVQFK	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	GPIKFNVWDTAGQEK	1688.8	1689.8	1688.9	1689.9
90.0	4.0	4.0	22.2	2.0	99.0	SNYNFEKPFLWLAR	1783.9	1784.9	1783.9	1784.9
147.0	5.0	5.0	20.4	2.0	99.0	KKNLQYYDISAK	1469.8	1470.8	1469.8	1470.8
147.0	5.0	5.0	20.4	1.7	98.0	SNYNFEKPFLWLAR	1783.9	1784.9	1783.9	1784.9
147.0	5.0	5.0	20.4	1.2	94.0	NVPNWHR	921.5	922.5	921.5	922.5
147.0	5.0 RS26_HUMAN	5.0	20.4	0.1 nal protein S	24.1	AAQGEPQVQFK sapiens (Human)	1243.6	1244.6	1243.6	1244.6
178.0	2.0	2.0 5.7	29.6 51.3	2.0	99.0 99.0	DISEASVFDAYVLPK DISEASVFDAYVLPK	1652.8 1652.8	1653.8 1653.8	1652.8 1652.8	1653.8 1653.8
222.0	5.7	5.7	51.3	2.0	99.0	LHYCVSCAIHSK	1473.7	1474.7	1473.7	1474.7
222.0		5.7	51.3	1.7	98.0	NIVEAAAVR	941.5	942.5	941.5	942.5
292.0	2.0	2.0	30.4	2.0	99.0	FRPAGAAPRPPPKPM	1588.9	1589.9	1588.9	1589.9
534.0	GBB1_HUMAN 2.0 2.0	2.0	Guanine nuc	2.0	99.0	G(I)/G(S)/G(T) subunit beta 1 (Transduci ELAGHTGYLSCCR	1522.7	1523.7	1522.7	1523.7
	PPIA_HUMAN	2.0				ELAGHTGYLSCCR A (EC 5.2.1.8) (PPI ase A) (Rotamase A) (C				
27.0	24.9	24.9	81.8	2.0	99.0	ALSTGEKGFGYK	1256.6	1257.6	1256.6	1257.6
27.0	24.9	24.9	81.8	2.0	99.0	ALSTGEKGFGYKGSCFHR	2000.9	2002.0	2001.0	2002.0
27.0	24.9	24.9	81.8	2.0	99.0	EGMNIVEAMER	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	GFGYKGSCFHR	1314.6	1315.6	1314.6	1315.6
27.0	24.9	24.9	81.8	2.0	99.0	HTGPGILSMANAGPNTNGSQFFICTAK	2791.3	2792.3	2791.3	2792.3
27.0	24.9	24.9	81.8	2.0	99.0	IIPGFMCQGGDFTR IIPGFMCQGGDFTRHNGTGGK	1597.7	1598.7	1597.7	1598.7
27.0	24.9	24.9	81.8	2.0	99.0		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	VKEGMNIVEAMER	1504.7	1505.7	1504.7	1505.7
27.0	24.9	24.9	81.8	2.0	99.0	VNPTVFFDIAVDGEPLGR	1945.0	1946.0	1945.0	1946.0
27.0	24.9	24.9	81.8		99.0	VSFELFADKVPK	1378.7	1379.8	1378.7	1379.8
27.0	24.9	24.9	81.8	0.9	87.0	KITIADCGQLE	1246.6	1247.6	1246.6	1247.6
27.0	24.9	24.9	81.8		99.0	GFGYKGSCFHR	1314.6	1315.6	1314.6	1315.6
27.0	24.9	24.9	81.8	0.0	83.0	GFGYKGSCFHR	1466.6	1467.6	1466.6	1467.6
27.0	24.9	24.9	81.8		99.0	SIYGEKFEDENFILK	1832.9	1833.9	1830.9	1831.9
27.0 27.0 27.0	24.9 24.9	24.9 24.9	81.8 81.8	0.0	99.0 99.0	VKEGMNIVEAMER VNPTVFFDIAVDGEPLGR	1506.8 1987.0	1507.8 1988.0	1504.7 1987.0	1505.7 1988.0
17.0 17.0	16.0 16.0	16.0 16.0	57.0 57.0	2.0 2.0	99.0 99.0 99.0	ALSTGEKGFGYK FEDENFILK	1256.6 1153.6	1988.0 1257.6 1154.6	1256.6 1153.6	1257.6 1154.6
17.0	16.0	16.0	57.0	2.0	99.0 99.0 99.0	GFGYKGSCFHR	1314.6	1315.6	1314.6	1315.6
17.0	16.0	16.0	57.0	2.0	99.0	IIPGFMCQGGDFTR	1597.7	1598.7	1597.7	1598.7
17.0	16.0	16.0	57.0	2.0		SIYGEKFEDENFILK	1830.9	1831.9	1830.9	1831.9
17.0	16.0	16.0	57.0	2.0	99.0	VKEGMNIVEAMER	1504.7	1505.7	1504.7	1505.7
17.0	16.0	16.0	57.0		99.0	VNPTVFFDIAVDGEPLGR	1987.0	1988.0	1987.0	1988.0
17.0	16.0	16.0	57.0	2.0	99.0	VSFELFADKVPK	1378.7	1379.7	1378.7	1379.8
87.0	8.7	8.7	45.5		99.0	GFGYKGSCFHR	1314.6	1315.6	1314.6	1315.6
87.0	8.7	8.7	45.5	2.0	99.0	IIPGFMCQGGDFTR	1597.7	1598.7	1597.7	1598.7
87.0	8.7	8.7	45.5	2.0	99.0	SIYGEKFEDENFILK	1830.9	1831.9	1830.9	1831.9
87.0	8.7	8.7	45.5	2.0	99.0	VKEGMNIVEAMER	1501.7	1502.7	1504.7	1505.7

87.0 87.0 87.0 87.0 87.0	8.7 8.7 8.7 8.7	8.7 8.7 8.7 8.7 8.7	45.5 45.5 45.5 45.5 45.5	0.7 0.0 0.0 0.0 0.0	79.0 99.0 91.0 99.0 99.0	VNPTVFFDIAVDGEPLGR GFGYKGSCFHR GFGYKGSCFHR SIYGEKFEDENFILK VKEGMNIVEAMER	1987.0 1314.6 1315.6 1834.9 1504.7	1988.0 1315.6 1316.7 1835.9 1505.7	1987.0 1314.6 1314.6 1830.9 1504.7	1988.0 1315.6 1315.6 1831.9 1505.7
P62942 FI 174.0	KB1A_HUMAN 2.0	2.0	FK506-bindi 40.7	ng protein 1 2.0	99.0	.8) (Peptidyl-prolyl cis-trans isomerase) (GWEEGVAQMSVGQR	PPI ase) (Rotamase) 1532.7) (12 kDa FKBP) 1533.7	(FKBP-12) (Imm 1532.7	nunophilin FKBP1 1533.7
215.0	6.0	6.0	29.6	2.0	99.0	GVQVETISPGDGR	1313.7	1314.7	1313.7	1314.7
215.0	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 R 372.0		2.8	40S riboson 55.0		527a - Homo 98.0	o sapiens (Human) CCLTYCFNKPEDK	1716.7	1717.7	1716.7	1717.7
372.0	2.8	2.8	55.0	0.6	77.0	YYKVDENGKISR	1471.8	1472.8	1471.7	1472.7
372.0	2.8		55.0	0.5	67.0	ECPSDECGAGVFMASHFDR	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	ECPSDECGAGVFMASHFDR	2170.8	2171.9	2170.9	2171.9
157.0	4.6	4.6	55.0	0.6	74.0	YYKVDENGKISR	1471.7	1472.7	1471.7	1472.7
P63104 1-	433Z_HUMAN 22.8	22.8	14-3-3 prote 65.7			kinase C inhibitor protein 1) (KCIP-1) - Ho AKLAEQAERYDDMAACMK			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	DSTLIMQLLR	1188.7	1189.7	1188.7	1189.7
34.0	22.8	22.8	65.7	2.0	99.0	FLIPNASQAESKVFYLK	1954.1	1955.1	1954.1	1955.1
34.0	22.8	22.8	65.7	2.0	99.0	GIVDQSQQAYQEAFEISKK	2168.1	2169.1	2168.1	2169.1
34.0	22.8	22.8	65.7	2.0	99.0	KEMQPTHPIR	1235.6	1236.7	1235.6	1236.7
34.0	22.8	22.8	65.7	2.0	99.0	MDKNELVQK	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	YDDMAACMK	1103.4	1104.4	1103.4	1104.4
34.0	22.8	22.8	65.7	2.0	99.0	YLAEVAAGDDKK	1278.6	1279.7	1278.6	1279.7
34.0	22.8	22.8	65.7	0.6	72.0	VVSSIEQKTEGAEKKQQMAR	2246.2	2247.2	2246.2	2247.2
34.0	22.8	22.8	65.7	0.1	25.0	MKGDYYR	931.4	932.4	931.4	932.4
67.0	5.1	5.1	35.1	2.0	99.0	GIVDQSQQAYQEAFEISKK	2168.1	2169.1	2168.1	2169.1
67.0	5.1	5.1	35.1		99.0	NLLSVAYKNVVGAR	1502.9	1503.9	1502.9	1503.9
67.0	5.1	5.1	35.1	1.0	91.0	DSTLIMQLLR	1188.7	1189.7	1188.7	1189.7
56.0	13.3	13.3	51.4	2.0	99.0	GIVDQSQQAYQEAFEISKK	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		99.0	VVSSIEQKTEGAEKKQQMAR	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	EMQPTHPIR	1107.6	1108.6	1107.5	1108.6
56.0	13.3	13.3	51.4	1.5	97.0	KEMQPTHPIR	1235.6	1236.7	1235.6	1236.7
56.0	13.3	13.3	51.4	1.2	94.0	DSTLIMQLLR	1188.7	1189.7	1188.7	1189.7
56.0	13.3	13.3	51.4	0.7	81.0	MDKNELVQK	1145.6	1146.6	1145.6	1146.6
56.0	13.3	13.3	51.4	0.5	68.0	TAFDEAIAELDTLSEESYK	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 G 533.0 382.0	2.0 1.7	2.0 1.7	4.1 8.5	leotide-bind 2.0 1.7	ding protein 99.0 98.0	subunit beta 2-like 1 (Guanine nucleotide LTRDETNYGIPOR LTRDETNYGIPOR	-binding protein sub 1561.8 1561.8	ounit beta-like p 1562.8 1562.8	rotein 12.3) (Red 1561.8 1561.8	ceptor of activate 1562.8 1562.8
	CTG_HUMAN 54.2	54.2	Actin, cytopl		amma-actin) 99.0		975.4	976.4	975.4	976.4
4.0	54.2	54.2	69.9	2.0	99.0	AVFPSIVGRP	1041.6	1042.6	1041.6	1042.6
4.0	54.2	54.2	69.9	2.0	99.0	AVFPSIVGRPR	1197.7	1198.7	1197.7	1198.7
4.0	54.2	54.2	69.9	2.0	99.0	CYVALDFEQEMATAASSSSLEK	2549.0	2550.0	2549.0	2550.0
4.0	54.2	54.2	69.9		99.0	DLYANTVLSGGTTMYPGIADR	2214.0	2215.1	2214.1	2215.1
4.0	54.2	54.2	69.9	2.0	99.0	EEEIAALVIDNGSGMCK	1876.9	1877.9	1876.9	1877.9
4.0	54.2	54.2	69.9	2.0	99.0	EITALAPSTMK	1160.6	1161.6	1160.6	1161.6
4.0	54.2	54.2	69.9	2.0	99.0	GYSFTTTAER	1131.5	1132.5	1131.5	1132.5
4.0	54.2	54.2	69.9	2.0	99.0	GYSFTTTAEREIVRDIK	1985.1	1986.1	1985.0	1986.0
4.0	54.2	54.2	69.9	2.0	99.0	HQGVMVGMGQK	1170.6	1171.6	1170.6	1171.6
4.0	54.2	54.2	69.9	2.0	99.0	HQGVMVGMGQKDSYVGDEAQSK	2350.1	2351.1	2350.1	2351.1
4.0	54.2	54.2	69.9	2.0	99.0	HQGVMVGMGQKDSYVGDEAQSKR	2506.2	2507.2	2506.2	2507.2
4.0 4.0 4.0	54.2 54.2 54.2	54.2 54.2 54.2	69.9 69.9 69.9	2.0 2.0 2.0	99.0 99.0 99.0	IKIIAPPER IWHHTFYNELR	1035.6 1514.7 2342.2	1036.7 1515.7	1035.6 1514.7	1036.7 1515.7
4.0 4.0 4.0	54.2 54.2 54.2	54.2 54.2 54.2	69.9 69.9	2.0 2.0 2.0	99.0 99.0	KDLYANTVLSGGTTMYPGIADR MQKEITALAPSTMK QEYDESGPSIVHR	1547.8 1515.7	2343.2 1548.8 1516.7	2342.1 1547.8 1515.7	2343.1 1548.8 1516.7
4.0	54.2	54.2	69.9	2.0	99.0	QEYDESGPSIVHRK	1643.8	1644.8	1643.8	1644.8
4.0	54.2	54.2	69.9	2.0	99.0	SYELPDGQVITIGNER	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	1953.1	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	YPIEHGIVTNWDDMEK	1959.9	1960.9	1959.9	1960.9
4.0	54.2	54.2	69.9	1.7	98.0	GYSFTTTAEREIVR	1628.8	1629.8	1628.8	1629.8
4.0	54.2	54.2	69.9	1.4	96.0	SYELPDGOVITIGNERFR	2093.1	2094.1	2093.1	2094.1
4.0	54.2	54.2	69.9	1.3	95.0	GYSFTTTAEREIVRDIKEK	2242.2	2243.2	2242.2	2243.2
4.0	54.2	54.2	69.9		94.0	VAPEEHPVLLTEAPLNPKANREK	2551.4	2552.4	2551.4	2552.4
4.0	54.2	54.2	69.9	1.1	92.0	RGILTLK	799.5	800.5	799.5	800.5
4.0	54.2	54.2	69.9	1.0	89.0	IWHHTFYNE	1245.5	1246.6	1245.6	1246.6
4.0	54.2	54.2	69.9	0.9	86.0	IKIIAPPERK	1163.7	1164.8	1163.7	1164.7
4.0	54.2	54.2	69.9	0.8	83.0	IIAPPERK	922.6	923.6	922.6	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 4.0 4.0	54.2 54.2 54.2	54.2 54.2	69.9 69.9	0.1 0.1	28.4 28.1	SLSTFQQMWISK EEEIAALVIDNGSGMCKA	1454.7 2028.9	1455.7 2029.9	1454.7 2028.8	1455.7 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	LDLAGRDLTDYLMK	1622.8	1623.8	1622.8	1623.8
4.0	54.2	54.2	69.9	0.0	96.0	AGFAGDDAPR	978.5	979.5	975.4	976.4
4.0	54.2	54.2	69.9	0.0	99.0	EEEIAALVIDNGSGMCK	1877.8	1878.8	1877.8	1878.8
4.0	54.2	54.2	69.9	0.0	99.0	EEEIAALVIDNGSGMCK	2029.9	2030.9	2029.8	2030.8
4.0	54.2	54.2	69.9	0.0	99.0	EEEIAALVIDNGSGMCK	2029.8	2030.9	2029.8	2030.8
4.0	54.2	54.2	69.9	0.0	86.0	GYSFTTTAEREIVRDIKEK	2243.2	2244.2	2242.2	2243.2
4.0	54.2	54.2	69.9		99.0	HQGVMVGMGQK	1186.6	1187.6	1186.6	1187.6
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMVGMGQK	1182.6	1183.6	1182.6	1183.6
4.0	54.2	54.2	69.9		99.0	HQGVMVGMGQK	1172.6	1173.6	1170.6	1171.6
4.0	54.2	54.2	69.9	0.0	29.0	HQGVMVGMGQK	1186.6	1187.6	1186.6	1187.6
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSK	2366.1	2367.1	2366.1	2367.1
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSK	2394.1	2395.1	2394.1	2395.1
4.0 4.0 4.0	54.2 54.2 54.2	54.2 54.2 54.2	69.9 69.9	0.0	99.0 99.0 99.0	HQGVMVGMGQKDSYVGDEAQSK HQGVMVGMGQKDSYVGDEAQSK HQGVMVGMGQKDSYVGDEAQSK	2366.1 2378.1	2367.1 2367.1 2379.1	2366.1 2378.1	2367.1 2367.1 2379.1
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSKR	2522.2	2523.2	2522.2	2523.2
4.0	54.2	54.2	69.9		99.0	HQGVMVGMGQKDSYVGDEAQSKR	2522.2	2523.2	2522.2	2523.2
4.0	54.2	54.2	69.9	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSKR	2534.2	2535.2	2534.2	2535.2
4.0	54.2	54.2	69.9		99.0	HQGVMVGMGQKDSYVGDEAQSKR	2518.2	2519.2	2518.2	2519.2
4.0	54.2	54.2	69.9	0.0	95.0	HQGVMVGMGQKDSYVGDEAQSKR	2538.2	2539.2	2538.2	2539.2
4.0	54.2	54.2	69.9	0.0	99.0	IKIIAPPER	1035.6	1036.7	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 4.0	54.2 54.2	54.2 54.2	69.9 69.9	0.0	99.0 99.0	IWHHTFYNELR IWHHTFYNELR	1516.7 1516.7 1530.7	1517.7 1517.7 1531.7	1514.7 1530.7	1515.7 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		99.0	IWHHTFYNELR	1515.7	1516.7	1515.7	1516.7
4.0	54.2	54.2	69.9	0.0	56.0	IWHHTFYNELR	1499.7	1500.7	1499.7	1500.7
4.0	54.2	54.2	69.9		44.0	IWHHTFYNELR	1470.7	1471.7	1470.7	1471.7
4.0	54.2	54.2	69.9	0.0	99.0	QEYDESGPSIVHR	1498.7	1499.7	1498.7	1499.7
4.0	54.2	54.2	69.9	0.0	99.0	QEYDESGPSIVHRK	1626.8	1627.8	1626.8	1627.8
4.0	54.2	54.2	69.9	0.0	99.0	SYELPDGQVITIGNER	1789.9	1790.9	1789.9	1790.9
4.0 4.0 4.0	54.2 54.2 54.2	54.2 54.2 54.2	69.9 69.9	0.0 0.0	99.0 95.0	SYELPDGQVITIGNER SYELPDGQVITIGNER SYELPDGQVITIGNER	1789.9 1790.9 1786.0	1790.9 1791.9 1787.0	1789.9 1790.9 1785.9	1790.9 1791.9 1786.9
4.0	54.2	54.2	69.9	0.0	99.0	YPIEHGIVTNWDDMEK	1945.9	1946.9	1945.9	1946.9
154.0	2.0	31.4	66.4	2.0	99.0	EEEIAALVIDNGSGMCK	1877.8	1878.8	1877.8	1878.8
154.0 154.0	2.0 2.0	31.4 31.4	66.4 66.4	0.0	99.0 99.0	AVFPSIVGRPR DLTDYLMK DLYANTULSCOTTMYDCIADD	1197.7 997.5	1198.7 998.5	1197.7 997.5	1198.7 998.5
154.0	2.0	31.4	66.4	0.0	99.0	DLYANTVLSGGTTMYPGIADR	2214.1	2215.1	2214.1	2215.1
154.0	2.0	31.4	66.4	0.0	99.0	EEEIAALVIDNGSGMCK	1876.9	1877.9	1876.9	1877.9
154.0	2.0	31.4	66.4	0.0	99.0	EEEIAALVIDNGSGMCK	2029.9	2030.9	2029.8	2030.8
154.0	2.0	31.4	66.4	0.0	99.0	EEEIAALVIDNGSGMCK	1892.9	1893.9	1892.8	1893.9
154.0	2.0	31.4	66.4		99.0	EEEIAALVIDNGSGMCK	1877.9	1878.9	1877.8	1878.8

						OVOCETTA COCUMO				
154.0	2.0	31.4	66.4	0.0	98.0	GYSFTTTAEREIVR	1628.8	1629.8	1628.8	1629.8
154.0	2.0	31.4	66.4	0.0	99.0	HQGVMVGMGQK	1170.6	1171.6	1170.6	1171.6
154.0	2.0	31.4	66.4	0.0	94.0	HQGVMVGMGQK	1171.6	1172.6	1170.6	1171.6
154.0	2.0	31.4	66.4	0.0	22.0	HQGVMVGMGQK	1186.6	1187.6	1186.6	1187.6
154.0	2.0	31.4	66.4	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSK	2350.1	2351.1	2350.1	2351.1
154.0	2.0	31.4	66.4	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSKR	2506.2	2507.2	2506.1	2507.1
154.0	2.0	31.4	66.4	0.0	96.0	HQGVMVGMGQKDSYVGDEAQSKR	2506.2	2507.2	2506.2	2507.2
154.0	2.0	31.4	66.4	0.0	89.0	IKIIAPPER	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		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		99.0	LCYVALDFEQEMATAASSSSLEK	2549.0	2550.0	2549.1	2550.1
154.0 154.0	2.0	31.4 31.4	66.4 66.4	0.0	36.0 99.0	QEYDESGPSIVHR QEYDESGPSIVHRK	1496.7 1643.8	1497.7 1644.8	1496.7 1643.8	1497.7 1644.8
154.0 154.0	2.0	31.4 31.4	66.4 66.4	0.0	74.0 99.0	QEYDESGPSIVHRK SYELPDGQVITIGNER	1626.8 1789.9	1627.8 1790.9	1626.8 1789.9	1627.8 1790.9
154.0 154.0	2.0	31.4 31.4 31.4	66.4	0.0	99.0 64.0	VAPEEHPVLLTEAPLNPK VAPEEHPVLLTEAPLNPKANR	1764.4 1953.1 2294.2	1954.1 2295.3	1953.1 2294.2	1954.1 2295.2
154.0	2.0	31.4	66.4 66.4	0.0	99.0	VAPEEHPVLLTEAPLNPKANREK	2551.4	2552.4	2551.4	2552.4
154.0	2.0	31.4	66.4	0.0	99.0	YPIEHGIVTNWDDMEK	1959.9	1960.9	1959.9	1960.9
5.0	50.7	50.7	69.1	2.0	99.0	AGFAGDDAPR	975.4	976.5	975.4	976.4
5.0	50.7	50.7	69.1	2.0	99.0	AVFPSIVGRPR	1197.7	1198.7	1197.7	1198.7
5.0	50.7	50.7	69.1	2.0	99.0	CYVALDFEQEMATAASSSSLEK	2549.0	2550.0	2549.0	2550.0
5.0	50.7	50.7	69.1	2.0	99.0	DLYANTVLSGGTTMYPGIADR	2214.1	2215.1	2214.1	2215.1
5.0	50.7	50.7	69.1	2.0	99.0	EEEIAALVIDNGSGMCK	1877.8	1878.8	1877.8	1878.8
5.0	50.7	50.7	69.1	2.0	99.0	GILTLKYPIEHGIVTNWDDMEK	2585.3	2586.3	2585.3	2586.3
5.0	50.7	50.7	69.1	2.0	99.0	GYSFTTTAER	1131.5	1132.5	1131.5	1132.5
5.0	50.7	50.7	69.1	2.0	99.0	GYSFTTTAEREIVR	1628.8	1629.8	1628.8	1629.8
5.0	50.7	50.7	69.1	2.0	99.0	GYSFTTTAEREIVRDIKEK	2242.2	2243.2	2242.2	2243.2
5.0	50.7	50.7	69.1	2.0	99.0	HQGVMVGMGQK	1170.6	1171.6	1170.6	1171.6
5.0	50.7	50.7	69.1	2.0	99.0	HQGVMVGMGQKDSYVGDEAQSK	2350.1	2351.1	2350.1	2351.1
5.0	50.7	50.7	69.1	2.0	99.0	HQGVMVGMGQKDSYVGDEAQSKR	2506.2	2507.2	2506.2	2507.2
5.0	50.7	50.7	69.1		99.0	IKIIAPPER	1035.7	1036.7	1035.6	1036.7
5.0 5.0	50.7 50.7	50.7 50.7	69.1 69.1	2.0	99.0 99.0	IKIIAPPERK IWHHTFYNELR	1163.7	1164.8	1163.7	1164.7
5.0	50.7	50.7	69.1	2.0	99.0	KDLYANTVLSGGTTMYPGIADR	1515.7 2342.2	1516.7 2343.2	1515.7 2342.2	1516.7 2343.2
5.0	50.7	50.7	69.1	2.0	99.0	MQKEITALAPSTMK	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	1785.9	1786.9	1789.9	1790.9
5.0	50.7	50.7	69.1	2.0	99.0	VAPEEHPVLLTEAPLNPK	1953.0	1954.1	1953.1	1954.1
5.0	50.7	50.7	69.1	2.0	99.0	VAPEEHPVLLTEAPLNPKANR	2294.2	2295.2	2294.2	2295.2
5.0	50.7	50.7	69.1	2.0	99.0	YPIEHGIVTNWDDMEK	1975.9	1976.9	1975.9	1976.9
5.0	50.7	50.7	69.1	1.5	97.0	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	1351.7	1350.6	1351.6
5.0	50.7	50.7	69.1	0.2	30.0	DSYVGDEAQSKR	1353.6	1354.6	1353.6	1354.6
5.0	50.7	50.7	69.1	0.0	99.0	EEEIAALVIDNGSGMCK	1876.9	1877.9	1876.9	1877.9
5.0	50.7	50.7	69.1	0.0	94.0	EEEIAALVIDNGSGMCK	1875.8	1876.8	1875.8	1876.8
5.0	50.7	50.7	69.1		27.0	EEEIAALVIDNGSGMCK	1893.9	1895.0	1893.8	1894.8
5.0	50.7	50.7	69.1	0.0	99.0	HQGVMVGMGQK	1173.6	1174.6	1170.6	1171.6
5.0	50.7	50.7	69.1	0.0	99.0	HQGVMVGMGQK	1186.6	1187.6	1186.6	1187.6
5.0	50.7	50.7	69.1		99.0	HQGVMVGMGQK	1182.6	1183.6	1182.6	1183.6
5.0	50.7	50.7	69.1	0.0	99.0	HQGVMVGMGQKDSYVGDEAQSKR	2522.2	2523.2	2522.2	2523.2
5.0	50.7	50.7	69.1		99.0	HQGVMVGMGQKDSYVGDEAQSKR	2518.2	2519.2	2518.2	2519.2
5.0	50.7	50.7	69.1	0.0	96.0	HQGVMVGMGQKDSYVGDEAQSKR	2522.2	2523.2	2522.2	2523.2
5.0	50.7	50.7	69.1	0.0	99.0	IKIIAPPER	1035.7	1036.7	1035.6	1036.7
5.0	50.7	50.7	69.1	0.0	95.0	IKIIAPPERK	1163.7	1164.8	1163.7	1164.7
5.0	50.7	50.7	69.1		99.0	IWHHTFYNELR	1516.7	1517.7	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		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		99.0	IWHHTFYNELR	1512.8	1513.8	1514.7	1515.7
5.0	50.7	50.7	69.1	0.0	97.0	IWHHTFYNELR	1515.7	1516.7	1515.7	1516.7
5.0	50.7	50.7	69.1	0.0	99.0	QEYDESGPSIVHR	1498.7	1499.7	1498.7	1499.7
5.0	50.7 50.7	50.7 50.7	69.1 69.1	0.0	97.0 99.0	QEYDESGPSIVHR QEYDESGPSIVHRK	1498.7 1643.8	1499.7 1644.8	1498.7 1643.8	1499.7 1644.8
5.0	50.7	50.7	69.1	0.0	99.0	QEYDESGPSIVHRK	1642.8	1643.8	1643.8	1644.8
5.0	50.7	50.7	69.1		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		99.0	SYELPDGQVITIGNER	1789.9	1790.9	1789.9	1790.9
5.0 5.0	50.7 50.7	50.7 50.7	69.1 69.1	0.0	99.0 99.0	SYELPDGQVITIGNER SYELPDGQVITIGNER	1789.9 1802.9	1790.9 1803.9	1789.9 1802.9	1790.9 1803.9
5.0 5.0	50.7 50.7	50.7 50.7	69.1 69.1	0.0	99.0	SYELPDGQVITIGNER YPIEHGIVTNWDDMEK	1790.9 1959.9	1791.9 1960.9	1790.9 1959.9	1791.9 1960.9
P63279 UB0 497.0	2.0	2.0	7.0	2.0	99.0	C 6.3.2) (SUMO-protein ligase) (Ubiquitir GTPWEGGLFK	1090.5	1091.6	1090.5	1091.6
173.0 P67936 TPN		2.0		2.0 n alpha-4 cha		GTPWEGGLFK nyosin-4) (TM30p1) - Homo sapiens (Huma		1091.6	1090.5	1091.6
39.0	21.0	21.0	45.6	2.0	99.0	AMKDEEKMEIQEMQLK	1979.9	1980.9	1979.9	1980.9
39.0	21.0	21.0	45.6	2.0	99.0	HIAEEADRKYEEVAR	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	IQALQQQADEAEDRAQGLQR	2267.1	2268.1	2267.1	2268.1
39.0	21.0	21.0	45.6	2.0	99.0	IQLVEEELDR	1242.6	1243.6	1242.6	1243.7
39.0	21.0	21.0	45.6	2.0	99.0	IQLVEEELDRAQER	1726.9	1727.9	1726.9	1727.9
39.0	21.0	21.0	45.6	2.0	99.0	KIQALQQQADEAEDR	1741.9	1742.9	1741.9	1742.9
39.0	21.0	21.0	45.6	2.0	99.0	KIQALQQQADEAEDRAQGLQR	2395.2	2396.2	2395.2	2396.2
39.0	21.0	21.0	45.6	2.0	99.0	LATALOKLEEAEKAADESER	2201.1	2202.1	2201.1	2202.1
39.0	21.0	21.0	45.6	2.0	99.0	RIQLVEEELDRAQER	1883.0	1884.0	1883.0	1884.0
39.0	21.0	21.0	45.6	1.0	89.0	LEEAEKAADESER	1475.7	1476.7	1475.7	1476.7
39.0	21.0	21.0	45.6		99.0	HIAEEADRKYEEVAR	1826.9	1827.9	1826.9	1827.9
39.0	21.0	21.0	45.6	0.0	74.0	HIAEEADRKYEEVAR	1814.9	1815.9	1814.9	1815.9
39.0	21.0	21.0	45.6		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	IQLVEEELDRAQER	1726.9	1727.9	1726.9	1727.9
78.0	4.5	4.5	44.4	2.0	99.0	KIQALQQQADEAEDR	1769.9	1770.9	1769.9	1770.9
78.0	4.5	4.5	44.4	0.5	67.0	LATALQKLEEAEKAADESER	2201.1	2202.1	2201.1	2202.1
57.0	13.2	13.2	49.6	2.0	99.0	IQLVEEELDRAQER	1726.9	1727.9	1726.9	1727.9
57.0	13.2	13.2	49.6	2.0	99.0	KIQALQQQADEAEDR	1741.9	1742.9	1741.9	1742.9
57.0	13.2	13.2	49.6	2.0	99.0	KIQALQQQADEAEDRAQGLQR	2395.2	2396.2	2395.2	2396.2
57.0	13.2	13.2	49.6	2.0	99.0	LATALQKLEEAEKAADESER	2201.1	2202.1	2201.1	2202.1
57.0	13.2	13.2	49.6	2.0	99.0	RIQLVEEELDRAQER	1883.0	1884.0	1883.0	1884.0
57.0	13.2	13.2	49.6	1.1	92.0	RIQLVEEELDR	1398.7	1399.8	1398.7	1399.8
57.0	13.2	13.2	49.6	0.8	83.0	LEEAEKAADESER	1475.7	1476.7	1475.7	1476.7
57.0	13.2	13.2	49.6	0.8	83.0	REKAEGDVAALNRR	1583.8	1584.9	1583.8	1584.9
57.0	13.2	13.2	49.6	0.3	50.0	HIAEEADRKYEEVAR	1814.9	1815.9	1814.9	1815.9
57.0	13.2	13.2	49.6	0.1	25.0	IQALQQQADEAEDR	1613.8	1614.8	1613.8	1614.8
57.0	13.2	13.2	49.6	0.1	23.7	AGLNSLEAVKR	1199.7	1200.7	1199.7	1200.7
57.0	13.2	13.2	49.6	0.0	99.0	KIQALQQQADEAEDR	1769.9	1770.9	1769.9	1770.9
P68104 EF1		12.0		factor 1-alpha		Ipha-1) (Elongation factor 1 A-1) (eEF1A-1 GSFKYAWVLDK				
91.0 91.0 91.0	12.0 12.0 12.0	12.0 12.0 12.0	21.4 21.4 21.4	2.0 2.0 2.0	99.0 99.0	IGGIGTVPVGR QTVAVGVIK	1024.6 913.6	1025.6 914.6	1024.6 913.6	1025.6 914.6
91.0	12.0	12.0	21.4	2.0	99.0	SGDAAIVDMVPGKPMCVESFSDYPPLGR	2994.4	2995.4	2994.4	2995.4
91.0	12.0	12.0	21.4	2.0	99.0	VETGVLKPGMVVTFAPVNVTTEVK	2514.4	2515.4	2514.3	2515.3
91.0	12.0	12.0	21.4	2.0	99.0	YYVTIIDAPGHRDFIK	1907.0	1908.0	1907.0	1908.0
91.0	12.0	12.0	21.4	0.0	90.0	IGGIGTVPVGR	1024.6	1025.6	1024.6	1025.6
129.0	2.3	2.3	10.2	2.0	99.0	GSFKYAWVLDK	1340.7	1341.7	1340.7	1341.7
129.0	2.3	2.3	10.2	0.2	32.0	YYVTIIDAPGHR	1403.7	1404.7	1403.7	1404.7
90.0	8.2	8.2	22.1	2.0	99.0	IGGIGTVPVGR	1024.6	1025.6	1024.6	1025.6
90.0	8.2	8.2	22.1	2.0	99.0	QTVAVGVIK	913.6	914.6	913.6	914.6
90.0	8.2	8.2	22.1	2.0	99.0	VETGVLKPGMVVTFAPVNVTTEVK	2514.4	2515.4	2514.4	2515.4

90.0	8.2	8.2	22.1	2.0	99.0	YYVTIIDAPGHRDFIK	1907.0	1908.0	1907.0	1908.0
90.0	8.2	8.2	22.1	0.2	42.0	STTTGHLIYK	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
33.0	TBAK_HUMAN 23.4	23.4	38.6	2.0	99.0	ha-tubulin ubiquitous) (Tubulin K-alpha-1) AVCMLSNTTAIAEAWAR	1863.9	1864.9	1863.9	1864.9
33.0	23.4	23.4	38.6	2.0	99.0	AVFVDLEPTVIDEVR	1700.9	1701.9	1700.9	1701.9
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	2496.1	2497.1
33.0	23.4	23.4	38.6	2.0	99.0	VGINYQPPTVVPGGDLAK	1824.0	1825.0	1824.0	1825.0
33.0	23.4	23.4	38.6	2.0	99.0	YMACCLLYR	1248.5	1249.6	1248.5	1249.6
33.0	23.4	23.4	38.6	2.0	99.0	YMACCLLYRGDVVPK	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	1739.8	1740.9
33.0	23.4	23.4	38.6	1.3	95.0	AFVHWYVGEGMEEGEFSEAR	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	OLFHPEOLITGK	1409.8	1410.8	1409.8	1410.8
33.0	23.4	23.4	38.6	0.0	94.0	OLFHPEOLITGKEDAANNYAR	2397.2	2398.2	2397.2	2398.2
49.0	15.5	15.5	29.9	2.0	99.0	AFVHWYVGEGMEEGEFSEAR	2329.0	2330.0	2329.0	2330.0
49.0	15.5	15.5	29.9	2.0	99.0	AVCMLSNTTAIAEAWAR	1863.9	1864.9	1863.9	1864.9
49.0	15.5	15.5	29.9	2.0	99.0	AVFVDLEPTVIDEVR	1700.9	1701.9	1700.9	1701.9
49.0	15.5	15.5	29.9	2.0	99.0	LDHKFDLMYAKR	1535.8	1536.8	1535.8	1536.8
49.0	15.5	15.5	29.9	2.0	99.0	QLFHPEQLITGK	1392.7	1393.7	1392.7	1393.7
49.0	15.5	15.5	29.9	2.0	99.0	QLFHPEQLITGKEDAANNYAR	2397.2	2398.2	2397.2	2398.2
49.0	15.5	15.5	29.9	2.0	99.0	YMACCLLYR	1248.5	1249.6	1248.5	1249.6
49.0	15.5	15.5	29.9	1.5	97.0	YMACCLLYRGDVVPK	1843.9	1844.9	1843.9	1844.9
49.0	15.5 H31_HUMAN	15.5	29.9	0.0	99.0 3/b) (H3/d	QLFHPEQLITGKEDAANNYAR	2414.2	2415.2	2414.2	2415.2
154.0	7.9	7.9	41.2	2.0	99.0	EIAODFKTDLR	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	KOLATKAAR	1027.6	1028.6	1027.7	1028.7
154.0	7.9	7.9	41.2		99.0	EIAODEKTDLR	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		99.0	EIAQDFKTDLR	1334.7	1335.7	1334.7	1335.7
112.0	6.9	6.9	37.5	2.0	99.0	KSAPATGGVKKPHR	1488.9	1489.9	1488.9	1489.9
112.0	6.9	6.9	37.5	2.0	99.0	YRPGTVALR	1031.6	1032.6	1031.6	1032.6
112.0	6.9	6.9	37.5	0.7	80.0	KLPFQR	787.5	788.5	787.5	788.5
112.0	6.9	6.9	37.5	0.1	23.0	STELLIR	830.5	831.5	830.5	831.5
112.0	6.9	6.9	37.5	0.0	99.0	EIAQDFKTDLR	1348.7	1349.7	1348.7	1349.7
112.0	6.9	6.9	37.5	0.0	53.0	EIAQDFKTDLR	1362.7	1363.7	1362.7	1363.7
112.0	6.9	6.9	37.5	0.0	41.0	KLPFQR	787.5	788.5	787.5	788.5
139.0	2.1	2.1	19.1	2.0	99.0	EIAQDFKTDLR	1334.6	1335.6	1334.7	1335.7
139.0		2.1	19.1	0.1	24.0	STELLIR	830.5	831.5	830.5	831.5
369.0	GSTO1_HUMAN	2.9	14.5	e transferase	99.0	C 2.5.1.18) (GSTO 1-1) - Homo sapiens (Hu VPSLVGSFIR	1073.6	1074.6	1073.6	1074.6
369.0	2.9	2.9	14.5	0.6	75.0	SLGKGSAPPGPVPEGSIR	1704.9	1705.9	1704.9	1705.9
369.0	2.9	2.9	14.5	0.3	46.0	GSAPPGPVPEGSIR	1319.7	1320.7	1319.7	1320.7
188.0	2.0	2.0	3.3	2.0	99.0	NKPEWFFK	1094.6	1095.6	1094.6	1095.6
146.0	5.1	5.1	28.6	2.0	99.0	SLGKGSAPPGPVPEGSIR	1704.9	1705.9	1704.9	1705.9
146.0	5.1	5.1	28.6	2.0	99.0	VPSLVGSFIR	1073.6	1074.6	1073.6	1074.6
146.0	5.1	5.1	28.6	0.7	78.0	NKPEWFFK	1094.6	1095.6	1094.6	1095.6
146.0	5.1	5.1	28.6	0.3	46.0	GIRHEVININLK	1404.8	1405.8	1404.8	1405.8
146.0	5.1	5.1	28.6	0.1	23.0	GSAPPGPVPEGSIR	1319.7	1320.7	1319.7	1320.7
P80295 1 459.0	MT1I_HUMAN 2.0	4.0	Metallothic 52.5	onein-1I (MT-1 2.0	99.0	othionein-II) - Homo sapiens (Human) MDPNCSCAAGVSCTCAGSCK	2263.8	2264.8	2263.8	2264.8
459.0	2.0	4.0	52.5	0.0	99.0	MDPNCSCAAGVSCTCAGSCK	2233.8	2234.8	2233.8	2234.8
459.0	2.0	4.0	52.5	0.0	99.0	SCCSCCPVGCAK	1444.5	1445.5	1444.5	1445.5
459.0	2.0	4.0	52.5	0.0	99.0	SCCSCCPVGCAK	1447.5	1448.5	1444.5	1445.5
459.0	2.0	4.0	52.5		99.0	SCCSCCPVGCAK	1447.5	1448.5	1444.5	1445.5
304.0	2.0	6.0	54.1	2.0	99.0	MDPNCSCAAGVSCTCAGSCK	2263.8	2264.8	2263.8	2264.8
304.0		6.0	54.1	0.0	99.0	KSCCSCCPVGCAK	1573.6	1574.6	1572.6	1573.6
304.0 304.0	2.0	6.0 6.0	54.1 54.1	0.0	99.0 99.0	SCCSCCPVGCAK SCCSCCPVGCAK	1444.5 1446.5	1445.5 1447.5	1444.5 1444.5	1445.5 1445.5
304.0 182.0	2.0	6.0	54.1 53.2	0.0	99.0 99.0	SCCSCCPVGCAK SCCSCCPVGCAK	1446.5 1444.5	1447.5 1445.5	1444.5 1444.5	1445.5 1445.5
P84103 5 279.0		4.0	Splicing fa		serine-rich					
279.0 313.0	4.0	4.0 2.0	37.8 46.3	2.0	99.0 99.0	NPPGFAFVEFEDPRDAADAVR AFGYYGPLR	2319.1 1042.5	2320.1 1043.5	2319.1 1042.5	2320.1 1043.5
	CLH1_HUMAN 2.3	2.3	Clathrin he			lomo sapiens (Human) FLRENPYYDSR	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		99.0	IHEGCEEPATHNALAK	1775.8	1776.8	1775.8	1776.8
234.0	2.5 HNRPU_HUMAN	2.5	3.5	0.5 eous nuclear r	68.0	NNRPSEGPLQTR	1384.6	1385.7	1384.7	1385.7
93.0	11.9	11.9	23.1	2.0	99.0	GHGEQOPOPPATOQOOPOOR	2395.1	2396.1	2395.1	2396.1
93.0	11.9	11.9	23.1	2.0	99.0	GYFEYIEENKYSR	1696.8	1697.8	1696.8	1697.8
93.0	11.9	11.9	23.1	2.0	99.0	KMCLFAGFQR	1256.6	1257.6	1256.6	1257.6
93.0	11.9	11.9	23.1		99.0	MCLFAGFQR	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	FIEIAAR	818.5	819.5	818.5	819.5
93.0 93.0	11.9 11.9	11.9 11.9	23.1	0.2	31.0 98.0	RGNMPQRGGGGGGGGGGYPYPR SSGPTSLFAVTVAPPGAR	2303.1 1711.9	2304.1 1712.9	2303.1 1713.9	2304.1 1714.9
140.0	5.7	5.7	20.6	2.0	99.0	FIEIAAR	818.5	819.5	818.5	819.5
140.0 140.0 Q01082	5.7 5.7 SPTB2_HUMAN	5.7 5.7	20.6 20.6 Spectrip be	2.0 1.7 eta chain, brai	99.0 98.0	MCLFAGFQR GYFEYIEENKYSR in page-grythroid beta chain 1) (Reta-II spe	1128.5 1696.8 ectrip) (Fodrip bet	1129.5 1697.8 2 chain) - Homo	1128.5 1696.8	1129.5 1697.8
119.0 119.0	9.6 9.6	9.6 9.6	8.6 8.6	eta chain, brai 2.0 2.0	n 1 (Specti 99.0 99.0	in, non-erythroid beta chain 1) (Beta-II spe DLDDFQSWLSR EVDDLEQWIAER	1380.6 1501.7	1381.6 1502.7	1380.6 1501.7	1381.6 1502.7
119.0	9.6	9.6	8.6	2.0	99.0	FMELLEPLNER	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	DASVAEAWLLGQEPYLSSR	2091.0	2092.0	2091.0	2092.0
119.0 119.0	9.6 9.6 9.6	9.6 9.6	8.6 8.6 8.6	0.5 0.1 0.0	70.0 27.0 37.0	WVNSHLAR LQAAYAGDKADDIQKR	981.5 1761.9	982.5 1762.9	981.5 1761.9	982.5 1762.9
119.0 255.0	2.2	9.6 2.2	7.9	2.0	99.0	FYHDAKEIFGR DASVAEAWLLGQEPYLSSR	1381.7 2091.0	1382.7 2092.1	1381.7 2091.0	1382.7 2092.0
	SET_HUMAN	2.2	7.9 Protein SE		35.0 e 2A inhibi	AEHERELALR tor 12PP2A) (1-2PP2A) (Template-activating				
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		99.0	IDFYFDENPYFENKVLSK	2267.1	2268.1	2267.1	2268.1
61.0	16.1	16.1	15.2	2.0	99.0	SGYRIDFYFDENPYFENK	2303.0	2304.1	2303.0	2304.0
61.0	16.1	16.1	15.2		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	YNKLRQPFFQKR	1623.9	1624.9	1623.9	1624.9
61.0	16.1	16.1	15.2	1.5	97.0	LRQPFFQKR	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	LRQPFFQK	1062.6	1063.6	1062.6	1063.6
61.0	16.1	16.1	15.2	0.0	99.0	VEVTEFEDIK	1208.6	1209.6	1207.6	1208.6
127.0	6.0	6.0	22.8	2.0	99.0	IDFYFDENPYFENK	1839.8	1840.8	1839.8	1840.8
127.0	6.0	6.0	22.8	2.0	99.0	LRQPFFQKR	1218.7	1219.7	1218.7	1219.7
127.0 Q01469		6.0	22.8 Fatty acid-	2.0 binding protei	99.0 n, epiderm	VEVTEFEDIKSGYR al (E-FABP) (Psoriasis-associated fatty acid	1670.8 -binding protein h	1671.8 omolog) (PA-FA	1670.8 BP) - Homo sapie	
176.0	6.5	6.5	57.8	2.0	99.0	ATVQQLEGR	1042.5	1043.5	1042.5	1043.5
176.0	6.5	6.5	57.8	2.0	99.0	TTQFSCTLGEKFEETTADGRK	2405.1	2406.1	2405.1	2406.1
176.0	6.5	6.5	57.8	1.3	95.0	TTQFSCTLGEKFEETTADGR TQTVCNFTDGALVQHQEWDGKESTITR	2277.0	2278.0	2277.0	2278.0
176.0	6.5	6.5	57.8	1.2	93.0		3120.4	3121.5	3120.5	3121.5
226.0	2.9	2.9	31.9	2.0	99.0	ATVQQLEGR	1042.5	1043.6	1042.5	1043.5
226.0	2.9	2.9	31.9	0.7	81.0	TQTVCNFTDGALVQHQEWDGKESTITR	3120.5	3121.5	3120.5	3121.5
	2.9 CAP1_HUMAN	2.9		0.2 yclase-associa			888.4	889.4	888.4	889.4
121.0	9.6	9.6	16.2	2.0	99.0	ADMONLVER	1116.5	1117.5	1116.5	1117.5
121.0	9.6	9.6	16.2	2.0	99.0	AVGRLEAVSHTSDMHR	1764.9	1765.9	1764.9	1765.9
121.0		9.6	16.2	2.0	99.0	SGPKPFSAPKPQTSPSPK	1837.0	1838.0	1837.0	1838.0

121.0 121.0	9.6 9.6	9.6 9.6	16.2 16.2	2.0 1.5	99.0 97.0	SGPKPFSAPKPQTSPSPKR LEAVSHTSDMHR	1993.1 1381.6	1994.1 1382.7	1993.1 1381.6	1994.1 1382.6
56.0 56.0	6.0 6.0	6.0 6.0	14.5 14.5	2.0 2.0	99.0 99.0	ADMQNLVER SGPKPFSAPKPQTSPSPK	1116.5 1837.0	1117.5 1838.0	1116.5 1837.0	1117.5 1838.0
56.0 110.0	6.0 7.1	6.0 7.1	14.5 21.1	2.0 2.0	99.0 99.0	SSLFAQINQGESITHALK ADMQNLVER	1927.0 1116.5	1928.0 1117.5	1927.0 1116.5	1928.0 1117.5
110.0 110.0	7.1 7.1	7.1 7.1	21.1 21.1	2.0	99.0 99.0	LEAVSHTSDMHR SGPKPFSAPKPQTSPSPK	1381.6 1837.0	1382.7 1838.0	1381.6 1837.0	1382.6 1838.0
110.0	7.1	7.1	21.1 RNA-binding	1.0	91.0	THKNPALKAQSGPVR cogene) (Ewing sarcoma breakpoint region 1 pr	1602.9	1603.9	1602.9	1603.9
268.0	EWS_HUMAN 4.1	4.1	25.8	2.0	99.0	AAVEWFDGKDFQGSK	1683.8	1684.8	1683.8	1684.8
268.0 268.0	4.1 4.1	4.1 4.1	25.8 25.8	2.0 0.1	99.0 25.0	AGDWQCPNPGCGNQNFAWR GGRGGDRGGFRGGRGMDRGGFGGGRR	2233.9 2582.2	2234.9 2583.2	2233.9 2582.2	2234.9 2583.2
115.0 115.0	2.8 2.8	2.8 2.8	23.6 23.6	2.0 0.8	99.0 85.0	AAVEWFDGKDFQGSK GGGRGGMGSAGER	1683.8 1177.6	1684.8 1178.6	1683.8 1177.5	1684.8 1178.5
0.218 Q02818	2.0 NUCB1_HUMAN	2.0	16.8 Nucleobindin	2.0 n-1 precurso	99.0 or (CALNUC)	AGDWQCPNPGCGNQNFAWR - Homo sapiens (Human)	2233.9	2234.9	2233.9	2234.9
271.0 271.0	4.1 4.1	4.1 4.1	18.2 18.2	2.0 2.0	99.0 99.0	DLAQYDAAHHEEFKR KQQQQQQGHKAPAAHPEGQLK	1828.9 2464.3	1829.9 2465.3	1828.8 2464.3	1829.9 2465.3
271.0	4.1	4.1	18.2	0.1	21.0	AORLSOETEALGR DLAQYDAAHHEEFKR	1460.7	1461.7	1460.7	1461.7
150.0 150.0	4.7 4.7	4.7 4.7	23.4 23.4	2.0	99.0 99.0	QFEHLDPQNQHTFEAR	1828.9 1978.9	1829.9 1979.9	1828.8 1978.9	1829.9 1979.9
150.0 150.0	4.7 4.7	4.7 4.7	23.4 23.4	0.4 0.1	58.0 29.0	DLELLIQTATR YEMLKEHER	1271.7 1233.6	1272.7 1234.6	1271.7 1233.6	1272.7 1234.6
150.0 150.0	4.7 4.7	4.7 4.7	23.4 23.4	0.1 0.0	26.0 97.0	EMEEERLRMR DLAQYDAAHHEEFKR	1357.7 1828.8	1358.7 1829.9	1357.7 1828.8	1358.7 1829.9
Q02878 F	RL6_HUMAN 3.2	3.2	60S ribosoma	al protein L 2.0	6 (TAX-resp 99.0	onsive enhancer element-binding protein 107 AIPQLQGYLR	(TAXREB107) 1157.7	(Neoplasm-relat	ed protein C140) 1157.7) - Homo sapiens 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 Q06033 I		2.0	12.8 Inter-alpha-1		99.0 bitor heavy	AIPQLQGYLR chain H3 precursor (ITI heavy chain H3) (Inte				
116.0 116.0	9.7 9.7	9.7 9.7	7.3 7.3	2.0 2.0	99.0 99.0	DYIFGNYIER FAHNVVTMR	1289.6 1043.6	1290.6 1044.6	1289.6 1043.6	1290.6 1044.6
116.0 116.0	9.7 9.7	9.7 9.7	7.3 7.3	2.0 2.0	99.0 99.0	GHVSFKPSLDQQR KGHVSFKPSLDQQR	1497.7 1625.9	1498.7 1626.9	1497.8 1625.9	1498.8 1626.9
116.0 100.0	9.7 3.5	9.7 3.5	7.3 8.6	1.7 2.0	98.0 99.0	VTFELTYEELLKR FAHNVVTMR	1639.9 1043.6	1640.9 1044.6	1639.9 1043.6	1640.9 1044.6
100.0 92.0	3.5 8.1	3.5 8.1	8.6 13.8	1.5	97.0 99.0	DYIFGNYIER DYIFGNYIER	1289.6 1289.6	1290.6 1290.6	1289.6 1289.6	1290.6 1290.6
92.0	8.1	8.1	13.8	2.0	99.0	FAHNVVTMR KGHVSFKPSLDQQR	1043.6	1044.6	1043.6	1044.6
92.0 92.0	8.1 8.1	8.1 8.1	13.8 13.8	2.0 2.0	99.0 99.0	VTFELTYEELLKR	1625.9 1639.9	1626.9 1640.9	1625.9 1639.9	1626.9 1640.9
Q06323 F	PSME1_HUMAN 14.7	14.7	Proteasome a 38.2	2.0	99.0	Init 1 (Proteasome activator 28-alpha subunit) AAKQPHVGDYR	1240.6	1241.6	1240.6	ic protease subu 1241.6
68.0 68.0	14.7 14.7	14.7 14.7	38.2 38.2	2.0 2.0	99.0 99.0	LEGFHTQISK NAYAVLYDIILK	1158.6 1394.8	1159.6 1395.8	1158.6 1394.8	1159.6 1395.8
68.0 68.0	14.7 14.7	14.7 14.7	38.2 38.2	2.0	99.0 99.0	OLVHELDEAEYRDIR OPHVGDYR	1884.9 953.4	1885.9 954.4	1884.9 953.4	1885.9 954.4
68.0 68.0	14.7 14.7 14.7	14.7	38.2 38.2 38.2	2.0	99.0 98.0	YFSERGDAVTK LMVMEIR	1271.6 890.5	1272.6 891.5	1271.6 890.5	1272.6 891.5
68.0	14.7	14.7	38.2	1.0	91.0	IVVLLQR	839.6	840.6	839.6	840.6
50.0 50.0	6.3 6.3	6.3 6.3	26.9 26.9	2.0 2.0	99.0 99.0	IVVLLQR NAYAVLYDIILK	839.6 1394.8	840.6 1395.8	839.6 1394.8	840.6 1395.8
50.0 50.0	6.3 6.3	6.3 6.3	26.9 26.9	2.0 0.3	99.0 49.0	QLVHELDEAEYR LMVMEIR	1500.7 890.5	1501.7 891.5	1500.7 890.5	1501.7 891.5
59.0 59.0	12.9 12.9	12.9 12.9	34.1 34.1	2.0 2.0	99.0 99.0	AAKQPHVGDYR IEDGNNFGVAVQEK	1240.6 1519.7	1241.6 1520.7	1240.6 1519.7	1241.6 1520.7
59.0 59.0	12.9 12.9	12.9 12.9	34.1 34.1	2.0	99.0 99.0	IVVLLQR QLVHELDEAEYR	839.6 1483.7	840.6 1484.7	839.6 1483.7	840.6 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 59.0	12.9 12.9	12.9 12.9	34.1 34.1	1.4 0.9	96.0 88.0	NAYAVLYDIILK LMVMEIR	1394.8 890.5	1395.8 891.5	1394.8 890.5	1395.8 891.5
59.0	12.9	12.9	34.1	0.4	57.0	YFSERGDAVTK	1271.6	1272.6	1271.6	1272.6
59.0	12.9	12.9	34.1	0.2	41.0	QPHVGDYR	953.4	954.4	953.4	954.4
		12.9 12.9								
59.0 59.0 59.0 QO6830 F	12.9 12.9 12.9 PRDX1_HUMAN	12.9 12.9 12.9	34.1 34.1 34.1 Peroxiredoxi	0.2 0.0 0.0 n-1 (EC 1.1	41.0 97.0 93.0 1.1.15) (Th	QPHVGDYR QLVHELDEAEYR QLVHELDEAEYRDIR ioredoxin peroxidase 2) (Thioredoxin-depende	953.4 1500.7 1884.9 nt peroxide rea	954.4 1501.7 1885.9 ductase 2) (Prolif	953.4 1500.7 1884.9 eration-associate	954.4 1501.7 1885.9 ed gene protein)
59.0 59.0 59.0 Q06830 48.0 48.0	12.9 12.9 12.9 12.9 PRDX1_HUMAN 18.3 18.3	12.9 12.9 12.9 18.3 18.3	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3	0.2 0.0 0.0 n-1 (EC 1.1 2.0 2.0	41.0 97.0 93.0 1.1.15) (Th 99.0 99.0	OPHVGDYR QLVHELDEAEYR QLVHELDEAEYRDIR Ioredoxin peroxidase 2) (Thioredoxin-depende ATAVMPDGQFKDISLSDYK ATAVMPDGGFKDISLSDYKGK	953.4 1500.7 1884.9 nt peroxide red 2085.0 2270.1	954.4 1501.7 1885.9 ductase 2) (Prolif 2086.0 2271.1	953.4 1500.7 1884.9 eration-associate 2085.0 2270.1	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1
59.0 59.0 59.0 QO6830 I 48.0 48.0 48.0	12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3	0.2 0.0 0.0 0.1 (EC 1.1 2.0 2.0 2.0 2.0	41.0 97.0 93.0 1.1.15) (Th 99.0 99.0 99.0	OPHVGDYR QLVHELDEAEYR QLVHELDEAEYRDIR IOredoxin peroxidase 2) (Thioredoxin-depende ATAVMPDGOFKDISLSDVK ATAVMPDGOFKDISLSDVKGK GLIDDKGILR LIGHPAPNFK	953.4 1500.7 1884.9 nt peroxide red 2085.0 2270.1 1358.8 979.5	954.4 1501.7 1885.9 ductase 2) (Prolif 2086.0 2271.1 1359.8 980.5	953.4 1500.7 1884.9 eration-associate 2085.0 2270.1 1358.8 979.5	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5
59.0 59.0 59.0 QO6830 I 48.0 48.0 48.0 48.0 48.0	12.9 12.9 12.9 12.9 PRDX1_HUMAN 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 9eroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3	0.2 0.0 0.0 0.1 10-1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 93.0 1.1.15) (Th 99.0 99.0 99.0 99.0 99.0 99.0	OPHVGDYR QLVHELDEAEYR QLVHELDEAEYRDIR IOredoxin peroxidase 2) (Thioredoxin-depende ATAVMPDGOFKDISLSDVK ATAVMPDGOFKDISLSDVKGK GLFIIDDKGLIR IGHPAPNFK KOGGLGPMNIPLVSDPKR LVOAFOFTDK	953.4 1500.7 1884.9 nt peroxide red 2085.0 2270.1 1358.8 979.5 1906.0 1195.6	954.4 1501.7 1885.9 ductase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6	953.4 1500.7 1884.9 eration-associate 2085.0 2270.1 1358.8 979.5 1906.0 1195.6	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6
59.0 59.0 59.0 006830 48.0 48.0 48.0 48.0 48.0 48.0	12.9 12.9 12.9 PRDX1_HUMAN 18.3 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.0 10.0 1.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 93.0 1.1.15) (Th 99.0 99.0 99.0 99.0 99.0 99.0 99.0	OPHVGDYR QLVHELDEAEYR QLVHELDEAEYRDIR IOredoxin peroxidase 2) (Thioredoxin-depende ATAVMPDGOFKDISLSDVK ATAVMPDGOFKDISLSDVKK GLFIIDDKGILR IGHPAPNFK KOGGLGPMNIPLVSDPKR LVQAFOFTDK QITVNDLPVGR TIAQDVGVK	953.4 1500.7 1884.9 nt peroxide red 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6	954.4 1501.7 1885.9 ductase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6
59.0 59.0 59.0 90.6830 48.0 48.0 48.0 48.0 48.0 48.0 48.0	12.9 12.9 12.9 PRDX1_HUMAN 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3	0.2 0.0 0.0 0.1 10-1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 93.0 1.1.15) (Th 99.0 99.0 99.0 99.0 99.0 99.0	OPHVGDYR OLVHELDEAEYR OLVHELDEAEYRDIR JOTEDOXIN PEROXIGESE 2) (Thioredoxin-depende ATAM/PDGOFKDISLSDYK ATAM/PDGOFKDISLSDYKGK GLFIIDDKGUR IGHPAPNFK KOGGLGPMNIPLVSDPKR LVOAFOFTOK OITVNDLPVGR	953.4 1500.7 1884.9 nt peroxide red 2085.0 2270.1 1388.8 979.5 1906.0 1195.6 1210.7	954.4 1501.7 1885.9 Cluctase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0	953.4 1500.7 1884.9 Ceration-associate 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7
59.0 59.0 59.0 OCO6830 I 48.0 48.0 48.0 48.0 48.0 48.0 48.0 48.0	12.9 12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.1 1.1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 93.0 1.1.15) (Th 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	OPHVGDYR QLVHELDEAEYR QLVHELDEAEYRDIR JOTECOMIN PEROXICIASE 2) (Thioredoxin-depende ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYKGK GLFIIDDKGILR IGHPAPNFK KOGGLGPMNIPLVSDPKR LVQAFOFTDK QITVNDLPVGR TIAQDYGVLKADEGISFR ATAVMPDGOFK ATAVMPDGOFK ATAVMPDGOFKDISLSDYK	953.4 1500.7 1884.9 nt peroxide rec 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0	954.4 1501.7 1885.9 Guctase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0	953.4 1500.7 1884.9 eration-associate 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0
59.0 59.0 59.0 006830 48.0 48.0 48.0 48.0 48.0 48.0 48.0 48.0	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.1 1-1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 93.0 1.1.15) (Th 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	OPHVGDYR QLVHELDEAEYR QLVHELDEAEYRDIR JORDON OPTONICIONE ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYKGK GLFIIDDKGILR IGHPAPNFK KOGGLGPMNIPLVSDPKR LVQAFOFTDK QITVNDLPVGR TIAQDYCVLK ATAVMPDGOFK ATAVMPDGOFK ATAVMPDGOFK ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYKGK IGHPAPNFK	953.4 1500.7 1884.9 nt peroxide rev 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5	954.4 1501.7 1885.9 Suctase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1	963.4 1500.7 1884.9 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 116.6 2085.0 2270.1 979.5	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 980.5
59.0 59.0 59.0 006830 48.0 48.0 48.0 48.0 48.0 48.0 48.0 25.0 25.0 25.0 25.0	12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 12.3 12.3 12.3 12.3 12.3	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.0 0.1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 93.0 1.1.15) (Th 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	OPHVGDYR QLVHELDEAEYR QLVHELDEAEYRDIR Oredoxin peroxidase 2) (Thioredoxin-depende ATAVMPDGOFKDISLSDVK ATAVMPDGOFKDISLSDVKGK GLFIIDDKGGLR IGHPAPNEK KOGGLGPMNIPLVSDPKR LVQAFOFTOK QITVNDLPVGR TIAQDYGVLKADEGISFR ATAVMPDGOFK ATAVMPDGOFK ATAVMPDGOFK GATAVMPDGOFKDISLSDVK IGHPAPNEK KOGGLGPMNIPLVSDPKR LVGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	953.4 1500.7 1884.9 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 116.6 2085.0 2270.1 979.5 1906.0	954.4 1501.7 1885.9 20uctase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 2086.0 2271.1 980.5 1907.1	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 2085.0 2270.1 979.5 1906.0 1195.6	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 2086.0 2271.1 980.5 1907.1 1196.6
59.0 59.0 59.0 48.0 48.0 48.0 48.0 48.0 48.0 25.0 25.0 25.0 25.0 25.0 25.0	12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3 12	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.0 0.1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 93.0 1.1.15) 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.0	OPHVGDYR QLYHELDEAEYR QLYHELDEAEYR QLYHELDEAEYRDIR Oredoxin peroxidase 2) (Thioredoxin-depende ATAVMPDGOFKDISLSDVK ATAVMPDGOFKDISLSDVKGK GLFIIDDKGILR IGHPAPNEK KOGGLGPMNIPLVSDPKR LVOAFOFTDK OITVNDLPVGR TIAQDYCVLKADEGISFR ATAVMPDGOFK ATAVMPDGOFK ATAVMPDGOFKDISLSDVK ATAVMPDGOFKDISLSDVK GLTPAPNEK KOGGLGPMNIPLVSDPKR LVOAFOFTDK IGHPAPNEK KOGGLGPMNIPLVSDPKR LVOAFOFTDK IGHPAPNEK KOGGLGPMNIPLVSDPKR LVOAFOFTDK QITVNDLPVGR TIAQDYCVLKADEGISFR	953.4 1500.7 1884.9 nt peroxide res 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5 1906.0 1195.6 1210.7 1195.6	954.4 1501.7 1885.9 20uctase 2) (Prolif 2086.0 2271.1 13559.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 2086.0 2271.1 980.5 1907.1 1196.6 1211.7	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5 1906.0 1195.6 1210.7 195.6 1210.7	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 2086.0 2271.1 980.5 1907.1 1196.6 1211.7 1980.5
59.0 59.0 QO6830 48.0 48.0 48.0 48.0 48.0 48.0 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3 12	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.0 0.0 1.0 1.0 1.0 1.0	41.0 97.0 93.0 11.1.15) (Th 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	OPHVGDYR OLYHELDEAEYR QLVHELDEAEYR QLVHELDEAEYRIR Oredoxin peroxidase 2) (Thioredoxin-depende ATAWMPDGOFKDISLSDYKGK GLFIIDDKGLIR IGHPAPNEK KOGGLGPMNIPLVSDPKR LVQAFOFTDK OITVNDLPVGR TIAQDYGVLKADEGISFR ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK IGHPAPNEK KOGGLGPMNIPLVSDPK LVQAFOFTDK OITVNDLPVGR TIAQDYGVLKADEGISFR ATAWMPDGOFKDISLSDYK ATAWMPDGOFK	953.4 1500.7 1884.9 10 peroxide rev 2095.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5 1906.0 1195.6 1210.7 1996.0 1195.6	954.4 1501.7 1885.9 20uctase 2) (Prolif 2086.0 2271.1 13559.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 2086.0 2271.1 980.5 1907.1 1196.6 1211.7 1983.0 2085.1	953.4 1590.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5 1906.0 1195.6 1210.7 1982.0 1195.6 1210.7 1982.0 1195.6 1210.7 1982.0 1163.6	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 2086.0 2271.1 980.5 1907.1 1196.6 1211.7 1983.0 2086.0 1196.6
59.0 59.0 59.0 90.6830 Jt 48.0 48.0 48.0 48.0 48.0 48.0 25.0 25.0 25.0 25.0 25.0 25.0 25.0	12.9 12.9 12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3 12	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.0 0.1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 93.0 11.115) (Th 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	OPHVGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYRIR ORGOXIN PEROXIdase 2) (Thioredoxin-depende ATAWMPDGOFKDISLSDYKCK GLFIIDDKGILR IGHPAPNEK KOGGLGPMNIPLVSDPKR LVQAFOFTOK OITVNDLPVCR TIAQDYGVLK ATAWMPDGOFKDISLSDYK	953.4 1500.7 1894.9 nt peroxide rev 2095.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5 1906.0 1195.6 1210.7 1996.0 1195.6 2270.1 979.5 1906.0 1195.6 2270.1	954.4 1501.7 1885.9 2006.0 2271.1 13559.8 980.5 1907.0 1196.6 12211.7 1107.6 1983.0 2086.0 2271.1 980.5 1907.1 1196.6 2211.7 1196.6 2211.7 1196.6 2271.1 1196.6 2271.1	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1196.6 11982.0 1163.6 2085.0 2270.1 979.5 1906.0 1195.6 1210.7 1979.5 1906.0 1195.6 1210.7 1982.0 1163.6 2085.0 2	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 1980.5 1907.1 1196.6 1211.7 1196.6 1211.7 1980.5 1907.1 1196.6 1211.7 1983.0 2086.0 1164.6 2086.0 2271.1
59.0 59.0 006830]1 48.0 48.0 48.0 48.0 48.0 25.0 25.0 25.0 25.0 25.0 25.0 48.0 48.0 48.0 48.0 48.0 48.0 48.0 48	12.9 12.9 12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3 12	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	02 00 00 00 00 00 00 00 20 20 20 20 20 2	41.0 97.0 93.0 93.0 99.0 99.0 99.0 99.0 99.0 99	OPHVGDYR OLVHELDEAEYR QLVHELDEAEYR QLVHELDEAEYRDIR ORGOXIN PEROXIGIASE 2) (Thioredoxin-depende ATAWMPDGOFKDISLSDVK ATAWMPDGOFKDISLSDVKCK GLFIIDDKGILR IGHPAPNEK KOGGLGPMNIPLVSDPKR LVOAFOFTOK OITVNDLPVGR TIAQDYGVLK TIAQDYGVLK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK KOGGLGPMNIPLVSDPKR LVOAFOFTOK LVOAFOFTOK OITVNDLPVGR TIAQDYGVLKADEGISER ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYKGK GLFIIDDKGILR IGHPAPNEK	953.4 1500.7 1884.9 11 peroxide rec 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5 1906.0 1193.0 1106.6 1210.7 1106.6 1210.7 1106.6 1210.7 1106.6 1210.7	954.4 1501.7 185.9 2006.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 2271.1 1980.5 1907.1 1196.6 1211.7	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 1970.5 1906.0 1195.6 1210.7 1163.6 2085.0 2270.1 1982.0 1163.6 2085.0	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 2086.0 2271.1 980.5 1907.1 1196.6 1211.7 1198.3.0 1164.6 2086.0 2271.1 1980.5 1907.1 1196.6 1211.7 1983.0 2086.0 1164.6 2086.0 2086.0 2086.0
59.0 59.0 99.0 48.0 48.0 48.0 48.0 48.0 48.0 25.0 25.0 25.0 25.0 25.0 25.0 41.0 41.0	12.9 12.9 12.9 12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3 12	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	02 00 00 00 00 00 00 00 00 00 00 00 00 0	41.0 97.0 97.0 1.1.15) (Th 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	OPHVGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYRDR OORDOOR OF CONTROL OF CONTROL ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYKGK GLFIIDDKGILR IGHPANFK KOGGLGPMNIPLVSDPKR LVOAFOFTDK OITVNDLPVGR TIAADDYCVLK TIAADDYCVLKADEGISFR ATAVMPDGOFKDISLSDYKGK GLFIPANFK KOGGLGPMNIPLVSDPKR LVOAFOFTDK OITVNDLPVGR TIAADDYCVLKADEGISFR ATAVMPDGOFKDISLSDYKGK GLFPANFK KOGGLGPMNIPLVSDPKR LVOAFOFTDK OITVNDLPVGR TIAADDYGVLKADEGISFR ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDY	953.4 1500.7 1884.9 1 peroxide ret 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5 1906.0 1193.6 1210.7 1982.0 2270.1 2084.1 1163.6 2085.0 2270.1 379.5 1906.0	954.4 1501.7 1885.9 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 1980.5 1907.1 1196.6 1211.7 11983.0 2085.1 1196.6 2271.1 1164.6 2086.0 2271.1 1559.8 979.5	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 2085.0 2270.1 979.5 1906.0 1195.6 1210.7 1163.6 2085.0 2270.1 1982.0 1163.6 2085.0 2270.1 1982.0 1163.6 2085.0 2270.1 1982.0 1163.6 2085.0 2270.1 1982.0 1163.6 2085.0 2770.1 1982.0 2085.0 2770.1 1982.0 2085.0 2770.1 1982.0 2085.0 2770.1 1982.0 2085.0 2770.1 1982.0 2085.0 2770.1 1982.0 2085.0 2770.1 2085.0 2770.1	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 2086.0 2271.1 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 2086.0 2271.1 1196.6 1211.7 1983.0 1164.6 2086.0 2271.1 1359.8
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59.0 59.0 CO683O]I 48.0 48.0 48.0 48.0 48.0 48.0 59.0 25.0 25.0 25.0 25.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0 61.0 CO838O]I 436.0 CO2906]I	12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.0 0.1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 97.0 99.0	OPHYGDYR OLYHELDEAEYR OLYHELDEAEYROR OUTHELDEAEYROR OTHER OF THE STANDARD OF	953.4 1500.7 1884.9 11 percolde rec 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 1996.0 1195.6 1210.7 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1982.0 1195.6 1210.7 1982.0 2084.1 1163.6 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 2270.1 1982.0 2085.0 1195.6 11	954.4 1501.7 1885.9 ductase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 1196.6 1211.7 1883.0 164.6 2086.0 2271.1 1196.6 1211.7 1883.0 164.6 1211.7 1883.0 164.6 1211.7 1883.0 164.6 1211.7 1883.0 165.1 164.6 1211.7 1883.0 165.1 164.6 165.1 164.6 165.1 164.6 165.1 164.6 165.1 165.8 170.1	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2270.1 979.5 1906.0 1195.6 1210.7 1168.6 2270.1 1979.5 1906.0 1195.6 1210.7 1168.6 2270.1 1982.0 2085.0 1195.6 1193.6 1882.0 2770.1 1982.0 1195.6 1193.6 1882.0 279.5 1906.0 1195.6 1193.6 1882.0 270.1 1358.8 979.5 1906.0 1195.6 1195.6 1195.7 1196.6 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1195.7 1196.8 1196.	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 2086.0 2271.1 1983.0 1164.6 1281.7 1983.0 1164.6 1211.7 1196.6 1211.7 1196.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1280.5 1907.1 1196.6 1280.0 1196.6 1280.0 1196.6 1194.6 1898.0 1196.7 1196.6 1194.6 1198.0 1196.6 1194.6 1198.0 1196.6 1
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59.0 59.0 59.0 69.0 48.0 48.0 48.0 48.0 48.0 48.0 59.0 25.0 25.0 25.0 25.0 25.0 25.0 25.0 25	12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.1 0.2 0.0 0.0 0.1 0.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	41.0 97.0 17.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.	OPHYGDYR OLYHELDEAEYR OLYHELDEAEYR OLYHELDEAEYRDR OFFORD FORWIGHSE 2) (Thioredoxin-depende ATAVMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYKK ATAWMPDGOFKDISLSDYKK GLFIIDDKGILR IGHPANHK KOGGLGPMNIPLVSDPKR LVOAFOFTOK OITVNDLPYGR TIAODYCVLK TIAODYCVLK ATAWMPDGOFKDISLSDYK ATAWMPDGOFK	953.4 1500.7 1884.9 11 peroxide ret 2085.0 2270.1 3358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5 1906.0 11982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1982.0 2084.1 1183.6 1982.0 2270.1 1982.0 2270.1 1982.0 2084.1 1183.6 1982.0 2270.1 1985.6 1982.0 2270.1 1985.6 1982.0 2270.1 1356.8 978.5 1995.0 1195.6 1195.7 119	954.4 1501.7 1885.9 1885.9 1901.7 1885.9 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 1286.0 2271.1 1986.6 1211.7 1196.6 1211.7 1196.6 1211.7 1196.6 1211.7 11983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1196.6 1297.1 1196.6 1194.7 1983.0 2085.1 1196.6 1194.7 1983.0 2080.5 1211.7 1206.6 1598.7 1206.6 1598.7 1206.6 1598.7 1206.6 1598.7 1206.6 1328.7 1206.6 1206.7 1206.6 1206.7 1206.6 1206.7 1206.6 1206.7 1206.6 1206.7 1206.6 1206.7 120	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1282.0 1163.6 2085.0 2270.1 979.5 1906.0 1195.6 1210.7 1108.8 1982.0 2085.0 1270.1 1982.0 1195.6 1210.7 11982.0 1195.6 1210.7 11982.0 1195.6 1210.7 11982.0 2085.0 1195.6 1210.7 11982.0 2085.0 1195.6 1210.7 11982.0 2085.0 1195.6 1210.7 11982.0 2085.0 1195.6 1210.7 11982.0 2085.0 1195.6 1210.7 1210.7 1210.7 1210.7 1210.7 1220.5 1227.6 956.6 2670.2 983.6 3011.2 1755.9 11442.7	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 2086.0 2271.1 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 2086.0 2271.1 1196.6 1211.7 1983.0 2086.0 1211.7 1983.0 2086.0 1211.7 1983.0 980.5 1907.1 1196.6 1194.6 1983.0 980.5 1907.1 1196.6 1194.6 1983.0 980.5 1907.1 1196.6 1983.0 980.5 1907.1 1196.6 1983.0 980.5 1907.1 1196.6 1983.0 980.5 1907.1 1196.6 1983.0 980.5 11907.1 1196.6 1194.6 11983.0 1211.7 00.0 00.0 00.0 00.0 00.0 00.0 00.0
59.0 59.0 006830]t 48.0 48.0 48.0 48.0 48.0 59.0 25.0 25.0 25.0 25.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0 60.0 60.0 60.0 60.0	12.9 12.9 12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3 12	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.1-1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 97.0 99.0 99.0 99.0 99.0 99.0 99	OPHVGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYRDIR IOROGIN PEROXIGIASE 2) (Thioredoxin-depende ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK GLFIIDDKGILR IGHPAPNEK KOGGLGPMNIPLYSDPKR LVOAFOFTOK OITVNDLPVGR TIAODYGVLK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDY ATAWMPGOFKDISLSDY ATAWMPGOFKDISLSDY ATAWMPGOFKDISLSDY ATAWMPGOFKDISLSDY ATAMMPGOFKDISLSD	953.4 1500.7 1884.9 11 peroxide rev 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2270.1 1992.0 1163.6 2270.1 1998.0 1195.6 1210.7 1982.0 2270.1 1163.6 2085.0 2270.1 1163.6 2085.0 2270.1 1193.6 11	954.4 1501.7 1885.9 ductase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 1983.0 1164.6 1208.5 1907.1 1196.6 1211.7 1983.0 2085.1 1164.6 2086.0 2271.1 1983.0 1164.6 2086.0 2271.1 1983.0 1164.6 2085.1 1164.6 2085.1 1164.6 2085.1 1196.6 1211.7 1983.0 100.2 100	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1195.6 1195.0 1195.6 1195.0 1195.6 1210.7 1196.0 1195.6 1210.7 1982.0 2270.1 1979.5 1195.6 1195.6 1195.6 1195.6 1195.6 1195.6 1195.6 1195.6 1195.6 1195.6 1195.6 1195.7 1210.7 10 Mac-2 BP) (1 2451.1 1205.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7 12451.1 1255.5 1210.7	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 1983.0 1164.6 1211.7 11983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1286.0 1196.6 1194.6 1983.0 980.5 1907.1 1196.6 1194.6 1983.0 980.5 1211.7 MAC2BP) (Tumor 2452.1 1206.6 1598.7 ein 76) (DRBP76 1328.6 1596.7 2671.2 984.6 3012.2 984.6 3012.2 1756.9
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59.0 59.0 59.0 63.0] 48.0 48.0 48.0 48.0 48.0 59.0 25.0 25.0 25.0 25.0 41.0 41.0 41.0 41.0 41.0 41.0 60.0 60.0 60.0 60.0 60.0 60.0 60.0 6	12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	02 02 02 02 02 02 02 02 02 02 02 02 02 0	41.0 97.0 13.0 11.1.15) (Th 99.0 99.0 99.0 99.0 99.0 99.0 99.0 99.	OPHVGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYRDR OTER OF THE CONTROLL OF THE	953.4 1500.7 1884.9 11 peroxide ret 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 1992.0 1163.6 2085.0 2270.1 1992.0 1163.6 2085.0 2270.1 1992.0 1195.6 1210.7 1982.0 2270.1 1196.0 1210.7 1982.0 2270.1 1358.8 978.5 1906.0 1195.6 119	954.4 1501.7 1885.9 ductase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 2271.1 11983.0 1164.6 12211.7 1196.6 1211.7 1196.5 1907.1 1196.6 1211.7 1983.0 2085.1 1164.6 2086.0 2271.1 1164.6 1285.1 1164.6 1285.1 1164.6 1285.1 1164.6 1285.1 1164.6 1285.1 1164.6 1285.1 1164.6 1285.1 1164.6 1285.1 1164.6 1285.1 1285.8 1907.1 11983.0 1271.1 1285.8 1907.1 11983.0 1196.6 1194.7 1983.0 1196.6 1194.7 1983.0 1196.6 1194.7 11983.0 1196.6 1194.7 11983.0 1196.6 1194.7 11983.0 1196.6 1194.7 11983.0 1196.6 1194.7 1196.8 1196.6 1196.7 1196.8 1196.6 1196.7 1196.8 1196.6 1196.7 1196.8 1196.6 1196.7 1196.8 1196.	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 1979.5 1906.0 1195.6 1210.7 1182.0 2085.0 1210.7 1182.0 1163.6 2270.1 1982.0 1195.6 1210.7 1182.0 1163.6 1982.0 1195.6 1193.6 1982.0 1195.6 1193.6 1982.0 1995.0 1195.6 1193.6 1982.0 1995.0 1195.6 1193.6 1982.0 1995.0 1195.5 1195.7 1	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 1996.5 1907.1 1196.6 1211.7 11983.0 1164.6 2086.0 2271.1 1196.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1280.0 1164.6 1280.0 1164.6 1280.0 1164.6 1280.0 1271.1 1206.6 1194.6 1383.0 1211.7 1206.6 1598.7 1211.7 1206.6 1598.7 1328.6 957.6 957.6 957.6 957.6 957.6 957.6 944.3 1398.6 1444.7 1707.4 984.6 1756.9 984.6 1756.9 1726.8
59.0 59.0 59.0 63.0] 48.0 48.0 48.0 48.0 48.0 59.0 25.0 25.0 25.0 25.0 41.0 41.0 41.0 41.0 41.0 41.0 60.0 60.0 60.0 60.0 60.0 60.0 60.0 6	12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9	12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.1 0.2 0.0 0.2 0.0 0.2 0.0 0.0 0.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0	41.0 97.0 97.0 99.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0 90.0	OPHYGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYRDR OTERORIC OF THE CONTROLL ON THE CONTROLL OF THE CONTROLL OF THE CONTROLL ON	953.4 1500.7 1884.9 11 percolde ret 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 1982.0 1153.6 1210.7 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1196.6 1210.7 1982.0 2270.1 1358.8 978.5 1906.0 1195.6 1195.7 1210.7 121	954.4 1501.7 1885.9 ductase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1288.0 1164.6 2086.0 2271.1 1983.0 1164.6 1211.7 1983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1196.6 1211.7 1983.0 2085.1 1907.1 11559.8 979.5 1907.1 11559.8 979.5 1907.1 1196.6 1398.7 1211.7 1983.0 2080.5 1194.7 1983.0 2211.7 1983.0 221.7 1983.0 221.7 1983.0 221.7 1983.0 221.7 1983.0 2452.1 1206.6 1598.7 2452.1 2452.1 1206.6 1598.7 1598.7 1598.7 1598.7 1756.9 1443.7 1398.6 1444.7 1756.9 20plyydrolase) (L	953.4 1500.7 1884.9 eration-associate 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2285.0 1295.5 1906.0 1195.6 1210.7 1982.0 2085.0 1295.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1195.6 1320.6	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1283.0 1164.6 1298.3 1196.6 1211.7 1198.3 1196.6 1211.7 1983.0 2086.0 2271.1 1196.6 1211.7 1983.0 2086.0 2271.1 1196.6 1211.7 1983.0 2086.0 1164.6 1298.0 1164.6 1298.0 1164.6 1298.0 1164.6 1298.0 1164.6 1298.0 1164.6 1298.0 1164.6 1298.0 1164.6 1298.0 1164.6 1298.0 1164.6 1298.0 1164.6 1298.0 1
59.0 59.0 59.0 63.0] 48.0 48.0 48.0 48.0 48.0 59.0 25.0 25.0 25.0 25.0 41.0 41.0 41.0 41.0 41.0 41.0 60.0 60.0 60.0 60.0 60.0 60.0 60.0 6	12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9	12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 12.3 12.3 12.3 12.3 12.3 12.3 12.3 12	34.1 34.1 34.1 34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.1 0.2 0.0 0.0 0.2 0.0 0.0 0.0 0.0 0.0 0.0	41.0 97.0 97.0 99.0 99.0 99.0 99.0 99.0 99	OPHYGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYR OF CONTROL OF CONTROL ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDYK GLFIIDDKGLIR IGHPAPNEK KOGGLGPMNIPLVSDPKR LVOAFOFTOK OITVNDLPYGR TIAODYGVLK TIAODYGVLKADEGISFR ATAWMPDGOFKDISLSDYK ATAWMPDGOFKDISLSDY ATAWMPDGOFKDISLSDY ATAWMPDGOFKDISLSDY ATAWMPDGOFKDISLSDY ATAWMPDGOFKDISLSDY ATAWMPDGOFKDISLSDY ATAWMPDGOFKDI	953.4 1500.7 1884.9 11 peroxide ret 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 979.5 1906.0 1163.6 2085.0 2270.1 1982.0 1183.6 1210.7 1982.0 1195.6 1210.7 1982.0 1195.6 1210.7 1982.0 1195.6 1210.7 1982.0 1195.6 1210.7 1982.0 1195.6 1210.7 1982.0 1195.6 1210.7 1982.0 1195.6	954.4 1501.7 1885.9 1885.9 1901.7 1885.9 2086.0 2271.1 13559.8 980.5 1907.0 1196.6 1211.7 1107.6 1288.0 1164.6 2286.0 2271.1 11983.0 1164.6 1288.0 1298.5 1907.1 1196.6 1211.7 1183.0 2085.1 1164.6 2086.0 2271.1 1196.6 1211.7 1983.0 2085.1 1194.7 1983.0 2085.1 1164.6 2086.0 2271.1 1196.6 1211.7 1983.0 2085.1 1164.6 2086.0 2271.1 1359.8 979.5 1907.1 1196.6 1194.7 1283.0 980.5 1211.7 1206.6 1598.7 00uble-stranded F 1328.7 957.5 2671.2 984.6 3012.2 1756.9 1443.7 1398.6 1444.7 707.4 984.6 1726.8 1726.8 1726.8 1726.8 1726.8	953.4 1500.7 1884.9 eration-associate 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 1979.5 1906.0 1195.6 1210.7 1182.0 2085.0 2270.1 1982.0 1195.6 1210.7 1183.6 2085.0 1195.6 1210.7 1183.6 1882.0 2770.1 1358.8 979.5 1906.0 1195.6 1193.6 1892.0 270.1 1358.8 979.5 1906.0 1195.6 1193.6 1892.0 275.1 1210.7 1210	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 2086.0 2271.1 1983.0 1164.6 2086.0 2271.1 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1980.5 1907.1 1196.6 1194.6 1198.0 1211.7 1196.6 1194.6 1198.0 1211.7 1206.6 1598.7 1211.7 1328.6 957.6 957.6 1328.6 957.6 1328.6 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8
59.0 59.0 59.0 60.0 60.0 60.0 60.0 60.0 60.0 60.0 6	12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.1-1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 97.0 99.0 99.0 99.0 99.0 99.0 99	OPHVGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYROR OOR OF CONTROL OF CONTROL OF CONTROL	953.4 1500.7 1884.9 11 peroxide rec 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2270.1 1992.0 1195.6 1210.7 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1163.6 2270.1 1163.6 2270.1 1163.6 2270.1 1163.6 1210.7 1982.0 2270.1 1195.6 1210.7 1982.0 2270.1 1358.8 978.5 1906.0 1195.6 1193.6 1982.0 979.5 1210.7 1982.0 979.5 1210.7 1982.0 979.5 1210.7 1982.0 979.5 1210.7 1982.0 979.5 1210.7 1982.0 979.5 1210.7 1982.0 979.5 1210.7 1983.6 1983.6 1983.6 1983.6 1983.6 1983.6 1983.6 1983.6 1983.6 1983.6 1983.6 1983.6 1755.9 1015.9	954.4 1501.7 1885.9 ductase 2) (Prolif 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 2086.0 2271.1 1983.0 1164.6 2086.0 2271.1 1996.6 1211.7 1983.0 2085.1 1196.6 1211.7 1893.0 2085.1 1196.6 1211.7 1893.0 2085.1 1196.6 1211.7 1893.0 2085.1 1196.6 1211.7 1893.0 2085.1 1196.6 1211.7 1893.0 2086.0 2271.1 1206.6 1398.7 150.1 1983.0 2080.5 1194.7 1983.0 2080.5 1194.7 1983.0 2080.5 1194.7 1983.0 2080.5 1194.7 1983.0 2080.5 1194.7 1983.0 2080.5 1194.7 1983.0 2080.5 1194.7 1196.6 1194.7 1198.7 1206.6 1398.7 2452.1 1206.6 1398.7 2452.1 1206.6 1398.7 1206.6 1398.7 1206.9 1443.7 1398.6 1444.7 177.0 1766.9 1726.8 1724.9 1726.8	953.4 1500.7 1884.9 eration-associate 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 199.5 1906.0 1195.6 1210.7 1982.0 2085.0 1296.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1195.6 1320.6 2670.2 283.6 3011.2 1327.6 956.6 2670.2 983.6 3011.2 1755.9 1442.7 1397.6 1443.7 706.4 983.6 1725.8 1725.8	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1283.0 1164.6 1298.0 2271.1 1983.0 2086.0 2271.1 196.6 1211.7 1983.0 2086.0 2271.1 196.6 1211.7 1983.0 2086.0 2271.1 196.6 1211.7 1983.0 2086.0 2271.1 195.6 1211.7 1983.0 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1983.0 2086.0 2271.1 1359.8 980.5 1907.6 1194.6 1983.0 286.0 1164.6 1983.0 106.6 1957.6 194.6 1983.0 174.6 1983.0 174.6 1983.0 175.6 1983.0 174.6 1983.0 175.6 1983.0 175.6 1983.0 176.6 1984.6 176.6 176.6 177.7 176.8 176.8 176.8 176.8 176.8 176.8 176.8
59.0 59.0 CO683O] 48.0 48.0 48.0 48.0 48.0 59.0 25.0 25.0 25.0 25.0 41.0 41.0 41.0 41.0 41.0 41.0 60.0 60.0 60.0 60.0 60.0 60.0 60.0 6	12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 97.0 99.0 99.0 99.0 99.0 99.0 99	OPHVGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYROR OUTHELDEAEYRDR OTERORITION	953.4 1500.7 1884.9 1184.9 1185.6 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 1979.5 1906.0 1195.6 1210.7 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1982.0 2270.1 1983.0 2270.1 1183.6 1210.7 1982.0 2270.1 1183.6 1295.0 1295.0 1195.6 1193	954.4 1501.7 1885.9 1885.9 1901.7 1885.9 1902.0 1196.6 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 1983.0 1164.6 2086.0 1211.7 1196.3 1001.1 1196.6 1211.7 1196.3 1001.1 1196.6 1211.7 11983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1211.7 1983.0 1211.7 1983.0 1211.7 1983.0 1001.1 1359.8 1979.5 1907.1 1196.6 1194.7 1983.0 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 1206.6 1598.7 1001.1 10	953.4 1500.7 1884.9 eration-associate 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 1979.5 1906.0 1195.6 1210.7 1982.0 2085.0 1195.6 1210.7 1982.0 1183.6 2085.0 1183.6 1982.0 1183.6 1982.0 1183.6 1982.0 1183.6 1982.0 1183.6 1982.0 1183.6 1983.6 1983.6 1983.6 1983.6 1983.6 1983.6 2755.9 11442.7 1327.6	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 980.5 1907.1 1196.6 1211.7 11983.0 1164.6 2086.0 2271.1 1196.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1283.0 1164.6 1283.0 1164.6 1283.0 11750.8 180.5 1211.7 1206.6 1598.7 121.7 1206.6 1598.7 121.7 1206.6 1598.7 1328.6 1597.6 1328.6 1597.6 1328.6 1597.6 1328.6 1597.6 1328.6 1597.6 1328.6 1597.6 1328.6 1597.6 1328.6 1597.6 1328.6 1597.6 1328.6 1597.6 1597.6 1756.9 1443.7 1756.9 1443.7 1756.9 1756.9 1756.9 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8
59.0 59.0 CO683O]I 48.0 48.0 48.0 48.0 48.0 59.0 25.0 25.0 25.0 25.0 41.0 41.0 41.0 41.0 41.0 41.0 41.0 60.0 60.0 60.0 60.0 60.0 60.0 60.0 6	12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9	12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.0 0.1 0.1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 97.0 99.0 99.0 99.0 99.0 99.0 99	OPHVGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYROR OUTHELDEAEYRDR OTER OF THE STANDARD OF THE S	953.4 1500.7 1884.9 1500.7 1884.9 1884	954.4 1501.7 1885.9 1201.7 1885.9 1201.7 1885.9 1201.7 13559.8 1907.0 1196.6 1211.7 1107.6 1983.0 1164.6 1286.0 1271.1 1983.0 1164.6 1286.0 1271.1 1983.0 1164.6 1286.0 1271.1 1196.6 1286.0 1271.1 1196.6 1286.0 1271.1 1196.6 1286.0 1271.1 1196.6 1286.0 1271.7 1883.0 1285.1 1164.6 1286.0 1271.1 1286.0 1271.1 1286.0 1271.1 1286.0 1286.0 1271.1 1286.0 1286.0 1271.1 1286.0 1286.0 1297.1 1298.0 12	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2085.0 2270.1 1979.5 1163.6 2085.0 1195.6 1210.7 1182.0 1163.6 2085.0 1195.6 1210.7 1982.0 1163.6 2270.1 1979.5 1163.6 1210.7 1982.0 1163.6 1210.7 1982.0 1163.6 1285.0 1195.6 1195.8 1175.8 1175.8 1175.8 1175.8 1196.0 2581.4 3112.4	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1983.0 1164.6 2086.0 2271.1 1980.5 1907.1 1196.6 1211.7 11983.0 1164.6 2086.0 2271.1 1196.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1983.0 1175.9 1907.1 1196.6 1196.6 1196.6 1196.6 1196.6 1196.6 1196.7 121.7 1206.6 1598.7 121.7 1206.6 1598.7 121.7 1398.6 1328.6 1338.6 1338.6 1338.6 1348.7 134
59.0 59.0 59.0 60.0 48.0 48.0 48.0 48.0 48.0 48.0 55.0 25.0 25.0 25.0 25.0 25.0 25.0 25	12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9	12.9 12.9 12.9 12.9 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	34.1 34.1 34.1 34.1 34.1 34.1 Peroxiredoxi 55.3 55.3 55.3 55.3 55.3 55.3 55.3 55.	0.2 0.0 0.2 0.0 0.1 (EC 1.1 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	41.0 97.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19	OPHYGDYR OLVHELDEAEYR OLVHELDEAEYR OLVHELDEAEYROR OLVHELDEAEYRDR OFFORD FORWIGHSE 2) (Thioredoxin-depende ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDYK GLFIIDDKGLIR IGHPAPNEK KOGGLGPMNIPLVSDPKR LVOAFOFTOK OITVNDLPYGR TIAODYGVLK ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDY ATAVMPDGOFKDISLSDYK ATAVMPDGOFKDISLSDY ATAVMPDGOFKDISLSDY ATAVMPDGOFKDISLSDY ATAVMPDGOFKDISLSDY ATAVMPDGOFKDISLSDY ATAVMPDGOFKDISLSDY ATAVMPDGOF	953.4 1500.7 1884.9 11 peroxide ret 2035.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1982.0 1163.6 2025.0 2270.1 1992.0 1163.6 2025.0 2270.1 1992.0 1195.6 1210.7 1992.0 20270.1 1992.0 20270.1 1992.0 1195.6 1210.7 1992.0 1195.6 1196.0 1196.	954.4 1501.7 1885.9 1201.7 1885.9 2086.0 2271.1 1359.8 980.5 1907.0 1196.6 1211.7 1107.6 1288.0 1196.6 1288.0 12971.1 1983.0 1164.6 1288.0 1298.1 1196.6 1211.7 11983.0 2085.1 1196.6 1211.7 11983.0 2085.1 1196.6 1211.7 11983.0 2085.1 1194.7 1983.0 2085.1 1194.7 1983.0 2085.1 1194.7 1983.0 2085.1 1211.7 2-2-binding protei 12452.1 1206.6 1598.7 20uble-stranded F 1328.7 957.5 2671.2 984.6 3012.2 1756.9 1443.7 1398.6 1444.7 707.4 984.6 1726.8 1726.8 1726.8 991.5 991.5	953.4 1500.7 1884.9 eration-associat 2085.0 2270.1 1358.8 979.5 1906.0 1195.6 1210.7 1106.6 1282.0 1163.6 2085.0 2270.1 979.5 1906.0 1195.6 1210.7 11982.0 2085.0 2270.1 1979.5 1906.0 1195.6 1210.7 1182.0 2085.0 1195.6 1210.7 1183.6 182.0 2791.1 1358.8 979.5 1906.0 1195.6 1210.7 1195.6 1210.7 1195.6 1321.0 1195.6 1320.0 1195.6 1321.0 1338.8 979.5 1396.0 1195.6 1321.7 1398.0 1398.0 1398.0 1398.1 1399.6 1442.7 1397.6 1443.7 706.4 983.6 1397.6 1443.7 706.4 983.6 1755.9 1755.9 1755.8 1725.8	954.4 1501.7 1885.9 ed gene protein) 2086.0 2271.1 1359.8 980.5 1907.1 1196.6 1211.7 1107.6 1288.0 1164.6 1288.0 1271.1 1980.5 1907.1 1196.6 1211.7 1196.6 1211.7 1196.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1164.6 1211.7 1983.0 1208.0 1211.7 1983.0 1211.7 1983.0 1211.7 1983.0 1211.7 1983.0 1211.7 1983.0 1211.7 1359.8 190.5 1190.6 1194.6 1328.6 1591.7 1328.6 1591.7 1328.6 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8 1726.8

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	YDGSTIVPGEQGAEYQHFIQQCTDDVR	3112.4	3113.4	3112.4	3113.4
85.0	INRPD_HUMAN 12.2	12.2	Heterogened	ous nuclear 2.0	99.0	protein DO (hnRNP DO) (AU-rich element R FGEVVDCTLKLDPITGR	1919.0	1920.0	ns (Human) 1919.0	1920.0
85.0	12.2	12.2	35.2	2.0	99.0	GFCFITFK	1018.5	1019.5	1018.5	1019.5
85.0	12.2	12.2	35.2	2.0	99.0	GFCFITFKEEEPVKK	1857.9	1858.9	1857.9	1858.9
85.0	12.2	12.2	35.2	2.0	99.0	GFGFVLFK	913.5	914.5	913.5	914.5
85.0	12.2	12.2	35.2	2.0	99.0	IFVGGLSPDTPEEK	1487.7	1488.8	1487.8	1488.8
85.0	12.2	12.2	35.2	2.0	99.0	SRGFGFVLFK	1156.6	1157.6	1156.6	1157.6
85.0	12.2	12.2	35.2	0.1	21.0	IFVGGLSPDTPEEKIR	1756.9	1757.9	1756.9	1757.9
157.0	2.0	4.0	11.0	2.0	99.0	GFCFITFKEEEPVKK	1857.9	1858.9	1857.9	1858.9
157.0	2.0	4.0	11.0	0.0	99.0	GFGFVLFK	913.5	914.5	913.5	914.5
	F3A_HUMAN 8.2	8.2			nitiation fac	tor 3 subunit 10 (el F-3 theta) (el F3 p167) RGADDDRPSWR				
137.0	8.2	8.2	16.1	2.0	99.0	WGDRDSEGTWR	1363.6	1364.6	1363.6	1364.6
137.0	8.2	8.2	16.1		98.0	RGLDDDRGPWR	1341.7	1342.7	1341.7	1342.7
137.0	8.2	8.2	16.1	1.5	97.0	RGMDDDRGPR	1203.5	1204.5	1203.5	1204.5
137.0	8.2		16.1	0.8	83.0	EELEQREAELQKVR	1769.9	1770.9	1769.9	1770.9
137.0 137.0 137.0	8.2 8.2	8.2 8.2	16.1 16.1 16.1	0.1 0.0	25.0 96.0	DLRDDRDRRGPPLR WGDRDSEGTWR	1761.9 1363.6	1762.9 1364.6	1761.9 1363.6	17762.9 1364.6
404.0 Q14764IN	1.3	1.3	16.4	1.2	94.0	WGDRDSEGTWR	1363.6	1364.6	1363.6	1364.6
122.0	9.5 9.5	9.5	Major vault 13.9	2.0	99.0	ALQPLEEGEDEEKVSHQAGDHWLIR	2886.4	2887.4	2886.3	2887.3
122.0	9.5	9.5	13.9	2.0	99.0	VPHNAAVQVYDYR	1530.8	1531.8	1530.8	1531.8
122.0		9.5	13.9	1.3	95.0	ATEEFIIR	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	SLQPLAPR	880.5	881.5	880.5	881.5
122.0	9.5	9.5	13.9	0.6	77.0	DAQGLVLFDVTGQVR	1616.8	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	DAQGLVLFDVTGQVR	1616.9	1617.9	1616.9	1617.9
145.0	5.1	5.1	15.8	2.0	99.0	VPHNAAVQVYDYR	1530.8	1531.8	1530.8	1531.8
145.0	5.1	5.1	15.8	1.0	90.0	ATEEFIIR	1019.5	1020.5	1019.5	1020.5
Q14847 L 72.0	ASP1_HUMAN 14.1	14.1	LIM and SH3 37.9	3 domain pro 2.0	otein 1 (LAS 99.0	GP-1) (MLN 50) - Homo sapiens (Human) GFSVVADTPELQR	1417.7	1418.7	1417.7	1418.7
72.0	14.1	14.1	37.9	2.0	99.0	GYEKKPYCNAHYPK	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	LKOOSELOSOVR	1442.8	1443.8	1442.8	1443.8
72.0	14.1	14.1	37.9		99.0	NYKGYEKKPYCNAHYPK	2159.0	2160.0	2159.0	2160.0
72.0	14.1	14.1	37.9	2.0	99.0	QSFTMVADTPENLR	1590.7	1591.8	1590.7	1591.7
72.0	14.1	14.1	37.9		99.0	TQDQISNIKYHEEFEK	2007.9	2009.0	2008.0	2009.0
124.0 124.0	6.0	6.0	33.7 33.7	2.0	99.0 99.0	GKGFSVVADTPELQR	1602.8 2159.0	1603.8 2160.0	1602.8	1603.8 2160.0
124.0	6.0	6.0 6.0	33.7	2.0	99.0	NYKGYEKKPYCNAHYPK TQDQISNIKYHEEFEK	2008.0	2009.0	2159.0 2008.0	2009.0
78.0	NONO_HUMAN	15.9	33.3	2.0	99.0	er-binding protein (NonO protein) (54 kDa FACHSASLTVR	1247.6	1248.6	1247.6	1248.6
78.0	13.4	15.9	33.3	2.0	99.0	FAQPGSFEYEYAMR	1694.7	1695.7	1694.7	1695.7
78.0	13.4	15.9	33.3	2.0	99.0	HEHQVMLMR	1179.6	1180.6	1179.6	1180.6
78.0	13.4	15.9	33.3	2.0	99.0	RQQEGFKGTFPDAR	1635.8	1636.8	1635.8	1636.8
78.0	13.4	15.9	33.3	1.3	95.0	FGQAATMEGIGAIGGTPPAFNR	2162.0	2163.0	2162.1	2163.1
78.0	13.4	15.9	33.3	1.2	99.0	GIVEFSGKPAAR	1230.7	1231.7	1230.7	1231.7
78.0	13.4	15.9	33.3	1.2	99.0	MEELHNQEVQKR	1539.8	1540.8	1539.7	1540.8
78.0	13.4	15.9	33.3	1.1	99.0	RMEELHNOEVOKR	1695.9	1696.9	1695.8	1696.9
78.0	13.4	15.9	33.3	0.5	67.0	EQPPRFAQPGSFEYEYAMR	2302.0	2303.0	2302.0	2303.1
78.0	13.4	15.9	33.3	0.1	21.0	ALIEMEKQQQDQVDR	1829.9	1830.9	1829.9	1830.9
232.0	2.6	2.6	21.4	1.4	96.0	MEELHNQEVQKR	1539.7	1540.8	1539.7	1540.8
232.0 Q16181 S	2.6 SEPT7_HUMAN	2.6	21.4 Septin-7 (CI	1.2 DC10 proteir	93.0 homolog)	HEHQVMLMR - Homo sapiens (Human)	1179.6	1180.6	1179.6	1180.6
406.0	2.3	2.3	9.8	1.3	95.0	RROFEDEKANWEAQQR	2090.0	2091.0	2090.0	2091.0
406.0	2.3	2.3	9.8	0.6	74.0	QFEDEKANWEAQQR	1777.8	1778.8	1777.8	1778.8
406.0 406.0	2.3	2.3 2.3	9.8 9.8	0.3	48.0 20.0	FEDYLNAESR NLEGYVGFANLPNQVYR	1242.6 1953.0	1243.6 1954.0	1242.6 1953.0	1243.6 1954.0
206.0	3.5	3.5	10.3	2.0	99.0	QFEDEKANWEAQQR	1777.8	1778.8	1777.8	1778.8
206.0	3.5	3.5	10.3	1.5	97.0	NLEGYVGFANLPNQVYR	1953.0	1954.0	1953.0	1954.0
Q16555 E						n 2 (DRP-2) (Collapsin response mediator THNSSLEYNIFEGMECR				
336.0	3.5	3.5	5.9	2.0	99.0	THNSSLEYNIFEGMECR	2085.9	2086.9	2085.9	2086.9
336.0		3.5	5.9	1.5	97.0	VFNLYPR	907.5	908.5	907.5	908.5
	SCN1_HUMAN 2.5					a actin-bundling protein) (p55) - Homo sa YLAADKDGNVTCER		1611.7	1610.7	1611.7
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		99.0	NASCYFDIEWR	1459.6	1460.6	1459.6	1460.6
Q16881 T	RXR1_HUMAN	2.4	Thioredoxin	reductase 1	, cytoplasm	nic precursor (EC 1.8.1.9) (TR) (TR1) - Hon	no sapiens (Human)			
392.0 392.0	2.4	2.4	9.2 9.2	2.0 0.4	99.0 58.0	WGLGGTCVNVGCIPK VMVLDFVTPTPLGTR	1616.8 1644.9	1617.8 1645.9	1616.8 1644.9	1617.8 1645.9
	2.0 NBP_HUMAN	2.0				VEETVKHDWDR n (CNBP) (Zinc finger protein 9) - Homo sa		1413.7	1412.7	1413.7
353.0	3.2	3.2	43.5	2.0	99.0	EQCCYNCGKPGHLAR	1848.8	1849.8	1848.8	1849.8
353.0	3.2	3.2	43.5	1.2	94.0	CGESGHLAKDCDLQEDACYNCGR	2697.0	2698.0	2697.0	2698.0
	2.0 MLRM_HUMAN	2.0				EQCCYNCGKPGHLAR Insarcomeric (Myosin RLC) - Homo sapiens		1849.8	1848.8	1849.8
151.0	8.0	8.0	29.1	2.0	99.0	ELLTTMGDRFTDEEVDELYR	2431.1	2432.1	2431.1	2432.1
151.0	8.0	8.0	29.1	2.0	99.0	FTDEEVDELYR	1414.6	1415.6	1414.6	1415.6
151.0	8.0	8.0	29.1	2.0	99.0	GNFNYIEFTR	1259.6	1260.6	1259.6	1260.6
151.0	8.0	8.0	29.1	2.0	99.0	NAFACFDEEATGTIQEDYLR	2349.0	2350.0	2349.0	2350.0
146.0	2.1	2.1	17.4	2.0	99.0	GNFNYIEFTR	1259.6	1260.6	1259.6	1260.6
128.0	6.0	6.0	33.9	2.0	99.0	ELLTTMGDRFTDEEVDELYR	2431.2	2432.2	2431.1	2432.1
128.0	6.0	6.0	33.9	2.0	99.0	GNFNYIEFTR	1259.6	1260.6	1259.6	1260.6
128.0	6.0	6.0	33.9	2.0	99.0	NAFACFDEEATGTIQEDYLR	2349.0	2350.0	2349.0	2350.0
Q6FI 13 H 111.0	12A2A_HUMAN 3.1	3.1	Histone H2A 52.3	type 2-A (F 2.0	99.0	mo sapiens (Human) AGLQFPVGR	943.5	944.5	943.5	944.5
111.0	3.1	3.1	52.3	1.1	92.0	HLQLAIR	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	HLQLAIR	849.5	850.5	849.5	850.5
129.0	6.0	6.0	39.2		99.0	NDEELNKLLGR	1299.7	1300.7	1299.7	1300.7
	132_HUMAN 7.9		Histone H3.2			no sapiens (Human) EIAQDFKTDLR	1334.6	1335.6	1334.7	1335.7
154.0 154.0 154.0	7.9 7.9	7.9 7.9	41.2 41.2 41.2	2.0 2.0 2.0	99.0 99.0	KSAPATGGVKKPHR STELLIR	1488.9 830.5	1489.9 831.5	1488.9 830.5	1489.9 831.5
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 7.9	7.9 7.9 7.9	41.2 41.2 41.2	0.0	99.0 99.0	EIAQDFKTDLR	1348.7	1349.7	1348.7	1349.7
154.0 112.0	6.9	6.9	37.5	0.0 2.0	99.0	KSAPATGGVKKPHR EIAQDFKTDLR	1474.9 1334.7	1475.9 1335.7	1474.8 1334.7	1475.8 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		99.0	YRPGTVALR	1031.6	1032.6	1031.6	1032.6
112.0	6.9	6.9	37.5	0.7	80.0	KLPFQR	787.5	788.5	787.5	788.5
112.0	6.9	6.9	37.5	0.1	23.0	STELLIR	830.5	831.5	830.5	831.5
112.0	6.9	6.9	37.5	0.0	99.0	EIAQDFKTDLR	1348.7	1349.7	1348.7	1349.7
112.0	6.9	6.9	37.5	0.0	53.0	EIAQDFKTDLR	1362.7	1363.7	1362.7	1363.7
112.0	6.9	6.9	37.5	0.0	41.0	KLPFQR	787.5	788.5	787.5	788.5
139.0	2.1	2.1	19.1	2.0	99.0	EIAQDFKTDLR	1334.6	1335.6	1334.7	1335.7
139.0	2.1 JRP2_HUMAN	2.1	19.1 Unc-112-rel	0.1	24.0	STELLIR 3) (MIG2-like) - Homo sapiens (Human)	830.5	831.5	830.5	831.5
409.0	2.2	2.2	12.7	2.0	99.0	LLVPSPEGMSEIYLR	1702.9	1703.9	1702.9	1703.9
409.0	2.2	2.2	12.7	0.2	36.0	VVLAGGVAPALFR	1268.8	1269.8	1268.8	1269.8
319.0	2.0 IRB4_HUMAN	2.0	9.9	2.0	99.0	VVLAGGVAPALFR eptor subfamily B member 4 precursor (Le	1268.8	1269.8	1268.8	1269.8
327.0	3.7	3.7	7.1	2.0	99.0	SPMDTFLLIK	1163.6	1164.6	1163.6	1164.6
327.0	3.7	3.7	7.1	1.7	98.0	FSIPSMTEDYAGR	1472.7	1473.7	1472.7	1473.7
191.0										
	1.9	1.9	5.1	1.7	98.0	SPMDTFLLIK	1163.6	1164.6	1163.6	1164.6
191.0 260.0 260.0										

260.0	2.2 HS105_HUMAN	2.2	16.7	0.3 protein 105 k	46.0	SPMDTFLLIK hock 110 kDa protein) (Antigen NY-CO-25)	1163.6	1164.6	1163.6	1164.6
290.0 290.0	4.0 4.0	4.0 4.0	6.9 6.9	2.0 2.0	99.0 99.0	GCALQCAILSPAFK NAVEEYVYEFR	1534.8 1401.6	1535.8 1402.6	1534.8 1401.6	1535.8 1402.6
290.0	4.0	4.0	6.9	0.0	99.0	NAVEEYVYEFR	1417.7	1418.7	1417.7	1418.7
194.0 194.0	1.7 1.7	1.7 1.7	10.7 10.7	1.7 0.0	98.0 97.0	NAVEEYVYEFR NAVEEYVYEFR	1417.7 1401.6	1418.7 1402.6	1417.7 1401.6	1418.7 1402.6
	2.0 GALM_HUMAN	2.0	9.6 Aldose 1-epi			NAVEEYVYEFR alactose mutarotase) - Homo sapiens (Hum		1418.7	1417.7	1418.7
148.0 148.0	8.0 8.0	8.0 8.0	19.3 19.3	2.0 2.0	99.0 99.0	FQLQSDLLR GFDKVLWTPR	1118.6 1217.7	1119.6 1218.7	1118.6 1217.7	1119.6 1218.7
148.0 148.0	8.0 8.0	8.0 8.0	19.3 19.3	2.0	99.0 99.0	HSGFCLETQNWPDAVNQPR QPYFGAVIGR	2255.0 1106.6	2256.0 1107.6	2255.0 1106.6	2256.0 1107.6
274.0 Q96CX2	2.1	2.1	14.0 BTB/POZ do	2.0	99.0	HSGFCLETQNWPDAVNQPR	2255.0	2256.0	2255.0	2256.0
474.0	2.0	2.0	7.4	2.0	99.0	EAEYFELPELVR	1493.7	1494.8	1493.7	1494.7
139.0 139.0	5.7 5.7	5.7 5.7	25.5 25.5	2.0 2.0	99.0 99.0	DLQLVLPDYFPER MFTQQQPQELAR	1603.8 1475.7	1604.8 1476.7	1603.8 1475.7	1604.8 1476.7
139.0 Q96EP5	5.7 DAZP1_HUMAN	5.7	25.5 DAZ-associa		98.0 (Deleted i	EAEYFELPELVR n azoospermia-associated protein 1) - Hom			1493.7	1494.7
283.0 283.0	4.0 4.0	4.0 4.0	11.3 11.3	2.0 2.0	99.0 99.0	LFVGGLDWSTTQETLR SQAPGQPGASQWGSR	1821.9 1512.7	1822.9 1513.7	1821.9 1512.7	1822.9 1513.7
395.0 Q961U4	1.5 ABHEB_HUMAN	1.5	7.6 Abhydrolase	1.4 domain-con	96.0 taining pro	SQAPGQPGASQWGSR tein 14B (EC 3) (CCG1-interacting fact	1512.7 or B) - Homo sapier	1513.7 ns (Human)	1512.7	1513.7
308.0 308.0	4.0 4.0	4.0 4.0	11.4 11.4	2.0 2.0	99.0 99.0	FSSETWONLGTLHR FSVLLLHGIR	1674.8 1153.7	1675.8 1154.7	1674.8 1153.7	1675.8 1154.7
236.0 236.0	2.5	2.5	11.4 11.4	2.0	99.0 66.0	FSSETWQNLGTLHR FSVLLLHGIR	1674.8	1675.8 1154.7	1674.8 1153.7	1675.8
Q96KP4	CNDP2_HUMAN	2.5	Cytosolic nor	nspecific dip	eptidase (C	NDP dipeptidase 2) (Glutamate carboxype		1) - Homo sapi	ens (Human)	1154.7
347.0 347.0	3.3 3.3	3.3 3.3	8.4 8.4	2.0 1.3	99.0 95.0	WVAIQSVSAWPEKR TGQEIPVNVR	1655.9 1111.6	1656.9 1112.6	1655.9 1111.6	1656.9 1112.6
253.0 253.0	2.2 2.2	2.2 2.2	7.4 7.4	2.0 0.1	99.0 26.0	TVFGVEPDLTR TGQEIPVNVR	1232.6 1111.6	1233.7 1112.6	1232.6 1111.6	1233.6 1112.6
Q99497 120.0	PARK7_HUMAN 9.6	9.6	Protein DJ-1 28.6	(Oncogene	DJ1) (Parki 99.0	nson disease protein 7) - Homo sapiens (H DKMMNGGHYTYSENRVEK	uman) 2159.0	2160.0	2158.9	2159.9
120.0 120.0		9.6 9.6	28.6 28.6	2.0 2.0	99.0 99.0	GAEEMETVIPVDVMR GAEEMETVIPVDVMRR	1674.8 1830.9	1675.8 1831.9	1674.8 1830.9	1675.8 1831.9
120.0 120.0		9.6 9.6	28.6 28.6	2.0	99.0 97.0	MMNGGHYTYSENR VTVAGLAGKDPVQCSR	1559.6 1656.9	1560.6 1657.9	1559.6 1656.9	1560.6 1657.9
266.0 266.0	2.1 2.1	2.1	20.1 20.1	1.4	96.0 80.0	AGIKVTVAGLAGKDPVQCSR MMNGGHYTYSENRVEK	2026.1 1915.8	2027.1 1916.8	2026.1 1915.8	2027.1 1916.8
177.0 Q9BRA2	2.0	2.0	14.8 Thioredoxin-	2.0	99.0	GAEEMETVIPVDVMR hioredoxin-related protein) (TRP14) (Protein)	1674.8	1675.8	1674.8	1675.8
307.0	4.0	4.0	19.5	2.0	99.0	TIFAYFTGSK	1133.6	1134.6	1133.6	1134.6
307.0 358.0	4.0 2.0	4.0 2.0	19.5 11.4	2.0	99.0 99.0	YEEVSVSGFEEFHR YEEVSVSGFEEFHR	1713.8 1713.8	1714.8 1714.8	1713.8 1713.8	1714.8 1714.8
213.0	SH3L3_HUMAN 6.0	6.0	SH3 domain- 31.2	2.0	amic acid-r 99.0	ich-like protein 3 (SH3 domain-binding pro IQYQLVDISQDNALR	1774.9	1775.9	1774.9	1775.9
213.0 213.0		6.0 6.0	31.2 31.2	2.0 2.0	99.0 99.0	IQYQLVDISQDNALRDEMR VYSTSVTGSR	2306.1 1055.5	2307.1 1056.5	2306.1 1055.5	2307.1 1056.5
176.0 340.0	2.0 2.0	2.0 2.0	20.4 49.5	2.0 2.0	99.0 99.0	IQYQLVDISQDNALRDEMR IQYQLVDISQDNALRDEMR	2306.1 2306.1	2307.1 2307.1	2306.1 2306.1	2307.1 2307.1
Q9NUV9 105.0	GIMA4_HUMAN 10.4	10.4	GTPase I MAI	P family mer 2.0	nber 4 (I mr 99.0	nunity-associated protein 4) (Immunity-as AAQYGSMSFNPSTPGASYGPGR	sociated nucleotide 2244.0	2245.0 (hl	AN1) - Homo sapi 2244.0	iens (Human) 2245.0
105.0 105.0	10.4 10.4	10.4 10.4	24.9 24.9	2.0	99.0 99.0	AEEEIQKQTQAMQELHR AQLLGLIQR	2068.0 1010.6	2069.0 1011.6	2068.0 1010.6	2069.0 1011.6
105.0 105.0	10.4 10.4	10.4 10.4	24.9 24.9	2.0 2.0	99.0 99.0	KLAEQEAHYAVR LAEQEAHYAVR	1413.7 1285.6	1414.7 1286.6	1413.7 1285.6	1414.7 1286.6
105.0 213.0	10.4	10.4	24.9 23.1	0.4 1.3	57.0 95.0	SFMILIFTR LAEQEAHYAVR	1126.6 1285.6	1127.6 1286.6	1126.6 1285.6	1127.6 1286.6
118.0	6.4	6.4	26.1	2.0	99.0	IREEYEEKIR	1363.7	1364.7	1363.7	1364.7
118.0 118.0	6.4 6.4	6.4 6.4	26.1 26.1	2.0 1.3	99.0 95.0	LAEQEAHYAVR IREEYEEKIRKLEDKVEQEKR	1285.6 2771.5	1286.7 2772.5	1285.6 2771.5	1286.6 2772.5
118.0 118.0	6.4 6.4	6.4 6.4	26.1 26.1	0.6 0.5	73.0 71.0	KLAEQEAHYAVR SFMILIFTR	1413.7 1126.6	1414.7 1127.6	1413.7 1126.6	1414.7 1127.6
Q9NY33 185.0	6.2	6.2	Dipeptidyl-pe 15.7	2.0	99.0	(Dipeptidyl-peptidase III) (DPP III) (Dip LEGSDVQLLEYEASAAGLIR	2133.0	2134.0	2133.1	2134.1
185.0 185.0	6.2 6.2	6.2 6.2	15.7 15.7	2.0 2.0	99.0 99.0	LFKEVDGEGKPYYEVR VILGSEAAQQHPEEVR	1928.0 1761.9	1929.0 1762.9	1928.0 1761.9	1929.0 1762.9
170.0 171.0	2.0 4.0	2.0 4.0	6.1 11.9	2.0 2.0	99.0 99.0	LAQDFLDSQNLSAYNTR LFKEVDGEGKPYYEVR	1954.9 1928.0	1956.0 1929.0	1954.9 1928.0	1955.9 1929.0
171.0 Q9NYL9	4.0 TMOD3_HUMAN	4.0	11.9 Tropomoduli	2.0 in-3 (Ubiquit	99.0 ous tropom	LYAYHLSR odulin) (U-Tmod) - Homo sapiens (Human	1021.5	1022.5	1021.5	1022.5
305.0 305.0	4.0 4.0	4.0 4.0	7.1 7.1	2.0 2.0	99.0 99.0	FGYOFTOOGPR SNDPVATAFAEMLK	1327.6 1492.7	1328.6 1493.7	1327.6 1492.7	1328.6 1493.7
330.0 Q9P258	2.0	2.0	11.6 Protein RCC2	2.0	99.0	FGYQFTQQGPR n of 60 kDa) (RCC1-like protein TD-60) - H	1327.7	1328.7	1327.6	1328.6
273.0 273.0	4.1 4.1	4.1 4.1	8.2 8.2	2.0	99.0 99.0	NLGONLWGPHR VESWGEGGYGR	1290.7 1231.6	1291.7 1232.6	1290.7 1231.6	1291.7 1232.6
211.0 211.0	3.2 3.2	3.2 3.2	10.5 10.5	2.0	99.0 94.0	NLGQNLWGPHR YGCLAGVR	1290.7 894.4	1291.7 895.4	1290.7 894.4	1291.7 895.4
	CATZ_HUMAN	8.0	Cathepsin Z		C 3.4.22)	(Cathepsin X) (Cathepsin P) - Homo sapier NQHIPQYCGSCWAHASTSAMADR		2648.1	2647.1	2648.1
145.0	8.0	8.0	24.8	2.0	99.0 99.0	NSWGEPWGER NVDGVNYASITR	1216.5	1217.5	1216.5	1217.5
145.0 145.0	8.0	8.0	24.8 24.8	2.0 2.0	99.0	YNLAIEEHCTFGDPIV	1307.7 1876.9	1308.7 1877.9	1307.6 1876.9	1308.7 1877.9
99.0 99.0	3.7 3.7	3.7	11.6 11.6	2.0 1.7	99.0 98.0	YNLAIEEHCTFGDPIV NSWGEPWGER	1876.9 1216.5	1877.9 1217.5	1876.9 1216.5	1877.9 1217.5
113.0 113.0	6.8 6.8	6.8 6.8	38.9 38.9	2.0 2.0	99.0 99.0	NSWGEPWGER NVDGVNYASITR	1217.5 1307.6	1218.5 1308.7	1217.5 1307.6	1218.5 1308.7
113.0 113.0	6.8 6.8	6.8 6.8	38.9 38.9	2.0 0.4	99.0 58.0	YNLAIEEHCTFGDPIV DLPKSWDWR	1876.9 1201.6	1877.9 1202.6	1876.9 1201.6	1877.9 1202.6
113.0 113.0	6.8 6.8	6.8 6.8	38.9 38.9	0.2	35.0 32.0	NQHIPQYCGSCWAHASTSAMADR NSWGEPWGERGWLR	2647.1 1728.8	2648.1 1729.8	2647.1 1728.8	2648.1 1729.8
113.0 Q9UJU6	6.8	6.8	38.9 Drebrin-like	0.0	98.0 3 domain-co	NSWGEPWGER ontaining protein 7) (Drebrin-F) (Cervical S	1216.5	1217.5	1216.5	1217.5
248.0 248.0	4.7	4.7 4.7	22.6 22.6	2.0	99.0 99.0	SPTDWALFTYEGNSNDIR TWEQQQEVVSR	2084.9 1388.7	2086.0 1389.7	2084.9 1388.7	2086.0 1389.7
248.0	4.7	4.7	22.6	0.6	72.0	FVLINWTGEGVNDVRK	1846.0	1847.0	1846.0	1847.0
248.0 223.0	3.0	4.7 3.0	22.6 17.0	0.1 2.0	25.0 99.0	FVLINWTGEGVNDVR SPTDWALFTYEGNSNDIR	1717.9 2085.0	1718.9 2086.0	1717.9 2084.9	1718.9 2086.0
223.0 Q9UL46		3.0				TWEQQQEVVSR nit 2 (Proteasome activator 28-subunit bet				
182.0 182.0	6.2 6.2	6.2 6.2	26.4 26.4	2.0 2.0	99.0 99.0	ALVHERDEAAYGELR ASKETHVMDYR	1727.9 1335.6	1728.9 1336.6	1727.9 1335.6	1728.9 1336.6
182.0 182.0	6.2	6.2 6.2	26.4 26.4	2.0 0.2	99.0 32.0	QNLFQEAEEFLYR IVNPKGEEKPSMY	1685.8 1490.7	1686.8 1491.7	1685.8 1490.7	1686.8 1491.8
182.0 163.0	6.2	6.2 2.0	26.4 16.3	0.0 2.0	99.0 99.0	QNLFQEAEEFLYR ALVHERDEAAYGELR	1668.8 1727.9	1669.8 1728.9	1668.8 1727.9	1669.8 1728.9
95.0 95.0	8.1 8.1	8.1 8.1	26.4 26.4	2.0 2.0	99.0 99.0	ALVHERDEAAYGELR ASKETHVMDYR	1727.9 1335.6	1728.9 1336.6	1727.9 1335.6	1728.9 1336.6
95.0 95.0	8.1 8.1	8.1 8.1	26.4 26.4	2.0	99.0 99.0	IVNPKGEEKPSMY QNLFQEAEEFLYR	1490.7 1685.8	1491.8 1686.8	1490.7 1685.8	1491.8 1686.8
95.0 Q9ULV4	8.1	8.1	26.4 Coronin-1C (0.0	99.0 (hCRNN4) -	QNLFQEAEEFLYR Homo sapiens (Human)	1668.7	1669.8	1668.8	1669.8
223.0	5.7	6.0 6.0	18.1 18.1	2.0	99.0 99.0	AIFLADGNVFTTGFSR VGIVAWHPTAR	1714.9 1205.7	1715.9 1206.7	1714.9 1205.7	1715.9 1206.7
223.0	5.7	6.0	18.1	1.7	98.0	VTWDSSFCAVNPR	1537.7	1538.7	1537.7	1538.7
223.0 200.0	1.5	6.0 1.8	18.1 17.3	0.0 1.5	47.0 97.0	FFKLHER AIFLADGNVFTTGFSR	991.5 1714.9	992.5 1715.9	991.5 1714.9	992.5 1715.9
200.0 198.0	3.7	1.8 4.0	17.3 14.6	2.0	47.0 99.0	FFKLHER VGIVAWHPTAR	991.5 1205.7	992.5 1206.7	991.5 1205.7	992.5 1206.7
198.0 198.0	3.7	4.0 4.0	14.6 14.6	1.7 0.0	98.0 49.0	VTWDSSFCAVNPR FFKLHER	1537.7 991.5	1538.7 992.5	1537.7 991.5	1538.7 992.5
198.0	3.7 PA2G4_HUMAN	4.0	14.6	0.0	47.0	FFKLHER (Cell cycle protein p38-2G4 homolog) (hG	991.5 (4-1) (ErbB3-bindin	992.5	991.5	992.5

174.0	6.5	6.5	18.8	2.0	99.0	FDAMPFTLR	1096.5	1097.5	1096.5	1097.5
174.0	6.5	6.5	18.8	2.0	99.0	HELLOPFNVLYEK	1628.9	1629.9	1628.9	1629.9
174.0	6.5	6.5	18.8	2.0	99.0	LVKPGNONTQVTEAWNK	1926.0	1927.0	1926.0	1927.0
174.0	6.5	6.5	18.8	0.4	61.0	AFFSEVER	983.5	984.5	983.5	984.5
174.0	6.5	6.5	18.8	0.1	23.0	TTIYKRDPSKQYGLK	1797.0	1798.0	1797.0	1798.0
288.0	2.0	2.0	6.3	2.0	99.0	AFFSEVER	983.5	984.5	983.5	984.5
	N1_HUMAN	2.0	Talin-1 - Ho			ALLOEVER	303.3	304.3	303.3	304.5
67.0	14.8	14.8	8.8	2.0	99.0	ACKEAAYHPEVAPDVR	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	LHTDDELNWLDHGR	1719.8	1720.8	1719.8	1720.8
67.0	14.8	14.8	8.8	2.0	99.0	TMQFEPSTMVYDACR	1834.8	1835.8	1834.8	1835.8
67.0	14.8	14.8	8.8	2.0	99.0	VGAIPANALDDGQWSQGLISAAR	2309.2	2310.2	2309.2	2310.2
67.0	14.8	14.8	8.8	2.0	99.0	VVAPTISSPVCQEQLVEAGR	2139.1	2140.1	2139.1	2140.1
67.0	14.8	14.8	8.8	0.7	80.0	AVAEQIPLLVQGVR	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	TMQFEPSTMVYDACR	1834.8	1835.8	1834.8	1835.8
75.0	9.8	9.8	7.6	2.0	99.0	VVAPTISSPVCQEQLVEAGR	2139.1	2140.1	2139.1	2140.1
75.0	9.8	9.8	7.6	1.7	98.0	AVAEQIPLLVQGVR	1491.9	1492.9	1491.9	1492.9
75.0	9.8	9.8	7.6	0.9	87.0	ASAGPQPLLVQSCK	1454.7	1455.7	1454.8	1455.8
75.0	9.8	9.8	7.6	0.5	65.0	KSTVLQQQYNR	1363.7	1364.7	1363.7	1364.7
75.0	9.8	9.8	7.6	0.4	64.0	EAAYHPEVAPDVR	1452.7	1453.7	1452.7	1453.7
75.0	9.8	9.8	7.6	0.2	32.0	ACKEAAYHPEVAPDVR	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 R	BM8A_HUMAN		RNA-binding	protein 8A	(RNA-bindi	ng motif protein 8A) (Ribonucleoprote	in RBM8A) (RNA-binding	protein Y14)	(Binder of OVCA1	-1) (BOV-1) - Ho
485.0	2.0	2.0	18.4	2.0	99.0	MREDYDSVEQDGDEPGPQR	2221.9	2222.9	2221.9	2222.9
328.0	2.0	2.0	27.0	2.0	99.0	MREDYDSVEQDGDEPGPQR	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

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

^{*} 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	
II 4bata	24.44	0.4 - 0.0	0.047	
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	$1,339.4 \pm 793.9$	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.