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**Could zona pellucida binding protein 2 (ZPBP2) or proteins containing BX7B motifs in human sperm have hyaluronic acid binding or recognition properties?**

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Key Words:	Hyaluronic acid (HA), Hyaluronic Acid Binding Protein (HABP), Link module, LC-MS/MS, BX7B motif

1           **Could zona pellucida binding protein 2 (ZBP2) or several proteins containing BX7B**  
2           **motifs in human sperm have hyaluronic acid binding or recognition properties?**

3  
4           **Running title: Identification and characterisation of putative sperm Hyaladherins using mass**  
5           **spectrometry**

6  
7                           **F. Torabi, O. A. Bogle, J. M. Estanyol, R. Oliva, D. Miller**

8           **Abstract**

9           **Background:** Hyaluronic acid binding proteins (hyaladherins) can bind hyaluronic acid (HA)  
10           surrounding the cumulus-oophorus complex, are distinct from hyases such as PH 20 (SPAM1) and  
11           are expressed by mature spermatozoa. Although HABP1 and CD44 are reasonably well  
12           characterised hyaladherins and the former has been implicated in sperm-oocyte interactions, the  
13           overall significance of sperm hyaladherins for male fertility is still poorly understood.

14           **Methods:** As information on sperm hyaladherins is limited, a protein affinity 'panning' procedure was  
15           used to facilitate their enrichment by partitioning of whole sperm protein homogenates (N=4) into  
16           binding and non-binding fractions and their subsequent characterisation by liquid chromatography  
17           tandem mass spectrometry (LC-MS/MS). Sequences of proteins from both fractions were submitted  
18           to PDBsum to look for orthologous entries (PDB codes) and all returned codes were queried against  
19           the matching protein using SAS (Sequences Annotated by Structure) looking for structural  
20           similarities between them. A systematic search for other common features of hyaladherins was also  
21           undertaken.

22           **Results:** The presence of BX7B sequence motifs found in several well-described hyaladherins  
23           including RHAMM was used to assess efficacy of potential hyaladherin partitioning by the HA  
24           substrate. The data showed that 50% (14/28) and 34.5% (28/81) of proteins in the bound and  
25           unbound fractions, respectively, contained these motifs (one-tailed Z score = 1.45; p = 0.074),  
26           indicating weak discrimination by the substrate. Querying PDBsum with sequences for all bound  
27           proteins returned several PDB codes matching ZBP2 with the HA-binding Link domain of the  
28           hyaladherin, CD44. Western blot analysis confirmed the affinity partitioning of proteins indicated by

29 the LC-MS/MS results with ADAM32 (containing two BX7B motifs) and ZPBP2 (containing a Link-  
30 like HA-binding domain) present only in the binding fraction.

31

## 32 **Discussion and Conclusions**

33 The protein extraction methods or the HA substrate used to pan them in this study were probably  
34 not ideal, as hyaladherins expected to be present in sperm homogenates (such as CD44 and  
35 RHAMM) were not detected. The results, however, provide evidence that ZPBP2, found only in the  
36 bound fraction may have hyaladherin-like properties, which may reflect the evolutionary background  
37 context of contemporary sperm–egg interaction mechanisms.

38 **Keywords:** Hyaluronic acid (HA), Hyaladherins, CD44, Link module, BX7B motif, ZPBP2, ADAM32.

39

40

## 41 **Introduction**

42 In natural reproductive cycles, ejaculated spermatozoa encounter physiological selection pressures  
43 during their journey across the female reproductive tract, where sperm encounter several biological  
44 ‘checkpoints’, ensuring that only the ‘fitter’ cells reach the oocyte (Ikawa *et al.* , 2010, Suarez and  
45 Pacey, 2006). In assisted reproductive technologies (ART), the success of embryo development and  
46 pregnancy outcome also depends on sperm quality (Sakkas *et al.* , 2000) and the selection of viable  
47 sperm, including sperm with high DNA integrity and chromatin maturity is crucial (Hekmatdoost *et al.*  
48 , 2009). To a large extent, sperm selection for ART particularly with ICSI depends on the  
49 embryologists’ experience of picking the best sperm and is based on microscopic parameters of  
50 sperm motility, viability and morphology. Sperm abnormalities, however, particularly those occurring  
51 at the molecular level cannot always be detected by microscopic observation alone (Palermo *et al.* ,  
52 1992). Celik-Ozenci *et al.* (2004), for example, showed sperm with normal motility and morphology  
53 may have chromosomal abnormalities and ICSI provides no barrier preventing sperm with chromatin  
54 and other defects from participating in the fertilisation process. Negative effects on ICSI outcomes of  
55 the use of poor quality sperm may include miscarriage, an increased risk of congenital abnormalities  
56 and childhood cancer (Celik-Ozenci *et al.* , 2004, Gopalkrishnan *et al.* , 2000, Halliday, 2012, Jaleel

57 and Khan, 2013, Larsen *et al.* , 2013). These issues have led to the development of alternative  
58 methods of sperm selection for ICSI based on functional properties, potentially mimicking the natural  
59 processes occurring in the reproductive tract of healthy individuals and sperm binding to hyaluronic  
60 acid (HA) is one such method.

61

62 HA is a non-sulphated glycosaminoglycan with numerous biological functions in the extracellular  
63 matrix and on the cell surface (Amemiya *et al.* , 2005). HA is abundant in the female reproductive  
64 tract and may be involved in sperm-egg interactions (Ghosh *et al.* , 2007). The cumulus oophorus  
65 complex (COC) is also HA-rich (Zhuo and Kimata, 2001) and HA permeates the zona pellucida and  
66 the perivitelline space of mammalian oocytes (Vandevoort *et al.* , 1997). During *in vivo* fertilisation,  
67 mature spermatozoa bind hyaluronic acid in the extracellular matrix of the COC via hyaladherins  
68 and subsequently release unrelated hyases (for example, PH20/SPAM1) facilitating HA digestion  
69 and penetration of the cumulus mass. Immature spermatozoa, however, do not bind to HA or may  
70 bind it more weakly (Huszar *et al.* , 2003, Nasr-Esfahani *et al.* , 2008).

71

72 Hyaladherins including CD44 (Bajorath *et al.* , 1998, Underhill, 1992) and RHAMM (Hardwick *et al.* ,  
73 1992, Yang *et al.* , 1994), both present in ejaculate spermatozoa (Amaral *et al.* , 2014) are  
74 categorised by whether they contain a Link domain or module (a sequence of ~100 amino acids  
75 composed of two alpha-helices, two triple-stranded anti-parallel beta-sheets and two disulphide  
76 bonds (Barta *et al.* , 1993) or a BX7B motif (where the "B"s are arginine (R) or lysine (K) residues  
77 and the "X" is a sequence of seven non-acidic and at least one basic amino acids), a covalent bond  
78 or combinations thereof (Amemiya *et al.*, 2005, Day and Prestwich, 2002, Yang *et al.* , 1994). CD44,  
79 for example, contains both a Link module and a BX7B motif.

80

81 Investigating sperm hyaladherins is justified in relation to understanding the fertilisation potential of  
82 sperm and the causes of male infertility. A previous study in our laboratory provided evidence for the  
83 complexity of hyaladherin expression in ejaculate human spermatozoa and showed that sperm  
84 binding to HA was enhanced by capacitation (Torabi *et al.* , 2016) and may involve unknown

85 hyaladherins. To improve our understanding, proteins extracted from washed and homogenised  
86 ejaculate human spermatozoa were subjected to affinity panning on a HA-coated surface (Amemiya  
87 *et al.*, 2005). Adherent (binding) and non-binding proteins were recovered and subsequently  
88 characterised by tandem mass spectrometry (LC-MS/MS).

89

## 90 **Materials and methods**

### 91 Reagents used

92 Ethylenediaminetetraacetic acid (EDTA), Triton-X100, Acrylamide/Bis-acrylamide, 30% solution,  
93 Sodium dodecyl sulphate (SDS), Ammonium persulfate (APS) and *N,N,N',N'*-  
94 Tetramethylethylenediamine (TEMED) were obtained from Sigma-Aldrich (UK). PVDF membranes  
95 and Amicon Ultra-0.5 mL and 15 mL centrifugal filter units were obtained from Millipore (UK). Pierce  
96 BCA protein assay kit, Pierce™ protein-free (PBS/TBS) blocking buffer were obtained from Thermo  
97 Fisher Scientific (UK). Tris Base and NaCl were purchased from Fisher Scientific (UK). Protease  
98 inhibitor cocktail was purchased from Cell Signalling Technology (UK). ColorPlus prestained protein  
99 ladder was acquired from New England Biolabs (UK). Clarity™ western ECL substrate and Bradford  
100 protein assay reagent were purchased from Bio-Rad (UK). HA-coated dishes were purchased from  
101 Biocoat (USA). The monoclonal anti-ZPBP2 antibody was purchased from antibodies-online. The  
102 monoclonal anti-ADAM32 (sc-376738) and anti-Alpha tubulin (SC-5286) antibodies were obtained  
103 from Santa Cruz Biotechnology. Water for mass spectrometry containing 0.1% formic acid (LC-MS  
104 Chromasolv®) was from Honeywell (Seelze, Germany) and the acetonitrile from Fluka. The rest of  
105 the reagents were supplied by Sigma-Aldrich (St. Louis, MO) unless otherwise stated.

106

### 107 Ethical approval

108 The study was considered and nationally approved by the relevant UK Integrated Research  
109 Application System (IRAS) Ethics Committee (NRES 12\_NE\_0192) on 13 January 2013 and locally  
110 approved by the University of Leeds' School of Medicine Research Ethics Committee  
111 (SoMREC/13/017) on 28 November 2013.

112

### 113 Semen analysis

114 A schematic of the experimental plan is shown in Figure 1. Human semen samples were obtained  
115 ethically from young male volunteers (18-25 years of age) of unproven fertility by masturbation into  
116 sterile, tissue culture grade universal containers after 3 days abstinence. Collected semen samples  
117 were immediately liquefied for 30 minutes at 37 °C. The semen parameters related to each sample  
118 are shown in Table 1. After liquefaction, all samples were checked for volume, sperm concentration,  
119 sperm morphology and the number of round cells according to the WHO (World Health  
120 Organisation) criteria (2010) and following, where appropriate, the guidelines recommended by  
121 Bjorndahl et al (Bjorndahl *et al.* , 2016). Only those with normal semen parameters as defined by  
122 WHO criteria were included in the study.

123

### 124 Sperm preparation

125 To maximise the recovery of sperm, liquefied semen samples were centrifuged through a 60%  
126 density cushion of SupraSperm™ using special inserts (ProInsert-Nidacon, Sweden) to remove any  
127 round cell contamination at 300 ×g for 20 minutes. A pellet retrieval pipette (ProInsert kit) was used  
128 to aspirate sperm pellets which were then resuspended and washed in PBS (pH: 7.2) followed by  
129 centrifugation at 300 × g for 10 minutes (two repeated washes). Sperm motility and morphology  
130 were assessed using a Leitz Laborlux 12 light microscope and the sperm pellets were used for  
131 further protein extraction.

132

### 133 Protein extraction and affinity panning of sperm proteins

134 To reduce costs while as far as possible retaining sample heterogeneity, two aliquots of each  
135 sample were pooled into two (~2 × 10<sup>8</sup> sperm in total, each) combined samples (C1 and C2) and  
136 extracted separately in 500 µL of a mild lysis buffer (150 mM NaCl, 20 mM Tris-HCl (pH: 8), 2mM  
137 EDTA, 1x protease inhibitor cocktail, 0.5% Triton X-100) (D'Cruz *et al.* , 1993). The suspensions  
138 were sonicated on ice for 15 seconds on, 40 seconds off, at an amplitude of 10 microns. The  
139 sonication was repeated four times. Samples were incubated on ice for 1h with constant shaking.  
140 To recover extracted soluble proteins, samples were centrifuged at 16000 ×g for 20 minutes and

141 supernatants were aspirated and transferred into fresh tubes. Pellets were discarded. Protein  
142 quantification was performed using the Pierce BCA protein assay kit according to manufacturer's  
143 instruction (Thermo Fisher Scientific, UK). HA-coated dishes (Biocoat, USA) were used to pan for  
144 proteins in the sample homogenates (C1 and C2) with an affinity for hyaluronic acid. To block non-  
145 specific binding, dishes were treated beforehand with 1.5 mL of Pierce™ protein-free (PBS) blocking  
146 buffer (Thermo Fisher Scientific, UK) for 30 minutes at room temperature (RT) with gentle shaking.  
147 Dishes were then washed twice with 2 mL of phosphate buffered saline (PBS). Extracted proteins  
148 from the sperm of two different men were used and loaded on to separate HA-coated dishes at a  
149 concentration of 1.5 mg/mL. Dishes were incubated for 75 minutes at RT with gentle shaking after  
150 which, non-binding proteins were decanted for frozen storage at -80°C.

151

152 To minimise non-specific contamination of the binding fractions, dishes were washed with 1.5 mL  
153 PBS (four times for one minute each wash). Bound proteins were then recovered by incubating the  
154 plate surface with 400 µL of a pre-heated (95°C) Laemmli-based buffer containing 0.125 M Tris-HCl  
155 (pH: 6.8), 4%w/v SDS and 10%v/v 2-mercaptoethanol for 5 minutes with gentle shaking. Bound  
156 proteins were aspirated using a pipette. Both protein fractions (HA-binding and non-binding) were  
157 processed through Amicon Ultra-15 mL centrifugal desalting filters (3 kDa) according to  
158 manufacturer's instruction (Millipore, UK). The proteins were then concentrated using Amicon's  
159 Ultra-0.5 mL centrifugal filters according to manufacturer's instruction (Millipore, UK). A final volume  
160 (40 µL) was obtained after concentration and 30 µL of each was precipitated using TCA-acetone  
161 (see below). Ten (10 µl) aliquots were stored at -80°C for western blot analysis (see below).

162

### 163 Protein precipitation

164 To precipitate proteins, one volume of 100% (w/v) TCA was added to four volumes of the protein  
165 solution (final conc of 20% TCA) from both HA-binding and non-binding samples. All samples were  
166 incubated for 20 minutes at 4°C and centrifuged at 19000 xg for 5 minutes. Supernatants were  
167 discarded. Pellets were washed with 200 µL of ice-cold acetone and centrifuged at 19000 xg for 5

168 minutes at 4°C (twice, with washing between). Pellets were dried and stored at -80°C before  
169 sequencing by LC-MS/MS as outlined below.

170

#### 171 Liquid chromatography-tandem mass spectrometry (LC-MS/MS)

172 Proteins were digested with trypsin (Promega, Madison, WI) at 37°C overnight according to the  
173 manufacturer's recommendations. Tryptic peptides were separated by means of nano liquid  
174 chromatography using an Eksigent NanoLC AS2 ultra (AB SCIEX) with a flow rate of 400 nL/min, an  
175 EASY C18 trap column (5 µm, 120 µm, 100 µm inner diameter × 2 cm in length), and an EASY C18  
176 analytical column (3 µm, 120 µm, 75 µm inner diameter × 10 cm in length). The following linear  
177 gradient, using solvent B (97% acetonitrile, 0.1% formic acid) and solvent A (3% acetonitrile, 0.1%  
178 formic acid), was employed: 5%–40% buffer B (65 min); 40%–100% buffer B (5 min). MS/MS  
179 analysis was performed using an LTQ Orbitrap Velos (Thermo Fisher Scientific) with a  
180 nanoelectrospray ion source with precursor ion selection in the Orbitrap at 30,000 of resolution,  
181 selecting the 15 most intense precursor ions, with a collision energy of 35 in positive ion mode.  
182 MS/MS data acquisition was completed using Xcalibur 2.1 (Thermo Fisher Scientific). Figure 1  
183 shows a schematic illustration of the study plan.

184

185

#### 186 Protein identification, quantification and analysis

187 Proteome Discoverer 1.4 (ThermoFisher Scientific) was used to characterise all proteins. Database  
188 searching included all entries from the *Homo sapiens* UniProtKB/Swiss-Prot database (release 02-  
189 2015) using SEQUEST version 28.0 (Thermo Fisher Scientific). A 1% FDR and at least one (≥1)  
190 unique peptide per protein were the criteria used for protein identification. The dissociated or  
191 'ungrouping' of proteins from their respective families was used during the quantification process in  
192 order to avoid possible ambiguities associated with different isoforms of the same protein.

193

194 Identified proteins in binding and non-binding fractions from the two individual samples were  
195 compared and checked against the whole human sperm proteome (Amaral *et al.*, 2014) and only

196 those present in this database were included for further analysis. Additional information about the  
197 identified proteins was obtained using UniProtKB/Swiss-Prot, and BioMart - Ensembl. DAVID  
198 Bioinformatics Resources 6.8 was used for functional ontological annotation clustering (Huang *et al.*  
199 , 2007).

200

201 PDBsum was used to align amino acid sequences of identified proteins with sequences for which  
202 structural information is available (Laskowski, 2001, 2009, Laskowski *et al.* , 2005). The SAS  
203 (Sequences annotated by structure) server was then used ([http://www.ebi.ac.uk/thornton-](http://www.ebi.ac.uk/thornton-srv/databases/sas/)  
204 [srv/databases/sas/](http://www.ebi.ac.uk/thornton-srv/databases/sas/)) to determine the structural similarities between identified proteins in HA-binding  
205 and non-binding fractions with the hyaluronic acid binding domain of CD44 (highlighted by  
206 PDBsum). SAS annotates protein residues according to residue type (polar, non-polar, aliphatic and  
207 aromatic), secondary structure (alpha-helix, beta-strand, turn and coil), inter-molecular contacts  
208 (number of hydrogen bonds, total contacts, nucleic acid contacts and metal ions contacts to ligand),  
209 active sites and residue similarity (Milburn *et al.* , 1998). Sequence similarities were computed using  
210 the PAM250 log odds scores matrix with FASTA used as the sequence search method and  
211 presented as a simple pairwise comparisons. The colouring of residue similarity signifies identical  
212 amino acid types (red) down to conservative, semi-conservative and dissimilar residues using a  
213 spectrum ranging from orange through to blue. In addition, a Z-score and an E-value for sequence  
214 similarity were computed (Pagni and Jongeneel, 2001).

215

#### 216 Western blot analysis

217 To verify the results of LC-MS/MS experiments, 15 µg of binding and non-binding proteins from  
218 each sample were resolved by SDS PAGE and western blotted. Samples were dissolved and  
219 diluted 1:1 with 2x Laemmli buffer (4% SDS, 10% 2-mercaptoethanol, 20% glycerol, 0.004%  
220 bromophenol blue, 0.125 M Tris-HCl (pH: 6.8)) and boiled for 5 minutes at 95°C. The proteins were  
221 separated on a 10% gel at 120 V for 100 minutes in 1x SDS running buffer (25 mM Tris-base, 190  
222 mM Glycine, 0.1% SDS). Proteins were then transferred to PVDF membranes at 250 mA for 90  
223 minutes in 1x transfer buffer (25 mM Tris-base, 190 mM Glycine, and 20% methanol). The

224 membrane was blocked with Pierce™ protein-free (TBS) blocking buffer (Thermo Fisher Scientific,  
225 UK) for 1h at RT with constant shaking and then probed with antibodies to two proteins specific to  
226 the binding fraction, zona pellucida binding protein 2 (ZPBP2) and ADAM32 (200 µg/mL) at a  
227 primary antibody concentration of 1/500 and 1/200, respectively overnight at 4°C. An alpha tubulin  
228 antibody (200 µg/mL at a final concentration of 1/2000) was used as a control for proteins present in  
229 both fractions and as a loading control. Membranes were washed three times with TBS containing  
230 0.1% Tween-20 for 15 minutes each and incubated with 1:1000 dilution of relevant HRP-conjugated  
231 secondary antibodies for 1h at RT (all primary and secondary antibodies were diluted in Pierce™  
232 protein-free (TBS)). Membranes were washed as described above and the Clarity western ECL  
233 substrate was used to visualise protein bands (Bio-Rad, UK).

234

## 235 **Results**

### 236 Identification of proteins in HA-binding and non-binding fractions

237 LC-MS/MS data resulted in the identification of 180 (sample C1) and 227 (sample C2) proteins in  
238 HA-binding fractions and 466 (sample C1) and 563 (sample C2) proteins in non-binding fractions,  
239 respectively (Figure 2A). As shown in Figure 2BI, 45 proteins were common and specific (no  
240 overlaps with non-binding fractions) to both HA-binding fractions and had records in the human  
241 sperm proteome database (Amaral *et al.*, 2014) of which 28 had ≥1 unique peptides per protein.  
242 One hundred and twenty-nine (129) proteins were common to both non-binding fractions with 81  
243 recorded in the human sperm proteome database and represented by ≥1 unique peptides (Figure  
244 2BII). A list of all mass spectrometry data can be found in Suppl Tables 1-4. Additional information  
245 about the identified proteins was obtained using UniProtKB/Swiss-Prot, and BioMart - Ensembl.  
246 Table 2 lists proteins in the binding fractions. The equivalent list from the non-binding fractions is  
247 shown in Suppl Table 5.

248

249 An ontology analysis was undertaken to determine whether binding and non-binding proteins carried  
250 distinct functional signatures indicating a potential HA affinity effect. Following submission to DAVID,  
251 results suggested distinct signatures with the bound fraction carrying a weak enrichment for

252 secreted proteins although a stronger enrichment in the unbound fraction was found for chaperone  
253 and chaperone-like proteins (Suppl Tables 6 and 7).

254

#### 255 Alignment of the sequences of HA-binding and non-binding proteins using PDBsum and SAS

256 The amino acid sequences of the 28 proteins in the HA-binding fractions were submitted to  
257 PDBsum, which generates lists of structural features (PDB codes) conserved between proteins. One  
258 protein (ZPBP2) contained a sequence motif bearing similarity to the Link module of CD44, while 14  
259 others (50% in total; Table 2) contained BX7B sequences. Twenty-eight (28) proteins (34.5%; Suppl  
260 Table 5) from the non-binding fraction also contained the BXB7 motif indicating a slight enrichment  
261 for proteins containing the motif in the binding fractions (one-tailed Z score = 1.45;  $p = 0.074$ ). No  
262 proteins containing a Link-like sequence were present in the non-binding fraction. Proteins with  
263 multiple ( $\geq 2$ ) BX7B motifs, including ADAM32 (Uniprot QBTC27) with two and Midkine (Uniprot  
264 P21741) with four of which the latter is known to bind HA and other glycosaminoglycans  
265 (<http://www.ebi.ac.uk/QuickGO/GProtein?ac=P21741>), were more abundant in the binding (25%)  
266 versus the non-binding (15%) fractions although this difference was not significant (one-tailed Z  
267 score = 1.22;  $p = 0.111$ ). Hence, the trends suggest that HA binding motifs may have influenced the  
268 partitioning of the two populations. Charge differences between proteins were also explored as an  
269 alternative partitioning mechanism. Net charge is dictated by proteins' pI and as HA carries a net  
270 negative charge at pH 8.0 (the pH of the extraction buffer), basic proteins with a net positive charge  
271 could have electrostatically interacted with the substrate. Twenty (71.4%) of the proteins in the  
272 binding fraction compared with 21 (26%) in the non-binding fraction were likely to carry a net  
273 positive charge, a strongly significant difference, suggesting that charge effects may also have  
274 influenced the partitioning of proteins in the fractions (one-tailed Z score = 4.28;  $p < 0001$ ).

275

276 Of all the proteins in the binding fractions, ZPBP2 which contains a sequence motif with similarities  
277 to the Link module found in CD44 was flagged as one of the more interesting. ZPBP2 (also known  
278 as ZPBPL) was first reported in 2003 from an in silico search of a region on human chromosome  
279 17q12 that is frequently amplified in breast and stomach cancers (Katoh and Katoh, 2003). Figure

280 3A shows the alignment between ZBPB2 and CD44 (PDB code 2i83, residues 21 – 178) with a  
281 32.7% sequence identity and 69% overall similarity covering a 55 amino acid overlap. Unlike CD44  
282 where the Link module is close to the amino-terminal end, the equivalent sequence in ZBPB2 is  
283 located towards the carboxyl-terminal end. There were no proteins with a sequence resembling the  
284 Link module in the non-binding fractions. The 2i83 PDB code comparison is shown because it  
285 corresponds with the CD44's HA-binding form although other valid codes representing a similar  
286 residue overlap were also flagged (Table 3) (Liu and Finzel, 2014, Takeda *et al.*, 2006, Teriete *et al.*  
287 , 2004). As ZBPB2 may have hyaladherin properties based on sequence similarities with the Link  
288 domain, further structural similarities were investigated using the Sequences Annotated by Structure  
289 (SAS) server (Milburn *et al.*, 1998). This resource checks for the number of contacts between the  
290 protein and its presumptive ligand based on secondary structure prediction and was used to scan  
291 the homologous HA binding motif on ZBPB2. The PROSITE secondary structure alignment  
292 (PS01241) for 2i83 (<http://prosite.expasy.org/cgi-bin/prosite/prosite-search-ac?PS01241>) with  
293 ZBPB2 is shown in Figure 3B. Residues in ZBPB2 conserved with those in CD44 within the HA  
294 binding domain, included Arg46/246, Ala49/249, Phe56/256, Asn57/257, Thr59/259, Leu60/260,  
295 Pro61/261, Met63/263, Leu70/270, Cys78/278, Arg79/279, Gly81/281, Phe82/282, Arg91/287,  
296 His93/289, Asn95/291, Cys98/292, Ala99/293, Thr109/303, Thr117/311, Ser123/317). Boxes  
297 indicate conserved residues involved in ligand binding and the stars indicate conserved cysteine  
298 residues.

299

300 PDB was also used to check whether the Link module that could influence the partitioning of  
301 proteins into binding and non-binding fractions was present in any of the 81 proteins common to the  
302 non-binding fractions. None returned a PDB code. We also aligned the sequences of ten putative  
303 HA-binding proteins containing the Link module (Table 4\*) and eleven, randomly selected proteins  
304 from the non-binding fraction (Table 4<sup>†</sup>) without evidence for a Link module. SAS was then used to  
305 look for any existing structural similarities between them and the CD44 motifs flagged by the PDB  
306 codes, (4pz3, 4pz4, 1uuh, 1poz and 2i83; Table 3). When aligned with these sequences, the first

307 seven proteins in the list had the highest Z-scores (123-321) and lowest E-values ( $4.5e^{-16}$ - $2.2e^{-5}$ ).  
308 The next three proteins had lower Z-scores (50.6 -112.1) and higher E-values ( $1.9e^{-4}$ - 0.38). The  
309 eleven proteins in the non-binding fraction (Table 4<sup>‡</sup>) occasionally showed higher percentage  
310 identities with the CD44 Link module (PLIN3 for example). Similarly, human axonemal dynein light  
311 intermediate polypeptide 1 (O14645) also showed a high % identity with sequences represented by  
312 PDB codes 4pz3 and 1uuh but with a far lower Z score and high E value. Relative Z-scores and E-  
313 values give more accurate predictions of structural relationships between proteins than percentage  
314 identity and although not reported to contain a Link module hitherto, ZPBP2 is included in Table 4  
315 because it was flagged by PDB / SAS and has a relatively high Z-score with correspondingly low E-  
316 value.

317

#### 318 Western blotting to confirm the results of proteomics

319 To confirm the results obtained by LC-MS/MS, western blotting was performed using antibodies  
320 against ZPBP2, ADAM32 and alpha tubulin on binding and non-binding fractions from the four  
321 samples individually and independently processed prior to combining for proteomic analysis.  
322 ADAM32 was chosen because it has two BX7B motifs. Antibodies against ZPBP2 and ADAM32  
323 detected protein bands at approximately 38 kDa and 85 kDa, respectively in binding fractions (lanes  
324 2, 4, 6, 8), consistent with our sequencing and partitioning data (Figure 4). Additional bands at ~36  
325 kDa and 42 kDa were revealed using the antibody to ZPBP2. No signals were detected in non-  
326 binding fractions (Lanes 1, 3, 5, 7). The antibody against alpha-tubulin (present in both fractions  
327 and used here as a loading control) detected a single band at approximately 50 kDa in all samples.

328

#### 329 **Discussion**

330 The present study was conducted to search for novel hyaladherins in human sperm by allowing the  
331 soluble proteins extracted from homogenised sperm to interact with a HA-coated surface before  
332 their recovery and characterisation by tandem mass spectrometry (LC-MS/MS). This simple affinity  
333 panning process (Amemiya *et al.*, 2005) resulted in the identification and selection for further  
334 analysis of 28 proteins from the binding fractions including one containing a sequence related to the

335 HA-binding domain of CD44 (Liu and Finzel, 2014, Takeda *et al.*, 2006, Teriete *et al.*, 2004) that  
336 was identified as ZPBP2. Based on the proportion of positively charged proteins in the binding  
337 versus non-binding fractions of extracted sperm proteins, electrostatic attraction is also likely to have  
338 played a role in the outcomes of the panning process (Lenormand *et al.*, 2008, Purcell *et al.*,  
339 2014). Nonetheless, a conformational change in conjunction with the overall charge of a protein  
340 could also favour interaction with HA, which is known to be transitory in nature (Kohda *et al.*, 1996,  
341 Liu and Finzel, 2014, Misra *et al.*, 2015).

342

343 SAS determines and applies unique identifiers from different crystallographic (X-ray or Nuclear  
344 Magnetic Resonance) submissions, which in the case of the ZPBP2 included five records (PDB  
345 codes 4pz3, 1uuu, 4pz4, 2i83 and 1poz) relating to the HA-binding (Link) domain of CD44 (Liu and  
346 Finzel, 2014, Takeda *et al.*, 2006, Teriete *et al.*, 2004). CD44 is one of the better understood  
347 hyaladherins and is a type I transmembrane protein located on the surface of many different cell  
348 types including mammalian sperm as reported previously (Bains *et al.*, 2002). Its location on the  
349 sperm surface has also been shown to alter during and following capacitation and the acrosome  
350 reaction (Torabi *et al.*, 2016). CD44 has many different isoforms due to alternative splicing in the  
351 proximal region of the extracellular domain and also shows evidence of post-translational  
352 modifications (Oliferenko *et al.*, 2000, Toole, 2004). CD44 probably binds HA through a disulphide-  
353 bond stabilized HA-binding domain (HABD) located within the Link module (Takeda *et al.*, 2006) and  
354 the peptide sequence in ZPBP2 bearing similarity to the Link domain of CD44 is based on the  
355 latter's ligand bound configuration (Bajorath *et al.*, 1998) and retains two of the cysteine residues  
356 thought to be responsible for stabilising the HABD.

357

358 Both ZPBP1 and ZPBP2 are located on the acrosome and the role of the former in binding the zona  
359 pellucida is already documented (Mori *et al.*, 1993, Mori *et al.*, 1995). Both proteins belong to the  
360 immunoglobulin like domain containing family (Lin *et al.*, 2007) and are co-designated by sequence  
361 similarity, sharing a similar, amino-terminal signal sequence and a carboxyl-terminal zona binding  
362 homologous domain (ZBHD) with 15 conserved cysteine residues (Kato and Kato, 2003). Loss of

363 either protein leads to disruption of acrosome formation and sperm morphology (ZPBP1/2) and to  
364 male mouse sterility (ZPBP1) or subfertility (ZPBP2; Lin et al., 2007). The ZPHD and putative Link  
365 domains, overlap (Figure 3A) and share common features, notably the two conserved cysteines  
366 (Figure 3A; stars) supporting the latter's disulphide linked HA-binding configuration (Teriete *et al.*,  
367 2004).

368

369 Excepting teleosts, which have no ZPBPs and use a completely distinct process for fertilisation  
370 (Morisawa, 1999), the ZPHD domain is conserved across all vertebrate species (Lin et al., 2007).  
371 Amphibians express just one ZPBP, which is more similar to mammalian ZPBP2 than to ZPBP1 (Lin  
372 et al., 2007), explaining PDPsum's 'failure' to report homology with ZPBP1. These data suggest  
373 that the recognition of zona pellucida protein 2 (ZP2) by either of the ZPBPs and of HA by  
374 hyaladherins containing the Link module like CD44, may utilise similar mechanisms. Hence, zona  
375 recognition by amphibian sperm ZPBPs could have arisen via an earlier HA-binding (or lectin  
376 binding) property that was partially conserved during the likely gene duplication event that gave rise  
377 to ZPBP1 (Lin et al., 2007; Kohda et al., 1996). The original ZPBPs of primitive vertebrates may not  
378 have had time to evolve the more specific sperm-egg interactions seen in modern mammals.  
379 Alongside CD44, however, they may still have hyaladherin-like properties. In the human, ZPBP2 has  
380 at least two known isoforms of 338 (38.6) kDa and 316 (36.2 kDa) amino acids, respectively, both of  
381 which contain the ZPHD sequence. These and an additional band at ~42 kDa that may represent a  
382 novel isoform of this protein (Lin *et al.*, 2007) were only detected in the binding fractions by western  
383 blotting (Figure 4).

384

385 The Link module present in CD44 is also present in several other hyaladherins including TSG-6,  
386 versican, link protein, brevican, aggrecan and neurican, which were not detected in either binding or  
387 non-binding fractions. The BX7B motif has been reported in RHAMM, CD44, and the hyaluronidase,  
388 HABP1 (C1QBP) among others (Day and Prestwich, 2002, Yang *et al.*, 1994). Midkine (MK) is a  
389 secreted growth factor rich in basic amino acids and cysteine with a molecular mass of  
390 approximately 13 kDa (Jono and Ando, 2010). The two BX7B motifs in ADAM32 and the four in

391 Midkine as well as the proteins' net positive charge may help explain their presence in the binding  
392 fraction. ADAM32 has been identified as a type I non-catalytic metalloprotease-like transmembrane  
393 protein (Wolfsberg *et al.* , 1995). The protein is expressed during spermatogenesis and processed  
394 during epididymal maturation to become localised on the sperm surface (Kim *et al.* , 2006). Western  
395 blot analysis confirmed that ADAM32 was confined to the binding fractions. To date 29 ADAMs have  
396 been identified of which 15 are expressed in testis (Primakoff and Myles, 2000). This suggests a  
397 specific relationship between ADAM function, spermatogenesis and fertilisation. ADAM2 (fertilin  
398 beta) and ADAM3 (cyritestin) interact with integrin in the egg plasma membrane of mouse oocytes  
399 (Wassarman *et al.* , 2001).

400

401 The absence of known sperm hyaladherins, including CD44, RHAMM and C1QBP in any of the  
402 extract fractions as well as the presence of BX7B motifs in some proteins from the non-binding  
403 fractions was surprising and warrants further consideration (Bajorath *et al.*, 1998, Hardwick *et al.*,  
404 1992, Underhill, 1992, Yang *et al.*, 1994). One possibility is that the transient and dynamic binding  
405 reported between hyaladherins and hyaluronic acid that facilitates cell adhesion and migration  
406 relating to conformational changes in protein structure was responsible (Kohda *et al.*, 1996, Liu and  
407 Finzel, 2014, Misra *et al.*, 2015). HA-binding proteins without the required conformational  
408 configuration may well have been extracted by our methods but were in the wrong conformational  
409 arrangement to permit efficient enrichment by HA-binding. Alternatively, the missing hyaladherins  
410 may not have been sufficiently abundant in either fraction to be detectable by the LC-MS/MS  
411 method used. CD44, for example, is not listed in the most recent and comprehensive human sperm  
412 proteome (Amaral *et al.*, 2014). Moreover, the mild solvent used in the extraction process, designed  
413 to preserve tertiary structure, may have failed to access these proteins, which were lost in the  
414 insoluble pellets following sperm homogenisation. Membrane anchoring could also have rendered  
415 many proteins inaccessible under the extraction conditions used here (Gupta *et al.* , 1991). Finally,  
416 BX7B motifs may not be universally involved in HA-binding, with only RHAMM having been shown  
417 to have an absolute requirement for them to date (Day, 2000, Yang *et al.*, 1994). Work is in  
418 progress to isolate proteins from sperm permitted to undergo capacitation beforehand where

419 conformational or localisation changes to hyaladherins, increasing access to the extraction solvent,  
420 may have occurred (Torabi et al, 2016). Modification of the HA substrate may also improve its  
421 capacity to recognise and bind hyaladherins and experiments are also underway exploring this  
422 possibility.

423

424 Just one protein (ZPBP2) present only in HA-binding fractions contained a Link-like module.  
425 Regardless of the efficacy of the panning process itself, the uncovering of a structural relationship  
426 between ZPBP2 and CD44 is noteworthy and suggests that the general HA-sperm recognition  
427 process occurring in the cumulus-oophorus complex may predate the appearance of more  
428 specialised protein-protein, sperm-zona interactions in this context. The synthesis of larger  
429 quantities of both isoforms of ZPBP2 is warranted to more fully study their structural and possible  
430 HA-binding characteristics, their relationship to hyaladherins and involvement in male infertility.

431

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437 the MRC, NHS, NIHR or the Department of Health.

438

439

440 **Figures and Tables.**

441 Figure 1. Flow chart of experimental design.

442

443 Figure 2. Venn diagrams illustrating overlaps between **(A)** HA-binding and non-binding proteins in  
444 samples from two combined (C1 and C2) sperm samples from four volunteer donors of unproven  
445 fertility and **(B)** overlaps between combined HA-binding **(I)** and non-binding proteins **(II)** from these  
446 samples.

447

448 Figure 3. Homology between the ligand (HA) bound form of CD44 (PDB code 2i83, 158 amino  
449 acids) and ZPBP2; 338 amino acids). Panel **A** shows the best residue alignment of ZPBP2 with  
450 2i83. Blue dashed lines indicate alignment adjustment spacing of 2i83 which means the residue  
451 numbers in panels A and B will not necessarily correspond. Boxes border residues implicated in  
452 ligand binding. Residue conservation is denoted by colours ranging from red (identical) to least  
453 conserved (blue). Panel **B** shows the predicted secondary structure (helices and strands) of ZPBP2  
454 with the confidence for helix and strand predictions denoted by green shading (darker shade means  
455 higher confidence). Red shading signifies the Link domain signature of CD44 with the small shaded  
456 bars indicating the strongest drivers of predicted secondary structure. Stars indicate the cysteines  
457 thought to be critical to the HA-binding configuration of the Link module.

458

459 Figure 4. Western blotting on binding (lanes 2, 4, 6, 8) and non-binding (lanes 1, 3, 5, 7) proteins in  
460 the four samples (1 - 4) used in these experiments with antibodies directed against ZPBP2 and  
461 ADAM32. Alpha-tubulin, present in both binding and non-binding fractions was used as a loading  
462 control. Lane 9 shows rainbow Mr calibration standards.

463

464 Table 1. Semen parameters of young male volunteers (unproven fertility) participating in the study.

465

466 Table 2. Proteins in both (C1 and C2) binding fractions with  $\geq 1$  unique identifying peptide and with  
467 no overlap with proteins in the non-binding fractions. Numbers in parenthesis indicate the number of  
468 BX7B motifs found in the protein sequence. N/D is not detected.

469

470 Table 3. PDB codes for sequences matching ZPBP2 ([http://www.ebi.ac.uk/thornton-](http://www.ebi.ac.uk/thornton-srv/databases/cgi-bin/pdbsum/GetPage.pl?pdbcode=index.html)  
471 [srv/databases/cgi-bin/pdbsum/GetPage.pl?pdbcode=index.html](http://www.ebi.ac.uk/thornton-srv/databases/cgi-bin/pdbsum/GetPage.pl?pdbcode=index.html)).

472

473 Table 4. List of 10\* binding proteins containing and 11<sup>‡</sup> randomly selected proteins from the non-  
474 binding fraction without the Link module. SAS was used to look for any existing structural similarities  
475 with the PDB flagged CD44 motifs (Table 3). ZPBP2 is included in Table 4 because it was flagged  
476 by PDB / SAS and has relatively high Z-scores and low E-values.

477

478 Suppl Table 1. Full LC-MS/MS data for proteins detected in the HA-binding fractions (C1).

479

480 Suppl Table 2. Full LC-MS/MS data for proteins detected in the HA-binding fractions (C2).

481

482 Suppl Table 3. Full LC-MS/MS data for proteins detected in the non-binding fractions (C1).

483

484 Suppl Table 4. Full LC-MS/MS data for proteins detected in the non-binding fractions (C2).

485

486 Suppl Table 5. Proteins found in both non-binding fractions and no overlap with the corresponding  
487 binding fractions.

488

489 Suppl Table 6. Functional annotation clustering of binding proteins using DAVID Bioinformatics  
490 Resources 6.8

491

492 Suppl Table 7. Functional annotation clustering of non-binding proteins using DAVID Bioinformatics  
493 Resources 6.

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- 616
- 617
- 618

1 **Could zona pellucida binding protein 2 (ZBP2) or several proteins containing BX7B**  
2 **motifs in human sperm have hyaluronic acid binding or recognition properties?**

3  
4 **Running title: Identification and characterisation of putative sperm Hyaladherins using mass**  
5 **spectrometry**

6  
7 **F. Torabi, O. A. Bogle, J. M. Estanyol, R. Oliva, D. Miller**

8 **Abstract**

9 **Background:** Hyaluronic acid binding proteins (hyaladherins) can bind hyaluronic acid (HA)  
10 surrounding the cumulus-oophorus complex, are distinct from hyases such as PH 20 (SPAM1) and  
11 are expressed by mature spermatozoa. Although HABP1 and CD44 are reasonably well  
12 characterised hyaladherins and the former has been implicated in sperm-oocyte interactions, the  
13 overall significance of sperm hyaladherins for male fertility is still poorly understood.

14 **Methods:** As information on sperm hyaladherins is limited, a protein affinity 'panning' procedure was  
15 used to facilitate their enrichment by partitioning of whole sperm protein homogenates (N=4) into  
16 binding and non-binding fractions and their subsequent characterisation by liquid chromatography  
17 tandem mass spectrometry (LC-MS/MS). Sequences of proteins from both fractions were submitted  
18 to PDBsum to look for orthologous entries (PDB codes) and all returned codes were queried against  
19 the matching protein using SAS (Sequences Annotated by Structure) looking for structural  
20 similarities between them. A systematic search for other common features of hyaladherins was also  
21 undertaken.

22 **Results:** The presence of BX7B sequence motifs found in several well-described hyaladherins  
23 including RHAMM was used to assess efficacy of potential hyaladherin partitioning by the HA  
24 substrate. The data showed that 50% (14/28) and 34.5% (28/81) of proteins in the bound and  
25 unbound fractions, respectively, contained these motifs (one-tailed Z score = 1.45; p = 0.074),  
26 indicating weak discrimination by the substrate. Querying PDBsum with sequences for all bound  
27 proteins returned several PDB codes matching ZBP2 with the HA-binding Link domain of the  
28 hyaladherin, CD44. Western blot analysis confirmed the affinity partitioning of proteins indicated by

29 the LC-MS/MS results with ADAM32 (containing two BX7B motifs) and ZPBP2 (containing a Link-  
30 like HA-binding domain) present only in the binding fraction.

31

## 32 **Discussion and Conclusions**

33 The protein extraction methods or the HA substrate used to pan them in this study were probably  
34 not ideal, as hyaladherins expected to be present in sperm homogenates (such as CD44 and  
35 RHAMM) were not detected. The results, however, provide evidence that ZPBP2, found only in the  
36 bound fraction may have hyaladherin-like properties, which may reflect the evolutionary background  
37 context of contemporary sperm–egg interaction mechanisms.

38 **Keywords:** Hyaluronic acid (HA), Hyaladherins, CD44, Link module, BX7B motif, ZPBP2, ADAM32.

39

40

## 41 **Introduction**

42 In natural reproductive cycles, ejaculated spermatozoa encounter physiological selection pressures  
43 during their journey across the female reproductive tract, where sperm encounter several biological  
44 ‘checkpoints’, ensuring that only the ‘fitter’ cells reach the oocyte (Ikawa *et al.* , 2010, Suarez and  
45 Pacey, 2006). In assisted reproductive technologies (ART), the success of embryo development and  
46 pregnancy outcome also depends on sperm quality (Sakkas *et al.* , 2000) and the selection of viable  
47 sperm, including sperm with high DNA integrity and chromatin maturity is crucial (Hekmatdoost *et al.*  
48 , 2009). To a large extent, sperm selection for ART particularly with ICSI depends on the  
49 embryologists’ experience of picking the best sperm and is based on microscopic parameters of  
50 sperm motility, viability and morphology. Sperm abnormalities, however, particularly those occurring  
51 at the molecular level cannot always be detected by microscopic observation alone (Palermo *et al.* ,  
52 1992). Celik-Ozenci *et al.* (2004), for example, showed sperm with normal motility and morphology  
53 may have chromosomal abnormalities and ICSI provides no barrier preventing sperm with chromatin  
54 and other defects from participating in the fertilisation process. Negative effects on ICSI outcomes of  
55 the use of poor quality sperm may include miscarriage, an increased risk of congenital abnormalities  
56 and childhood cancer (Celik-Ozenci *et al.* , 2004, Gopalkrishnan *et al.* , 2000, Halliday, 2012, Jaleel

57 and Khan, 2013, Larsen *et al.* , 2013). These issues have led to the development of alternative  
58 methods of sperm selection for ICSI based on functional properties, potentially mimicking the natural  
59 processes occurring in the reproductive tract of healthy individuals and sperm binding to hyaluronic  
60 acid (HA) is one such method.

61

62 HA is a non-sulphated glycosaminoglycan with numerous biological functions in the extracellular  
63 matrix and on the cell surface (Amemiya *et al.* , 2005). HA is abundant in the female reproductive  
64 tract and may be involved in sperm-egg interactions (Ghosh *et al.* , 2007). The cumulus oophorus  
65 complex (COC) is also HA-rich (Zhuo and Kimata, 2001) and HA permeates the zona pellucida and  
66 the perivitelline space of mammalian oocytes (Vandevoort *et al.* , 1997). During *in vivo* fertilisation,  
67 mature spermatozoa bind hyaluronic acid in the extracellular matrix of the COC via hyaladherins  
68 and subsequently release unrelated hyases (for example, PH20/SPAM1) facilitating HA digestion  
69 and penetration of the cumulus mass. Immature spermatozoa, however, do not bind to HA or may  
70 bind it more weakly (Huszar *et al.* , 2003, Nasr-Esfahani *et al.* , 2008).

71

72 Hyaladherins including CD44 (Bajorath *et al.* , 1998, Underhill, 1992) and RHAMM (Hardwick *et al.* ,  
73 1992, Yang *et al.* , 1994), both present in ejaculate spermatozoa (Amaral *et al.* , 2014) are  
74 categorised by whether they contain a Link domain or module (a sequence of ~100 amino acids  
75 composed of two alpha-helices, two triple-stranded anti-parallel beta-sheets and two disulphide  
76 bonds (Barta *et al.* , 1993) or a BX7B motif (where the "B"s are arginine (R) or lysine (K) residues  
77 and the "X" is a sequence of seven non-acidic and at least one basic amino acids), a covalent bond  
78 or combinations thereof (Amemiya *et al.*, 2005, Day and Prestwich, 2002, Yang *et al.* , 1994). CD44,  
79 for example, contains both a Link module and a BX7B motif.

80

81 Investigating sperm hyaladherins is justified in relation to understanding the fertilisation potential of  
82 sperm and the causes of male infertility. A previous study in our laboratory provided evidence for the  
83 complexity of hyaladherin expression in ejaculate human spermatozoa and showed that sperm  
84 binding to HA was enhanced by capacitation (Torabi *et al.* , 2016) and may involve unknown

85 hyaladherins. To improve our understanding, proteins extracted from washed and homogenised  
86 ejaculate human spermatozoa were subjected to affinity panning on a HA-coated surface (Amemiya  
87 *et al.*, 2005). Adherent (binding) and non-binding proteins were recovered and subsequently  
88 characterised by tandem mass spectrometry (LC-MS/MS).

89

## 90 **Materials and methods**

### 91 Reagents used

92 Ethylenediaminetetraacetic acid (EDTA), Triton-X100, Acrylamide/Bis-acrylamide, 30% solution,  
93 Sodium dodecyl sulphate (SDS), Ammonium persulfate (APS) and *N,N,N',N'*-  
94 Tetramethylethylenediamine (TEMED) were obtained from Sigma-Aldrich (UK). PVDF membranes  
95 and Amicon Ultra-0.5 mL and 15 mL centrifugal filter units were obtained from Millipore (UK). Pierce  
96 BCA protein assay kit, Pierce™ protein-free (PBS/TBS) blocking buffer were obtained from Thermo  
97 Fisher Scientific (UK). Tris Base and NaCl were purchased from Fisher Scientific (UK). Protease  
98 inhibitor cocktail was purchased from Cell Signalling Technology (UK). ColorPlus prestained protein  
99 ladder was acquired from New England Biolabs (UK). Clarity™ western ECL substrate and Bradford  
100 protein assay reagent were purchased from Bio-Rad (UK). HA-coated dishes were purchased from  
101 Biocoat (USA). The monoclonal anti-ZPBP2 antibody was purchased from antibodies-online. The  
102 monoclonal anti-ADAM32 (sc-376738) and anti-Alpha tubulin (SC-5286) antibodies were obtained  
103 from Santa Cruz Biotechnology. Water for mass spectrometry containing 0.1% formic acid (LC-MS  
104 Chromasolv®) was from Honeywell (Seelze, Germany) and the acetonitrile from Fluka. The rest of  
105 the reagents were supplied by Sigma-Aldrich (St. Louis, MO) unless otherwise stated.

106

### 107 Ethical approval

108 The study was considered and nationally approved by the relevant UK Integrated Research  
109 Application System (IRAS) Ethics Committee (NRES 12\_NE\_0192) on 13 January 2013 and locally  
110 approved by the University of Leeds' School of Medicine Research Ethics Committee  
111 (SoMREC/13/017) on 28 November 2013.

112

### 113 Semen analysis

114 A schematic of the experimental plan is shown in Figure 1. Human semen samples were obtained  
115 ethically from young male volunteers (18-25 years of age) of unproven fertility by masturbation into  
116 sterile, tissue culture grade universal containers after 3 days abstinence. Collected semen samples  
117 were immediately liquefied for 30 minutes at 37 °C. The semen parameters related to each sample  
118 are shown in Table 1. After liquefaction, all samples were checked for volume, sperm concentration,  
119 sperm morphology and the number of round cells according to the WHO (World Health  
120 Organisation) criteria (2010) and following, where appropriate, the guidelines recommended by  
121 Bjorndahl et al (Bjorndahl *et al.* , 2016). Only those with normal semen parameters as defined by  
122 WHO criteria were included in the study.

123

### 124 Sperm preparation

125 To maximise the recovery of sperm, liquefied semen samples were centrifuged through a 60%  
126 density cushion of SupraSperm™ using special inserts (ProInsert-Nidacon, Sweden) to remove any  
127 round cell contamination at 300 ×g for 20 minutes. A pellet retrieval pipette (ProInsert kit) was used  
128 to aspirate sperm pellets which were then resuspended and washed in PBS (pH: 7.2) followed by  
129 centrifugation at 300 × g for 10 minutes (two repeated washes). Sperm motility and morphology  
130 were assessed using a Leitz Laborlux 12 light microscope and the sperm pellets were used for  
131 further protein extraction.

132

### 133 Protein extraction and affinity panning of sperm proteins

134 To reduce costs while as far as possible retaining sample heterogeneity, two aliquots of each  
135 sample were pooled into two (~2 × 10<sup>8</sup> sperm in total, each) combined samples (C1 and C2) and  
136 extracted separately in 500 µL of a mild lysis buffer (150 mM NaCl, 20 mM Tris-HCl (pH: 8), 2mM  
137 EDTA, 1x protease inhibitor cocktail, 0.5% Triton X-100) (D'Cruz *et al.* , 1993). The suspensions  
138 were sonicated on ice for 15 seconds on, 40 seconds off, at an amplitude of 10 microns. The  
139 sonication was repeated four times. Samples were incubated on ice for 1h with constant shaking.  
140 To recover extracted soluble proteins, samples were centrifuged at 16000 ×g for 20 minutes and

141 supernatants were aspirated and transferred into fresh tubes. Pellets were discarded. Protein  
142 quantification was performed using the Pierce BCA protein assay kit according to manufacturer's  
143 instruction (Thermo Fisher Scientific, UK). HA-coated dishes (Biocoat, USA) were used to pan for  
144 proteins in the sample homogenates (C1 and C2) with an affinity for hyaluronic acid. To block non-  
145 specific binding, dishes were treated beforehand with 1.5 mL of Pierce™ protein-free (PBS) blocking  
146 buffer (Thermo Fisher Scientific, UK) for 30 minutes at room temperature (RT) with gentle shaking.  
147 Dishes were then washed twice with 2 mL of phosphate buffered saline (PBS). Extracted proteins  
148 from the sperm of two different men were used and loaded on to separate HA-coated dishes at a  
149 concentration of 1.5 mg/mL. Dishes were incubated for 75 minutes at RT with gentle shaking after  
150 which, non-binding proteins were decanted for frozen storage at -80°C.

151

152 To minimise non-specific contamination of the binding fractions, dishes were washed with 1.5 mL  
153 PBS (four times for one minute each wash). Bound proteins were then recovered by incubating the  
154 plate surface with 400 µL of a pre-heated (95°C) Laemmli-based buffer containing 0.125 M Tris-HCl  
155 (pH: 6.8), 4%w/v SDS and 10%v/v 2-mercaptoethanol for 5 minutes with gentle shaking. Bound  
156 proteins were aspirated using a pipette. Both protein fractions (HA-binding and non-binding) were  
157 processed through Amicon Ultra-15 mL centrifugal desalting filters (3 kDa) according to  
158 manufacturer's instruction (Millipore, UK). The proteins were then concentrated using Amicon's  
159 Ultra-0.5 mL centrifugal filters according to manufacturer's instruction (Millipore, UK). A final volume  
160 (40 µL) was obtained after concentration and 30 µL of each was precipitated using TCA-acetone  
161 (see below). Ten (10 µl) aliquots were stored at -80°C for western blot analysis (see below).

162

### 163 Protein precipitation

164 To precipitate proteins, one volume of 100% (w/v) TCA was added to four volumes of the protein  
165 solution (final conc of 20% TCA) from both HA-binding and non-binding samples. All samples were  
166 incubated for 20 minutes at 4°C and centrifuged at 19000 xg for 5 minutes. Supernatants were  
167 discarded. Pellets were washed with 200 µL of ice-cold acetone and centrifuged at 19000 xg for 5

168 minutes at 4°C (twice, with washing between). Pellets were dried and stored at -80°C before  
169 sequencing by LC-MS/MS as outlined below.

170

#### 171 Liquid chromatography-tandem mass spectrometry (LC-MS/MS)

172 Proteins were digested with trypsin (Promega, Madison, WI) at 37°C overnight according to the  
173 manufacturer's recommendations. Tryptic peptides were separated by means of nano liquid  
174 chromatography using an Eksigent NanoLC AS2 ultra (AB SCIEX) with a flow rate of 400 nL/min, an  
175 EASY C18 trap column (5 µm, 120 µm, 100 µm inner diameter × 2 cm in length), and an EASY C18  
176 analytical column (3 µm, 120 µm, 75 µm inner diameter × 10 cm in length). The following linear  
177 gradient, using solvent B (97% acetonitrile, 0.1% formic acid) and solvent A (3% acetonitrile, 0.1%  
178 formic acid), was employed: 5%–40% buffer B (65 min); 40%–100% buffer B (5 min). MS/MS  
179 analysis was performed using an LTQ Orbitrap Velos (Thermo Fisher Scientific) with a  
180 nanoelectrospray ion source with precursor ion selection in the Orbitrap at 30,000 of resolution,  
181 selecting the 15 most intense precursor ions, with a collision energy of 35 in positive ion mode.  
182 MS/MS data acquisition was completed using Xcalibur 2.1 (Thermo Fisher Scientific). Figure 1  
183 shows a schematic illustration of the study plan.

184

185

#### 186 Protein identification, quantification and analysis

187 Proteome Discoverer 1.4 (ThermoFisher Scientific) was used to characterise all proteins. Database  
188 searching included all entries from the *Homo sapiens* UniProtKB/Swiss-Prot database (release 02-  
189 2015) using SEQUEST version 28.0 (Thermo Fisher Scientific). A 1% FDR and at least one (≥1)  
190 unique peptide per protein were the criteria used for protein identification. The dissociated or  
191 'ungrouping' of proteins from their respective families was used during the quantification process in  
192 order to avoid possible ambiguities associated with different isoforms of the same protein.

193

194 Identified proteins in binding and non-binding fractions from the two individual samples were  
195 compared and checked against the whole human sperm proteome (Amaral *et al.*, 2014) and only

196 those present in this database were included for further analysis. Additional information about the  
197 identified proteins was obtained using UniProtKB/Swiss-Prot, and BioMart - Ensembl. DAVID  
198 Bioinformatics Resources 6.8 was used for functional ontological annotation clustering (Huang *et al.*  
199 , 2007).

200

201 PDBsum was used to align amino acid sequences of identified proteins with sequences for which  
202 structural information is available (Laskowski, 2001, 2009, Laskowski *et al.* , 2005). The SAS  
203 (Sequences annotated by structure) server was then used ([http://www.ebi.ac.uk/thornton-](http://www.ebi.ac.uk/thornton-srv/databases/sas/)  
204 [srv/databases/sas/](http://www.ebi.ac.uk/thornton-srv/databases/sas/)) to determine the structural similarities between identified proteins in HA-binding  
205 and non-binding fractions with the hyaluronic acid binding domain of CD44 (highlighted by  
206 PDBsum). SAS annotates protein residues according to residue type (polar, non-polar, aliphatic and  
207 aromatic), secondary structure (alpha-helix, beta-strand, turn and coil), inter-molecular contacts  
208 (number of hydrogen bonds, total contacts, nucleic acid contacts and metal ions contacts to ligand),  
209 active sites and residue similarity (Milburn *et al.* , 1998). Sequence similarities were computed using  
210 the PAM250 log odds scores matrix with FASTA used as the sequence search method and  
211 presented as a simple pairwise comparisons. The colouring of residue similarity signifies identical  
212 amino acid types (red) down to conservative, semi-conservative and dissimilar residues using a  
213 spectrum ranging from orange through to blue. In addition, a Z-score and an E-value for sequence  
214 similarity were computed (Pagni and Jongeneel, 2001).

215

#### 216 Western blot analysis

217 To verify the results of LC-MS/MS experiments, 15 µg of binding and non-binding proteins from  
218 each sample were resolved by SDS PAGE and western blotted. Samples were dissolved and  
219 diluted 1:1 with 2x Laemmli buffer (4% SDS, 10% 2-mercaptoethanol, 20% glycerol, 0.004%  
220 bromophenol blue, 0.125 M Tris-HCl (pH: 6.8)) and boiled for 5 minutes at 95°C. The proteins were  
221 separated on a 10% gel at 120 V for 100 minutes in 1x SDS running buffer (25 mM Tris-base, 190  
222 mM Glycine, 0.1% SDS). Proteins were then transferred to PVDF membranes at 250 mA for 90  
223 minutes in 1x transfer buffer (25 mM Tris-base, 190 mM Glycine, and 20% methanol). The

224 membrane was blocked with Pierce™ protein-free (TBS) blocking buffer (Thermo Fisher Scientific,  
225 UK) for 1h at RT with constant shaking and then probed with antibodies to two proteins specific to  
226 the binding fraction, zona pellucida binding protein 2 (ZPBP2) and ADAM32 (200 µg/mL) at a  
227 primary antibody concentration of 1/500 and 1/200, respectively overnight at 4°C. An alpha tubulin  
228 antibody (200 µg/mL at a final concentration of 1/2000) was used as a control for proteins present in  
229 both fractions and as a loading control. Membranes were washed three times with TBS containing  
230 0.1% Tween-20 for 15 minutes each and incubated with 1:1000 dilution of relevant HRP-conjugated  
231 secondary antibodies for 1h at RT (all primary and secondary antibodies were diluted in Pierce™  
232 protein-free (TBS)). Membranes were washed as described above and the Clarity western ECL  
233 substrate was used to visualise protein bands (Bio-Rad, UK).

234

## 235 **Results**

### 236 Identification of proteins in HA-binding and non-binding fractions

237 LC-MS/MS data resulted in the identification of 180 (sample C1) and 227 (sample C2) proteins in  
238 HA-binding fractions and 466 (sample C1) and 563 (sample C2) proteins in non-binding fractions,  
239 respectively (Figure 2A). As shown in Figure 2BI, 45 proteins were common and specific (no  
240 overlaps with non-binding fractions) to both HA-binding fractions and had records in the human  
241 sperm proteome database (Amaral *et al.*, 2014) of which 28 had  $\geq 1$  unique peptides per protein.  
242 One hundred and twenty-nine (129) proteins were common to both non-binding fractions with 81  
243 recorded in the human sperm proteome database and represented by  $\geq 1$  unique peptides (Figure  
244 2BII). A list of all mass spectrometry data can be found in Suppl Tables 1-4. Additional information  
245 about the identified proteins was obtained using UniProtKB/Swiss-Prot, and BioMart - Ensembl.  
246 Table 2 lists proteins in the binding fractions. The equivalent list from the non-binding fractions is  
247 shown in Suppl Table 5.

248

249 An ontology analysis was undertaken to determine whether binding and non-binding proteins carried  
250 distinct functional signatures indicating a potential HA affinity effect. Following submission to DAVID,  
251 results suggested distinct signatures with the bound fraction carrying a weak enrichment for

252 secreted proteins although a stronger enrichment in the unbound fraction was found for chaperone  
253 and chaperone-like proteins (Suppl Tables 6 and 7).

254

#### 255 Alignment of the sequences of HA-binding and non-binding proteins using PDBsum and SAS

256 The amino acid sequences of the 28 proteins in the HA-binding fractions were submitted to  
257 PDBsum, which generates lists of structural features (PDB codes) conserved between proteins. One  
258 protein (ZPBP2) contained a sequence motif bearing similarity to the Link module of CD44, while 14  
259 others (50% in total; Table 2) contained BX7B sequences. Twenty-eight (28) proteins (34.5%; Suppl  
260 Table 5) from the non-binding fraction also contained the BXB7 motif indicating a slight enrichment  
261 for proteins containing the motif in the binding fractions (one-tailed Z score = 1.45;  $p = 0.074$ ). No  
262 proteins containing a Link-like sequence were present in the non-binding fraction. Proteins with  
263 multiple ( $\geq 2$ ) BX7B motifs, including ADAM32 (Uniprot QBTC27) with two and Midkine (Uniprot  
264 P21741) with four of which the latter is known to bind HA and other glycosaminoglycans  
265 (<http://www.ebi.ac.uk/QuickGO/GProtein?ac=P21741>), were more abundant in the binding (25%)  
266 versus the non-binding (15%) fractions although this difference was not significant (one-tailed Z  
267 score = 1.22;  $p = 0.111$ ). Hence, the trends suggest that HA binding motifs may have influenced the  
268 partitioning of the two populations. Charge differences between proteins were also explored as an  
269 alternative partitioning mechanism. Net charge is dictated by proteins'  $pI$  and as HA carries a net  
270 negative charge at pH 8.0 (the pH of the extraction buffer), basic proteins with a net positive charge  
271 could have electrostatically interacted with the substrate. Twenty (71.4%) of the proteins in the  
272 binding fraction compared with 21 (26%) in the non-binding fraction were likely to carry a net  
273 positive charge, a strongly significant difference, suggesting that charge effects may also have  
274 influenced the partitioning of proteins in the fractions (one-tailed Z score = 4.28;  $p < 0001$ ).

275

276 Of all the proteins in the binding fractions, ZPBP2 which contains a sequence motif with similarities  
277 to the Link module found in CD44 was flagged as one of the more interesting. ZPBP2 (also known  
278 as ZPBPL) was first reported in 2003 from an in silico search of a region on human chromosome  
279 17q12 that is frequently amplified in breast and stomach cancers (Katoh and Katoh, 2003). Figure

280 3A shows the alignment between ZBPB2 and CD44 (PDB code 2i83, residues 21 – 178) with a  
281 32.7% sequence identity and 69% overall similarity covering a 55 amino acid overlap. Unlike CD44  
282 where the Link module is close to the amino-terminal end, the equivalent sequence in ZBPB2 is  
283 located towards the carboxyl-terminal end. There were no proteins with a sequence resembling the  
284 Link module in the non-binding fractions. The 2i83 PDB code comparison is shown because it  
285 corresponds with the CD44's HA-binding form although other valid codes representing a similar  
286 residue overlap were also flagged (Table 3) (Liu and Finzel, 2014, Takeda *et al.*, 2006, Teriete *et al.*  
287 , 2004). As ZBPB2 may have hyaladherin properties based on sequence similarities with the Link  
288 domain, further structural similarities were investigated using the Sequences Annotated by Structure  
289 (SAS) server (Milburn *et al.*, 1998). This resource checks for the number of contacts between the  
290 protein and its presumptive ligand based on secondary structure prediction and was used to scan  
291 the homologous HA binding motif on ZBPB2. The PROSITE secondary structure alignment  
292 (PS01241) for 2i83 (<http://prosite.expasy.org/cgi-bin/prosite/prosite-search-ac?PS01241>) with  
293 ZBPB2 is shown in Figure 3B. Residues in ZBPB2 conserved with those in CD44 within the HA  
294 binding domain, included Arg46/246, Ala49/249, Phe56/256, Asn57/257, Thr59/259, Leu60/260,  
295 Pro61/261, Met63/263, Leu70/270, Cys78/278, Arg79/279, Gly81/281, Phe82/282, Arg91/287,  
296 His93/289, Asn95/291, Cys98/292, Ala99/293, Thr109/303, Thr117/311, Ser123/317). Boxes  
297 indicate conserved residues involved in ligand binding and the stars indicate conserved cysteine  
298 residues.

299

300 PDB was also used to check whether the Link module that could influence the partitioning of  
301 proteins into binding and non-binding fractions was present in any of the 81 proteins common to the  
302 non-binding fractions. None returned a PDB code. We also aligned the sequences of ten putative  
303 HA-binding proteins containing the Link module (Table 4\*) and eleven, randomly selected proteins  
304 from the non-binding fraction (Table 4<sup>†</sup>) without evidence for a Link module. SAS was then used to  
305 look for any existing structural similarities between them and the CD44 motifs flagged by the PDB  
306 codes, (4pz3, 4pz4, 1uuh, 1poz and 2i83; Table 3). When aligned with these sequences, the first

307 seven proteins in the list had the highest Z-scores (123-321) and lowest E-values ( $4.5e^{-16}$ - $2.2e^{-5}$ ).  
308 The next three proteins had lower Z-scores (50.6 -112.1) and higher E-values ( $1.9e^{-4}$ - 0.38). The  
309 eleven proteins in the non-binding fraction (Table 4<sup>‡</sup>) occasionally showed higher percentage  
310 identities with the CD44 Link module (PLIN3 for example). Similarly, human axonemal dynein light  
311 intermediate polypeptide 1 (O14645) also showed a high % identity with sequences represented by  
312 PDB codes 4pz3 and 1uuh but with a far lower Z score and high E value. Relative Z-scores and E-  
313 values give more accurate predictions of structural relationships between proteins than percentage  
314 identity and although not reported to contain a Link module hitherto, ZPBP2 is included in Table 4  
315 because it was flagged by PDB / SAS and has a relatively high Z-score with correspondingly low E-  
316 value.

317

#### 318 Western blotting to confirm the results of proteomics

319 To confirm the results obtained by LC-MS/MS, western blotting was performed using antibodies  
320 against ZPBP2, ADAM32 and alpha tubulin on binding and non-binding fractions from the four  
321 samples individually and independently processed prior to combining for proteomic analysis.  
322 ADAM32 was chosen because it has two BX7B motifs. Antibodies against ZPBP2 and ADAM32  
323 detected protein bands at approximately 38 kDa and 85 kDa, respectively in binding fractions (lanes  
324 2, 4, 6, 8), consistent with our sequencing and partitioning data (Figure 4). Additional bands at ~36  
325 kDa and 42 kDa were revealed using the antibody to ZPBP2. No signals were detected in non-  
326 binding fractions (Lanes 1, 3, 5, 7). The antibody against alpha-tubulin (present in both fractions  
327 and used here as a loading control) detected a single band at approximately 50 kDa in all samples.

328

#### 329 **Discussion**

330 The present study was conducted to search for novel hyaladherins in human sperm by allowing the  
331 soluble proteins extracted from homogenised sperm to interact with a HA-coated surface before  
332 their recovery and characterisation by tandem mass spectrometry (LC-MS/MS). This simple affinity  
333 panning process (Amemiya *et al.*, 2005) resulted in the identification and selection for further  
334 analysis of 28 proteins from the binding fractions including one containing a sequence related to the

335 HA-binding domain of CD44 (Liu and Finzel, 2014, Takeda *et al.*, 2006, Teriete *et al.*, 2004) that  
336 was identified as ZPBP2. Based on the proportion of positively charged proteins in the binding  
337 versus non-binding fractions of extracted sperm proteins, electrostatic attraction is also likely to have  
338 played a role in the outcomes of the panning process (Lenormand *et al.*, 2008, Purcell *et al.*,  
339 2014). Nonetheless, a conformational change in conjunction with the overall charge of a protein  
340 could also favour interaction with HA, which is known to be transitory in nature (Kohda *et al.*, 1996,  
341 Liu and Finzel, 2014, Misra *et al.*, 2015).

342

343 SAS determines and applies unique identifiers from different crystallographic (X-ray or Nuclear  
344 Magnetic Resonance) submissions, which in the case of the ZPBP2 included five records (PDB  
345 codes 4pz3, 1uuu, 4pz4, 2i83 and 1poz) relating to the HA-binding (Link) domain of CD44 (Liu and  
346 Finzel, 2014, Takeda *et al.*, 2006, Teriete *et al.*, 2004). CD44 is one of the better understood  
347 hyaladherins and is a type I transmembrane protein located on the surface of many different cell  
348 types including mammalian sperm as reported previously (Bains *et al.*, 2002). Its location on the  
349 sperm surface has also been shown to alter during and following capacitation and the acrosome  
350 reaction (Torabi *et al.*, 2016). CD44 has many different isoforms due to alternative splicing in the  
351 proximal region of the extracellular domain and also shows evidence of post-translational  
352 modifications (Oliferenko *et al.*, 2000, Toole, 2004). CD44 probably binds HA through a disulphide-  
353 bond stabilized HA-binding domain (HABD) located within the Link module (Takeda *et al.*, 2006) and  
354 the peptide sequence in ZPBP2 bearing similarity to the Link domain of CD44 is based on the  
355 latter's ligand bound configuration (Bajorath *et al.*, 1998) and retains two of the cysteine residues  
356 thought to be responsible for stabilising the HABD.

357

358 Both ZPBP1 and ZPBP2 are located on the acrosome and the role of the former in binding the zona  
359 pellucida is already documented (Mori *et al.*, 1993, Mori *et al.*, 1995). Both proteins belong to the  
360 immunoglobulin like domain containing family (Lin *et al.*, 2007) and are co-designated by sequence  
361 similarity, sharing a similar, amino-terminal signal sequence and a carboxyl-terminal zona binding  
362 homologous domain (ZBHD) with 15 conserved cysteine residues (Kato and Kato, 2003). Loss of

363 either protein leads to disruption of acrosome formation and sperm morphology (ZPBP1/2) and to  
364 male mouse sterility (ZPBP1) or subfertility (ZPBP2; Lin et al., 2007). The ZPHD and putative Link  
365 domains, overlap (Figure 3A) and share common features, notably the two conserved cysteines  
366 (Figure 3A; stars) supporting the latter's disulphide linked HA-binding configuration (Teriete *et al.*,  
367 2004).

368

369 Excepting teleosts, which have no ZPBPs and use a completely distinct process for fertilisation  
370 (Morisawa, 1999), the ZPHD domain is conserved across all vertebrate species (Lin et al., 2007).  
371 Amphibians express just one ZPBP, which is more similar to mammalian ZPBP2 than to ZPBP1 (Lin  
372 et al., 2007), explaining PDPsum's 'failure' to report homology with ZPBP1. These data suggest  
373 that the recognition of zona pellucida protein 2 (ZP2) by either of the ZPBPs and of HA by  
374 hyaladherins containing the Link module like CD44, may utilise similar mechanisms. Hence, zona  
375 recognition by amphibian sperm ZPBPs could have arisen via an earlier HA-binding (or lectin  
376 binding) property that was partially conserved during the likely gene duplication event that gave rise  
377 to ZPBP1 (Lin et al., 2007; Kohda et al., 1996). The original ZPBPs of primitive vertebrates may not  
378 have had time to evolve the more specific sperm-egg interactions seen in modern mammals.  
379 Alongside CD44, however, they may still have hyaladherin-like properties. In the human, ZPBP2 has  
380 at least two known isoforms of 338 (38.6) kDa and 316 (36.2 kDa) amino acids, respectively, both of  
381 which contain the ZPHD sequence. These and an additional band at ~42 kDa that may represent a  
382 novel isoform of this protein (Lin *et al.*, 2007) were only detected in the binding fractions by western  
383 blotting (Figure 4).

384

385 The Link module present in CD44 is also present in several other hyaladherins including TSG-6,  
386 versican, link protein, brevican, aggrecan and neurican, which were not detected in either binding or  
387 non-binding fractions. The BX7B motif has been reported in RHAMM, CD44, and the hyaluronidase,  
388 HABP1 (C1QBP) among others (Day and Prestwich, 2002, Yang *et al.*, 1994). Midkine (MK) is a  
389 secreted growth factor rich in basic amino acids and cysteine with a molecular mass of  
390 approximately 13 kDa (Jono and Ando, 2010). The two BX7B motifs in ADAM32 and the four in

391 Midkine as well as the proteins' net positive charge may help explain their presence in the binding  
392 fraction. ADAM32 has been identified as a type I non-catalytic metalloprotease-like transmembrane  
393 protein (Wolfsberg *et al.* , 1995). The protein is expressed during spermatogenesis and processed  
394 during epididymal maturation to become localised on the sperm surface (Kim *et al.* , 2006). Western  
395 blot analysis confirmed that ADAM32 was confined to the binding fractions. To date 29 ADAMs have  
396 been identified of which 15 are expressed in testis (Primakoff and Myles, 2000). This suggests a  
397 specific relationship between ADAM function, spermatogenesis and fertilisation. ADAM2 (fertilin  
398 beta) and ADAM3 (cyritestin) interact with integrin in the egg plasma membrane of mouse oocytes  
399 (Wassarman *et al.* , 2001).

400

401 The absence of known sperm hyaladherins, including CD44, RHAMM and C1QBP in any of the  
402 extract fractions **as well as the presence of BX7B motifs in some proteins from the non-binding**  
403 **fractions** was surprising and warrants further consideration (Bajorath *et al.*, 1998, Hardwick *et al.*,  
404 1992, Underhill, 1992, Yang *et al.*, 1994). One possibility is that the transient and dynamic binding  
405 reported between hyaladherins and hyaluronic acid that facilitates cell adhesion and migration  
406 relating to conformational changes in protein structure was responsible (Kohda *et al.*, 1996, Liu and  
407 Finzel, 2014, Misra *et al.*, 2015). HA-binding proteins without the required conformational  
408 configuration may well have been extracted by our methods **but were in the wrong conformational**  
409 **arrangement to permit efficient enrichment by HA-binding. Alternatively, the missing hyaladherins**  
410 **may not have been** sufficiently abundant in either fraction to be detectable by the LC-MS/MS  
411 method used. **CD44, for example, is not listed in the most recent and comprehensive human sperm**  
412 **proteome (Amaral *et al.*, 2014). Moreover, the mild solvent used in the** extraction process, designed  
413 to preserve tertiary structure, may have failed to access these proteins, which were lost in the  
414 insoluble pellets following sperm homogenisation. Membrane anchoring **could also** have rendered  
415 many proteins inaccessible under the extraction conditions used here (Gupta *et al.* , 1991). **Finally,**  
416 **BX7B motifs may not be universally involved in HA-binding, with only RHAMM having been shown**  
417 **to have an absolute requirement for them to date (Day, 2000, Yang *et al.*, 1994).** Work is in  
418 progress to isolate proteins from sperm permitted to undergo capacitation beforehand where

419 conformational or localisation changes to hyaladherins, increasing access to the extraction solvent,  
420 may have occurred (Torabi et al, 2016). Modification of the HA substrate may also improve its  
421 capacity to recognise and bind hyaladherins and experiments are also underway exploring this  
422 possibility.

423

424 Just one protein (ZPBP2) present only in HA-binding fractions contained a Link-like module.  
425 Regardless of the efficacy of the panning process itself, the uncovering of a structural relationship  
426 between ZPBP2 and CD44 is noteworthy and suggests that the general HA-sperm recognition  
427 process occurring in the cumulus-oophorus complex may predate the appearance of more  
428 specialised protein-protein, sperm-zona interactions in this context. The synthesis of larger  
429 quantities of both isoforms of ZPBP2 is warranted to more fully study their structural and possible  
430 HA-binding characteristics, their relationship to hyaladherins and involvement in male infertility.

431

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436 34). The views expressed in this publication are those of the author(s) and not necessarily those of  
437 the MRC, NHS, NIHR or the Department of Health.

438

439

440 **Figures and Tables.**

441 Figure 1. Flow chart of experimental design.

442

443 Figure 2. Venn diagrams illustrating overlaps between **(A)** HA-binding and non-binding proteins in  
444 samples from two combined (C1 and C2) sperm samples from four volunteer donors of unproven  
445 fertility and **(B)** overlaps between combined HA-binding **(I)** and non-binding proteins **(II)** from these  
446 samples.

447

448 Figure 3. Homology between the ligand (HA) bound form of CD44 (PDB code 2i83, 158 amino  
449 acids) and ZPBP2; 338 amino acids). Panel **A** shows the best residue alignment of ZPBP2 with  
450 2i83. Blue dashed lines indicate alignment adjustment spacing of 2i83 which means the residue  
451 numbers in panels A and B will not necessarily correspond. Boxes border residues implicated in  
452 ligand binding. Residue conservation is denoted by colours ranging from red (identical) to least  
453 conserved (blue). Panel **B** shows the predicted secondary structure (helices and strands) of ZPBP2  
454 with the confidence for helix and strand predictions denoted by green shading (darker shade means  
455 higher confidence). Red shading signifies the Link domain signature of CD44 with the small shaded  
456 bars indicating the strongest drivers of predicted secondary structure. Stars indicate the cysteines  
457 thought to be critical to the HA-binding configuration of the Link module.

458

459 Figure 4. Western blotting on binding (lanes 2, 4, 6, 8) and non-binding (lanes 1, 3, 5, 7) proteins in  
460 the four samples (1 - 4) used in these experiments with antibodies directed against ZPBP2 and  
461 ADAM32. Alpha-tubulin, present in both binding and non-binding fractions was used as a loading  
462 control. Lane 9 shows rainbow Mr calibration standards.

463

464 Table 1. Semen parameters of young male volunteers (unproven fertility) participating in the study.

465

466 Table 2. Proteins in both (C1 and C2) binding fractions with  $\geq 1$  unique identifying peptide and with  
467 no overlap with proteins in the non-binding fractions. Numbers in parenthesis indicate the number of  
468 BX7B motifs found in the protein sequence. N/D is not detected.

469

470 Table 3. PDB codes for sequences matching ZPBP2 ([http://www.ebi.ac.uk/thornton-](http://www.ebi.ac.uk/thornton-srv/databases/cgi-bin/pdbsum/GetPage.pl?pdbcode=index.html)  
471 [srv/databases/cgi-bin/pdbsum/GetPage.pl?pdbcode=index.html](http://www.ebi.ac.uk/thornton-srv/databases/cgi-bin/pdbsum/GetPage.pl?pdbcode=index.html)).

472

473 Table 4. List of 10\* binding proteins containing and 11<sup>‡</sup> randomly selected proteins from the non-  
474 binding fraction without the Link module. SAS was used to look for any existing structural similarities  
475 with the PDB flagged CD44 motifs (Table 3). ZPBP2 is included in Table 4 because it was flagged  
476 by PDB / SAS and has relatively high Z-scores and low E-values.

477

478 Suppl Table 1. Full LC-MS/MS data for proteins detected in the HA-binding fractions (C1).

479

480 Suppl Table 2. Full LC-MS/MS data for proteins detected in the HA-binding fractions (C2).

481

482 Suppl Table 3. Full LC-MS/MS data for proteins detected in the non-binding fractions (C1).

483

484 Suppl Table 4. Full LC-MS/MS data for proteins detected in the non-binding fractions (C2).

485

486 Suppl Table 5. Proteins found in both non-binding fractions and no overlap with the corresponding  
487 binding fractions.

488

489 Suppl Table 6. Functional annotation clustering of binding proteins using DAVID Bioinformatics  
490 Resources 6.8

491

492 Suppl Table 7. Functional annotation clustering of non-binding proteins using DAVID Bioinformatics  
493 Resources 6.

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- 616
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re: MHR-17-0162.R1

"Zona pellucida binding protein 2 (ZPBP2) and several proteins containing BX7B motifs in human sperm may have hyaluronic acid binding or recognition properties"

Your manuscript has now been reviewed and the comments of the Reviewers and the Associate Editor are inserted below. We are pleased to inform you that the reviewer(s) have recommended publication, but also suggest some minor revisions to your manuscript. Each of these comments should be answered in a revised manuscript before it can be formally accepted.

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Associate Editor

Comments to the Author:

The authors have addressed most of the reviewers' critiques. However, there is still one comment that requires more discussion. The authors should add a paragraph to the discussion carefully discussing the fact that not all BX7B containing proteins are found in the bound fractions. One possibility to explain the data is that affinity purification methods and mass spectrometry are strong techniques for positive identification. However, these methods are not strong to discard candidates. Alternatively, findings in this manuscript indicates that BX7B domains are not sufficient for binding and other yet unidentified motifs are also needed.

[We are grateful for the suggestions. In response, we have substantially modified the relevant sections in the Discussion along the lines suggested \(lines 401-417\), which we now believe places our results in better context. We have also deleted one](#)

reference by Yang et al (1993) in favour of their later (1994) paper (Identification of a common hyaluronan binding motif in the hyaluronan binding proteins RHAMM, CD44 and link protein), EMBO J, 13, 286-296. This was the first report establishing a role for the BX7B motif in RHAMM for HA-binding.

Editorial Office:

Please add a statement of authors roles and any potential conflicts of interest to the main manuscript file.

An updated version that includes any missing signatures has been added.

Reviewer: 1

Comments to the Author

In my view the major concern I expressed on the original version has not been resolved. The presence or absence of a BX7B motif has no relationship to binding properties of the studied proteins.

The reviewer's comment is understood. We appreciate better that with the possible exception of RHAMM, the role of the BX7B motif remains unresolved and that this could well account for our findings on the partitioning of BX7B containing proteins. We have added a comment to this effect in the revised discussion (lines 401-417) specifically on lines 415-417. In an additional step towards reconciliation in this regard, we have changed the report's title to a question, which we hope will further assuage your concerns.

Table 1.

Sample	Volunteer Age	Sperm concentration (million/mL)	Total sperm count ( $\times 10^6$ )	Semen volume (mL)	Sperm motility (%)
D1	28	233	349.5	1.5	92
D2	36	200	300	1.5	90
D3	19	251	1204.8	4.8	87
D4	20	179	716	4	61
<b>Mean <math>\pm</math> SD</b>	<b>26 <math>\pm</math> 8</b>	<b>216 <math>\pm</math> 32.34</b>	<b>643 <math>\pm</math> 418</b>	<b>3 <math>\pm</math> 1.70</b>	<b>83 <math>\pm</math> 14.5</b>

Table 2

UniProt/SwissProt Accession	Description	UniProt Gene Name	Potential HA-binding domain (N)
A4D1T9	protease, serine, 37	PRSS37	BX7B(1)
P03973	Antileukoproteinase, secretory leukocyte peptidase inhibitor	SLPI	BX7B (1)
P05109	S100 calcium binding protein A8	S100A8	BX7B (1)
P13647	Keratin, type II cytoskeletal 5	KRT5	N/D
P20155	serine protease inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	SPINK2	N/D
P21741	midkine (neurite growth-promoting factor 2)	MDK	BX7B (4)
P35663	cylicin, basic protein of sperm head cytoskeleton 1	CYLC1	BX7B (6)
P62987	ubiquitin A-52 residue ribosomal protein fusion product 1	UBA52	BX7B (1)
P99999	cytochrome c, somatic	CYCS	BX7B (1)
Q00796	sorbitol dehydrogenase	SORD	N/D
Q13618	cullin 3	CUL3	BX7B (2)
Q16568	CART prepropeptide	CARTPT	N/D
Q16836	hydroxyacyl-CoA dehydrogenase	HADH	N/D
Q6NUT2	Probable C-mannosyltransferase	DPY19L2	BX7B (2)
Q6P4A8	phospholipase B domain containing 1	PLBD1	BX7B (1)
Q6UWM5	GLIPR1-like protein 1	GLIPR1L1	N/D
Q6X784	zona pellucida binding protein 2	ZBP2	Link-like domain
Q86YZ3	hornerin	HRNR	N/D
Q8N5Q1	family with sequence similarity 71, member E2	FAM71E2	BX7B (3)
Q8TC27	ADAM metallopeptidase domain 32	ADAM32	BX7B (2)
Q8WZ59	transmembrane protein 190	TMEM190	N/D
Q96KX0	lysozyme-like 4	LYZA	N/D
Q96QH8	sperm acrosome associated 5B	SPACA5	N/D
Q9BVA1	tubulin, beta 2B class IIb	TUBB2B	N/D
Q9BWH2	FUN14 domain containing 2	FUNDC2	BX7B (1)
Q9NPJ3	acyl-CoA thioesterase 13	ACOT13	N/D
Q9UII2	ATPase inhibitory factor 1	ATPIF1	N/D
Q9Y6A4	cilia and flagella associated protein 20	CFAP20	BX7B (3)

N/D: Not detected.

Table 3

PDB code	Model	Length	%-identity	AA overlap	Z-score	Ligands	Protein name
<b>4pz3(A)</b>	X-ray 1.08Å	150	32.7	55	116.4	ALA-ALA-ALA-VAL, PEG, EDO, MES.	High-resolution crystal structure of the human cd44 hyaluronan domain complex with undefined peptides.
<b>1uuh(A)</b>	X-ray 2.20Å	150	32.7	55	116.4		Hyaluronan binding domain of human cd44.
<b>4pz4(A)</b>	X-ray 1.60Å	154	32.7	55	116.2	SO4, PEG, GOL, EDO, DMS.	High-resolution crystal structure of the human cd44 hyaluronan domain in new space group.
<b>2i83(A)</b>	NMR	158	32.7	55	116.1		Hyaluronan-binding domain of cd44 in its ligand-bound form.
<b>1poz(A)</b>	NMR	159	32.7	55	116.0		Solution structure of the hyaluronan binding domain of human cd44.

Table 4:

PDB code	Smith Waterman Score	% Identity	a.a Overlap	Seq length	Z-score	E-value	Protein name/UniProt accession number
4pz4 (a.a 18-171)	227	35	120	227	279.5	9.2e-14	TSG6_Human tumor necrosis factor-inducible gene 6 protein (P98066) *
4pz3(a.a 18-170)	227	35	120	227	279.9	8.8e-14	
1uuh(a.a 20-178)	227	35	120	227	279.9	8.8e-14	
2i83 (a.a 21-178)	227	35	120	227	279.2	9.6e-14	
1poz (a.a 20-178)	227	35	120	227	279.1	9.7e-14	
4pz4 (a.a 18-171)	259	32.6	138	322	317.6	7e-16	LYVE1_Human Lymphatic vessel endothelial hyaluronic acid receptor 1 (Q9Y5Y7) *
4pz3(a.a 18-170)	259	32.6	138	322	318	6.7e-16	
1uuh(a.a 20-178)	259	32.6	138	322	318	6.7e-16	
2i83 (a.a 21-178)	262	32.3	158	322	321	4.5e-16	
1poz (a.a 20-178)	262	32.3	158	322	320	4.6e-16	
4pz4 (a.a 18-171)	148	26.2	103	862	173	7.9e-08	Human putative uncharacterized protein DKFZp434E0321 (Fragment)( CAB61358) (Q9UF98) *
4pz3(a.a 18-170)	148	26.2	103	862	173.4	7.5e-08	
1uuh(a.a 20-178)	148	26.2	103	862	173.4	7.5e-08	
2i83 (a.a 21-178)	148	26.2	103	862	172.7	8.3e-08	
1poz (a.a 20-178)	148	26.2	103	862	172.6	8.4e-08	

4pz4 (a.a 18-171)	154	29.8	94	2415	173.1	7.8e-08	Human Aggrecan core protein (P16112) *
4pz3(a.a 18-170)	154	29.8	94	2415	173.5	7.4e-08	
1uuh(a.a 20-178)	154	29.8	94	2415	173.5	7.4e-08	
2i83 (a.a 21-178)	154	29.8	94	2415	172.6	8.3e-08	
1poz (a.a 20-178)	154	29.8	94	2415	172.5	8.4e-08	
4pz4 (a.a 18-171)	123	26.1	88	340	149.6	1.6e-06	Human Hyaluronan and proteoglycan link protein 2 (BRAL1) (Q9GZV7) *
4pz3(a.a 18-170)	123	26.1	88	340	150	1.5e-06	
1uuh(a.a 20-178)	123	26.1	88	340	150	1.5e-06	
2i83 (a.a 21-178)	123	26.1	88	340	123	1.7e-06	
1poz (a.a 20-178)	123	26.1	88	340	149.2	1.7e-06	
4pz4 (a.a 18-171)	182	31.4	102	2570	207.2	9.9e-10	HUMAN Stabilin-1 (Q9NY15) *
4pz3(a.a 18-170)	182	31.4	102	2570	207.6	9.3e-19	
1uuh(a.a 20-178)	182	31.4	102	2570	207.6	9.3e-10	
2i83 (a.a 21-178)	182	31.4	102	2570	206.7	1e-09	
1poz (a.a 20-178)	182	31.4	102	2570	206.7	1e-09	
4pz4 (a.a 18-171)	115	25.5	94	1321	129.3	2.2e-05	Human Neurocan core protein (O14594) *
4pz3(a.a 18-170)	115	25.5	94	1321	129.7	2e-05	
1uuh(a.a 20-178)	115	25.5	94	1321	129.7	2e-05	

2i83 (a.a 21-178)	115	25.5	94	1321	128.9	2.3e-05	
1poz (a.a 20-178)	115	25.5	94	1321	128.8	2.3e-05	
4pz4 (a.a 18-171)	123	24.3	107	911	65.4	0.075	Human Brevican core protein (Q96GW7) *
4pz3(a.a 18-170)	123	24.3	107	911	65.8	0.071	
1uuh(a.a 20-178	123	24.3	107	911	65.8	0.071	
2i83 (a.a 21-178)	123	24.3	107	911	65.1	0.078	
1poz (a.a 20-178)	123	24.3	107	911	65	0.079	
4pz4 (a.a 18-171)	123	27.8	108	3396	111.6	0.00021	Human Versican core protein (P13611) *
4pz3(a.a 18-170)	123	27.8	108	3396	112.1	0.00019	
1uuh(a.a 20-178	123	27.8	108	3396	112.1	0.00019	
2i83 (a.a 21-178)	123	27.8	108	3396	111.2	0.00022	
1poz (a.a 20-178)	123	27.8	108	3396	111.2	0.00022	
4pz4 (a.a 18-171)	61	26.2	61	629	51	0.39	Human Sushi domain-containing protein 5 (KIAA0527) (O60279) *
4pz3(a.a 18-170)	61	26.2	61	629	51.4	0.38	
1uuh(a.a 20-178	61	26.2	61	629	51.4	0.38	
2i83 (a.a 21-178)	61	26.2	61	629	50.6	0.4	
1poz (a.a 20-178)	61	26.2	61	629	50.6	0.41	

4pz4 (a.a 18-171)	88	32.7	55	316	107	3.7e-04 (0.00037)	Zona pellucida binding protein 2 (ZPBP2 ) (Q6X784) *?
4pz3(a.a 18-170)	88	32.7	55	316	107.5	3.5e-4	
1uuh(a.a 20-178)	88	32.7	55	316	107.5	3.5e-4	
2i83 (a.a 21-178)	88	32.7	55	316	106.8	3.8e-04	
1poz (a.a 20-178)	88	32.7	55	316	106.7	3.9e-04	
4pz4 (a.a 18-171)	40	20.7	29	215	38	0.93	Human sperm acrosome membrane-associated protein 3 (Q81XA5) ‡
4pz3(a.a 18-170)	40	20.7	29	215	38.3	0.92	
1uuh(a.a 20-178)	40	20.7	29	215	38.3	0.92	
2i83 (a.a 21-178)	40	20.7	29	215	37.7	0.93	
1poz (a.a 20-178)	40	20.7	29	215	37.6	0.94	
4pz4 (a.a 18-171)	58	25	92	548	39.8	0.88	Human T-complex protein 1 subunit theta (P50990) ‡
4pz3(a.a 18-170)	58	25	92	548	40.1	0.86	
1uuh(a.a 20-178)	58	25	92	548	40	0.86	
2i83 (a.a 21-178)	58	225	92	548	39.4	0.89	
1poz (a.a 20-178)	58	25	92	548	39.3	0.89	
4pz4 (a.a 18-171)	46	23.4	64	170	52.7	0.33	CAMP_Human Cathelicidin antimicrobial peptide
4pz3(a.a 18-170)	46	23.4	64	170	53	0.32	

1uuh(a.a 20-178)	46	23.4	64	170	53	0.32	(P49913) ‡
2i83 (a.a 21-178)	46	23.4	64	170	52.4	0.34	
1poz (a.a 20-178)	46	23.4	64	170	52.3	0.34	
4pz4 (a.a 18-171)	39	23.5	34	258	42.4	0.77	Human Axonemal dynein light intermediate polypeptide 1 (O14645) ‡
4pz3(a.a 18-170)	34	55.6	9	258	42.7	0.76	
1uuh(a.a 20-178)	34	55.6	9	258	42.7	0.76	
2i83 (a.a 21-178)	39	23.5	34	258	42.1	0.79	
1poz (a.a 20-178)	39	23.5	34	258	42	0.79	
4pz4 (a.a 18-171)	49	38.9	18	434	33	0.99	PLIN3_HUMAN Perilipin-3 O60664 ‡
4pz3(a.a 18-170)	49	38.9	18	434	33.4	0.99	
1uuh(a.a 20-178)	49	38.9	18	434	33.4	0.99	
2i83 (a.a 21-178)	49	38.9	18	434	32.7	0.99	
1poz (a.a 20-178)	49	38.9	18	434	32.6	0.99	
4pz4 (a.a 18-171)	53	23.9	67	148	71.5	0.035	LYZL6_HUMAN Lysozyme-like protein 6 (O75951) ‡
4pz3(a.a 18-170)	50	28.1	64	148	63.2	0.099	
1uuh(a.a 20-178)	50	28.1	64	148	63.2	0.099	
2i83 (a.a 21-178)	50	28.1	64	148	62.6	0.11	
1poz (a.a 20-178)	50	28.1	64	148	62.5	0.11	

4pz4 (a.a 18-171)	38	25	32	150	52.8	0.32	Human Cytochrome c oxidase subunit 5A, mitochondrial (P20674) †
4pz3(a.a 18-170)	38	25	32	150	53.1	0.31	
1uuh(a.a 20-178)	38	25	32	150	53.1	0.31	
2i83 (a.a 21-178)	38	25	32	150	52.6	0.33	
1poz (a.a 20-178)	38	25	32	150	52.5	0.33	
4pz4 (a.a 18-171)	45	23.3	43	381	50.1	0.43	Human Putative heat shock protein HSP 90-beta 2 (Q58FF8) †
4pz3(a.a 18-170)	45	23.3	43	381	50.4	0.41	
1uuh(a.a 20-178)	45	23.3	43	381	50.4	0.41	
2i83 (a.a 21-178)	45	23.3	43	381	49.8	0.44	
1poz (a.a 20-178)	45	23.3	43	381	49.7	0.44	
4pz4 (a.a 18-171)	33	17.4	46	369	24.5	1	Human Hsc70-interacting protein (P50502) †
4pz3(a.a 18-170)	33	17.4	46	369	24.8	1	
1uuh(a.a 20-178)	33	17.4	46	369	24.8	1	
2i83 (a.a 21-178)	36	19.4	36	369	40.2	0.86	
1poz (a.a 20-178)	36	19.4	36	369	40.1	0.86	
4pz4 (a.a 18-171)	41	25.4	59	378	30.4	1	
4pz3(a.a 18-170)	41	25.4	59	378	30.8	1	

1uuh(a.a 20-178)	41	25.4	59	378	30.8	1	Human Hsp90 co-chaperone Cdc37 (Q16543) ‡
2i83 (a.a 21-178)	41	25.4	59	378	30.1	1	
1poz (a.a 20-178)	41	25.4	59	378	30	1	
4pz4 (a.a 18-171)	41	24	75	507	24.4	1	ARSA_HUMAN Arylsulfatase A (P15289) ‡
4pz3(a.a 18-170)	38	22	50	507	39.5	0.88	
1uuh(a.a 20-178)	38	22	50	507	39.5	0.88	
2i83 (a.a 21-178)	42	23.7	76	507	40	0.87	
1poz (a.a 20-178)	42	23.7	76	507	39.9	0.87	

Suppl Table 1

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
P99999	Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2 - [CYC_HUMAN]	170.64	66.67	1	9	9	55	105	11.7	9.57
P10323	Acrosin OS=Homo sapiens GN=ACR PE=2 SV=4 - [ACRO_HUMAN]	97.90	31.35	1	10	10	36	421	45.8	9.07
P04279	Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2 - [SEMG1_HUMAN]	80.29	35.28	1	10	13	27	462	52.1	9.29
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	68.98	38.87	1	13	15	21	584	58.8	5.21
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	64.86	25.16	1	11	13	21	644	66.0	8.12
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]	58.94	32.26	1	12	12	21	558	63.1	8.32
P07205	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3 - [PGK2_HUMAN]	55.16	46.76	1	11	14	21	417	44.8	8.54
Q02383	Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1 - [SEMG2_HUMAN]	52.39	23.88	1	7	10	15	582	65.4	9.07
P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	48.75	38.79	1	13	14	18	531	57.9	7.84
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	48.51	28.09	1	10	10	15	623	62.0	5.24
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	47.85	31.92	1	9	12	16	639	65.4	8.00
Q8NEB7	Acrosin-binding protein OS=Homo sapiens GN=ACRBP PE=2 SV=1 - [ACRBP_HUMAN]	36.73	17.13	1	6	6	10	543	61.3	5.16
P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3 - [AATM_HUMAN]	31.94	26.28	1	10	10	14	430	47.5	9.01
P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]	27.60	18.62	1	5	8	10	639	70.0	5.74
Q9UII2	ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1 PE=1 SV=1 - [ATIF1_HUMAN]	25.65	9.43	1	1	1	7	106	12.2	9.35
Q5JQC9	A-kinase anchor protein 4 OS=Homo sapiens GN=AKAP4 PE=1 SV=1 - [AKAP4_HUMAN]	24.45	11.71	1	8	8	8	854	94.4	6.96

Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	24.40	39.17	1	6	6	7	314	34.3	8.85
P07864	L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=1 SV=4 - [LDHC_HUMAN]	22.88	27.71	1	6	7	8	332	36.3	7.46
Q99798	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 - [ACON_HUMAN]	20.16	12.05	1	5	5	5	780	85.4	7.61
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	17.03	25.97	1	4	4	5	335	36.0	8.46
P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]	15.92	6.56	1	0	3	5	564	60.0	8.00
P25685	DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4 - [DNJB1_HUMAN]	14.78	15.59	1	5	6	6	340	38.0	8.63
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	14.04	23.35	1	5	5	7	364	39.4	8.09
P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN]	13.55	6.27	1	1	3	4	590	62.3	7.74
P20155	Serine protease inhibitor Kazal-type 2 OS=Homo sapiens GN=SPINK2 PE=1 SV=2 - [ISK2_HUMAN]	13.22	35.71	1	2	2	4	84	9.3	9.00
Q7Z4W2	Lysozyme-like protein 2 OS=Homo sapiens GN=LYZL2 PE=2 SV=2 - [LYZL2_HUMAN]	12.91	26.35	1	1	2	4	148	16.6	7.84
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	12.00	15.98	1	4	4	5	338	35.5	8.68
P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN]	10.76	4.79	1	0	2	3	564	60.0	8.00
P48668	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN]	10.76	4.79	1	0	2	3	564	60.0	8.00
P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN]	10.76	49.12	1	4	4	4	114	13.2	6.13
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	10.76	9.83	1	0	3	4	417	44.6	8.10
Q9NPJ3	Acyl-coenzyme A thioesterase 13 OS=Homo sapiens GN=ACOT13 PE=1 SV=1 - [ACO13_HUMAN]	10.53	44.29	1	3	3	3	140	15.0	9.14
O75969	A-kinase anchor protein 3 OS=Homo sapiens GN=AKAP3 PE=1 SV=2 - [AKAP3_HUMAN]	10.13	3.75	1	2	2	3	853	94.7	6.18
P00761	Trypsin OS=Sus scrofa PE=1 SV=1 - [TRYP_PIG]	9.47	14.29	1	3	3	4	231	24.4	7.18

P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]	9.18	7.84	1	0	4	4	472	51.5	5.16
Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMAN]	9.15	4.46	1	3	3	4	2850	282.2	10.04
Q6UWQ5	Lysozyme-like protein 1 OS=Homo sapiens GN=LYZL1 PE=2 SV=2 - [LYZL1_HUMAN]	8.50	25.00	1	1	2	3	148	16.6	8.05
Q9BS86	Zona pellucida-binding protein 1 OS=Homo sapiens GN=ZPBP PE=2 SV=1 - [ZPBP1_HUMAN]	8.24	15.67	1	3	3	3	351	40.1	9.28
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]	8.15	7.54	1	0	2	3	451	50.1	5.06
P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 - [TBA4A_HUMAN]	8.15	7.59	1	0	2	3	448	49.9	5.06
Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 - [TBA3C_HUMAN]	8.15	7.56	1	0	2	3	450	49.9	5.10
Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2 - [TBA3E_HUMAN]	8.15	7.56	1	0	2	3	450	49.8	5.14
Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 - [TBA1A_HUMAN]	8.15	7.54	1	0	2	3	451	50.1	5.06
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	8.15	7.57	1	0	2	3	449	49.9	5.10
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	8.14	4.33	1	2	2	2	763	82.9	9.04
A6NC86	phospholipase A2 inhibitor and Ly6/PLAUR domain- containing protein OS=Homo sapiens GN=PINLYP PE=2 SV=3 - [PINLY_HUMAN]	8.10	31.86	1	3	3	3	204	21.9	7.99
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	7.76	6.97	1	0	3	4	646	70.9	5.52
Q6X784	Zona pellucida-binding protein 2 OS=Homo sapiens GN=ZPBP2 PE=2 SV=1 - [ZPBP2_HUMAN]	7.68	10.36	1	2	2	2	338	38.6	7.78
O95678	Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN]	7.45	2.18	1	0	1	2	551	59.5	7.74
Q5XKE5	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2 - [K2C79_HUMAN]	7.45	3.93	1	0	2	3	535	57.8	7.20
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]	7.34	8.13	1	1	2	2	332	36.7	8.27

P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN]	7.10	5.71	1	0	3	3	473	51.2	5.05
Q9BWH2	FUN14 domain-containing protein 2 OS=Homo sapiens GN=FUNDC2 PE=1 SV=2 - [FUND2_HUMAN]	7.04	21.69	1	2	2	2	189	20.7	9.73
Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN]	6.78	6.48	1	0	3	3	432	48.1	5.02
P42785	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE=1 SV=1 - [PCP_HUMAN]	6.69	4.03	1	2	2	3	496	55.8	7.21
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	6.16	4.20	1	1	1	2	357	38.3	7.97
Q96E40	Uncharacterized protein C9orf9 OS=Homo sapiens GN=C9orf9 PE=2 SV=1 - [CI009_HUMAN]	5.97	22.07	1	3	3	4	222	25.1	9.13
P55145	Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens GN=MANF PE=1 SV=3 - [MANF_HUMAN]	5.88	17.58	1	2	2	2	182	20.7	8.69
Q9UDY4	DnaJ homolog subfamily B member 4 OS=Homo sapiens GN=DNAJB4 PE=1 SV=1 - [DNJB4_HUMAN]	5.81	8.90	1	1	2	2	337	37.8	8.50
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	5.77	4.74	1	1	2	2	654	72.3	5.16
P62736	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 - [ACTA_HUMAN]	5.66	9.02	1	0	2	2	377	42.0	5.39
P63267	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 - [ACTH_HUMAN]	5.66	9.04	1	0	2	2	376	41.8	5.48
P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]	5.66	9.02	1	0	2	2	377	42.0	5.39
P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]	5.66	9.02	1	0	2	2	377	42.0	5.39
Q6P4A8	Phospholipase B-like 1 OS=Homo sapiens GN=PLBD1 PE=1 SV=2 - [PLBL1_HUMAN]	5.60	4.16	1	1	1	1	553	63.2	9.06
O14556	Glyceraldehyde-3-phosphate dehydrogenase, testis- specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2 - [G3PT_HUMAN]	5.19	6.62	1	2	2	3	408	44.5	8.19
P43155	Carnitine O-acetyltransferase OS=Homo sapiens GN=CRAT PE=1 SV=5 - [CACP_HUMAN]	5.19	4.31	1	2	2	2	626	70.8	8.44
Q8TDB8	Solute carrier family 2, facilitated glucose transporter member 14 OS=Homo sapiens GN=SLC2A14 PE=2 SV=1 -	5.16	4.42	1	1	2	2	520	56.3	7.83

	[GTR14_HUMAN]									
Q9UKX2	Myosin-2 OS=Homo sapiens GN=MYH2 PE=1 SV=1 - [MYH2_HUMAN]	5.01	2.01	1	0	3	3	1941	222.9	5.82
Q9Y623	Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2 - [MYH4_HUMAN]	5.01	2.01	1	0	3	3	1939	222.9	5.85
P13646	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4 - [K1C13_HUMAN]	4.75	4.37	1	0	2	2	458	49.6	4.96
Q9Y6A4	Cilia- and flagella-associated protein 20 OS=Homo sapiens GN=CFAP20 PE=1 SV=1 - [CFA20_HUMAN]	4.71	10.88	1	2	2	2	193	22.8	9.76
P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	4.69	4.50	1	0	2	2	400	44.1	5.14
P19012	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN]	4.69	3.95	1	0	2	2	456	49.2	4.77
Q9NY65	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 - [TBA8_HUMAN]	4.25	4.01	1	0	1	1	449	50.1	5.06
Q6UWM5	GLIPR1-like protein 1 OS=Homo sapiens GN=GLIPR1L1 PE=1 SV=2 - [GPRL1_HUMAN]	4.24	3.72	1	1	1	3	242	27.1	8.21
P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	4.23	7.88	1	0	2	2	444	49.6	4.88
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]	4.23	7.88	1	0	2	2	444	49.6	4.89
P68371	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]	4.23	7.87	1	0	2	2	445	49.8	4.89
Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]	4.23	7.87	1	0	2	2	445	49.9	4.89
Q9BVA1	Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]	4.23	7.87	1	0	2	2	445	49.9	4.89
P09622	Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 - [DLDH_HUMAN]	4.21	4.91	1	2	2	2	509	54.1	7.85
Q14CN4	Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72 PE=1 SV=2 - [K2C72_HUMAN]	4.21	2.35	1	0	1	1	511	55.8	6.89
Q3SY84	Keratin, type II cytoskeletal 71 OS=Homo sapiens GN=KRT71 PE=1 SV=3 - [K2C71_HUMAN]	4.21	2.29	1	0	1	1	523	57.3	6.61
Q7RTS7	Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2 - [K2C74_HUMAN]	4.21	2.27	1	0	1	1	529	57.8	7.71
Q86Y46	Keratin, type II cytoskeletal 73 OS=Homo sapiens	4.21	2.22	1	0	1	1	540	58.9	7.23

	GN=KRT73 PE=1 SV=1 - [K2C73_HUMAN]									
P35663	Cylicin-1 OS=Homo sapiens GN=CYL1 PE=2 SV=2 - [CYLC1_HUMAN]	4.19	4.76	1	2	2	2	651	74.2	9.67
P03973	Antileukoproteinase OS=Homo sapiens GN=SLPI PE=1 SV=2 - [SLPI_HUMAN]	4.00	18.94	1	2	2	2	132	14.3	8.75
Q96HR9	Receptor expression-enhancing protein 6 OS=Homo sapiens GN=REEP6 PE=1 SV=1 - [REEP6_HUMAN]	3.97	7.07	1	1	1	1	184	20.7	8.56
P21741	Midkine OS=Homo sapiens GN=MDK PE=1 SV=1 - [MK_HUMAN]	3.95	13.99	1	2	2	2	143	15.6	9.79
Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	3.88	6.76	1	1	1	1	429	47.1	9.14
P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1 - [S10A8_HUMAN]	3.87	8.60	1	1	1	2	93	10.8	7.03
Q5BJF6	Outer dense fiber protein 2 OS=Homo sapiens GN=ODF2 PE=1 SV=1 - [ODFP2_HUMAN]	3.87	1.69	1	1	1	1	829	95.3	7.62
Q7Z794	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3 - [K2C1B_HUMAN]	3.86	2.08	1	0	1	1	578	61.9	5.99
Q96A08	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3 - [H2B1A_HUMAN]	3.81	11.81	1	1	1	1	127	14.2	10.32
A4D1T9	Probable inactive serine protease 37 OS=Homo sapiens GN=PRSS37 PE=2 SV=1 - [PRS37_HUMAN]	3.72	9.36	1	1	1	1	235	26.4	8.87
Q96KX0	Lysozyme-like protein 4 OS=Homo sapiens GN=LYZL4 PE=2 SV=1 - [LYZL4_HUMAN]	3.61	15.07	1	2	2	2	146	16.4	8.28
P34931	Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2 - [HS71L_HUMAN]	3.45	4.52	1	0	2	2	641	70.3	6.02
A5A3E0	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]	3.18	1.49	1	0	1	1	1075	121.4	6.20
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	3.18	4.27	1	0	1	1	375	41.7	5.48
P63261	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]	3.18	4.27	1	0	1	1	375	41.8	5.48
Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]	3.18	4.26	1	0	1	1	376	42.0	5.59
Q6S8J3	POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]	3.18	1.49	1	0	1	1	1075	121.3	6.20

Q9BYX7	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - [ACTBM_HUMAN]	3.18	4.27	1	0	1	1	375	42.0	6.33
P12882	Myosin-1 OS=Homo sapiens GN=MYH1 PE=1 SV=3 - [MYH1_HUMAN]	3.15	1.50	1	0	2	2	1939	223.0	5.74
P13535	Myosin-8 OS=Homo sapiens GN=MYH8 PE=1 SV=3 - [MYH8_HUMAN]	3.15	0.93	1	0	1	1	1937	222.6	5.74
P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6 - [TRFL_HUMAN]	3.12	2.68	1	1	1	1	710	78.1	8.12
Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]	3.04	4.05	1	1	1	1	543	59.3	7.65
Q16568	Cocaine- and amphetamine-regulated transcript protein OS=Homo sapiens GN=CARTPT PE=1 SV=1 - [CART_HUMAN]	3.02	18.97	1	2	2	2	116	12.8	8.25
P26640	Valine--tRNA ligase OS=Homo sapiens GN=VAR5 PE=1 SV=4 - [SYVC_HUMAN]	3.02	0.87	1	1	1	1	1264	140.4	7.59
P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	2.92	3.98	1	1	1	1	427	45.2	8.85
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	2.90	1.99	1	1	1	1	553	59.7	9.13
Q9HBV2	Sperm acrosome membrane-associated protein 1 OS=Homo sapiens GN=SPACA1 PE=1 SV=1 - [SACA1_HUMAN]	2.87	7.48	1	1	1	1	294	32.1	4.61
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]	2.85	1.86	1	1	1	1	645	72.9	5.07
Q9BUN1	Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1 - [MENT_HUMAN]	2.84	4.40	1	1	1	1	341	36.7	8.59
Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN]	2.78	3.18	1	1	1	1	440	48.1	5.08
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	2.75	1.52	1	1	1	1	658	73.7	8.18
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	2.75	3.59	1	0	1	1	334	36.6	6.05
Q6ZMR3	L-lactate dehydrogenase A-like 6A OS=Homo sapiens GN=LDHAL6A PE=2 SV=1 - [LDH6A_HUMAN]	2.75	3.61	1	0	1	1	332	36.5	6.99
P05976	Myosin light chain 1/3, skeletal muscle isoform OS=Homo sapiens GN=MYL1 PE=1 SV=3 - [MYL1_HUMAN]	2.71	5.67	1	1	1	1	194	21.1	5.03

Q8TC27	Disintegrin and metalloproteinase domain-containing protein 32 OS=Homo sapiens GN=ADAM32 PE=1 SV=2 - [ADA32_HUMAN]	2.57	2.03	1	1	1	1	787	87.9	5.55
Q5T9S5	Coiled-coil domain-containing protein 18 OS=Homo sapiens GN=CCDC18 PE=2 SV=1 - [CCD18_HUMAN]	2.46	0.69	1	1	1	1	1454	168.9	5.66
Q7Z3Y7	Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN]	2.40	1.94	1	0	1	1	464	50.5	5.47
Q7Z3Y8	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2 - [K1C27_HUMAN]	2.40	1.96	1	0	1	1	459	49.8	5.05
Q7Z3Y9	Keratin, type I cytoskeletal 26 OS=Homo sapiens GN=KRT26 PE=1 SV=2 - [K1C26_HUMAN]	2.40	1.92	1	0	1	1	468	51.9	4.92
Q7Z3Z0	Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1 - [K1C25_HUMAN]	2.40	2.00	1	0	1	1	450	49.3	5.08
Q8N4P6	Leucine-rich repeat-containing protein 71 OS=Homo sapiens GN=LRRC71 PE=2 SV=1 - [LRC71_HUMAN]	2.40	2.33	1	1	1	1	559	61.8	9.22
Q2M2I5	Keratin, type I cytoskeletal 24 OS=Homo sapiens GN=KRT24 PE=1 SV=1 - [K1C24_HUMAN]	2.38	2.10	1	0	1	1	525	55.1	4.96
P35900	Keratin, type I cytoskeletal 20 OS=Homo sapiens GN=KRT20 PE=1 SV=1 - [K1C20_HUMAN]	2.37	2.12	1	0	1	1	424	48.5	5.69
Q8N1A0	Keratin-like protein KRT222 OS=Homo sapiens GN=KRT222 PE=2 SV=1 - [KT222_HUMAN]	2.37	3.05	1	0	1	1	295	34.1	5.87
Q6NUT2	Probable C-mannosyltransferase DPY19L2 OS=Homo sapiens GN=DPY19L2 PE=1 SV=2 - [D19L2_HUMAN]	2.36	2.64	1	1	1	1	758	87.3	9.10
Q96M98	Parkin coregulated gene protein OS=Homo sapiens GN=PACRG PE=1 SV=2 - [PACRG_HUMAN]	2.36	4.73	1	1	1	1	296	33.3	8.21
Q8N5Q1	Putative protein FAM71E2 OS=Homo sapiens GN=FAM71E2 PE=5 SV=3 - [F71E2_HUMAN]	2.33	0.98	1	1	1	1	922	99.9	9.39
Q9BWS9	Chitinase domain-containing protein 1 OS=Homo sapiens GN=CHID1 PE=1 SV=1 - [CHID1_HUMAN]	2.31	6.11	1	1	1	1	393	44.9	8.63
Q1ZYL8	Izumo sperm-egg fusion protein 4 OS=Homo sapiens GN=IZUMO4 PE=2 SV=2 - [IZUM4_HUMAN]	2.30	6.03	1	1	1	1	232	26.5	7.46
	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	2.27	1.91	1	0	1	1	732	84.6	5.02
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	2.27	1.93	1	0	1	1	724	83.2	5.03
Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo	2.27	1.99	1	0	1	1	704	80.1	8.21

	sapiens GN=TRAP1 PE=1 SV=3 - [TRAP1_HUMAN]									
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	2.24	3.36	1	0	1	1	298	32.8	9.69
P12235	ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4 - [ADT1_HUMAN]	2.24	3.36	1	0	1	1	298	33.0	9.76
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	2.24	3.36	1	0	1	1	298	32.8	9.74
Q96QE4	Leucine-rich repeat-containing protein 37B OS=Homo sapiens GN=LRR37B PE=2 SV=3 - [LR37B_HUMAN]	2.23	1.90	1	1	1	1	947	105.5	4.91
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	2.18	2.22	1	0	1	1	496	53.9	7.20
Q9Y561	Low-density lipoprotein receptor-related protein 12 OS=Homo sapiens GN=LRP12 PE=1 SV=1 - [LRP12_HUMAN]	2.17	0.93	1	1	1	1	859	94.9	5.24
Q5T749	Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1 - [KPRP_HUMAN]	2.15	1.55	1	1	1	1	579	64.1	8.27
Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]	2.14	3.77	1	1	1	1	318	35.9	7.11
Q9H0R5	Guanylate-binding protein 3 OS=Homo sapiens GN=GBP3 PE=1 SV=3 - [GBP3_HUMAN]	2.14	1.51	1	1	1	1	595	68.1	6.51
Q9BY22	L-lactate dehydrogenase A-like 6B OS=Homo sapiens GN=LDHAL6B PE=1 SV=3 - [LDH6B_HUMAN]	2.14	3.15	1	1	1	1	381	41.9	8.65
P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - [SPB6_HUMAN]	2.12	3.99	1	1	1	1	376	42.6	5.27
Q96PU9	Outer dense fiber protein 3 OS=Homo sapiens GN=ODF3 PE=2 SV=1 - [ODF3A_HUMAN]	2.07	5.12	1	1	1	1	254	27.7	9.89
P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN]	2.07	10.00	1	1	1	1	110	11.3	6.54
P19367	Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 - [HXX1_HUMAN]	2.05	1.20	1	0	1	1	917	102.4	6.80
P52789	Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 - [HXX2_HUMAN]	2.05	1.20	1	0	1	1	917	102.3	6.05
Q8WZ59	Transmembrane protein 190 OS=Homo sapiens GN=TMEM190 PE=2 SV=1 - [TM190_HUMAN]	2.01	9.60	1	1	1	1	177	19.4	5.24
Q14093	Cylicin-2 OS=Homo sapiens GN=CYLC2 PE=2 SV=1 -	1.95	4.31	1	1	1	1	348	39.1	9.74

	[CYLC2_HUMAN]									
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2 - [CUL3_HUMAN]	1.91	1.95	1	1	1	1	768	88.9	8.48
P0CG47	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN]	1.82	11.79	1	0	1	1	229	25.7	7.43
P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]	1.82	5.77	1	0	1	1	156	18.0	9.64
P62987	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]	1.82	7.03	1	0	1	1	128	14.7	9.83
P0CG48	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]	1.82	11.82	1	0	1	1	685	77.0	7.66
Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	1.77	2.22	1	0	1	1	450	50.4	4.93
Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1 - [FILA2_HUMAN]	1.69	0.50	1	1	1	1	2391	247.9	8.31
O00221	NF-kappa-B inhibitor epsilon OS=Homo sapiens GN=NFKBIE PE=1 SV=3 - [IKBE_HUMAN]	0.00	8.20	1	1	1	1	500	52.8	6.68
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]	0.00	3.02	1	1	1	1	529	56.5	5.40
P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	0.00	2.03	1	0	1	1	641	70.0	5.66
P11055	Myosin-3 OS=Homo sapiens GN=MYH3 PE=1 SV=3 - [MYH3_HUMAN]	0.00	0.57	1	0	1	1	1940	223.8	5.81
P12035	Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 - [K2C3_HUMAN]	0.00	1.43	1	0	1	1	628	64.4	6.48
P12830	Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3 - [CADH1_HUMAN]	0.00	1.02	1	1	1	1	882	97.4	4.73
P17066	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2 - [HSP76_HUMAN]	0.00	2.02	1	0	1	1	643	71.0	6.14
P30613	Pyruvate kinase PKLR OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	0.00	1.92	1	0	1	1	574	61.8	7.74
P46019	Phosphorylase b kinase regulatory subunit alpha, liver isoform OS=Homo sapiens GN=PHKA2 PE=1 SV=1 - [KPB2_HUMAN]	0.00	3.32	1	1	1	1	1235	138.3	6.44
P48454	Serine/threonine-protein phosphatase 2B catalytic subunit gamma isoform OS=Homo sapiens GN=PPP3CC	0.00	2.34	1	1	1	1	512	58.1	6.98

	PE=1 SV=3 - [PP2BC_HUMAN]									
P48741	Putative heat shock 70 kDa protein 7 OS=Homo sapiens GN=HSPA7 PE=5 SV=2 - [HSP77_HUMAN]	0.00	3.54	1	0	1	1	367	40.2	7.87
P61626	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [LYSC_HUMAN]	0.00	5.41	1	1	1	1	148	16.5	9.16
Q01546	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K22O_HUMAN]	0.00	1.41	1	0	1	1	638	65.8	8.12
Q5HYC2	Uncharacterized protein KIAA2026 OS=Homo sapiens GN=KIAA2026 PE=2 SV=2 - [K2026_HUMAN]	0.00	0.33	1	1	1	1	2103	227.9	9.04
Q7Z442	Polycystic kidney disease protein 1-like 2 OS=Homo sapiens GN=PKD1L2 PE=1 SV=4 - [PK1L2_HUMAN]	0.00	1.10	1	1	1	1	2459	272.4	5.82
Q96QH8	Sperm acrosome-associated protein 5 OS=Homo sapiens GN=SPACA5 PE=2 SV=1 - [LYZL5_HUMAN]	0.00	4.40	1	1	1	1	159	17.9	6.42
Q9H9Y6	DNA-directed RNA polymerase I subunit RPA2 OS=Homo sapiens GN=POLR1B PE=1 SV=2 - [RPA2_HUMAN]	0.00	3.44	1	1	1	1	1135	128.1	7.83
Q9UFN0	Protein NipSnap homolog 3A OS=Homo sapiens GN=NIPSNAP3A PE=1 SV=2 - [NPS3A_HUMAN]	0.00	4.05	1	1	1	1	247	28.4	9.16

Suppl Table 2

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
P10323	Acrosin OS=Homo sapiens GN=ACR PE=2 SV=4 - [ACRO_HUMAN]	397.02	53.21	1	18	18	130	421	45.8	9.07
P99999	Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2 - [CYC_HUMAN]	364.45	75.24	1	14	14	120	105	11.7	9.57
P07205	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3 - [PGK2_HUMAN]	135.22	62.11	1	18	21	45	417	44.8	8.54
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]	130.00	42.29	1	17	17	50	558	63.1	8.32
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	117.06	40.07	1	17	17	35	584	58.8	5.21
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	111.18	48.45	1	17	21	36	644	66.0	8.12
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	84.34	44.91	1	15	20	28	639	65.4	8.00
P07864	L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=1 SV=4 - [LDHC_HUMAN]	75.32	60.24	1	13	14	26	332	36.3	7.46
P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	75.30	40.68	1	14	14	25	531	57.9	7.84
P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3 - [AATM_HUMAN]	57.01	42.56	1	12	12	20	430	47.5	9.01
P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6 - [TRFL_HUMAN]	54.29	29.44	1	15	15	19	710	78.1	8.12
Q9NPJ3	Acyl-coenzyme A thioesterase 13 OS=Homo sapiens GN=ACOT13 PE=1 SV=1 - [ACO13_HUMAN]	52.93	62.14	1	5	5	18	140	15.0	9.14
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	49.76	29.86	1	11	11	16	623	62.0	5.24
Q5JQC9	A-kinase anchor protein 4 OS=Homo sapiens	48.57	19.91	1	12	12	17	854	94.4	6.96

	GN=AKAP4 PE=1 SV=1 - [AKAP4_HUMAN]									
Q8NEB7	Acrosin-binding protein OS=Homo sapiens GN=ACRBP PE=2 SV=1 - [ACRBP_HUMAN]	45.90	18.23	1	6	6	14	543	61.3	5.16
Q6UWQ5	Lysozyme-like protein 1 OS=Homo sapiens GN=LYZL1 PE=2 SV=2 - [LYZL1_HUMAN]	45.58	26.35	1	2	3	12	148	16.6	8.05
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	45.16	35.44	1	8	8	14	364	39.4	8.09
Q02383	Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1 - [SEMG2_HUMAN]	44.42	22.16	1	7	8	15	582	65.4	9.07
Q9UII2	ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1 PE=1 SV=1 - [ATIF1_HUMAN]	42.69	17.92	1	5	5	15	106	12.2	9.35
P68371	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]	38.06	41.12	1	0	10	13	445	49.8	4.89
P04279	Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2 - [SEMG1_HUMAN]	38.04	25.76	1	8	9	13	462	52.1	9.29
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	33.58	48.41	1	8	8	10	314	34.3	8.85
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]	32.76	31.31	1	0	8	11	444	49.6	4.89
O14556	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2 - [G3PT_HUMAN]	30.93	41.91	1	9	9	13	408	44.5	8.19
P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	28.03	33.33	1	0	8	9	444	49.6	4.88
Q99798	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 - [ACON_HUMAN]	26.21	12.44	1	7	7	11	780	85.4	7.61
Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	25.86	21.78	1	0	7	10	450	50.4	4.93
Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]	24.60	25.17	1	0	7	9	445	49.9	4.89
Q9BVA1	Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 - [TBB2B_HUMAN]	24.60	25.17	1	0	7	9	445	49.9	4.89
Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens	23.18	20.67	1	0	5	7	450	49.9	5.10

	GN=TUBA3C PE=1 SV=3 - [TBA3C_HUMAN]									
Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2 - [TBA3E_HUMAN]	23.18	20.67	1	0	5	7	450	49.8	5.14
Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 - [TBA1A_HUMAN]	23.18	20.62	1	0	5	7	451	50.1	5.06
P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]	22.59	18.15	1	6	7	8	639	70.0	5.74
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	21.95	9.83	1	0	3	7	417	44.6	8.10
Q9BS86	Zona pellucida-binding protein 1 OS=Homo sapiens GN=ZPBP PE=2 SV=1 - [ZPBP1_HUMAN]	20.98	33.05	1	7	7	8	351	40.1	9.28
Q7Z4W2	Lysozyme-like protein 2 OS=Homo sapiens GN=LYZL2 PE=2 SV=2 - [LYZL2_HUMAN]	20.85	26.35	1	2	3	6	148	16.6	7.84
P36969	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Homo sapiens GN=GPX4 PE=1 SV=3 - [GPX4_HUMAN]	20.52	35.03	1	6	6	10	197	22.2	8.37
Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]	20.17	21.70	1	5	5	6	318	35.9	7.11
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]	19.78	17.52	1	0	4	6	451	50.1	5.06
P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 - [TBA4A_HUMAN]	19.78	17.63	1	0	4	6	448	49.9	5.06
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	17.45	12.25	1	0	3	5	449	49.9	5.10
Q96E40	Uncharacterized protein C9orf9 OS=Homo sapiens GN=C9orf9 PE=2 SV=1 - [CI009_HUMAN]	17.12	35.14	1	5	5	6	222	25.1	9.13
P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]	16.98	6.91	1	0	5	7	564	60.0	8.00
Q5VU65	Nuclear pore membrane glycoprotein 210-like OS=Homo sapiens GN=NUP210L PE=2 SV=1 - [P210L_HUMAN]	16.71	5.14	1	7	7	8	1888	210.5	7.50
P03973	Antileukoproteinase OS=Homo sapiens GN=SLPI PE=1 SV=2 - [SLPI_HUMAN]	16.71	11.36	1	2	2	6	132	14.3	8.75

P42785	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE=1 SV=1 - [PCP_HUMAN]	16.50	12.70	1	4	4	5	496	55.8	7.21
Q7Z794	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3 - [K2C1B_HUMAN]	15.56	3.46	1	0	2	6	578	61.9	5.99
Q1ZYL8	Izumo sperm-egg fusion protein 4 OS=Homo sapiens GN=IZUMO4 PE=2 SV=2 - [IZUM4_HUMAN]	15.27	24.14	1	3	3	5	232	26.5	7.46
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	15.26	20.20	1	5	5	7	510	54.6	8.76
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	15.25	8.06	1	2	5	6	732	84.6	5.02
A6NC86	phospholipase A2 inhibitor and Ly6/PLAUR domain-containing protein OS=Homo sapiens GN=PINLYP PE=2 SV=3 - [PINLY_HUMAN]	15.10	16.67	1	2	2	4	204	21.9	7.99
Q96KX0	Lysozyme-like protein 4 OS=Homo sapiens GN=LYZL4 PE=2 SV=1 - [LYZL4_HUMAN]	14.74	24.66	1	3	3	5	146	16.4	8.28
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]	14.31	11.45	1	2	3	5	332	36.7	8.27
Q9Y277	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1 - [VDAC3_HUMAN]	14.19	13.78	1	2	2	5	283	30.6	8.66
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	13.92	17.61	1	3	3	4	335	36.0	8.46
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	13.65	13.02	1	3	3	4	338	35.5	8.68
P00761	Trypsin OS=Sus scrofa PE=1 SV=1 - [TRYP_PIG]	12.66	16.45	1	3	3	8	231	24.4	7.18
O75969	A-kinase anchor protein 3 OS=Homo sapiens GN=AKAP3 PE=1 SV=2 - [AKAP3_HUMAN]	12.58	5.16	1	3	3	4	853	94.7	6.18
Q6P4A8	Phospholipase B-like 1 OS=Homo sapiens GN=PLBD1 PE=1 SV=2 - [PLBL1_HUMAN]	12.40	11.93	1	3	3	3	553	63.2	9.06
Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 -	11.70	16.50	1	3	3	4	303	33.3	7.97

	[MTCH2_HUMAN]									
O00233	26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3 - [PSMD9_HUMAN]	11.13	30.49	1	2	2	3	223	24.7	6.95
P61019	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 - [RAB2A_HUMAN]	10.88	23.58	1	3	4	4	212	23.5	6.54
Q5BJF6	Outer dense fiber protein 2 OS=Homo sapiens GN=ODF2 PE=1 SV=1 - [ODFP2_HUMAN]	10.69	4.58	1	3	3	4	829	95.3	7.62
P20155	Serine protease inhibitor Kazal-type 2 OS=Homo sapiens GN=SPINK2 PE=1 SV=2 - [ISK2_HUMAN]	10.61	26.19	1	1	1	2	84	9.3	9.00
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	10.23	5.97	1	2	2	4	553	59.7	9.13
A6NM11	Leucine-rich repeat-containing protein 37A2 OS=Homo sapiens GN=LRR37A2 PE=2 SV=2 - [L37A2_HUMAN]	10.18	1.88	1	0	2	3	1700	188.3	5.50
A6NMS7	Leucine-rich repeat-containing protein 37A OS=Homo sapiens GN=LRR37A PE=2 SV=3 - [L37A1_HUMAN]	10.18	1.88	1	0	2	3	1700	188.1	5.49
O60309	Leucine-rich repeat-containing protein 37A3 OS=Homo sapiens GN=LRR37A3 PE=2 SV=2 - [L37A3_HUMAN]	10.18	1.96	1	0	2	3	1634	180.5	5.31
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]	9.92	10.96	1	3	3	4	529	56.5	5.40
P19367	Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 - [HKK1_HUMAN]	9.66	6.54	1	4	4	4	917	102.4	6.80
P09622	Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 - [DLDH_HUMAN]	9.54	6.68	1	2	2	3	509	54.1	7.85
Q9BUN1	Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1 - [MENT_HUMAN]	9.37	6.74	1	2	2	3	341	36.7	8.59
P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]	9.17	8.26	1	1	3	4	472	51.5	5.16
Q8N5Q1	Putative protein FAM71E2 OS=Homo sapiens	9.10	2.93	1	2	2	3	922	99.9	9.39

	GN=FAM71E2 PE=5 SV=3 - [F71E2_HUMAN]									
P45880	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 - [VDAC2_HUMAN]	9.08	13.27	1	2	2	4	294	31.5	7.56
Q01546	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2 - [K22O_HUMAN]	8.84	2.82	1	0	4	4	638	65.8	8.12
P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN]	8.80	4.58	1	1	4	4	590	62.3	7.74
P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3 - [K2C6A_HUMAN]	8.69	5.14	1	0	4	4	564	60.0	8.00
P48668	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3 - [K2C6C_HUMAN]	8.69	5.14	1	0	4	4	564	60.0	8.00
Q16568	Cocaine- and amphetamine-regulated transcript protein OS=Homo sapiens GN=CARTPT PE=1 SV=1 - [CART_HUMAN]	8.67	14.66	1	2	2	3	116	12.8	8.25
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2 - [CUL3_HUMAN]	8.63	1.95	1	1	1	3	768	88.9	8.48
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [SDHA_HUMAN]	8.61	3.77	1	2	2	3	664	72.6	7.39
Q96QE4	Leucine-rich repeat-containing protein 37B OS=Homo sapiens GN=LRRC37B PE=2 SV=3 - [LR37B_HUMAN]	8.60	4.96	1	3	3	3	947	105.5	4.91
Q6NUT2	Probable C-mannosyltransferase DPY19L2 OS=Homo sapiens GN=DPY19L2 PE=1 SV=2 - [D19L2_HUMAN]	8.37	7.65	1	2	3	3	758	87.3	9.10
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	8.26	3.18	1	0	2	3	724	83.2	5.03
Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	8.10	9.19	1	0	3	3	446	49.8	4.88
Q9NY65	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 - [TBA8_HUMAN]	7.98	8.69	1	0	2	2	449	50.1	5.06
P04179	Superoxide dismutase [Mn], mitochondrial	7.97	6.76	1	1	1	3	222	24.7	8.25

	OS=Homo sapiens GN=SOD2 PE=1 SV=2 - [SODM_HUMAN]									
P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN]	7.66	26.32	1	2	2	2	114	13.2	6.13
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	7.61	3.59	1	0	1	3	334	36.6	6.05
Q6ZMR3	L-lactate dehydrogenase A-like 6A OS=Homo sapiens GN=LDHAL6A PE=2 SV=1 - [LDH6A_HUMAN]	7.61	3.61	1	0	1	3	332	36.5	6.99
Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMAN]	7.41	3.79	1	2	2	4	2850	282.2	10.04
P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7 - [K2C8_HUMAN]	7.06	3.93	1	0	2	3	483	53.7	5.59
P10909	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1 - [CLUS_HUMAN]	6.97	8.91	1	2	2	2	449	52.5	6.27
P55145	Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens GN=MANF PE=1 SV=3 - [MANF_HUMAN]	6.96	9.34	1	1	1	4	182	20.7	8.69
P34931	Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2 - [HS71L_HUMAN]	6.94	5.15	1	1	3	3	641	70.3	6.02
P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	6.81	8.53	1	0	2	2	434	47.0	7.71
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	6.81	8.53	1	0	2	2	434	47.1	7.39
A6NNZ2	Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 - [TBB8L_HUMAN]	6.75	9.46	1	0	2	2	444	49.5	4.86
Q3ZCM7	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]	6.75	9.46	1	0	2	2	444	49.7	4.89
P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2 - [EFTU_HUMAN]	6.63	3.76	1	1	1	2	452	49.5	7.61
P15259	Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3 - [PGAM2_HUMAN]	6.54	15.81	1	2	3	3	253	28.7	8.88
Q16698	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1 - [DECR_HUMAN]	6.50	6.57	1	1	1	2	335	36.0	9.28

O95678	Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN]	6.41	3.09	1	0	3	3	551	59.5	7.74
Q9BZX4	Ropporin-1B OS=Homo sapiens GN=ROPN1B PE=1 SV=1 - [ROP1B_HUMAN]	6.26	12.26	1	0	2	2	212	23.9	5.15
Q9HAT0	Ropporin-1A OS=Homo sapiens GN=ROPN1 PE=1 SV=2 - [ROP1A_HUMAN]	6.26	12.26	1	0	2	2	212	23.9	5.66
Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 - [UGPA_HUMAN]	6.05	2.76	1	1	1	4	508	56.9	8.15
P26436	Acrosomal protein SP-10 OS=Homo sapiens GN=ACRV1 PE=1 SV=2 - [ASPX_HUMAN]	6.05	8.68	1	2	2	3	265	28.1	4.69
Q6UWU2	Beta-galactosidase-1-like protein OS=Homo sapiens GN=GLB1L PE=2 SV=1 - [GLB1L_HUMAN]	5.79	5.35	1	4	4	5	654	74.1	8.92
A4D1T9	Probable inactive serine protease 37 OS=Homo sapiens GN=PRSS37 PE=2 SV=1 - [PRSS37_HUMAN]	5.65	15.32	1	2	2	3	235	26.4	8.87
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	5.58	1.83	1	1	1	2	763	82.9	9.04
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 - [TPIS_HUMAN]	5.27	9.09	1	2	2	2	286	30.8	5.92
P21266	Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3 - [GSTM3_HUMAN]	5.20	10.22	1	2	2	2	225	26.5	5.54
Q9BWH2	FUN14 domain-containing protein 2 OS=Homo sapiens GN=FUNDC2 PE=1 SV=2 - [FUND2_HUMAN]	5.19	12.70	1	2	2	2	189	20.7	9.73
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	5.15	21.36	1	2	2	2	103	11.4	11.36
P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	5.08	2.35	1	0	1	2	469	51.4	5.48
P14136	Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]	5.08	2.55	1	0	1	2	432	49.8	5.52
P19013	Keratin, type II cytoskeletal 4 OS=Homo sapiens	5.08	2.06	1	0	1	2	534	57.2	6.61

	GN=KRT4 PE=1 SV=4 - [K2C4_HUMAN]									
Q6KB66	Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2 - [K2C80_HUMAN]	5.08	2.43	1	0	1	2	452	50.5	5.67
O95563	Mitochondrial pyruvate carrier 2 OS=Homo sapiens GN=MPC2 PE=1 SV=1 - [MPC2_HUMAN]	4.93	9.45	1	1	1	2	127	14.3	10.43
P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	4.90	3.59	1	0	2	2	641	70.0	5.66
P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN]	4.69	4.23	1	0	2	2	473	51.2	5.05
Q9HBV2	Sperm acrosome membrane-associated protein 1 OS=Homo sapiens GN=SPACA1 PE=1 SV=1 - [SACA1_HUMAN]	4.56	9.52	1	2	2	2	294	32.1	4.61
Q96QH8	Sperm acrosome-associated protein 5 OS=Homo sapiens GN=SPACA5 PE=2 SV=1 - [LYZL5_HUMAN]	4.44	18.24	1	2	2	3	159	17.9	6.42
P12036	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4 - [NFH_HUMAN]	4.42	0.88	1	0	2	2	1026	112.4	6.18
Q7RTS7	Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=1 SV=2 - [K2C74_HUMAN]	4.42	1.70	1	0	2	2	529	57.8	7.71
Q86Y46	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1 - [K2C73_HUMAN]	4.42	1.67	1	0	2	2	540	58.9	7.23
P12035	Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3 - [K2C3_HUMAN]	4.42	1.43	1	0	2	2	628	64.4	6.48
Q9Y6A4	Cilia- and flagella-associated protein 20 OS=Homo sapiens GN=CFAP20 PE=1 SV=1 - [CFA20_HUMAN]	4.38	14.51	1	2	2	2	193	22.8	9.76
P09104	Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3 - [ENOG_HUMAN]	4.35	5.07	1	0	1	1	434	47.2	5.03
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 - [TCPO_HUMAN]	4.23	3.83	1	2	2	2	548	59.6	5.60
Q8NBX0	Saccharopine dehydrogenase-like	4.08	5.36	1	1	1	1	429	47.1	9.14

	oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]									
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1 - [PSA6_HUMAN]	4.07	9.35	1	2	2	2	246	27.4	6.76
P63167	Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 - [DYL1_HUMAN]	4.04	24.72	1	0	2	2	89	10.4	7.40
Q96FJ2	Dynein light chain 2, cytoplasmic OS=Homo sapiens GN=DYNLL2 PE=1 SV=1 - [DYL2_HUMAN]	4.04	24.72	1	0	2	2	89	10.3	7.37
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 - [TCPB_HUMAN]	3.96	5.05	1	2	2	2	535	57.5	6.46
P55084	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN]	3.81	4.22	1	2	2	2	474	51.3	9.41
Q8WUD1	Ras-related protein Rab-2B OS=Homo sapiens GN=RAB2B PE=1 SV=1 - [RAB2B_HUMAN]	3.66	6.02	1	0	1	1	216	24.2	7.83
Q6NXN4	Putative C-mannosyltransferase DPY19L2P1 OS=Homo sapiens GN=DPY19L2P1 PE=2 SV=1 - [D19P1_HUMAN]	3.66	7.85	1	0	1	1	242	28.0	9.85
Q8N807	Protein disulfide-isomerase-like protein of the testis OS=Homo sapiens GN=PDILT PE=1 SV=2 - [PDILT_HUMAN]	3.60	2.23	1	1	1	1	584	66.6	6.86
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	3.54	4.20	1	1	1	1	357	38.3	7.97
P24539	ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 - [AT5F1_HUMAN]	3.44	4.69	1	1	1	1	256	28.9	9.36
P84243	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 - [H33_HUMAN]	3.41	23.53	1	1	1	1	136	15.3	11.27
P49901	Sperm mitochondrial-associated cysteine-rich protein OS=Homo sapiens GN=SMCP PE=2 SV=2 - [MCSP_HUMAN]	3.34	27.59	1	2	2	2	116	12.8	8.07
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	3.29	2.46	1	1	1	1	609	69.3	6.28

Q5SRE5	Nucleoporin NUP188 homolog OS=Homo sapiens GN=NUP188 PE=1 SV=1 - [NU188_HUMAN]	3.23	0.91	1	1	1	1	1749	195.9	6.73
P49913	Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1 SV=1 - [CAMP_HUMAN]	3.20	7.65	1	1	1	1	170	19.3	9.41
O60361	Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1 - [NDK8_HUMAN]	3.19	12.41	1	0	1	2	137	15.5	8.57
P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]	3.19	11.18	1	0	1	2	152	17.1	6.19
P22392	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1 - [NDKB_HUMAN]	3.19	11.18	1	0	1	2	152	17.3	8.41
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	3.13	2.48	1	0	1	1	646	70.9	5.52
Q8TC27	Disintegrin and metalloproteinase domain-containing protein 32 OS=Homo sapiens GN=ADAM32 PE=1 SV=2 - [ADA32_HUMAN]	3.02	2.41	1	1	1	1	787	87.9	5.55
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1 - [COX41_HUMAN]	2.97	6.51	1	1	1	1	169	19.6	9.51
Q5FVE4	Long-chain-fatty-acid--CoA ligase ACSBG2 OS=Homo sapiens GN=ACSBG2 PE=1 SV=2 - [ACBG2_HUMAN]	2.68	2.85	1	1	1	1	666	74.3	8.46
P00414	Cytochrome c oxidase subunit 3 OS=Homo sapiens GN=MT-CO3 PE=1 SV=2 - [COX3_HUMAN]	2.67	5.36	1	1	1	1	261	29.9	7.31
P0CG47	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN]	2.64	11.79	1	0	1	1	229	25.7	7.43
P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 - [RS27A_HUMAN]	2.64	5.77	1	0	1	1	156	18.0	9.64
P62987	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 - [RL40_HUMAN]	2.64	7.03	1	0	1	1	128	14.7	9.83

P0CG48	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]	2.64	11.82	1	0	1	1	685	77.0	7.66
Q8WZ59	Transmembrane protein 190 OS=Homo sapiens GN=TMEM190 PE=2 SV=1 - [TM190_HUMAN]	2.64	7.91	1	1	1	1	177	19.4	5.24
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	2.51	2.60	1	0	1	1	462	50.1	9.01
Q05639	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 - [EF1A2_HUMAN]	2.51	2.59	1	0	1	1	463	50.4	9.03
Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 - [EF1A3_HUMAN]	2.51	2.60	1	0	1	1	462	50.2	9.07
P30042	ES1 protein homolog, mitochondrial OS=Homo sapiens GN=C21orf33 PE=1 SV=3 - [ES1_HUMAN]	2.48	3.73	1	1	1	1	268	28.2	8.27
Q6UW49	Sperm equatorial segment protein 1 OS=Homo sapiens GN=SPESP1 PE=1 SV=2 - [SPESP_HUMAN]	2.46	3.14	1	1	1	1	350	38.9	5.73
P23284	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2 - [PPIB_HUMAN]	2.45	5.09	1	1	1	1	216	23.7	9.41
Q6UWM5	GLIPR1-like protein 1 OS=Homo sapiens GN=GLIPR1L1 PE=1 SV=2 - [GPRL1_HUMAN]	2.41	3.72	1	1	1	1	242	27.1	8.21
Q58FG0	Putative heat shock protein HSP 90-alpha A5 OS=Homo sapiens GN=HSP90AA5P PE=1 SV=1 - [HS905_HUMAN]	2.34	4.49	1	0	1	1	334	38.7	6.57
P14555	Phospholipase A2, membrane associated OS=Homo sapiens GN=PLA2G2A PE=1 SV=2 - [PA2GA_HUMAN]	2.32	6.94	1	1	1	1	144	16.1	9.23
P0C8F1	Prostate and testis expressed protein 4 OS=Homo sapiens GN=PATE4 PE=2 SV=2 - [PATE4_HUMAN]	2.30	12.24	1	1	1	1	98	11.4	8.62
P18669	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 - [PGAM1_HUMAN]	2.26	4.33	1	0	1	1	254	28.8	7.18
P35663	Cylicin-1 OS=Homo sapiens GN=CYLC1 PE=2 SV=2 - [CYLC1_HUMAN]	2.25	2.46	1	1	1	1	651	74.2	9.67
Q9H4B7	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1 - [TBB1_HUMAN]	2.24	2.22	1	0	1	1	451	50.3	5.17

Q6X784	Zona pellucida-binding protein 2 OS=Homo sapiens GN=ZPBP2 PE=2 SV=1 - [ZPBP2_HUMAN]	2.21	2.96	1	1	1	1	338	38.6	7.78
P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	2.21	1.34	1	1	1	1	745	81.7	6.14
Q18PE1	Protein Dok-7 OS=Homo sapiens GN=DOK7 PE=1 SV=1 - [DOK7_HUMAN]	2.19	2.98	1	1	1	1	504	53.1	6.89
Q92523	Carnitine O-palmitoyltransferase 1, muscle isoform OS=Homo sapiens GN=CPT1B PE=2 SV=2 - [CPT1B_HUMAN]	2.16	1.42	1	1	1	1	772	87.7	8.62
P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1 - [S10A8_HUMAN]	2.15	11.83	1	1	1	1	93	10.8	7.03
Q58FF6	Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1 - [H90B4_HUMAN]	2.14	1.98	1	0	1	1	505	58.2	4.73
Q58FF7	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1 - [H90B3_HUMAN]	2.14	1.68	1	0	1	1	597	68.3	4.79
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	2.14	4.80	1	0	1	2	375	41.7	5.48
P63261	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 - [ACTG_HUMAN]	2.14	4.80	1	0	1	2	375	41.8	5.48
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	2.12	1.53	1	1	1	1	654	72.3	5.16
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]	2.12	1.24	1	1	1	1	645	72.9	5.07
P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	2.11	2.25	1	0	1	1	400	44.1	5.14
P19012	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN]	2.11	1.97	1	0	1	1	456	49.2	4.77
Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 -	2.11	2.08	1	0	1	1	432	48.1	5.02

	[K1C17_HUMAN]									
P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	2.11	2.34	1	1	1	1	427	45.2	8.85
P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Homo sapiens GN=PPIF PE=1 SV=1 - [PPIF_HUMAN]	2.09	3.86	1	1	1	1	207	22.0	9.38
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN]	2.01	1.78	1	1	1	1	505	56.7	6.35
O75952	Calcium-binding tyrosine phosphorylation-regulated protein OS=Homo sapiens GN=CABYR PE=1 SV=2 - [CABYR_HUMAN]	2.01	4.26	1	1	1	1	493	52.7	4.55
P17612	cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2 - [KAPCA_HUMAN]	1.94	2.56	1	0	1	1	351	40.6	8.79
P22694	cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB PE=1 SV=2 - [KAPCB_HUMAN]	1.94	2.56	1	0	1	1	351	40.6	8.78
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN]	1.94	4.56	1	1	1	1	263	28.5	6.92
Q8N1N4	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2 - [K2C78_HUMAN]	1.93	1.54	1	0	1	1	520	56.8	6.02
O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
P06899	Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3 - [H2B1J_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
P23527	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3 - [H2B1O_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
P33778	Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2 - [H2B1B_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
P57053	Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2 - [H2BFS_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.37
P58876	Histone H2B type 1-D OS=Homo sapiens	1.88	8.73	1	0	1	1	126	13.9	10.32

	GN=HIST1H2BD PE=1 SV=2 - [H2B1D_HUMAN]									
P62807	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4 - [H2B1C_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
Q16778	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3 - [H2B2E_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
Q5QNW6	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3 - [H2B2F_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
Q8N257	Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3 - [H2B3B_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
Q93079	Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3 - [H2B1H_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
Q96A08	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3 - [H2B1A_HUMAN]	1.88	8.66	1	0	1	1	127	14.2	10.32
Q99877	Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3 - [H2B1N_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
Q99879	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3 - [H2B1M_HUMAN]	1.88	8.73	1	0	1	1	126	14.0	10.32
Q99880	Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3 - [H2B1L_HUMAN]	1.88	8.73	1	0	1	1	126	13.9	10.32
P21741	Midkine OS=Homo sapiens GN=MDK PE=1 SV=1 - [MK_HUMAN]	1.86	6.99	1	1	1	1	143	15.6	9.79
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	1.85	4.62	1	1	1	1	260	29.2	7.40
Q15363	Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens GN=TMED2 PE=1 SV=1 - [TMED2_HUMAN]	1.75	4.48	1	1	1	1	201	22.7	5.17
P00403	Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1 - [COX2_HUMAN]	1.74	4.41	1	1	1	1	227	25.5	4.82
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	1.71	1.67	1	1	1	1	658	73.7	8.18
P16104	Histone H2AX OS=Homo sapiens GN=H2AFX PE=1 SV=2 - [H2AX_HUMAN]	1.69	16.08	1	0	1	1	143	15.1	10.74
Q8IUE6	Histone H2A type 2-B OS=Homo sapiens	1.69	17.69	1	0	1	1	130	14.0	10.89

	GN=HIST2H2AB PE=1 SV=3 - [H2A2B_HUMAN]									
Q96QV6	Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3 - [H2A1A_HUMAN]	1.69	17.56	1	0	1	1	131	14.2	10.86
P14625	Endoplasmic reticulum protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]	1.65	1.62	1	1	1	1	803	92.4	4.84
O75122	CLIP-associating protein 2 OS=Homo sapiens GN=CLASP2 PE=1 SV=2 - [CLAP2_HUMAN]	0.00	1.39	1	1	1	1	1294	141.0	8.47
P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	0.00	2.99	1	1	1	1	501	57.1	6.55
P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 - [ACADS_HUMAN]	0.00	2.43	1	1	1	1	412	44.3	7.99
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2 - [PSA2_HUMAN]	0.00	8.12	1	1	1	1	234	25.9	7.43
Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	0.00	1.66	1	1	1	1	362	40.1	9.38
Q86TL2	Transmembrane protein 110 OS=Homo sapiens GN=TMEM110 PE=2 SV=1 - [TM110_HUMAN]	0.00	15.99	1	1	1	1	294	33.2	8.15
Q9BYT9	Anoctamin-3 OS=Homo sapiens GN=ANO3 PE=1 SV=2 - [ANO3_HUMAN]	0.00	1.83	1	1	1	1	981	114.6	8.66
Q9UF56	F-box/LRR-repeat protein 17 OS=Homo sapiens GN=FBXL17 PE=2 SV=3 - [FXL17_HUMAN]	0.00	2.57	1	1	1	1	701	75.6	8.07

Suppl Table 3

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	Area	# AAs	MW [kDa]	calc. pI
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	84.18	33.18	1	3	9	32	1.649E4	434	47.1	7.39
Q5JQC9	A-kinase anchor protein 4 OS=Homo sapiens GN=AKAP4 PE=1 SV=1 - [AKAP4_HUMAN]	78.68	21.55	1	13	13	36	1.217E4	854	94.4	6.96
A6NM11	Leucine-rich repeat-containing protein 37A2 OS=Homo sapiens GN=LRRC37A2 PE=2 SV=2 - [L37A2_HUMAN]	67.35	13.65	1	1	15	24	3.200E4	1700	188.3	5.50
A6NMS7	Leucine-rich repeat-containing protein 37A OS=Homo sapiens GN=LRRC37A PE=2 SV=3 - [L37A1_HUMAN]	65.44	13.06	1	0	14	23	3.200E4	1700	188.1	5.49
Q8NEB7	Acrosin-binding protein OS=Homo sapiens GN=ACRBP PE=2 SV=1 - [ACRBP_HUMAN]	62.05	27.07	1	9	9	23	7.398E3	543	61.3	5.16
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	59.82	22.98	1	9	13	23	7.405E3	644	66.0	8.12
O60309	Leucine-rich repeat-containing protein 37A3 OS=Homo sapiens GN=LRRC37A3 PE=2 SV=2 - [L37A3_HUMAN]	55.70	12.61	1	0	13	20	3.200E4	1634	180.5	5.31
Q9XSJ4	Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4 - [ENOA_BOVIN]	54.39	23.04	1	0	6	17	2.647E3	434	47.3	6.80
P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]	54.29	25.67	1	1	14	22	7.250E3	639	70.0	5.74
Q9BUN1	Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1 - [MENT_HUMAN]	49.44	28.15	1	6	6	17	6.054E3	341	36.7	8.59
P34933	Heat shock-related 70 kDa protein 2 OS=Bos taurus GN=HSPA2 PE=2 SV=2 - [HSP72_BOVIN]	49.22	20.60	1	0	12	20	7.250E3	636	69.7	5.59
P04279	Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2 - [SEMG1_HUMAN]	46.34	27.27	1	11	11	17	3.458E3	462	52.1	9.29
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	44.69	29.36	1	1	13	19	1.266E4	654	72.3	5.16

Q0VCX2	78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1 - [GRP78_BOVIN]	42.15	27.02	1	0	12	17	1.266E4	655	72.4	5.16
P02769	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4 - [ALBU_BOVIN]	41.80	21.09	1	9	10	17	2.528E4	607	69.2	6.18
Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 - [TBA1A_HUMAN]	41.30	29.71	1	0	8	15	8.952E3	451	50.1	5.06
Q2HJ86	Tubulin alpha-1D chain OS=Bos taurus GN=TUBA1D PE=1 SV=1 - [TBA1D_BOVIN]	41.30	29.65	1	0	8	15	8.952E3	452	50.3	5.03
Q3MHM5	Tubulin beta-4B chain OS=Bos taurus GN=TUBB4B PE=2 SV=1 - [TBB4B_BOVIN]	40.87	18.43	1	0	7	14	4.721E3	445	49.8	4.89
Q6UW49	Sperm equatorial segment protein 1 OS=Homo sapiens GN=SPESP1 PE=1 SV=2 - [SPESP_HUMAN]	40.30	32.29	1	7	7	14	3.091E3	350	38.9	5.73
P62157	Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2 - [CALM_BOVIN]	39.94	44.30	1	6	7	16	1.399E4	149	16.8	4.22
Q96QE4	Leucine-rich repeat-containing protein 37B OS=Homo sapiens GN=LRR37B PE=2 SV=3 - [LR37B_HUMAN]	39.83	16.16	1	10	10	15	6.484E3	947	105.5	4.91
P81947	Tubulin alpha-1B chain OS=Bos taurus PE=1 SV=2 - [TBA1B_BOVIN]	39.38	29.71	1	0	8	14	8.952E3	451	50.1	5.06
Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 - [TBA3C_HUMAN]	38.93	29.78	1	0	8	14	8.952E3	450	49.9	5.10
Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2 - [TBA3E_HUMAN]	38.93	29.78	1	0	8	14	8.952E3	450	49.8	5.14
Q32KN8	Tubulin alpha-3 chain OS=Bos taurus GN=TUBA3 PE=2 SV=1 - [TBA3_BOVIN]	38.93	29.78	1	0	8	14	8.952E3	450	49.9	5.10
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	38.55	7.81	1	1	3	12	1.195E4	858	95.3	6.83
Q02383	Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1 - [SEMG2_HUMAN]	37.11	23.54	1	9	9	13	4.842E4	582	65.4	9.07
P60712	Actin, cytoplasmic 1 OS=Bos taurus GN=ACTB PE=1 SV=1 - [ACTB_BOVIN]	37.09	35.73	1	0	6	9	5.979E4	375	41.7	5.48
P63258	Actin, cytoplasmic 2 OS=Bos taurus GN=ACTG1 PE=1 SV=1 - [ACTG_BOVIN]	37.09	35.73	1	0	6	9	5.979E4	375	41.8	5.48
P68103	Elongation factor 1-alpha 1 OS=Bos taurus GN=EEF1A1 PE=1 SV=1 - [EF1A1_BOVIN]	36.86	17.10	1	0	4	11	2.760E4	462	50.1	9.01

Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 - [EF1A3_HUMAN]	36.86	17.10	1	0	4	11	2.760E4	462	50.2	9.07
Q3SYU2	Elongation factor 2 OS=Bos taurus GN=EEF2 PE=2 SV=3 - [EF2_BOVIN]	35.90	4.66	1	0	2	11	1.195E4	858	95.3	6.83
Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]	35.11	15.73	1	0	6	12	4.721E3	445	49.9	4.89
Q6B856	Tubulin beta-2B chain OS=Bos taurus GN=TUBB2B PE=1 SV=2 - [TBB2B_BOVIN]	35.11	15.73	1	0	6	12	4.721E3	445	49.9	4.89
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	35.06	18.15	1	4	8	14	7.516E3	584	58.8	5.21
P14625	Endoplasmic reticulum chaperone protein GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]	34.22	15.69	1	2	10	15	8.264E3	803	92.4	4.84
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	33.07	27.88	1	8	8	13	8.827E3	434	47.0	5.44
Q32PH8	Elongation factor 1-alpha 2 OS=Bos taurus GN=EEF1A2 PE=2 SV=1 - [EF1A2_BOVIN]	31.20	11.88	1	0	3	9	8.930E3	463	50.4	9.03
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	30.67	20.71	1	0	6	11	6.776E3	449	49.9	5.10
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	30.56	16.12	1	11	11	13	5.171E3	999	111.3	5.22
Q3ZCJ7	Tubulin alpha-1C chain OS=Bos taurus GN=TUBA1C PE=1 SV=1 - [TBA1C_BOVIN]	30.48	22.94	1	0	6	11	6.776E3	449	49.8	5.10
Q2T9S0	Tubulin beta-3 chain OS=Bos taurus GN=TUBB3 PE=2 SV=1 - [TBB3_BOVIN]	29.26	16.22	1	0	6	10		450	50.4	4.93
Q3ZBU7	Tubulin beta-4A chain OS=Bos taurus GN=TUBB4A PE=2 SV=1 - [TBB4A_BOVIN]	28.86	18.47	1	0	7	10	4.721E3	444	49.6	4.88
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	28.26	15.03	1	0	9	13	6.115E3	732	84.6	5.02
Q76LV2	Heat shock protein HSP 90-alpha OS=Bos taurus GN=HSP90AA1 PE=1 SV=3 - [HS90A_BOVIN]	28.26	15.01	1	0	9	13	6.115E3	733	84.7	5.01
P07205	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3 - [PGK2_HUMAN]	27.77	32.37	1	7	9	14	8.807E3	417	44.8	8.54

Q13561	Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4 - [DCTN2_HUMAN]	27.10	23.94	1	3	6	9		401	44.2	5.21
Q2HJ81	Tubulin beta-6 chain OS=Bos taurus GN=TUBB6 PE=2 SV=1 - [TBB6_BOVIN]	26.65	11.43	1	0	4	9		446	49.9	4.86
Q9HAT0	Ropporin-1A OS=Homo sapiens GN=ROPN1 PE=1 SV=2 - [ROP1A_HUMAN]	25.57	17.92	1	1	3	9	8.025E3	212	23.9	5.66
P81948	Tubulin alpha-4A chain OS=Bos taurus GN=TUBA4A PE=1 SV=2 - [TBA4A_BOVIN]	25.53	19.87	1	0	5	9	1.113E4	448	49.9	5.06
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	24.60	13.96	1	6	6	10	8.076E3	623	62.0	5.24
P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	24.47	20.61	1	2	6	9		427	45.2	8.85
Q95M18	Endoplasmin OS=Bos taurus GN=HSP90B1 PE=2 SV=1 - [ENPL_BOVIN]	24.10	11.44	1	0	8	12	8.582E3	804	92.4	4.84
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	24.04	18.26	1	1	7	10		553	59.7	9.13
P10909	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1 - [CLUS_HUMAN]	23.77	10.91	1	5	5	9	1.153E4	449	52.5	6.27
P15259	Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3 - [PGAM2_HUMAN]	22.78	31.62	1	2	6	9	1.207E4	253	28.7	8.88
Q9BZX4	Ropporin-1B OS=Homo sapiens GN=ROPN1B PE=1 SV=1 - [ROP1B_HUMAN]	22.60	12.26	1	0	2	8	8.025E3	212	23.9	5.15
P19483	ATP synthase subunit alpha, mitochondrial OS=Bos taurus GN=ATP5A1 PE=1 SV=1 - [ATPA_BOVIN]	22.33	15.91	1	0	6	9		553	59.7	9.19
Q2KJD0	Tubulin beta-5 chain OS=Bos taurus GN=TUBB5 PE=2 SV=1 - [TBB5_BOVIN]	21.87	14.64	1	0	6	8	4.721E3	444	49.6	4.89
Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	20.95	11.43	1	0	4	7		446	49.8	4.88
Q9H4B8	Dipeptidase 3 OS=Homo sapiens GN=DPEP3 PE=2 SV=2 - [DPEP3_HUMAN]	20.37	9.43	1	3	3	8		488	53.7	7.96
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN]	20.15	20.00	1	3	8	9	3.761E3	505	56.7	6.35

Q1ZYL8	Izumo sperm-egg fusion protein 4 OS=Homo sapiens GN=IZUMO4 PE=2 SV=2 - [IZUM4_HUMAN]	19.29	15.09	1	3	3	7	1.008E4	232	26.5	7.46
P14314	Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2 - [GLU2B_HUMAN]	19.26	16.48	1	6	6	10	2.408E3	528	59.4	4.41
P15289	Arylsulfatase A OS=Homo sapiens GN=ARSA PE=1 SV=3 - [ARSA_HUMAN]	19.03	9.27	1	3	3	7	6.340E3	507	53.6	6.07
Q7L266	Isoaspartyl peptidase/L-asparaginase OS=Homo sapiens GN=ASRGL1 PE=1 SV=2 - [ASGL1_HUMAN]	18.99	13.96	1	3	3	6		308	32.0	6.24
P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	18.49	9.22	1	0	2	5	3.186E3	434	47.0	7.71
P09104	Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3 - [ENOG_HUMAN]	18.49	9.22	1	0	2	5	3.186E3	434	47.2	5.03
Q3ZC09	Beta-enolase OS=Bos taurus GN=ENO3 PE=2 SV=1 - [ENOB_BOVIN]	18.49	9.22	1	0	2	5	3.186E3	434	47.1	7.72
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	17.92	23.67	1	1	5	7	1.624E4	338	35.5	8.68
P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	17.54	4.56	1	0	1	5	9.460E3	461	51.0	6.68
Q92176	Coronin-1A OS=Bos taurus GN=CORO1A PE=1 SV=3 - [COR1A_BOVIN]	17.54	4.56	1	0	1	5	9.460E3	461	50.9	6.68
O75969	A-kinase anchor protein 3 OS=Homo sapiens GN=AKAP3 PE=1 SV=2 - [AKAP3_HUMAN]	17.51	8.79	1	6	6	8	6.588E3	853	94.7	6.18
Q3ZCF0	Dynactin subunit 2 OS=Bos taurus GN=DCTN2 PE=2 SV=1 - [DCTN2_BOVIN]	17.38	12.66	1	0	3	5		403	44.3	5.16
P61019	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 - [RAB2A_HUMAN]	17.00	25.94	1	2	4	6		212	23.5	6.54
P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]	16.87	12.74	1	2	5	9	6.912E3	573	61.0	5.87
Q29RZ0	Acetyl-CoA acetyltransferase, mitochondrial OS=Bos taurus GN=ACAT1 PE=2 SV=1 - [THIL_BOVIN]	16.74	13.74	1	0	4	6		422	44.9	8.85
Q6S8J3	POTE ankyrin domain family member E	16.49	2.14	1	0	1	4	9.292E3	1075	121.3	6.20

	OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]										
P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2 - [H2A1B_HUMAN]	16.41	43.85	1	0	3	6	5.849E4	130	14.1	11.05
P0C0S9	Histone H2A type 1 OS=Bos taurus PE=1 SV=2 - [H2A1_BOVIN]	16.41	43.85	1	0	3	6	5.849E4	130	14.1	10.90
P20671	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2 - [H2A1D_HUMAN]	16.41	43.85	1	0	3	6	5.849E4	130	14.1	10.90
Q7L7L0	Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3 - [H2A3_HUMAN]	16.41	43.85	1	0	3	6	5.849E4	130	14.1	11.05
Q93077	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3 - [H2A1C_HUMAN]	16.41	43.85	1	0	3	6	5.849E4	130	14.1	11.05
Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3 - [H2A1H_HUMAN]	16.41	44.53	1	0	3	6	5.849E4	128	13.9	10.89
Q99878	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3 - [H2A1J_HUMAN]	16.41	44.53	1	0	3	6	5.849E4	128	13.9	10.89
Q3ZBX9	Histone H2A.J OS=Bos taurus GN=H2AFJ PE=2 SV=1 - [H2AJ_BOVIN]	16.41	44.19	1	0	3	6	5.849E4	129	14.0	10.90
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]	16.23	9.04	1	2	2	6	1.415E4	332	36.7	8.27
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	16.22	16.79	1	2	4	6	1.188E4	417	48.1	4.44
P12821	Angiotensin-converting enzyme OS=Homo sapiens GN=ACE PE=1 SV=1 - [ACE_HUMAN]	15.74	5.59	1	6	6	7	9.300E3	1306	149.6	6.39
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	14.93	14.88	1	3	3	5		336	35.3	8.13
P18669	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 - [PGAM1_HUMAN]	14.87	19.69	1	0	4	6	1.207E4	254	28.8	7.18
Q3SZ62	Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3 - [PGAM1_BOVIN]	14.87	19.69	1	0	4	6	1.207E4	254	28.8	7.18
Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 - [PARK7_HUMAN]	14.53	29.63	1	0	3	5		189	19.9	6.79
Q5E946	Protein DJ-1 OS=Bos taurus GN=PARK7 PE=2 SV=1 - [PARK7_BOVIN]	14.53	29.63	1	0	3	5		189	20.0	7.33
P06744	Glucose-6-phosphate isomerase OS=Homo	13.80	12.72	1	3	5	6	2.337E3	558	63.1	8.32

	sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]										
Q16698	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1 - [DECR_HUMAN]	13.64	15.82	1	4	4	5	1.478E4	335	36.0	9.28
P30086	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 - [PEBP1_HUMAN]	13.54	28.34	1	3	3	4	1.009E4	187	21.0	7.53
Q99798	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 - [ACON_HUMAN]	13.51	8.97	1	1	5	7	7.873E3	780	85.4	7.61
P38657	Protein disulfide-isomerase A3 OS=Bos taurus GN=PDIA3 PE=2 SV=1 - [PDIA3_BOVIN]	13.28	13.07	1	0	5	6	3.434E3	505	56.9	6.65
Q8TC56	Protein FAM71B OS=Homo sapiens GN=FAM71B PE=1 SV=2 - [FA71B_HUMAN]	13.27	8.93	1	3	3	5		605	64.7	9.48
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	13.06	7.36	1	3	4	7	5.013E3	639	65.4	8.00
P54709	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1 - [AT1B3_HUMAN]	13.02	17.92	1	4	4	6	6.669E3	279	31.5	8.35
P80303	Nucleobindin-2 OS=Homo sapiens GN=NUCB2 PE=1 SV=2 - [NUCB2_HUMAN]	12.98	12.38	1	4	4	6	1.505E4	420	50.2	5.12
A1A4R1	Histone H2A type 2-C OS=Bos taurus GN=HIST2H2AC PE=2 SV=1 - [H2A2C_BOVIN]	12.96	21.71	1	0	2	5		129	14.0	10.90
Q6F113	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3 - [H2A2A_HUMAN]	12.96	21.54	1	0	2	5		130	14.1	10.90
Q32LG3	Malate dehydrogenase, mitochondrial OS=Bos taurus GN=MDH2 PE=1 SV=1 - [MDHM_BOVIN]	12.86	17.16	1	0	4	5	5.267E3	338	35.6	8.54
P16104	Histone H2AX OS=Homo sapiens GN=H2AFX PE=1 SV=2 - [H2AX_HUMAN]	12.78	42.66	1	0	3	5	3.716E4	143	15.1	10.74
Q8IU66	Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3 - [H2A2B_HUMAN]	12.78	46.92	1	0	3	5	3.716E4	130	14.0	10.89
P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [RLA2_HUMAN]	12.56	45.22	1	0	2	4		115	11.7	4.54
P42899	60S acidic ribosomal protein P2 OS=Bos taurus GN=RPLP2 PE=3 SV=1 - [RLA2_BOVIN]	12.56	45.22	1	0	2	4		115	11.7	4.61
Q8WW22	DnaJ homolog subfamily A member 4	12.49	11.59	1	3	3	5		397	44.8	7.59

	OS=Homo sapiens GN=DNAJA4 PE=1 SV=1 - [DNJA4_HUMAN]										
O95757	Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3 - [HS74L_HUMAN]	12.40	3.22	1	2	2	6	8.961E3	839	94.5	5.88
Q9NY65	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 - [TBA8_HUMAN]	12.01	10.91	1	0	3	4	1.113E4	449	50.1	5.06
Q2HJB8	Tubulin alpha-8 chain OS=Bos taurus GN=TUBA8 PE=2 SV=1 - [TBA8_BOVIN]	12.01	10.91	1	0	3	4	1.113E4	449	50.0	5.20
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	11.94	7.91	1	0	2	5		417	44.6	8.10
Q3T0P6	Phosphoglycerate kinase 1 OS=Bos taurus GN=PGK1 PE=2 SV=3 - [PGK1_BOVIN]	11.94	7.91	1	0	2	5		417	44.5	8.27
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	11.50	9.60	1	0	5	5		646	70.9	5.52
P19120	Heat shock cognate 71 kDa protein OS=Bos taurus GN=HSPA8 PE=1 SV=2 - [HSP7C_BOVIN]	11.50	9.54	1	0	5	5		650	71.2	5.52
P34931	Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2 - [HS71L_HUMAN]	11.36	11.39	1	0	6	6		641	70.3	6.02
P0CB32	Heat shock 70 kDa protein 1-like OS=Bos taurus GN=HSPA1L PE=3 SV=1 - [HS71L_BOVIN]	11.36	11.39	1	0	6	6		641	70.3	6.20
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	11.34	14.84	1	3	3	4	3.892E3	364	39.4	8.09
P61603	10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=3 SV=2 - [CH10_BOVIN]	11.06	35.29	1	3	3	5		102	10.9	8.92
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3 - [TPIS_HUMAN]	10.97	13.64	1	2	3	4	5.403E3	286	30.8	5.92
P63103	14-3-3 protein zeta/delta OS=Bos taurus GN=YWHAZ PE=1 SV=1 - [1433Z_BOVIN]	10.83	17.14	1	2	3	4	8.093E3	245	27.7	4.79
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	10.76	4.11	1	1	2	4		609	69.3	6.28
O14556	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS	10.74	9.80	1	1	3	4	1.319E3	408	44.5	8.19

	PE=1 SV=2 - [G3PT_HUMAN]											
P15586	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3 - [GNS_HUMAN]	10.52	4.53	1	0	2	5	1.048E4	552	62.0	8.31	
Q1LZH9	N-acetylglucosamine-6-sulfatase OS=Bos taurus GN=GNS PE=2 SV=1 - [GNS_BOVIN]	10.52	4.46	1	0	2	5	1.048E4	560	62.7	8.43	
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	10.39	5.99	1	0	1	3	2.566E3	334	36.6	6.05	
Q5E9B1	L-lactate dehydrogenase B chain OS=Bos taurus GN=LDHB PE=2 SV=4 - [LDHB_BOVIN]	10.39	5.99	1	0	1	3	2.566E3	334	36.7	6.44	
P07864	L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=1 SV=4 - [LDHC_HUMAN]	10.28	18.37	1	5	5	5	5.922E3	332	36.3	7.46	
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 - [TCPB_HUMAN]	10.22	9.72	1	0	3	5	1.105E4	535	57.5	6.46	
Q3ZBH0	T-complex protein 1 subunit beta OS=Bos taurus GN=CCT2 PE=1 SV=3 - [TCPB_BOVIN]	10.22	9.72	1	0	3	5	1.105E4	535	57.4	6.64	
O75071	EF-hand calcium-binding domain-containing protein 14 OS=Homo sapiens GN=EFCAB14 PE=2 SV=1 - [EFC14_HUMAN]	10.14	10.30	1	4	4	5		495	55.0	6.32	
Q8IXA5	Sperm acrosome membrane-associated protein 3 OS=Homo sapiens GN=SPACA3 PE=1 SV=1 - [SACA3_HUMAN]	9.91	12.56	1	2	2	3		215	23.4	7.94	
Q8N0Y7	Probable phosphoglycerate mutase 4 OS=Homo sapiens GN=PGAM4 PE=2 SV=1 - [PGAM4_HUMAN]	9.79	9.45	1	0	2	4		254	28.8	6.65	
P57105	Synaptojanin-2-binding protein OS=Homo sapiens GN=SYNJ2BP PE=1 SV=2 - [SYJ2B_HUMAN]	9.70	24.83	1	0	3	4	8.297E3	145	15.9	6.30	
Q3T0C9	Synaptojanin-2-binding protein OS=Bos taurus GN=SYNJ2BP PE=2 SV=1 - [SYJ2B_BOVIN]	9.70	24.83	1	0	3	4	8.297E3	145	15.8	5.94	
P38646	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 - [GRP75_HUMAN]	9.69	2.50	1	0	1	3	6.993E3	679	73.6	6.16	
Q3ZCH0	Stress-70 protein, mitochondrial OS=Bos taurus GN=HSPA9 PE=2 SV=1 - [GRP75_BOVIN]	9.69	2.50	1	0	1	3	6.993E3	679	73.7	6.30	
P31081	60 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPD1 PE=1 SV=2 -	9.66	8.20	1	0	3	6		573	61.1	5.74	

	[CH60_BOVIN]										
O75390	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2 - [CISY_HUMAN]	9.41	5.79	1	0	2	3		466	51.7	8.32
Q29RK1	Citrate synthase, mitochondrial OS=Bos taurus GN=CS PE=1 SV=1 - [CISY_BOVIN]	9.41	5.79	1	0	2	3		466	51.7	8.12
P20674	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2 - [COX5A_HUMAN]	9.40	16.00	1	2	2	4		150	16.8	6.79
Q9HBV2	Sperm acrosome membrane-associated protein 1 OS=Homo sapiens GN=SPACA1 PE=1 SV=1 - [SACA1_HUMAN]	9.38	13.61	1	3	3	5	1.947E3	294	32.1	4.61
Q96QV6	Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3 - [H2A1A_HUMAN]	9.33	24.43	1	0	2	4	1.582E4	131	14.2	10.86
Q9H4A4	Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 - [AMPB_HUMAN]	9.31	2.92	1	1	1	3		650	72.5	5.74
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	9.25	15.38	1	3	3	6	5.221E3	260	29.2	7.40
P52193	Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2 - [CALR_BOVIN]	9.24	11.51	1	0	2	3	1.314E4	417	48.0	4.46
P30044	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 - [PRDX5_HUMAN]	9.19	12.15	1	1	2	4		214	22.1	8.70
P22695	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3 - [QCR2_HUMAN]	9.07	10.82	1	2	3	4	1.677E4	453	48.4	8.63
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	9.04	3.54	1	2	2	4		763	82.9	9.04
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	8.94	12.74	1	0	4	5	1.309E4	369	41.3	5.27
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]	8.92	19.66	1	1	7	8	8.961E3	529	56.5	5.40
P00829	ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2 - [ATPB_BOVIN]	8.92	16.29	1	0	6	7		528	56.2	5.27

Q8WUD1	Ras-related protein Rab-2B OS=Homo sapiens GN=RAB2B PE=1 SV=1 - [RAB2B_HUMAN]	8.81	11.57	1	0	2	3		216	24.2	7.83
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2 - [KAP2_HUMAN]	8.75	7.43	1	2	2	3		404	45.5	5.07
P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	8.70	8.89	1	0	5	5		641	70.0	5.66
Q27965	Heat shock 70 kDa protein 1B OS=Bos taurus GN=HSPA1B PE=2 SV=1 - [HS71B_BOVIN]	8.70	8.89	1	0	5	5		641	70.2	5.92
Q27975	Heat shock 70 kDa protein 1A OS=Bos taurus GN=HSPA1A PE=1 SV=2 - [HS71A_BOVIN]	8.70	8.89	1	0	5	5		641	70.2	5.92
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	8.69	4.42	1	0	3	4		724	83.2	5.03
Q76LV1	Heat shock protein HSP 90-beta OS=Bos taurus GN=HSP90AB1 PE=2 SV=3 - [HS90B_BOVIN]	8.69	4.42	1	0	3	4		724	83.2	5.03
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]	8.31	6.74	1	0	3	4	4.347E3	519	56.1	7.93
P00727	Cytosol aminopeptidase OS=Bos taurus GN=LAP3 PE=1 SV=3 - [AMPL_BOVIN]	8.31	6.74	1	0	3	4	4.347E3	519	56.3	6.48
P14927	Cytochrome b-c1 complex subunit 7 OS=Homo sapiens GN=UQCRB PE=1 SV=2 - [QCR7_HUMAN]	8.29	25.23	1	2	2	3	2.281E4	111	13.5	8.78
P59282	Tubulin polymerization-promoting protein family member 2 OS=Homo sapiens GN=TPPP2 PE=1 SV=2 - [TPPP2_HUMAN]	8.22	15.88	1	1	2	3	4.996E3	170	18.5	9.00
Q7Z794	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3 - [K2C1B_HUMAN]	8.20	4.15	1	1	2	4	5.013E3	578	61.9	5.99
Q9NQ60	Equatorin OS=Homo sapiens GN=EQTN PE=2 SV=2 - [EQTN_HUMAN]	8.16	13.27	1	3	3	4		294	32.8	5.00
P29401	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3 - [TKT_HUMAN]	8.13	3.37	1	0	1	3		623	67.8	7.66
Q6B855	Transketolase OS=Bos taurus GN=TKT PE=2 SV=1 - [TKT_BOVIN]	8.13	3.37	1	0	1	3		623	67.9	7.65

Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN]	8.01	10.00	1	3	3	4		440	48.1	5.08
O14950	Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 - [ML12B_HUMAN]	7.78	11.63	1	0	1	2		172	19.8	4.84
P19105	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 - [ML12A_HUMAN]	7.78	11.70	1	0	1	2		171	19.8	4.81
Q5E9E2	Myosin regulatory light polypeptide 9 OS=Bos taurus GN=MYL9 PE=2 SV=3 - [MYL9_BOVIN]	7.78	11.63	1	0	1	2		172	19.9	4.81
A4IF97	Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1 - [ML12B_BOVIN]	7.78	11.70	1	0	1	2		171	19.7	4.84
Q14568	Putative heat shock protein HSP 90-alpha A2 OS=Homo sapiens GN=HSP90AA2 PE=1 SV=2 - [HS902_HUMAN]	7.77	6.12	1	0	2	3	1.278E3	343	39.3	4.65
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	7.70	1.61	1	0	1	3		806	89.3	5.26
Q3ZBT1	Transitional endoplasmic reticulum ATPase OS=Bos taurus GN=VCP PE=2 SV=1 - [TERA_BOVIN]	7.70	1.61	1	0	1	3		806	89.3	5.26
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]	7.38	5.88	1	2	2	4	9.892E3	476	54.1	5.62
Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]	7.32	10.69	1	2	3	4	5.988E3	318	35.9	7.11
P12273	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1 - [PIP_HUMAN]	7.31	19.18	1	2	2	3		146	16.6	8.05
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	7.28	6.67	1	0	1	2		225	24.7	4.67
Q5E983	Elongation factor 1-beta OS=Bos taurus GN=EEF1B PE=2 SV=3 - [EF1B_BOVIN]	7.28	6.67	1	0	1	2		225	24.8	4.67
P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 - [TCPE_HUMAN]	7.23	3.33	1	1	1	3	1.258E4	541	59.6	5.66

P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	7.20	4.97	1	0	2	3	3.457E3	543	62.6	6.80
Q3ZBZ8	Stress-induced-phosphoprotein 1 OS=Bos taurus GN=STIP1 PE=2 SV=1 - [STIP1_BOVIN]	7.20	4.97	1	0	2	3	3.457E3	543	62.4	6.43
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [SDHA_HUMAN]	7.18	5.27	1	0	2	3		664	72.6	7.39
P31039	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Bos taurus GN=SDHA PE=1 SV=3 - [SDHA_BOVIN]	7.18	5.26	1	0	2	3		665	72.9	7.59
Q3ZBD7	Glucose-6-phosphate isomerase OS=Bos taurus GN=GPI PE=2 SV=4 - [G6PI_BOVIN]	7.10	5.39	1	0	2	3	2.337E3	557	62.8	7.71
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 - [TCPQ_HUMAN]	7.08	5.11	1	1	2	5		548	59.6	5.60
Q8TDB8	Solute carrier family 2, facilitated glucose transporter member 14 OS=Homo sapiens GN=SLC2A14 PE=2 SV=1 - [GTR14_HUMAN]	6.95	4.62	1	1	2	3	3.651E3	520	56.3	7.83
Q32KV0	Phosphoglycerate mutase 2 OS=Bos taurus GN=PGAM2 PE=2 SV=1 - [PGAM2_BOVIN]	6.84	12.65	1	0	3	3	1.207E4	253	28.7	8.88
P20004	Aconitate hydratase, mitochondrial OS=Bos taurus GN=ACO2 PE=1 SV=4 - [ACON_BOVIN]	6.79	7.18	1	0	4	4	7.873E3	780	85.3	7.83
Q15506	Sperm surface protein Sp17 OS=Homo sapiens GN=SPA17 PE=1 SV=1 - [SP17_HUMAN]	6.67	25.83	1	2	2	2		151	17.4	4.78
A6NNZ2	Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 - [TBB8L_HUMAN]	6.59	6.53	1	0	3	3	4.721E3	444	49.5	4.86
Q3ZCM7	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]	6.59	6.53	1	0	3	3	4.721E3	444	49.7	4.89
Q7Z6W1	Transmembrane and coiled-coil domain-containing protein 2 OS=Homo sapiens GN=TMCO2 PE=2 SV=1 - [TMCO2_HUMAN]	6.54	16.48	1	2	2	2	3.062E4	182	20.1	8.68
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]	6.47	3.71	1	2	2	2	1.290E4	944	106.8	6.14
Q6BCY4	NADH-cytochrome b5 reductase 2 OS=Homo sapiens GN=CYB5R2 PE=1 SV=1 - [NB5R2_HUMAN]	6.39	15.58	1	3	3	3	1.713E4	276	31.4	8.50

P06394	Keratin, type I cytoskeletal 10 OS=Bos taurus GN=KRT10 PE=3 SV=1 - [K1C10_BOVIN]	6.18	6.27	1	0	3	3	4.859E3	526	54.8	5.11
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	6.15	11.64	1	2	3	3	8.450E3	335	36.0	8.46
P38567	Hyaluronidase PH-20 OS=Homo sapiens GN=SPAM1 PE=1 SV=1 - [HYALP_HUMAN]	6.11	2.75	1	1	1	2		509	57.8	7.01
Q29S21	Keratin, type II cytoskeletal 7 OS=Bos taurus GN=KRT7 PE=2 SV=1 - [K2C7_BOVIN]	6.09	4.94	1	0	2	3		466	51.5	5.97
O75952	Calcium-binding tyrosine phosphorylation- regulated protein OS=Homo sapiens GN=CABYR PE=1 SV=2 - [CABYR_HUMAN]	6.08	5.88	1	2	2	2		493	52.7	4.55
Q9P0L0	Vesicle-associated membrane protein- associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3 - [VAPA_HUMAN]	5.87	5.62	1	0	2	2		249	27.9	8.62
Q0VCY1	Vesicle-associated membrane protein- associated protein A OS=Bos taurus GN=VAPA PE=2 SV=1 - [VAPA_BOVIN]	5.87	5.62	1	0	2	2		249	27.8	8.60
O15173	Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1 - [PGRC2_HUMAN]	5.87	8.52	1	1	1	2		223	23.8	4.88
Q96KW9	Protein SPACA7 OS=Homo sapiens GN=SPACA7 PE=2 SV=2 - [SPAC7_HUMAN]	5.81	23.59	1	3	3	4	3.174E3	195	21.5	4.78
Q8NFI4	Putative protein FAM10A5 OS=Homo sapiens GN=ST13P5 PE=5 SV=1 - [F10A5_HUMAN]	5.81	8.94	1	0	3	4	1.309E4	369	41.4	5.05
Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens GN=HINT2 PE=1 SV=1 - [HINT2_HUMAN]	5.60	24.54	1	1	3	4		163	17.2	9.16
O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	5.55	3.05	1	1	1	2		394	43.6	9.00
P20810	Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 - [ICAL_HUMAN]	5.55	2.40	1	1	1	2		708	76.5	5.07
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	5.34	33.00	1	0	2	2		100	11.3	8.79

Q2KJD2	Vesicle-associated membrane protein 3 OS=Bos taurus GN=VAMP3 PE=3 SV=1 - [VAMP3_BOVIN]	5.34	31.73	1	0	2	2		104	11.5	8.79
P29692	Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5 - [EF1D_HUMAN]	5.27	8.54	1	1	2	2		281	31.1	5.01
Q8IYT1	Protein FAM71A OS=Homo sapiens GN=FAM71A PE=2 SV=2 - [FA71A_HUMAN]	5.25	5.39	1	2	2	3	7.449E3	594	63.1	9.64
P02662	Alpha-S1-casein OS=Bos taurus GN=CSN1S1 PE=1 SV=2 - [CASA1_BOVIN]	5.24	13.08	1	2	2	2	1.428E4	214	24.5	5.02
O60884	DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1 - [DNJA2_HUMAN]	5.20	3.40	1	0	1	2		412	45.7	6.48
Q2HJ94	DnaJ homolog subfamily A member 2 OS=Bos taurus GN=DNAJA2 PE=2 SV=1 - [DNJA2_BOVIN]	5.20	3.40	1	0	1	2		412	45.7	6.48
Q2KJE5	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Bos taurus GN=GAPDHS PE=2 SV=1 - [G3PT_BOVIN]	5.07	6.33	1	0	2	2		395	43.3	8.12
O46375	Transthyretin OS=Bos taurus GN=TTR PE=1 SV=1 - [TTHY_BOVIN]	4.99	8.84	1	1	1	2	4.766E3	147	15.7	6.30
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCLH3 PE=1 SV=1 - [UCLH3_HUMAN]	4.93	6.96	1	0	1	2		230	26.2	4.92
Q2TBG8	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Bos taurus GN=UCLH3 PE=2 SV=1 - [UCLH3_BOVIN]	4.93	6.96	1	0	1	2		230	26.2	4.92
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	4.88	2.22	1	0	1	2	3.651E3	496	53.9	7.20
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]	4.86	16.88	1	1	2	2	3.241E3	154	15.9	6.13
Q9H0C2	ADP/ATP translocase 4 OS=Homo sapiens GN=SLC25A31 PE=2 SV=1 - [ADT4_HUMAN]	4.85	8.25	1	0	2	2		315	35.0	9.89
Q2YDD9	ADP/ATP translocase 4 OS=Bos taurus GN=SLC25A31 PE=2 SV=1 - [ADT4_BOVIN]	4.85	8.05	1	0	2	2		323	35.7	9.55
O75083	WD repeat-containing protein 1 OS=Homo	4.84	2.64	1	1	1	2		606	66.2	6.65

	sapiens GN=WDR1 PE=1 SV=4 - [WDR1_HUMAN]											
P18859	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 - [ATP5J_HUMAN]	4.77	26.85	1	2	2	2		108	12.6	9.52	
Q04837	Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1 - [SSBP_HUMAN]	4.77	10.14	1	1	1	2		148	17.2	9.60	
P02751	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4 - [FN1_HUMAN]	4.68	0.63	1	1	1	2	1.138E4	2386	262.5	5.71	
Q9BSF0	Small membrane A-kinase anchor protein OS=Homo sapiens GN=C2orf88 PE=1 SV=2 - [SMAKA_HUMAN]	4.66	26.32	1	2	2	2	1.227E4	95	11.0	4.87	
P49913	Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1 SV=1 - [CAMP_HUMAN]	4.63	20.00	1	2	2	2		170	19.3	9.41	
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4 - [PIMT_HUMAN]	4.62	8.37	1	0	1	2		227	24.6	7.21	
P15246	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Bos taurus GN=PCMT1 PE=1 SV=2 - [PIMT_BOVIN]	4.62	8.37	1	0	1	2		227	24.5	7.58	
P17066	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2 - [HSP76_HUMAN]	4.46	3.11	1	0	2	2		643	71.0	6.14	
Q58FF6	Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1 - [H90B4_HUMAN]	4.43	1.98	1	0	1	2		505	58.2	4.73	
Q58FF7	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1 - [H90B3_HUMAN]	4.43	1.68	1	0	1	2		597	68.3	4.79	
Q96M98	Parkin coregulated gene protein OS=Homo sapiens GN=PACRG PE=1 SV=2 - [PACRG_HUMAN]	4.43	9.12	1	2	2	3		296	33.3	8.21	
Q96E40	Uncharacterized protein C9orf9 OS=Homo sapiens GN=C9orf9 PE=2 SV=1 - [C1009_HUMAN]	4.43	5.86	1	1	1	2		222	25.1	9.13	

P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	4.43	2.29	1	0	1	2		437	50.1	6.67
Q3SZV3	Elongation factor 1-gamma OS=Bos taurus GN=EEF1G PE=2 SV=1 - [EF1G_BOVIN]	4.43	2.27	1	0	1	2		440	50.3	6.57
P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [SDHB_HUMAN]	4.42	4.29	1	0	1	2	1.215E4	280	31.6	8.76
Q3T189	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Bos taurus GN=SDHB PE=2 SV=1 - [SDHB_BOVIN]	4.42	4.29	1	0	1	2	1.215E4	280	31.5	8.60
Q8N4E7	Ferritin, mitochondrial OS=Homo sapiens GN=FTMT PE=1 SV=1 - [FTMT_HUMAN]	4.39	9.50	1	1	1	3		242	27.5	7.27
Q5BJF6	Outer dense fiber protein 2 OS=Homo sapiens GN=ODF2 PE=1 SV=1 - [ODFP2_HUMAN]	4.32	2.65	1	1	2	2	4.091E3	829	95.3	7.62
Q9Y2B0	Protein canopy homolog 2 OS=Homo sapiens GN=CNPY2 PE=1 SV=1 - [CNPY2_HUMAN]	4.27	8.79	1	1	1	2		182	20.6	4.92
P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7 - [K2C8_HUMAN]	4.25	2.28	1	0	1	2		483	53.7	5.59
P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	4.25	2.35	1	0	1	2		469	51.4	5.48
P14136	Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1 - [GFAP_HUMAN]	4.25	2.55	1	0	1	2		432	49.8	5.52
P19013	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4 - [K2C4_HUMAN]	4.25	2.06	1	0	1	2		534	57.2	6.61
Q6KB66	Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2 - [K2C80_HUMAN]	4.25	2.43	1	0	1	2		452	50.5	5.67
A0JND2	Keratin, type II cytoskeletal 80 OS=Bos taurus GN=KRT80 PE=2 SV=1 - [K2C80_BOVIN]	4.25	2.61	1	0	1	2		422	47.4	5.31
A7YWK3	Keratin, type II cytoskeletal 73 OS=Bos taurus GN=KRT73 PE=2 SV=1 - [K2C73_BOVIN]	4.25	2.04	1	0	1	2		540	58.8	7.23
P04263	Keratin, type II cytoskeletal 68 kDa, component IA (Fragment) OS=Bos taurus PE=2 SV=1 - [K2CA_BOVIN]	4.25	6.04	1	0	1	2		182	18.1	8.32
Q28115	Glial fibrillary acidic protein OS=Bos taurus GN=GFAP PE=1 SV=2 - [GFAP_BOVIN]	4.25	2.57	1	0	1	2		428	49.5	5.45

P07108	Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2 - [ACBP_HUMAN]	4.18	22.99	1	1	1	3	2.041E4	87	10.0	6.57
Q9H4B7	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1 - [TBB1_HUMAN]	4.18	4.43	1	0	2	2		451	50.3	5.17
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 - [QCR1_HUMAN]	4.10	2.08	1	1	1	2		480	52.6	6.37
P62739	Actin, aortic smooth muscle OS=Bos taurus GN=ACTA2 PE=1 SV=1 - [ACTA_BOVIN]	4.09	6.10	1	0	1	1		377	42.0	5.39
Q3ZC07	Actin, alpha cardiac muscle 1 OS=Bos taurus GN=ACTC1 PE=2 SV=1 - [ACTC_BOVIN]	4.09	6.10	1	0	1	1		377	42.0	5.39
Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]	4.09	10.90	1	1	2	2		376	42.0	5.59
P55084	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN]	3.98	2.74	1	0	1	2		474	51.3	9.41
O46629	Trifunctional enzyme subunit beta, mitochondrial OS=Bos taurus GN=HADHB PE=2 SV=1 - [ECHB_BOVIN]	3.98	2.74	1	0	1	2		475	51.3	9.32
Q9NQ48	Leucine zipper transcription factor-like protein 1 OS=Homo sapiens GN=LZTFL1 PE=1 SV=1 - [LZTL1_HUMAN]	3.76	8.70	1	1	2	2	7.002E3	299	34.6	5.36
O75190	DnaJ homolog subfamily B member 6 OS=Homo sapiens GN=DNAJB6 PE=1 SV=2 - [DNJB6_HUMAN]	3.75	7.06	1	0	2	2		326	36.1	9.16
Q0III6	DnaJ homolog subfamily B member 6 OS=Bos taurus GN=DNAJB6 PE=2 SV=1 - [DNJB6_BOVIN]	3.75	9.50	1	0	2	2		242	26.9	7.61
Q8SQ21	Histidine triad nucleotide-binding protein 2, mitochondrial OS=Bos taurus GN=HINT2 PE=2 SV=1 - [HINT2_BOVIN]	3.70	14.72	1	0	2	3		163	17.1	7.50
P62803	Histone H4 OS=Bos taurus PE=1 SV=2 - [H4_BOVIN]	3.67	19.42	1	2	2	2	1.003E4	103	11.4	11.36
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FUH1 PE=1 SV=3 - [FUMH_HUMAN]	3.67	4.31	1	2	2	2		510	54.6	8.76
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	3.59	1.07	1	1	1	1		1960	226.4	5.60

P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1 - [RD23B_HUMAN]	3.52	4.65	1	1	2	2		409	43.1	4.84
Q8TC71	Mitochondria-eating protein OS=Homo sapiens GN=SPATA18 PE=1 SV=1 - [MIEAP_HUMAN]	3.44	5.20	1	2	2	2	1.228E4	538	61.1	8.63
O95292	Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3 - [VAPB_HUMAN]	3.23	4.94	1	0	1	1		243	27.2	7.30
A2VDZ9	Vesicle-associated membrane protein-associated protein B OS=Bos taurus GN=VAPB PE=2 SV=1 - [VAPB_BOVIN]	3.23	4.94	1	0	1	1		243	27.1	7.30
P55145	Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens GN=MANF PE=1 SV=3 - [MANF_HUMAN]	3.20	8.24	1	1	1	1		182	20.7	8.69
Q8IZP2	Putative protein FAM10A4 OS=Homo sapiens GN=ST13P4 PE=5 SV=1 - [ST134_HUMAN]	3.13	5.83	1	0	1	1		240	27.4	5.08
P00442	Superoxide dismutase [Cu-Zn] OS=Bos taurus GN=SOD1 PE=1 SV=2 - [SODC_BOVIN]	3.03	7.89	1	0	1	1	3.241E3	152	15.7	6.32
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN]	3.01	10.00	1	1	1	1	1.954E4	140	15.0	8.27
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 - [PYR1_HUMAN]	2.99	1.12	1	1	1	1		2225	242.8	6.46
P62491	Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RB11A_HUMAN]	2.95	6.02	1	0	1	1		216	24.4	6.57
Q3MHP2	Ras-related protein Rab-11B OS=Bos taurus GN=RAB11B PE=2 SV=3 - [RB11B_BOVIN]	2.95	5.96	1	0	1	1		218	24.5	5.94
Q2TA29	Ras-related protein Rab-11A OS=Bos taurus GN=RAB11A PE=2 SV=3 - [RB11A_BOVIN]	2.95	6.02	1	0	1	1		216	24.5	6.57
P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	2.95	3.24	1	0	1	1	1.096E4	586	69.4	6.27
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	2.95	3.29	1	0	1	1	1.096E4	577	67.8	6.40
P35241	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1 - [RADI_HUMAN]	2.95	3.26	1	0	1	1	1.096E4	583	68.5	6.37
P31976	Ezrin OS=Bos taurus GN=EZR PE=1 SV=2 - [EZRI_BOVIN]	2.95	3.27	1	0	1	1	1.096E4	581	68.7	6.42

Q2HJ49	Moesin OS=Bos taurus GN=MSN PE=2 SV=3 - [MOES_BOVIN]	2.95	3.29	1	0	1	1	1.096E4	577	67.9	6.16
Q32LP2	Radixin OS=Bos taurus GN=RDX PE=2 SV=1 - [RADI_BOVIN]	2.95	3.26	1	0	1	1	1.096E4	583	68.5	6.27
Q8TAD1	Sperm protein associated with the nucleus on the X chromosome E OS=Homo sapiens GN=SPANXE PE=2 SV=1 - [SPNXE_HUMAN]	2.82	11.34	1	0	1	1	2.254E4	97	11.0	5.26
Q9BXN6	Sperm protein associated with the nucleus on the X chromosome D OS=Homo sapiens GN=SPANXD PE=2 SV=1 - [SPNXD_HUMAN]	2.82	11.34	1	0	1	1	2.254E4	97	11.0	6.11
Q9NS25	Sperm protein associated with the nucleus on the X chromosome B/F OS=Homo sapiens GN=SPANXB1 PE=2 SV=1 - [SPNXB_HUMAN]	2.82	10.68	1	0	1	1	2.254E4	103	11.8	6.15
Q9NS26	Sperm protein associated with the nucleus on the X chromosome A OS=Homo sapiens GN=SPANXA1 PE=2 SV=1 - [SPNXA_HUMAN]	2.82	11.34	1	0	1	1	2.254E4	97	11.0	5.10
Q9NY87	Sperm protein associated with the nucleus on the X chromosome C OS=Homo sapiens GN=SPANXC PE=2 SV=1 - [SPNXC_HUMAN]	2.82	11.34	1	0	1	1	2.254E4	97	11.0	5.10
P0CG47	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN]	2.79	20.96	1	0	1	1		229	25.7	7.43
P62992	Ubiquitin-40S ribosomal protein S27a OS=Bos taurus GN=RPS27A PE=1 SV=2 - [RS27A_BOVIN]	2.79	10.26	1	0	1	1		156	18.0	9.64
P63048	Ubiquitin-60S ribosomal protein L40 OS=Bos taurus GN=UBA52 PE=1 SV=2 - [RL40_BOVIN]	2.79	12.50	1	0	1	1		128	14.7	9.83
P0CG48	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]	2.79	21.02	1	0	1	1		685	77.0	7.66
P0CG53	Polyubiquitin-B OS=Bos taurus GN=UBB PE=1 SV=1 - [UBB_BOVIN]	2.79	20.98	1	0	1	1		305	34.3	7.47
P0CH28	Polyubiquitin-C OS=Bos taurus GN=UBC PE=1 SV=1 - [UBC_BOVIN]	2.79	20.87	1	0	1	1		690	77.5	7.66
Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens GN=ABHD10 PE=1 SV=1 - [ABHDA_HUMAN]	2.79	5.56	1	1	1	1		306	33.9	8.57
P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 - [TCPD_HUMAN]	2.79	2.60	1	1	1	1		539	57.9	7.83

P06702	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN]	2.77	24.56	1	2	2	2	3.491E3	114	13.2	6.13
Q9H853	Putative tubulin-like protein alpha-4B OS=Homo sapiens GN=TUBA4B PE=5 SV=2 - [TBA4B_HUMAN]	2.77	5.81	1	0	1	1		241	27.5	7.83
Q9HDC9	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2 - [APMAP_HUMAN]	2.76	2.88	1	1	1	1	1.217E4	416	46.5	6.16
P17174	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3 - [AATC_HUMAN]	2.72	3.63	1	1	1	1	1.764E4	413	46.2	7.01
P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]	2.71	1.77	1	0	1	1		564	60.0	8.00
O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3 - [ATP5H_HUMAN]	2.70	10.56	1	1	1	1	1.447E4	161	18.5	5.30
Q5E956	Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3 - [TPIS_BOVIN]	2.67	5.22	1	0	1	1	3.816E3	249	26.7	6.92
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	2.65	0.96	1	0	1	1		1675	191.5	5.69
P49951	Clathrin heavy chain 1 OS=Bos taurus GN=CLTC PE=1 SV=1 - [CLH1_BOVIN]	2.65	0.96	1	0	1	1		1675	191.5	5.69
P48741	Putative heat shock 70 kDa protein 7 OS=Homo sapiens GN=HSPA7 PE=5 SV=2 - [HSP77_HUMAN]	2.63	3.00	1	0	1	1		367	40.2	7.87
P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3 - [ODPB_HUMAN]	2.60	4.46	1	0	1	1		359	39.2	6.65
P11966	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Bos taurus GN=PDHB PE=1 SV=2 - [ODPB_BOVIN]	2.60	4.46	1	0	1	1		359	39.1	6.65
Q9NZ45	CDGSH iron-sulfur domain-containing protein 1 OS=Homo sapiens GN=CISD1 PE=1 SV=1 - [CISD1_HUMAN]	2.57	13.89	1	0	1	1	1.905E3	108	12.2	9.09
Q3ZBU2	CDGSH iron-sulfur domain-containing protein 1	2.57	14.15	1	0	1	1	1.905E3	106	12.0	9.09

	OS=Bos taurus GN=CISD1 PE=1 SV=1 - [CISD1_BOVIN]										
P09466	Glycodelin OS=Homo sapiens GN=PAEP PE=1 SV=2 - [PAEP_HUMAN]	2.55	7.78	1	1	1	1		180	20.6	5.57
Q9UBX1	Cathepsin F OS=Homo sapiens GN=CTSF PE=1 SV=1 - [CATF_HUMAN]	2.54	2.07	1	1	1	1		484	53.3	8.22
Q9UNZ2	NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2 - [NSF1C_HUMAN]	2.54	2.97	1	0	1	1		370	40.5	5.10
Q3SZC4	NSFL1 cofactor p47 OS=Bos taurus GN=NSFL1C PE=2 SV=1 - [NSF1C_BOVIN]	2.54	2.97	1	0	1	1		370	40.6	5.19
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]	2.52	1.86	1	1	1	1		645	72.9	5.07
Q58FF8	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2 - [H90B2_HUMAN]	2.50	2.36	1	0	1	1		381	44.3	4.84
Q16566	Calcium/calmodulin-dependent protein kinase type IV OS=Homo sapiens GN=CAMK4 PE=1 SV=1 - [KCC4_HUMAN]	2.48	2.96	1	1	1	1		473	51.9	5.82
Q2T9U2	Outer dense fiber protein 2 OS=Bos taurus GN=ODF2 PE=2 SV=1 - [ODFP2_BOVIN]	2.48	1.83	1	0	1	1		657	75.5	7.59
P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]	2.47	1.91	1	0	1	1		472	51.5	5.16
P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN]	2.47	1.90	1	0	1	1		473	51.2	5.05
Q7Z3Y7	Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN]	2.47	1.94	1	0	1	1		464	50.5	5.47
Q7Z3Y8	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2 - [K1C27_HUMAN]	2.47	1.96	1	0	1	1		459	49.8	5.05
Q7Z3Y9	Keratin, type I cytoskeletal 26 OS=Homo sapiens GN=KRT26 PE=1 SV=2 - [K1C26_HUMAN]	2.47	1.92	1	0	1	1		468	51.9	4.92

Q7Z3Z0	Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1 - [K1C25_HUMAN]	2.47	2.00	1	0	1	1		450	49.3	5.08
Q0P5J4	Keratin, type I cytoskeletal 25 OS=Bos taurus GN=KRT25 PE=2 SV=1 - [K1C25_BOVIN]	2.47	2.00	1	0	1	1		450	49.3	5.03
Q0P5J6	Keratin, type I cytoskeletal 27 OS=Bos taurus GN=KRT27 PE=2 SV=1 - [K1C27_BOVIN]	2.47	1.96	1	0	1	1		460	49.9	5.10
Q148H6	Keratin, type I cytoskeletal 28 OS=Bos taurus GN=KRT28 PE=2 SV=1 - [K1C28_BOVIN]	2.47	1.94	1	0	1	1		464	50.7	5.30
P26640	Valine--tRNA ligase OS=Homo sapiens GN=VAR5 PE=1 SV=4 - [SYVC_HUMAN]	2.45	1.27	1	1	1	1		1264	140.4	7.59
Q3SZI4	14-3-3 protein theta OS=Bos taurus GN=YWHAQ PE=2 SV=1 - [1433T_BOVIN]	2.44	4.08	1	0	1	1		245	27.7	4.78
P31946	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 - [1433B_HUMAN]	2.44	4.07	1	0	1	1		246	28.1	4.83
P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	2.44	4.03	1	0	1	1		248	27.8	4.74
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 - [1433G_HUMAN]	2.44	4.05	1	0	1	1		247	28.3	4.89
P62261	14-3-3 protein epsilon OS=Bos taurus GN=YWHAE PE=2 SV=1 - [1433E_BOVIN]	2.44	3.92	1	0	1	1		255	29.2	4.74
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	2.44	4.07	1	0	1	1		246	28.2	4.84
P68509	14-3-3 protein eta OS=Bos taurus GN=YWHAH PE=1 SV=2 - [1433F_BOVIN]	2.44	4.07	1	0	1	1		246	28.2	4.89
P68250	14-3-3 protein beta/alpha OS=Bos taurus GN=YWHAB PE=1 SV=2 - [1433B_BOVIN]	2.44	4.07	1	0	1	1		246	28.1	4.87
P68252	14-3-3 protein gamma OS=Bos taurus GN=YWHAG PE=1 SV=2 - [1433G_BOVIN]	2.44	4.05	1	0	1	1		247	28.2	4.89
Q0VC36	14-3-3 protein sigma OS=Bos taurus GN=SFN PE=2 SV=1 - [1433S_BOVIN]	2.44	4.03	1	0	1	1		248	27.8	4.72
Q3T077	Tubulin polymerization-promoting protein family member 2 OS=Bos taurus GN=TPPP2 PE=2 SV=1 - [TPPP2_BOVIN]	2.41	7.60	1	0	1	1		171	18.6	9.03
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo	2.40	2.78	1	1	1	1	8.442E3	575	58.9	7.49

	sapiens GN=DAK PE=1 SV=2 - [DHAK_HUMAN]										
P62820	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3 - [RAB1A_HUMAN]	2.40	9.27	1	0	1	1		205	22.7	6.21
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1 - [RAB1B_HUMAN]	2.40	9.45	1	0	1	1		201	22.2	5.73
Q2HJH2	Ras-related protein Rab-1B OS=Bos taurus GN=RAB1B PE=2 SV=1 - [RAB1B_BOVIN]	2.40	9.45	1	0	1	1		201	22.2	5.73
P14406	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens GN=COX7A2 PE=1 SV=1 - [CX7A2_HUMAN]	2.38	15.66	1	1	1	1		83	9.4	9.76
P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6 - [TRFL_HUMAN]	2.37	1.97	1	1	1	2		710	78.1	8.12
Q16563	Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 PE=1 SV=1 - [SYPL1_HUMAN]	2.33	4.25	1	1	1	2		259	28.5	8.43
P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN]	2.31	10.00	1	1	1	1		110	11.3	6.54
Q8WYR4	Radial spoke head 1 homolog OS=Homo sapiens GN=RSPH1 PE=1 SV=1 - [RSPH1_HUMAN]	2.30	5.18	1	1	1	2		309	35.1	4.63
P21266	Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3 - [GSTM3_HUMAN]	2.29	5.78	1	1	1	1		225	26.5	5.54
P10515	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLAT PE=1 SV=3 - [ODP2_HUMAN]	2.27	2.63	1	1	1	1		647	69.0	7.84
Q96C74	Ropporin-1-like protein OS=Homo sapiens GN=ROPN1L PE=1 SV=2 - [ROP1L_HUMAN]	2.27	7.83	1	1	1	1	1.142E4	230	26.1	7.72
A7YWG4	Gamma-glutamyl hydrolase OS=Bos taurus GN=GGH PE=2 SV=1 - [GGH_BOVIN]	2.26	3.14	1	0	1	1	7.389E3	318	35.7	9.06
P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3 - [AATM_HUMAN]	2.25	2.79	1	1	1	1		430	47.5	9.01
Q8TDM5	Sperm acrosome membrane-associated protein 4 OS=Homo sapiens GN=SPACA4 PE=1 SV=1 - [SACA4_HUMAN]	2.23	10.48	1	1	1	1		124	13.0	5.80

A5D989	Elongation factor 1-delta OS=Bos taurus GN=EEF1D PE=2 SV=2 - [EF1D_BOVIN]	2.19	4.29	1	0	1	1		280	31.1	5.06
Q96JQ2	Calmin OS=Homo sapiens GN=CLMN PE=1 SV=1 - [CLMN_HUMAN]	2.17	1.70	1	1	1	1	1.077E4	1002	111.6	4.94
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1 - [LETM1_HUMAN]	2.14	1.62	1	0	1	1		739	83.3	6.70
Q0VCA3	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Bos taurus GN=LETM1 PE=2 SV=1 - [LETM1_BOVIN]	2.14	1.64	1	0	1	1		732	81.8	6.73
P25686	DnaJ homolog subfamily B member 2 OS=Homo sapiens GN=DNAJB2 PE=1 SV=3 - [DNJB2_HUMAN]	2.14	3.09	1	0	1	1		324	35.6	5.95
Q8NHS0	DnaJ homolog subfamily B member 8 OS=Homo sapiens GN=DNAJB8 PE=1 SV=1 - [DNJB8_HUMAN]	2.14	9.91	1	1	2	2		232	25.7	6.42
P10096	Glyceraldehyde-3-phosphate dehydrogenase OS=Bos taurus GN=GAPDH PE=1 SV=4 - [G3P_BOVIN]	2.11	4.20	1	0	1	1	1.087E4	333	35.8	8.35
Q96IV0	Peptide-N(4)-(N-acetyl-beta- glucosaminy)asparagine amidase OS=Homo sapiens GN=NGLY1 PE=1 SV=1 - [NGLY1_HUMAN]	2.09	1.68	1	1	1	1		654	74.3	6.89
Q9P2E7	Protocadherin-10 OS=Homo sapiens GN=PCDH10 PE=2 SV=2 - [PCD10_HUMAN]	2.09	0.96	1	1	1	1		1040	112.9	4.87
P14174	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4 - [MIF_HUMAN]	2.07	7.83	1	1	1	1		115	12.5	7.88
Q53QW1	Uncharacterized protein C2orf57 OS=Homo sapiens GN=C2orf57 PE=2 SV=1 - [CB057_HUMAN]	2.07	3.80	1	1	1	1		395	41.6	5.12
P13646	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4 - [K1C13_HUMAN]	2.06	2.40	1	0	1	1		458	49.6	4.96
Q2M2I5	Keratin, type I cytoskeletal 24 OS=Homo sapiens GN=KRT24 PE=1 SV=1 -	2.06	2.10	1	0	1	1		525	55.1	4.96

	[K1C24_HUMAN]										
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	2.04	1.73	1	0	1	1		1101	120.8	7.33
Q32PF2	ATP-citrate synthase OS=Bos taurus GN=ACLY PE=2 SV=1 - [ACLY_BOVIN]	2.04	1.74	1	0	1	1		1091	119.7	7.24
Q96T88	E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1 - [UHRF1_HUMAN]	2.03	1.26	1	0	1	1		793	89.8	7.56
A7E320	E3 ubiquitin-protein ligase UHRF1 OS=Bos taurus GN=UHRF1 PE=2 SV=1 - [UHRF1_BOVIN]	2.03	1.27	1	0	1	1		786	88.3	8.00
Q86YB8	ERO1-like protein beta OS=Homo sapiens GN=ERO1LB PE=1 SV=2 - [ERO1B_HUMAN]	2.02	2.36	1	1	1	2		467	53.5	7.99
P61285	Dynein light chain 1, cytoplasmic OS=Bos taurus GN=DYNLL1 PE=1 SV=1 - [DYL1_BOVIN]	2.01	12.36	1	0	1	1	1.782E3	89	10.4	7.40
Q3MHR3	Dynein light chain 2, cytoplasmic OS=Bos taurus GN=DYNLL2 PE=3 SV=1 - [DYL2_BOVIN]	2.01	12.36	1	0	1	1	1.782E3	89	10.3	7.37
Q6STE5	SWI/SNF-related matrix-associated actin- dependent regulator of chromatin subfamily D member 3 OS=Homo sapiens GN=SMARCD3 PE=1 SV=1 - [SMRD3_HUMAN]	2.01	4.76	1	1	1	1		483	55.0	9.35
P30042	ES1 protein homolog, mitochondrial OS=Homo sapiens GN=C21orf33 PE=1 SV=3 - [ES1_HUMAN]	2.01	9.33	1	1	1	1		268	28.2	8.27
P46379	Large proline-rich protein BAG6 OS=Homo sapiens GN=BAG6 PE=1 SV=2 - [BAG6_HUMAN]	2.00	1.15	1	1	1	1		1132	119.3	5.60
Q3ZCI9	T-complex protein 1 subunit theta OS=Bos taurus GN=CCT8 PE=1 SV=3 - [TCPQ_BOVIN]	1.99	2.01	1	0	1	2		548	59.6	5.59
Q66GS9	Centrosomal protein of 135 kDa OS=Homo sapiens GN=CEP135 PE=1 SV=2 - [CP135_HUMAN]	1.96	0.88	1	0	1	1		1140	133.4	6.21
O75951	Lysozyme-like protein 6 OS=Homo sapiens GN=LYZL6 PE=2 SV=1 - [LYZL6_HUMAN]	1.93	6.08	1	1	1	1		148	16.9	6.14
P25325	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3 - [THTM_HUMAN]	1.92	4.38	1	1	1	1		297	33.2	6.60
P04179	Superoxide dismutase [Mn], mitochondrial	1.91	6.31	1	0	1	1		222	24.7	8.25

	OS=Homo sapiens GN=SOD2 PE=1 SV=2 - [SODM_HUMAN]										
P41976	Superoxide dismutase [Mn], mitochondrial OS=Bos taurus GN=SOD2 PE=2 SV=1 - [SODM_BOVIN]	1.91	6.31	1	0	1	1		222	24.6	8.54
P55854	Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=1 SV=2 - [SUMO3_HUMAN]	1.89	11.65	1	0	1	1	1.101E4	103	11.6	5.49
P61955	Small ubiquitin-related modifier 2 OS=Bos taurus GN=SUMO2 PE=3 SV=1 - [SUMO2_BOVIN]	1.89	12.63	1	0	1	1	1.101E4	95	10.9	5.50
Q6EEV6	Small ubiquitin-related modifier 4 OS=Homo sapiens GN=SUMO4 PE=1 SV=2 - [SUMO4_HUMAN]	1.89	12.63	1	0	1	1	1.101E4	95	10.7	7.18
Q17QV3	Small ubiquitin-related modifier 3 OS=Bos taurus GN=SUMO3 PE=3 SV=1 - [SUMO3_BOVIN]	1.89	11.54	1	0	1	1	1.101E4	104	11.7	5.95
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	1.86	1.82	1	0	1	1		658	73.7	8.18
Q2KJB7	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Bos taurus GN=CPT2 PE=2 SV=1 - [CPT2_BOVIN]	1.86	1.82	1	0	1	1		658	74.4	8.13
Q9BY14	Testis-expressed sequence 101 protein OS=Homo sapiens GN=TEX101 PE=2 SV=2 - [TX101_HUMAN]	1.85	5.62	1	1	1	1		249	26.6	4.94
Q08D91	Keratin, type II cytoskeletal 75 OS=Bos taurus GN=KRT75 PE=2 SV=1 - [K2C75_BOVIN]	1.85	2.21	1	0	1	1		543	59.0	7.65
Q5XQN5	Keratin, type II cytoskeletal 5 OS=Bos taurus GN=KRT5 PE=1 SV=1 - [K2C5_BOVIN]	1.85	2.00	1	0	1	1		601	62.9	7.81
P23004	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Bos taurus GN=UQCRC2 PE=1 SV=2 - [QCR2_BOVIN]	1.82	3.09	1	0	1	1	1.528E4	453	48.1	8.73
Q9Y371	Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 PE=1 SV=1 - [SHLB1_HUMAN]	1.81	3.56	1	0	1	1		365	40.8	6.04
Q32LM0	Endophilin-B1 OS=Bos taurus GN=SH3GLB1	1.81	3.56	1	0	1	1		365	40.8	6.20

	PE=2 SV=1 - [SHLB1_BOVIN]										
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX411 PE=1 SV=1 - [COX41_HUMAN]	1.81	7.10	1	1	1	1		169	19.6	9.51
O14645	Axonemal dynein light intermediate polypeptide 1 OS=Homo sapiens GN=DNAL11 PE=1 SV=2 - [IDLC_HUMAN]	1.80	11.24	1	2	2	2	8.760E3	258	29.6	8.50
Q8IYS8	Biorientation of chromosomes in cell division protein 1-like 2 OS=Homo sapiens GN=BOD1L2 PE=2 SV=2 - [BD1L2_HUMAN]	1.80	5.23	1	1	1	1	8.172E3	172	18.1	5.33
P37198	Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=3 - [NUP62_HUMAN]	1.78	4.60	1	2	2	2	4.443E3	522	53.2	5.31
O43169	Cytochrome b5 type B OS=Homo sapiens GN=CYB5B PE=1 SV=2 - [CYB5B_HUMAN]	1.78	8.22	1	1	1	1		146	16.3	4.97
P63027	Vesicle-associated membrane protein 2 OS=Homo sapiens GN=VAMP2 PE=1 SV=3 - [VAMP2_HUMAN]	1.78	14.66	1	0	1	1		116	12.7	8.13
P63026	Vesicle-associated membrane protein 2 OS=Bos taurus GN=VAMP2 PE=1 SV=2 - [VAMP2_BOVIN]	1.78	14.66	1	0	1	1		116	12.6	8.13
Q3ZBL4	Leucine zipper transcription factor-like protein 1 OS=Bos taurus GN=LZTFL1 PE=2 SV=1 - [LZTL1_BOVIN]	1.77	3.68	1	0	1	1	5.172E3	299	34.6	5.30
Q58FF3	Putative endoplasmic-like protein OS=Homo sapiens GN=HSP90B2P PE=5 SV=1 - [ENPLL_HUMAN]	1.77	2.51	1	0	1	1	6.525E3	399	45.8	5.26
Q58FG1	Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens GN=HSP90AA4P PE=5 SV=1 - [HS904_HUMAN]	1.76	3.11	1	0	1	1		418	47.7	5.19
Q86Y82	Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1 - [STX12_HUMAN]	1.75	5.43	1	1	1	1		276	31.6	5.59
Q14203	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3 - [DCTN1_HUMAN]	1.75	0.94	1	1	1	1		1278	141.6	5.81
Q9BVL2	Nucleoporin p58/p45 OS=Homo sapiens GN=NUPL1 PE=1 SV=1 - [NUPL1_HUMAN]	1.75	2.17	1	1	1	1		599	60.9	9.33

Q29RK4	UV excision repair protein RAD23 homolog B OS=Bos taurus GN=RAD23B PE=2 SV=1 - [RD23B_BOVIN]	1.71	2.21	1	0	1	1		408	43.1	4.84
P10323	Acrosin OS=Homo sapiens GN=ACR PE=2 SV=4 - [ACRO_HUMAN]	1.71	2.14	1	1	1	1		421	45.8	9.07
P27482	Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2 - [CALL3_HUMAN]	1.69	5.37	1	0	1	1		149	16.9	4.42
P25685	DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4 - [DNJB1_HUMAN]	1.69	6.76	1	0	2	2		340	38.0	8.63
Q3MI00	DnaJ homolog subfamily B member 1 OS=Bos taurus GN=DNAJB1 PE=2 SV=3 - [DNJB1_BOVIN]	1.69	6.76	1	0	2	2		340	38.2	8.63
Q8NHU3	Phosphatidylcholine:ceramide cholinephosphotransferase 2 OS=Homo sapiens GN=SGMS2 PE=1 SV=1 - [SMS2_HUMAN]	1.67	2.74	1	1	1	1		365	42.3	8.81
Q8N0W7	Fragile X mental retardation 1 neighbor protein OS=Homo sapiens GN=FMR1NB PE=1 SV=1 - [FMR1N_HUMAN]	1.67	3.53	1	1	1	1		255	29.2	8.94
Q5VZ72	Izumo sperm-egg fusion protein 3 OS=Homo sapiens GN=IZUMO3 PE=2 SV=4 - [IZUM3_HUMAN]	1.67	3.77	1	1	1	1	4.288E3	239	27.7	8.29
O43805	Sjoegren syndrome nuclear autoantigen 1 OS=Homo sapiens GN=SSNA1 PE=1 SV=2 - [SSNA1_HUMAN]	1.66	10.92	1	0	1	1		119	13.6	5.38
Q5E9C3	Sjoegren syndrome nuclear autoantigen 1 homolog OS=Bos taurus GN=SSNA1 PE=3 SV=1 - [SSNA1_BOVIN]	1.66	10.92	1	0	1	1		119	13.6	5.68
Q9BG11	Peroxiredoxin-5, mitochondrial OS=Bos taurus GN=PRDX5 PE=2 SV=2 - [PRDX5_BOVIN]	1.64	3.65	1	0	1	1		219	23.2	8.07
P22748	Carbonic anhydrase 4 OS=Homo sapiens GN=CA4 PE=1 SV=2 - [CAH4_HUMAN]	1.63	4.81	1	1	1	1		312	35.0	7.83
Q5GAN3	Probable inactive ribonuclease-like protein 13 OS=Homo sapiens GN=RNASE13 PE=2 SV=1 - [RNS13_HUMAN]	1.62	7.05	1	1	1	1		156	17.8	8.59
Q8WWF6	DnaJ homolog subfamily B member 3 OS=Homo sapiens GN=DNAJB3 PE=1 SV=1 -	1.62	8.97	1	0	1	1		145	16.5	4.94

	[DNJB3_HUMAN]											
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	1.62	4.91	1	0	1	1	1.184E4	224	25.0	6.38	
O77834	Peroxiredoxin-6 OS=Bos taurus GN=PRDX6 PE=1 SV=3 - [PRDX6_BOVIN]	1.62	4.91	1	0	1	1	1.184E4	224	25.1	6.38	
E9PGG2	Anomalous homeobox protein OS=Homo sapiens GN=ANHX PE=2 SV=1 - [ANHX_HUMAN]	0.00	3.43	1	1	1	1		379	41.7	5.38	
O15013	Rho guanine nucleotide exchange factor 10 OS=Homo sapiens GN=ARHGEF10 PE=1 SV=4 - [ARHGA_HUMAN]	0.00	1.02	1	1	1	1		1369	151.5	5.68	
O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
P06899	Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3 - [H2B1J_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
P0C0S4	Histone H2A.Z OS=Bos taurus GN=H2AFZ PE=1 SV=2 - [H2AZ_BOVIN]	0.00	7.03	1	0	1	1		128	13.5	10.58	
P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	0.00	4.33	1	1	1	2		531	57.9	7.84	
P18084	Integrin beta-5 OS=Homo sapiens GN=ITGB5 PE=1 SV=1 - [ITB5_HUMAN]	0.00	4.13	1	1	1	1		799	88.0	6.06	
P19367	Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 - [HKK1_HUMAN]	0.00	1.31	1	1	1	1		917	102.4	6.80	
P23527	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3 - [H2B1O_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	0.00	3.21	1	1	1	1		592	67.5	4.60	
P33778	Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2 - [H2B1B_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
P48047	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 - [ATPO_HUMAN]	0.00	6.57	1	1	1	1		213	23.3	9.96	
P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	0.00	1.41	1	1	1	1	8.106E3	919	103.2	5.72	
P57053	Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2 - [H2BFS_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.37	
P58876	Histone H2B type 1-D OS=Homo sapiens	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	

	GN=HIST1H2BD PE=1 SV=2 - [H2B1D_HUMAN]											
P62807	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4 - [H2B1C_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
Q13428	Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 - [TCOF_HUMAN]	0.00	2.69	1	1	1	1		1488	152.0	9.04	
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1 - [CDC37_HUMAN]	0.00	4.50	1	1	1	1		378	44.4	5.25	
Q16778	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3 - [H2B2E_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
Q5QNW6	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3 - [H2B2F_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
Q32LA7	Histone H2A.V OS=Bos taurus GN=H2AFV PE=2 SV=3 - [H2AV_BOVIN]	0.00	7.03	1	0	1	1		128	13.5	10.58	
Q86VQ3	Thioredoxin domain-containing protein 2 OS=Homo sapiens GN=TXND2 PE=1 SV=4 - [TXND2_HUMAN]	0.00	2.71	1	1	1	1		553	60.4	4.87	
Q8N257	Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3 - [H2B3B_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
Q93079	Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3 - [H2B1H_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
Q96A08	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3 - [H2B1A_HUMAN]	0.00	8.66	1	0	1	1	5.050E3	127	14.2	10.32	
Q96NT0	Coiled-coil domain-containing protein 115 OS=Homo sapiens GN=CCDC115 PE=1 SV=1 - [CC115_HUMAN]	0.00	3.89	1	1	1	1		180	19.7	6.95	
Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]	0.00	2.21	1	0	1	1		543	59.3	7.65	
Q99877	Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3 - [H2B1N_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
Q99879	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3 - [H2B1M_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	14.0	10.32	
Q99880	Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3 - [H2B1L_HUMAN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32	
Q9P225	Dynein heavy chain 2, axonemal OS=Homo sapiens GN=DNAH2 PE=2 SV=3 -	0.00	0.20	1	1	1	1		4427	507.4	6.37	

	[DYH2_HUMAN]										
A8MVZ5	Butyrophilin-like protein 10 OS=Homo sapiens GN=BTNL10 PE=5 SV=2 - [BTNLA_HUMAN]	0.00	4.12	1	1	1	1		291	32.6	8.34
Q2M2T1	Histone H2B type 1-K OS=Bos taurus GN=HIST1H2BK PE=1 SV=3 - [H2B1K_BOVIN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.29
Q2NKZ1	T-complex protein 1 subunit eta OS=Bos taurus GN=CCT7 PE=1 SV=1 - [TCPH_BOVIN]	0.00	2.21	1	0	1	1		543	59.4	7.20
Q32L48	Histone H2B type 1-N OS=Bos taurus GN=HIST1H2BN PE=1 SV=3 - [H2B1N_BOVIN]	0.00	8.73	1	0	1	1	5.050E3	126	13.9	10.32
Q32L97	Vesicle-associated membrane protein 4 OS=Bos taurus GN=VAMP4 PE=2 SV=1 - [VAMP4_BOVIN]	0.00	16.31	1	1	1	1		141	16.4	7.34

Suppl Table 4

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	Area	# AAs	MW [kDa]	calc. pI	8	
P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 - [HSP72_HUMAN]	139.86	48.20	1	2	25	56	3.146E5	639	70.0	5.74	TRUE	402
P34933	Heat shock-related 70 kDa protein 2 OS=Bos taurus GN=HSPA2 PE=2 SV=2 - [HSP72_BOVIN]	123.46	41.51	1	0	22	49	3.146E5	636	69.7	5.59	TRUE	402
Q5JQC9	A-kinase anchor protein 4 OS=Homo sapiens GN=AKAP4 PE=1 SV=1 - [AKAP4_HUMAN]	116.40	31.50	1	22	22	50	5.026E5	854	94.4	6.96	TRUE	402
A6NMS7	Leucine-rich repeat-containing protein 37A OS=Homo sapiens GN=LRRC37A PE=2 SV=3 - [L37A1_HUMAN]	79.66	13.35	1	1	16	32	1.188E6	1700	188.1	5.49	TRUE	402
A6NM11	Leucine-rich repeat-containing protein 37A2 OS=Homo sapiens GN=LRRC37A2 PE=2 SV=2 - [L37A2_HUMAN]	78.06	12.76	1	0	15	31	1.188E6	1700	188.3	5.50	TRUE	402
Q99798	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2 - [ACON_HUMAN]	68.36	31.54	1	7	16	25	1.335E5	780	85.4	7.61	TRUE	402
O60309	Leucine-rich repeat-containing protein 37A3 OS=Homo sapiens GN=LRRC37A3 PE=2 SV=2 - [L37A3_HUMAN]	64.29	11.32	1	0	13	26	1.188E6	1634	180.5	5.31	TRUE	402
P34931	Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2 - [HS71L_HUMAN]	63.44	30.42	1	2	14	25	3.175E5	641	70.3	6.02	TRUE	402
Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3 - [TBA3C_HUMAN]	63.41	34.00	1	0	9	22	2.421E5	450	49.9	5.10	TRUE	402
Q6PEY2	Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2 - [TBA3E_HUMAN]	63.41	34.00	1	0	9	22	2.421E5	450	49.8	5.14	TRUE	402
Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 - [TBA1A_HUMAN]	63.41	33.92	1	0	9	22	2.421E5	451	50.1	5.06	TRUE	402
Q2HJ86	Tubulin alpha-1D chain OS=Bos taurus GN=TUBA1D PE=1 SV=1 - [TBA1D_BOVIN]	63.41	33.85	1	0	9	22	2.421E5	452	50.3	5.03	TRUE	402

Q32KN8	Tubulin alpha-3 chain OS=Bos taurus GN=TUBA3 PE=2 SV=1 - [TBA3_BOVIN]	63.41	34.00	1	0	9	22	2.421E 5	450	49.9	5.10	TRUE	402
Q3MHM 5	Tubulin beta-4B chain OS=Bos taurus GN=TUBB4B PE=2 SV=1 - [TBB4B_BOVIN]	63.24	40.22	1	0	12	23	3.237E 5	445	49.8	4.89	TRUE	402
Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]	61.40	37.53	1	0	11	22	3.237E 5	445	49.9	4.89	TRUE	402
Q6B856	Tubulin beta-2B chain OS=Bos taurus GN=TUBB2B PE=1 SV=2 - [TBB2B_BOVIN]	61.40	37.53	1	0	11	22	3.237E 5	445	49.9	4.89	TRUE	402
P04279	Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2 - [SEMG1_HUMAN]	60.03	35.71	1	10	13	24	5.795E 4	462	52.1	9.29	FALSE	161
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5 - [HS90A_HUMAN]	58.61	25.55	1	0	17	25	5.664E 5	732	84.6	5.02	TRUE	402
Q76LV2	Heat shock protein HSP 90-alpha OS=Bos taurus GN=HSP90AA1 PE=1 SV=3 - [HS90A_BOVIN]	58.61	25.51	1	0	17	25	5.664E 5	733	84.7	5.01	TRUE	402
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	57.75	29.36	1	1	14	23	3.393E 5	654	72.3	5.16	TRUE	402
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	56.92	40.32	1	4	11	20	3.774E 5	434	47.1	7.39	TRUE	402
Q0VCX2	78 kDa glucose-regulated protein OS=Bos taurus GN=HSPA5 PE=2 SV=1 - [GRP78_BOVIN]	55.64	27.02	1	0	13	22	3.393E 5	655	72.4	5.16	TRUE	402
P81947	Tubulin alpha-1B chain OS=Bos taurus PE=1 SV=2 - [TBA1B_BOVIN]	55.47	31.04	1	0	8	18	1.248E 5	451	50.1	5.06	TRUE	402
Q2KJD0	Tubulin beta-5 chain OS=Bos taurus GN=TUBB5 PE=2 SV=1 - [TBB5_BOVIN]	55.40	36.49	1	0	11	21	1.935E 5	444	49.6	4.89	TRUE	402
Q3ZCJ7	Tubulin alpha-1C chain OS=Bos taurus GN=TUBA1C PE=1 SV=1 - [TBA1C_BOVIN]	55.17	27.17	1	0	7	18	2.329E 5	449	49.8	5.10	TRUE	402
POCB32	Heat shock 70 kDa protein 1-like OS=Bos taurus GN=HSPA1L PE=3 SV=1 - [HS71L_BOVIN]	54.51	24.49	1	0	12	22	3.175E 5	641	70.3	6.20	TRUE	402
O75969	A-kinase anchor protein 3 OS=Homo sapiens GN=AKAP3 PE=1 SV=2 - [AKAP3_HUMAN]	50.62	27.55	1	17	18	24	4.435E 5	853	94.7	6.18	TRUE	402
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 -	49.67	29.49	1	1	11	20	2.886E 5	529	56.5	5.40	TRUE	402

	[ATPB_HUMAN]												
P14625	Endoplasmic OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]	48.97	20.42	1	4	14	19	8.527E 4	803	92.4	4.84	TRUE	402
P81948	Tubulin alpha-4A chain OS=Bos taurus GN=TUBA4A PE=1 SV=2 - [TBA4A_BOVIN]	48.55	24.55	1	0	6	15	1.102E 5	448	49.9	5.06	TRUE	402
P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6 - [TRFL_HUMAN]	48.00	21.27	1	11	11	17	2.377E 5	710	78.1	8.12	FALSE	161
P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	47.94	23.09	1	1	10	18	3.175E 5	641	70.0	5.66	TRUE	402
P00829	ATP synthase subunit beta, mitochondrial OS=Bos taurus GN=ATP5B PE=1 SV=2 - [ATPB_BOVIN]	47.79	27.84	1	0	10	19	2.886E 5	528	56.2	5.27	TRUE	402
P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	47.41	38.88	1	6	11	19	8.252E 4	427	45.2	8.85	FALSE	161
Q8NEB7	Acrosin-binding protein OS=Homo sapiens GN=ACRBP PE=2 SV=1 - [ACRBP_HUMAN]	45.04	24.49	1	10	10	21	2.349E 6	543	61.3	5.16	TRUE	402
Q02383	Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1 - [SEMG2_HUMAN]	44.50	31.62	1	9	12	20	1.056E 5	582	65.4	9.07	FALSE	161
Q5BJF6	Outer dense fiber protein 2 OS=Homo sapiens GN=ODF2 PE=1 SV=1 - [ODFP2_HUMAN]	44.03	16.41	1	1	12	18	9.159E 4	829	95.3	7.62	TRUE	402
Q2T9U2	Outer dense fiber protein 2 OS=Bos taurus GN=ODF2 PE=2 SV=1 - [ODFP2_BOVIN]	44.03	19.18	1	0	11	17	9.159E 4	657	75.5	7.59	TRUE	402
O75952	Calcium-binding tyrosine phosphorylation-regulated protein OS=Homo sapiens GN=CABYR PE=1 SV=2 - [CABYR_HUMAN]	43.49	22.52	1	8	8	15	4.797E 5	493	52.7	4.55	TRUE	402
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	43.45	20.03	1	9	12	17	8.156E 4	644	66.0	8.12	FALSE	161
Q3ZBU7	Tubulin beta-4A chain OS=Bos taurus GN=TUBB4A PE=2 SV=1 - [TBB4A_BOVIN]	41.47	33.56	1	0	10	17	3.019E 5	444	49.6	4.88	TRUE	402
P62157	Calmodulin OS=Bos taurus GN=CALM PE=1 SV=2 - [CALM_BOVIN]	41.28	44.30	1	6	7	16	7.621E 5	149	16.8	4.22	TRUE	402
Q96QE4	Leucine-rich repeat-containing protein 37B OS=Homo sapiens GN=LRR37B PE=2 SV=3 - [LR37B_HUMAN]	41.16	17.21	1	11	11	16	3.792E 5	947	105. 5	4.91	TRUE	402

P20004	Aconitate hydratase, mitochondrial OS=Bos taurus GN=ACO2 PE=1 SV=4 - [ACON_BOVIN]	40.10	17.82	1	0	9	13	9.910E4	780	85.3	7.83	TRUE	402
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1 - [HYOU1_HUMAN]	39.55	14.61	1	9	9	16	6.529E4	999	111.3	5.22	TRUE	402
P07205	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3 - [PGK2_HUMAN]	38.23	29.02	1	6	8	13	3.113E5	417	44.8	8.54	FALSE	161
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	37.25	24.94	1	0	7	14	2.329E5	449	49.9	5.10	TRUE	402
Q27965	Heat shock 70 kDa protein 1B OS=Bos taurus GN=HSPA1B PE=2 SV=1 - [HS71B_BOVIN]	37.19	18.25	1	0	9	16	3.175E5	641	70.2	5.92	TRUE	402
Q27975	Heat shock 70 kDa protein 1A OS=Bos taurus GN=HSPA1A PE=1 SV=2 - [HS71A_BOVIN]	37.19	18.25	1	0	9	16	3.175E5	641	70.2	5.92	TRUE	402
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 - [TCPB_HUMAN]	35.50	18.32	1	2	6	12	7.592E4	535	57.5	6.46	TRUE	402
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	33.97	22.54	1	4	6	13	9.550E4	417	48.1	4.44	TRUE	402
P30086	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 - [PEBP1_HUMAN]	33.50	35.83	1	3	4	11	1.132E5	187	21.0	7.53	TRUE	402
Q7L266	Isoaspartyl peptidase/L-asparaginase OS=Homo sapiens GN=ASRGL1 PE=1 SV=2 - [ASGL1_HUMAN]	33.40	39.61	1	6	7	11	2.337E5	308	32.0	6.24	TRUE	402
Q2T9S0	Tubulin beta-3 chain OS=Bos taurus GN=TUBB3 PE=2 SV=1 - [TBB3_BOVIN]	32.98	23.78	1	0	8	10	2.105E5	450	50.4	4.93	TRUE	402
Q9HAT0	Ropporin-1A OS=Homo sapiens GN=ROPN1 PE=1 SV=2 - [ROP1A_HUMAN]	32.75	33.02	1	1	5	12	1.737E5	212	23.9	5.66	TRUE	402
Q6UW49	Sperm equatorial segment protein 1 OS=Homo sapiens GN=SPESP1 PE=1 SV=2 - [SPESP_HUMAN]	32.38	27.14	1	7	7	12	5.448E5	350	38.9	5.73	TRUE	402
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	32.30	39.64	1	4	9	15	6.092E5	338	35.5	8.68	FALSE	161
P15289	Arylsulfatase A OS=Homo sapiens GN=ARSA PE=1 SV=3 - [ARSA_HUMAN]	31.43	14.00	1	4	4	11	8.825E4	507	53.6	6.07	TRUE	402
Q95M18	Endoplasmic reticulum chaperone protein OS=Bos taurus GN=HSP90B1	31.42	12.69	1	0	10	13	2.979E5	804	92.4	4.84	TRUE	402

	PE=2 SV=1 - [ENPL_BOVIN]							4					
Q9XSJ4	Alpha-enolase OS=Bos taurus GN=ENO1 PE=1 SV=4 - [ENOA_BOVIN]	30.93	23.27	1	0	7	11	3.415E5	434	47.3	6.80	TRUE	402
P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN]	30.91	16.40	1	3	7	12	1.205E5	573	61.0	5.87	TRUE	402
Q8N4E7	Ferritin, mitochondrial OS=Homo sapiens GN=FTMT PE=1 SV=1 - [FTMT_HUMAN]	30.85	37.60	1	6	7	13	3.849E5	242	27.5	7.27	TRUE	402
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 - [ALDOA_HUMAN]	30.37	41.21	1	10	10	12	1.397E5	364	39.4	8.09	FALSE	161
P10909	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1 - [CLUS_HUMAN]	29.92	23.39	1	9	9	12	5.095E5	449	52.5	6.27	TRUE	402
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	29.83	28.27	1	4	6	10	1.970E5	336	35.3	8.13	FALSE	161
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	29.47	14.78	1	0	9	13	1.984E5	724	83.2	5.03	TRUE	402
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	29.36	18.15	1	4	8	12	7.720E4	584	58.8	5.21	TRUE	402
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	29.30	16.82	1	0	7	10	2.732E5	553	59.7	9.13	FALSE	161
P19483	ATP synthase subunit alpha, mitochondrial OS=Bos taurus GN=ATP5A1 PE=1 SV=1 - [ATPA_BOVIN]	29.30	16.82	1	0	7	10	2.732E5	553	59.7	9.19	FALSE	161
P63103	14-3-3 protein zeta/delta OS=Bos taurus GN=YWHAZ PE=1 SV=1 - [1433Z_BOVIN]	28.65	37.14	1	5	7	11	2.259E5	245	27.7	4.79	TRUE	402
Q9BZX4	Ropporin-1B OS=Homo sapiens GN=ROPN1B PE=1 SV=1 - [ROP1B_HUMAN]	28.26	27.83	1	1	5	10	1.775E5	212	23.9	5.15	TRUE	402
Q2HJ81	Tubulin beta-6 chain OS=Bos taurus GN=TUBB6 PE=2 SV=1 - [TBB6_BOVIN]	28.04	15.25	1	0	5	8	2.590E5	446	49.9	4.86	TRUE	402
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TP11 PE=1 SV=3 - [TPIS_HUMAN]	28.00	53.85	1	3	10	14	1.938E5	286	30.8	5.92	TRUE	402

P60712	Actin, cytoplasmic 1 OS=Bos taurus GN=ACTB PE=1 SV=1 - [ACTB_BOVIN]	27.78	26.13	1	0	6	10	6.884E 4	375	41.7	5.48	TRUE	402
P63258	Actin, cytoplasmic 2 OS=Bos taurus GN=ACTG1 PE=1 SV=1 - [ACTG_BOVIN]	27.78	26.13	1	0	6	10	6.884E 4	375	41.8	5.48	TRUE	402
Q76LV1	Heat shock protein HSP 90-beta OS=Bos taurus GN=HSP90AB1 PE=2 SV=3 - [HS90B_BOVIN]	27.74	13.12	1	0	8	12	1.984E 5	724	83.2	5.03	TRUE	402
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	26.29	12.41	1	0	6	10	1.167E 5	806	89.3	5.26	TRUE	402
Q3ZBT1	Transitional endoplasmic reticulum ATPase OS=Bos taurus GN=VCP PE=2 SV=1 - [TERA_BOVIN]	26.29	12.41	1	0	6	10	1.167E 5	806	89.3	5.26	TRUE	402
P15259	Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3 - [PGAM2_HUMAN]	25.94	47.04	1	3	8	11	3.831E 5	253	28.7	8.88	FALSE	161
Q13561	Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4 - [DCTN2_HUMAN]	25.76	22.44	1	3	6	8	1.114E 5	401	44.2	5.21	TRUE	402
O14556	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2 - [G3PT_HUMAN]	25.74	26.23	1	4	7	12	1.472E 5	408	44.5	8.19	FALSE	161
P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3 - [ODPB_HUMAN]	24.40	24.51	1	4	6	8	6.625E 4	359	39.2	6.65	TRUE	402
P61019	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1 - [RAB2A_HUMAN]	24.23	39.62	1	4	6	11	2.012E 5	212	23.5	6.54	TRUE	402
P30044	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4 - [PRDX5_HUMAN]	23.79	39.25	1	5	6	8	4.749E 4	214	22.1	8.70	FALSE	161
P52193	Calreticulin OS=Bos taurus GN=CALR PE=1 SV=2 - [CALR_BOVIN]	23.63	11.51	1	0	2	7	1.201E 5	417	48.0	4.46	TRUE	402
P19367	Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3 - [HKK1_HUMAN]	23.45	9.27	1	3	7	10	8.109E 4	917	102. 4	6.80	TRUE	402
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4 - [PDIA3_HUMAN]	23.11	24.36	1	4	9	10	3.423E 5	505	56.7	6.35	TRUE	402
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 -	22.36	11.76	1	0	7	10	5.632E 4	646	70.9	5.52	TRUE	402

	[HSP7C_HUMAN]												
P19120	Heat shock cognate 71 kDa protein OS=Bos taurus GN=HSPA8 PE=1 SV=2 - [HSP7C_BOVIN]	22.36	11.69	1	0	7	10	5.632E4	650	71.2	5.52	TRUE	402
Q29RZ0	Acetyl-CoA acetyltransferase, mitochondrial OS=Bos taurus GN=ACAT1 PE=2 SV=1 - [THIL_BOVIN]	21.80	18.48	1	0	5	9	5.229E4	422	44.9	8.85	FALSE	161
Q9NY65	Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1 - [TBA8_HUMAN]	21.34	18.49	1	0	5	7	2.421E5	449	50.1	5.06	TRUE	402
Q2HJB8	Tubulin alpha-8 chain OS=Bos taurus GN=TUBA8 PE=2 SV=1 - [TBA8_BOVIN]	21.34	18.49	1	0	5	7	2.421E5	449	50.0	5.20	TRUE	402
Q3ZBH0	T-complex protein 1 subunit beta OS=Bos taurus GN=CCT2 PE=1 SV=3 - [TCPB_BOVIN]	20.78	12.52	1	0	4	7	7.592E4	535	57.4	6.64	TRUE	402
Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]	20.16	22.64	1	5	6	8	1.150E5	318	35.9	7.11	TRUE	402
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]	20.10	15.41	1	4	6	10	8.420E4	519	56.1	7.93	TRUE	402
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]	19.67	32.47	1	3	4	6	5.830E5	154	15.9	6.13	TRUE	402
Q04837	Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1 - [SSBP_HUMAN]	19.65	38.51	1	4	4	7	2.278E5	148	17.2	9.60	FALSE	161
Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens GN=HINT2 PE=1 SV=1 - [HINT2_HUMAN]	19.36	47.24	1	2	5	8	1.968E5	163	17.2	9.16	FALSE	161
Q5E956	Triosephosphate isomerase OS=Bos taurus GN=TPI1 PE=2 SV=3 - [TPIS_BOVIN]	19.26	46.59	1	0	7	11	1.485E5	249	26.7	6.92	TRUE	402
Q9P0L0	Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3 - [VAPA_HUMAN]	19.16	15.66	1	0	4	7	4.821E5	249	27.9	8.62	FALSE	161
Q0VCY1	Vesicle-associated membrane protein-associated protein A OS=Bos taurus GN=VAPA PE=2 SV=1 - [VAPA_BOVIN]	19.16	15.66	1	0	4	7	4.821E5	249	27.8	8.60	FALSE	161
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	19.14	12.52	1	1	6	8	2.240E4	543	62.6	6.80	TRUE	402

P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	18.48	16.47	1	6	6	8	2.062E5	510	54.6	8.76	FALSE	161
Q32LG3	Malate dehydrogenase, mitochondrial OS=Bos taurus GN=MDH2 PE=1 SV=1 - [MDHM_BOVIN]	18.46	21.01	1	0	5	9	3.016E5	338	35.6	8.54	FALSE	161
Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	17.52	11.21	1	0	4	6	2.133E5	446	49.8	4.88	TRUE	402
P59282	Tubulin polymerization-promoting protein family member 2 OS=Homo sapiens GN=TPPP2 PE=1 SV=2 - [TPPP2_HUMAN]	17.23	27.65	1	3	3	6	3.471E4	170	18.5	9.00	FALSE	161
Q3ZCF0	Dynactin subunit 2 OS=Bos taurus GN=DCTN2 PE=2 SV=1 - [DCTN2_BOVIN]	17.10	12.66	1	0	3	5	7.101E4	403	44.3	5.16	TRUE	402
Q16698	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1 - [DECR_HUMAN]	16.98	27.16	1	6	6	7	2.177E5	335	36.0	9.28	FALSE	161
Q3ZBZ8	Stress-induced-phosphoprotein 1 OS=Bos taurus GN=STIP1 PE=2 SV=1 - [STIP1_BOVIN]	16.98	11.23	1	1	6	8	2.613E4	543	62.4	6.43	TRUE	402
Q8TC56	Protein FAM71B OS=Homo sapiens GN=FAM71B PE=1 SV=2 - [FA71B_HUMAN]	16.96	9.75	1	4	4	6	7.201E4	605	64.7	9.48	FALSE	161
P18669	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 - [PGAM1_HUMAN]	16.93	24.02	1	0	5	7	1.283E5	254	28.8	7.18	TRUE	402
Q3SZ62	Phosphoglycerate mutase 1 OS=Bos taurus GN=PGAM1 PE=2 SV=3 - [PGAM1_BOVIN]	16.93	24.02	1	0	5	7	1.283E5	254	28.8	7.18	TRUE	402
P15586	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3 - [GNS_HUMAN]	16.82	10.33	1	2	5	7	5.746E4	552	62.0	8.31	FALSE	161
Q1ZYL8	Izumo sperm-egg fusion protein 4 OS=Homo sapiens GN=IZUMO4 PE=2 SV=2 - [IZUM4_HUMAN]	16.46	15.09	1	3	3	7	7.943E5	232	26.5	7.46	TRUE	402
Q9HBV2	Sperm acrosome membrane-associated protein 1 OS=Homo sapiens GN=SPACA1 PE=1 SV=1 - [SACA1_HUMAN]	16.40	23.81	1	5	5	7	1.174E5	294	32.1	4.61	TRUE	402
P49913	Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1 SV=1 - [CAMP_HUMAN]	16.37	21.76	1	4	4	7	2.672E4	170	19.3	9.41	FALSE	161
P21266	Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3 -	16.25	32.89	1	6	6	10	5.312E4	225	26.5	5.54	TRUE	402

	[GSTM3_HUMAN]												
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	16.24	14.29	1	4	4	6	1.000E5	434	47.0	5.44	TRUE	402
P16104	Histone H2AX OS=Homo sapiens GN=H2AFX PE=1 SV=2 - [H2AX_HUMAN]	16.18	42.66	1	0	3	5	6.383E4	143	15.1	10.74	FALSE	161
Q8IU66	Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3 - [H2A2B_HUMAN]	16.18	46.92	1	0	3	5	6.383E4	130	14.0	10.89	FALSE	161
P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RD23B PE=1 SV=1 - [RD23B_HUMAN]	16.11	11.74	1	1	4	7	8.738E4	409	43.1	4.84	TRUE	402
Q8WYR4	Radial spoke head 1 homolog OS=Homo sapiens GN=RSPH1 PE=1 SV=1 - [RSPH1_HUMAN]	16.00	18.12	1	4	4	6	8.430E4	309	35.1	4.63	TRUE	402
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1 - [ETFA_HUMAN]	15.98	12.61	1	2	3	7	4.781E4	333	35.1	8.38	FALSE	161
Q9BUN1	Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1 - [MENT_HUMAN]	15.39	9.68	1	2	2	6	1.410E5	341	36.7	8.59	FALSE	161
A6NNZ2	Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1 - [TBB8L_HUMAN]	14.87	6.31	1	0	3	9	4.522E4	444	49.5	4.86	TRUE	402
Q3ZCM7	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]	14.87	6.31	1	0	3	9	4.522E4	444	49.7	4.89	TRUE	402
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4 - [TCPQ_HUMAN]	14.80	13.69	1	2	6	7	3.970E4	548	59.6	5.60	TRUE	402
P61603	10 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPE1 PE=3 SV=2 - [CH10_BOVIN]	14.59	35.29	1	3	3	6	1.328E6	102	10.9	8.92	FALSE	161
P12273	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1 - [PIP_HUMAN]	14.56	24.66	1	3	3	5	2.948E5	146	16.6	8.05	FALSE	161
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	14.56	11.40	1	5	5	7	6.261E4	623	62.0	5.24	TRUE	402
P07864	L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=1 SV=4 - [LDHC_HUMAN]	14.51	25.00	1	7	7	8	1.508E5	332	36.3	7.46	TRUE	402
P27595	Hexokinase-1 OS=Bos taurus GN=HK1 PE=2 SV=1 - [HXX1_BOVIN]	14.26	5.56	1	0	4	6	8.109E4	918	103.0	7.03	TRUE	402

Q29RK4	UV excision repair protein RAD23 homolog B OS=Bos taurus GN=RAD23B PE=2 SV=1 - [RD23B_BOVIN]	14.17	9.31	1	0	3	6	4.680E 4	408	43.1	4.84	TRUE	402
P55809	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1 - [SCOT1_HUMAN]	14.11	9.23	1	2	2	4	5.661E 4	520	56.1	7.46	TRUE	402
P10323	Acrosin OS=Homo sapiens GN=ACR PE=2 SV=4 - [ACRO_HUMAN]	14.10	10.21	1	4	4	7	3.523E 5	421	45.8	9.07	FALSE	161
P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	13.73	4.56	1	0	1	4	2.298E 4	461	51.0	6.68	TRUE	402
Q92176	Coronin-1A OS=Bos taurus GN=CORO1A PE=1 SV=3 - [COR1A_BOVIN]	13.73	4.56	1	0	1	4	2.298E 4	461	50.9	6.68	TRUE	402
Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 - [PDIA6_HUMAN]	13.54	10.45	1	3	3	5	5.444E 4	440	48.1	5.08	TRUE	402
O95757	Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3 - [HS74L_HUMAN]	13.42	8.22	1	6	6	8	1.011E 5	839	94.5	5.88	TRUE	402
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	13.42	14.67	1	1	2	4	9.433E 4	225	24.7	4.67	TRUE	402
Q6BCY4	NADH-cytochrome b5 reductase 2 OS=Homo sapiens GN=CYB5R2 PE=1 SV=1 - [NB5R2_HUMAN]	13.40	26.81	1	5	5	6	1.325E 5	276	31.4	8.50	FALSE	161
Q6S8J3	POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 - [POTEE_HUMAN]	13.30	5.21	1	0	4	5	4.410E 4	107 5	121. 3	6.20	TRUE	402
P38657	Protein disulfide-isomerase A3 OS=Bos taurus GN=PDIA3 PE=2 SV=1 - [PDIA3_BOVIN]	13.19	13.07	1	0	5	6	9.113E 4	505	56.9	6.65	TRUE	402
P11966	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Bos taurus GN=PDHB PE=1 SV=2 - [ODPB_BOVIN]	13.18	8.91	1	0	2	4	3.979E 4	359	39.1	6.65	TRUE	402
Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]	12.87	8.84	1	0	3	4	9.525E 4	543	59.3	7.65	TRUE	402
Q2NKZ1	T-complex protein 1 subunit eta OS=Bos taurus GN=CCT7 PE=1 SV=1 - [TCPH_BOVIN]	12.87	8.84	1	0	3	4	9.525E 4	543	59.4	7.20	TRUE	402
Q58FF8	Putative heat shock protein HSP 90-beta 2	12.87	11.81	1	0	4	6	1.536E	381	44.3	4.84	TRUE	402

	OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2 - [H90B2_HUMAN]							5					
P31081	60 kDa heat shock protein, mitochondrial OS=Bos taurus GN=HSPD1 PE=1 SV=2 - [CH60_BOVIN]	12.77	7.85	1	0	4	5	7.536E4	573	61.1	5.74	TRUE	402
P22695	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3 - [QCR2_HUMAN]	12.72	11.70	1	3	3	5	3.190E4	453	48.4	8.63	FALSE	161
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	12.65	12.64	1	5	6	6	4.672E4	609	69.3	6.28	TRUE	402
P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	12.61	11.30	1	4	4	5		531	57.9	7.84	TRUE	402
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2 - [F10A1_HUMAN]	12.59	20.05	1	0	6	8	1.128E5	369	41.3	5.27	TRUE	402
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [SDHA_HUMAN]	12.53	9.04	1	1	3	4	2.605E4	664	72.6	7.39	TRUE	402
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]	12.52	6.31	1	4	4	6	4.562E4	840	94.3	5.19	TRUE	402
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	12.32	6.73	1	2	4	5	3.224E4	639	65.4	8.00	FALSE	161
Q01469	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3 - [FABP5_HUMAN]	12.31	31.85	1	3	4	5	5.228E4	135	15.2	7.01	TRUE	402
P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2 - [H2A1B_HUMAN]	12.25	43.85	1	0	3	5	1.126E5	130	14.1	11.05	FALSE	161
P0C0S9	Histone H2A type 1 OS=Bos taurus PE=1 SV=2 - [H2A1_BOVIN]	12.25	43.85	1	0	3	5	1.126E5	130	14.1	10.90	FALSE	161
P20671	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2 - [H2A1D_HUMAN]	12.25	43.85	1	0	3	5	1.126E5	130	14.1	10.90	FALSE	161
Q7L7L0	Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3 - [H2A3_HUMAN]	12.25	43.85	1	0	3	5	1.126E5	130	14.1	11.05	FALSE	161
Q93077	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3 - [H2A1C_HUMAN]	12.25	43.85	1	0	3	5	1.126E5	130	14.1	11.05	FALSE	161

Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3 - [H2A1H_HUMAN]	12.25	44.53	1	0	3	5	1.126E 5	128	13.9	10.8 9	FALSE	161
Q99878	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3 - [H2A1J_HUMAN]	12.25	44.53	1	0	3	5	1.126E 5	128	13.9	10.8 9	FALSE	161
Q3ZBX9	Histone H2A.J OS=Bos taurus GN=H2AFJ PE=2 SV=1 - [H2AJ_BOVIN]	12.25	44.19	1	0	3	5	1.126E 5	129	14.0	10.9 0	FALSE	161
P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4 - [TCPG_HUMAN]	12.22	12.48	1	0	5	5	1.564E 5	545	60.5	6.49	TRUE	402
Q3T0K2	T-complex protein 1 subunit gamma OS=Bos taurus GN=CCT3 PE=1 SV=1 - [TCPG_BOVIN]	12.22	12.48	1	0	5	5	1.564E 5	545	60.5	6.80	TRUE	402
P54709	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1 - [AT1B3_HUMAN]	12.10	17.20	1	3	3	4	1.332E 5	279	31.5	8.35	FALSE	161
P30042	ES1 protein homolog, mitochondrial OS=Homo sapiens GN=C21orf33 PE=1 SV=3 - [ES1_HUMAN]	12.08	23.13	1	3	3	5	5.363E 4	268	28.2	8.27	FALSE	161
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	12.08	3.80	1	2	2	5	6.150E 4	763	82.9	9.04	FALSE	161
Q58FG0	Putative heat shock protein HSP 90-alpha A5 OS=Homo sapiens GN=HSP90AA5P PE=1 SV=1 - [HS905_HUMAN]	11.98	7.49	1	0	2	4	8.937E 4	334	38.7	6.57	TRUE	402
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	11.90	17.91	1	3	4	5	1.460E 5	335	36.0	8.46	FALSE	161
P07108	Acyl-CoA-binding protein OS=Homo sapiens GN=DBI PE=1 SV=2 - [ACBP_HUMAN]	11.78	50.57	1	2	3	6	1.004E 5	87	10.0	6.57	TRUE	402
P17174	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3 - [AATC_HUMAN]	11.48	14.04	1	4	4	5	2.364E 4	413	46.2	7.01	TRUE	402
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]	11.43	10.15	1	1	5	5	3.360E 4	463	51.1	5.64	TRUE	402
O75976	Carboxypeptidase D OS=Homo sapiens GN=CPD PE=1 SV=2 - [CBPD_HUMAN]	11.11	5.94	1	4	4	5	2.921E 4	138 0	152. 8	6.05	TRUE	402
P17066	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2 - [HSP76_HUMAN]	11.10	5.13	1	0	3	5		643	71.0	6.14	TRUE	402

P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]	11.02	8.81	1	0	3	4	5.971E 4	556	60.3	6.11	TRUE	402
Q32L40	T-complex protein 1 subunit alpha OS=Bos taurus GN=TCP1 PE=1 SV=1 - [TCPA_BOVIN]	11.02	8.81	1	0	3	4	5.971E 4	556	60.2	6.11	TRUE	402
Q32KV0	Phosphoglycerate mutase 2 OS=Bos taurus GN=PGAM2 PE=2 SV=1 - [PGAM2_BOVIN]	10.88	17.39	1	0	4	5	1.336E 5	253	28.7	8.88	FALSE	161
Q3ZC19	T-complex protein 1 subunit theta OS=Bos taurus GN=CCT8 PE=1 SV=3 - [TCPQ_BOVIN]	10.77	7.85	1	0	4	5	3.493E 4	548	59.6	5.59	TRUE	402
Q15506	Sperm surface protein Sp17 OS=Homo sapiens GN=SPA17 PE=1 SV=1 - [SP17_HUMAN]	10.63	35.76	1	4	4	4	2.869E 5	151	17.4	4.78	TRUE	402
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	10.45	7.91	1	0	2	3	1.349E 5	417	44.6	8.10	FALSE	161
Q3TOP6	Phosphoglycerate kinase 1 OS=Bos taurus GN=PGK1 PE=2 SV=3 - [PGK1_BOVIN]	10.45	7.91	1	0	2	3	1.349E 5	417	44.5	8.27	FALSE	161
P12821	Angiotensin-converting enzyme OS=Homo sapiens GN=ACE PE=1 SV=1 - [ACE_HUMAN]	10.37	3.45	1	4	4	5	1.373E 5	130 6	149. 6	6.39	TRUE	402
P61285	Dynein light chain 1, cytoplasmic OS=Bos taurus GN=DYNLL1 PE=1 SV=1 - [DYL1_BOVIN]	10.34	24.72	1	0	2	5	1.518E 5	89	10.4	7.40	TRUE	402
Q3MHR3	Dynein light chain 2, cytoplasmic OS=Bos taurus GN=DYNLL2 PE=3 SV=1 - [DYL2_BOVIN]	10.34	24.72	1	0	2	5	1.518E 5	89	10.3	7.37	TRUE	402
Q1LZH9	N-acetylglucosamine-6-sulfatase OS=Bos taurus GN=GNS PE=2 SV=1 - [GNS_BOVIN]	10.23	6.25	1	0	3	4	6.029E 4	560	62.7	8.43	FALSE	161
Q9UBX1	Cathepsin F OS=Homo sapiens GN=CTSF PE=1 SV=1 - [CATF_HUMAN]	10.07	7.85	1	4	4	5	7.783E 4	484	53.3	8.22	FALSE	161
Q2KJE5	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Bos taurus GN=GAPDHS PE=2 SV=1 - [G3PT_BOVIN]	10.04	9.87	1	0	3	4	1.037E 5	395	43.3	8.12	FALSE	161
Q8WW22	DnaJ homolog subfamily A member 4 OS=Homo sapiens GN=DNAJA4 PE=1 SV=1 - [DNJA4_HUMAN]	9.77	11.59	1	3	3	4	1.270E 5	397	44.8	7.59	TRUE	402
P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4 - [TCPD_HUMAN]	9.62	13.17	1	2	4	5	1.090E 5	539	57.9	7.83	TRUE	402
Q2TBU9	RuvB-like 2 OS=Bos taurus GN=RUVBL2 PE=2 SV=3 - [RUVB2_BOVIN]	9.59	7.56	1	0	4	4	2.606E 4	463	51.1	5.76	TRUE	402
Q8WUD1	Ras-related protein Rab-2B OS=Homo sapiens GN=RAB2B PE=1 SV=1 - [RAB2B_HUMAN]	9.57	11.57	1	0	2	4	2.463E 5	216	24.2	7.83	TRUE	402

Q58FF7	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1 - [H90B3_HUMAN]	9.50	5.70	1	0	3	5	1.536E5	597	68.3	4.79	TRUE	402
P14314	Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2 - [GLU2B_HUMAN]	9.49	10.61	1	4	4	7	1.094E5	528	59.4	4.41	TRUE	402
P25685	DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4 - [DNJB1_HUMAN]	9.44	9.71	1	1	3	4	6.780E4	340	38.0	8.63	FALSE	161
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3 - [PRS6A_HUMAN]	9.08	10.25	1	3	3	5	7.994E4	439	49.2	5.24	TRUE	402
P48741	Putative heat shock 70 kDa protein 7 OS=Homo sapiens GN=HSPA7 PE=5 SV=2 - [HSP77_HUMAN]	9.06	6.54	1	0	2	4		367	40.2	7.87	TRUE	402
Q9UJZ1	Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 - [STML2_HUMAN]	9.01	4.78	1	0	1	3	4.079E4	356	38.5	7.39	TRUE	402
Q32LL2	Stomatin-like protein 2, mitochondrial OS=Bos taurus GN=STOML2 PE=2 SV=1 - [STML2_BOVIN]	9.01	4.78	1	0	1	3	4.079E4	356	38.7	8.32	FALSE	161
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4 - [G6PI_HUMAN]	8.89	10.22	1	2	4	4	1.591E5	558	63.1	8.32	FALSE	161
P57105	Synaptojanin-2-binding protein OS=Homo sapiens GN=SYNJ2BP PE=1 SV=2 - [SYJ2B_HUMAN]	8.88	17.93	1	0	2	3	1.378E5	145	15.9	6.30	TRUE	402
Q3T0C9	Synaptojanin-2-binding protein OS=Bos taurus GN=SYNJ2BP PE=2 SV=1 - [SYJ2B_BOVIN]	8.88	17.93	1	0	2	3	1.378E5	145	15.8	5.94	TRUE	402
P31039	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Bos taurus GN=SDHA PE=1 SV=3 - [SDHA_BOVIN]	8.85	4.66	1	0	2	3	2.605E4	665	72.9	7.59	TRUE	402
P37198	Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=3 - [NUP62_HUMAN]	8.64	9.20	1	3	3	4	1.045E5	522	53.2	5.31	TRUE	402
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN]	8.63	4.55	1	1	1	2		440	49.2	6.21	TRUE	402

Q7Z4H3	HD domain-containing protein 2 OS=Homo sapiens GN=HDDC2 PE=1 SV=1 - [HDDC2_HUMAN]	8.63	22.06	1	2	3	4	2.824E4	204	23.4	5.49	TRUE	402
P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 - [TCPE_HUMAN]	8.35	7.58	1	2	2	3	9.123E4	541	59.6	5.66	TRUE	402
Q14568	Putative heat shock protein HSP 90-alpha A2 OS=Homo sapiens GN=HSP90AA2 PE=1 SV=2 - [HS902_HUMAN]	8.35	9.62	1	0	3	4		343	39.3	4.65	TRUE	402
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1 - [CDC37_HUMAN]	8.34	10.05	1	1	2	3	9.712E4	378	44.4	5.25	TRUE	402
P52209	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3 - [6PGD_HUMAN]	8.16	6.21	1	2	2	3	5.419E4	483	53.1	7.23	TRUE	402
P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3 - [ODPA_HUMAN]	8.15	8.46	1	0	3	4		390	43.3	8.06	FALSE	161
A7MB35	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Bos taurus GN=PDHA1 PE=2 SV=1 - [ODPA_BOVIN]	8.15	8.46	1	0	3	4		390	43.4	8.03	FALSE	161
Q5E983	Elongation factor 1-beta OS=Bos taurus GN=EEF1B PE=2 SV=3 - [EF1B_BOVIN]	8.14	6.67	1	0	1	2	9.433E4	225	24.8	4.67	TRUE	402
P18859	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 - [ATP5J_HUMAN]	7.99	22.22	1	2	2	3	1.681E5	108	12.6	9.52	FALSE	161
Q9H3G5	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2 - [CPVL_HUMAN]	7.96	12.18	1	4	4	5	1.665E5	476	54.1	5.62	TRUE	402
Q96JQ2	Calmin OS=Homo sapiens GN=CLMN PE=1 SV=1 - [CLMN_HUMAN]	7.95	2.79	1	2	2	3	3.358E4	1002	111.6	4.94	TRUE	402
Q8NF14	Putative protein FAM10A5 OS=Homo sapiens GN=ST13P5 PE=5 SV=1 - [F10A5_HUMAN]	7.95	11.65	1	0	4	5	1.762E4	369	41.4	5.05	TRUE	402
Q8IXA5	Sperm acrosome membrane-associated protein 3 OS=Homo sapiens GN=SPACA3 PE=1 SV=1 - [SACA3_HUMAN]	7.55	17.67	1	3	3	3		215	23.4	7.94	TRUE	402

Q96S96	Phosphatidylethanolamine-binding protein 4 OS=Homo sapiens GN=PEBP4 PE=1 SV=3 - [PEBP4_HUMAN]	7.46	14.10	1	2	2	3	4.996E4	227	25.7	6.54	TRUE	402
Q2KJE4	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Bos taurus GN=ETFA PE=2 SV=1 - [ETFA_BOVIN]	7.45	4.80	1	0	1	3	9.192E4	333	34.9	8.56	FALSE	161
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	7.42	5.99	1	0	1	3	2.004E4	334	36.6	6.05	TRUE	402
Q5E9B1	L-lactate dehydrogenase B chain OS=Bos taurus GN=LDHB PE=2 SV=4 - [LDHB_BOVIN]	7.42	5.99	1	0	1	3	2.004E4	334	36.7	6.44	TRUE	402
Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2 - [PARK7_HUMAN]	7.35	29.63	1	0	3	3		189	19.9	6.79	TRUE	402
Q5E946	Protein DJ-1 OS=Bos taurus GN=PARK7 PE=2 SV=1 - [PARK7_BOVIN]	7.35	29.63	1	0	3	3		189	20.0	7.33	TRUE	402
P14927	Cytochrome b-c1 complex subunit 7 OS=Homo sapiens GN=UQCRB PE=1 SV=2 - [QCR7_HUMAN]	7.31	11.71	1	1	1	2	7.861E4	111	13.5	8.78	FALSE	161
O14950	Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2 - [ML12B_HUMAN]	7.27	11.63	1	0	1	2	5.300E4	172	19.8	4.84	TRUE	402
P19105	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 - [ML12A_HUMAN]	7.27	11.70	1	0	1	2	5.300E4	171	19.8	4.81	TRUE	402
Q5E9E2	Myosin regulatory light polypeptide 9 OS=Bos taurus GN=MYL9 PE=2 SV=3 - [MYL9_BOVIN]	7.27	11.63	1	0	1	2	5.300E4	172	19.9	4.81	TRUE	402
A41F97	Myosin regulatory light chain 12B OS=Bos taurus GN=MYL12B PE=2 SV=1 - [ML12B_BOVIN]	7.27	11.70	1	0	1	2	5.300E4	171	19.7	4.84	TRUE	402
A5A3E0	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 - [POTEF_HUMAN]	7.19	3.07	1	0	3	3	1.760E4	1075	121.4	6.20	TRUE	402
Q2HJD7	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Bos taurus GN=HIBADH PE=2 SV=1 - [3HIDH_BOVIN]	7.14	13.69	1	1	3	3	9.693E3	336	35.4	8.13	FALSE	161
Q9NZ45	CDGSH iron-sulfur domain-containing protein 1 OS=Homo sapiens GN=CISD1 PE=1 SV=1 -	7.08	13.89	1	0	1	2	2.234E4	108	12.2	9.09	FALSE	161

	[CISD1_HUMAN]												
Q3ZBU2	CDGSH iron-sulfur domain-containing protein 1 OS=Bos taurus GN=CISD1 PE=1 SV=1 - [CISD1_BOVIN]	7.08	14.15	1	0	1	2	2.234E4	106	12.0	9.09	FALSE	161
O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3 - [ATP5H_HUMAN]	7.06	26.09	1	2	3	4	6.982E4	161	18.5	5.30	TRUE	402
O75390	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2 - [CISY_HUMAN]	7.02	3.43	1	0	1	2		466	51.7	8.32	FALSE	161
Q29RK1	Citrate synthase, mitochondrial OS=Bos taurus GN=CS PE=1 SV=1 - [CISY_BOVIN]	7.02	3.43	1	0	1	2		466	51.7	8.12	FALSE	161
Q86Y82	Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1 - [STX12_HUMAN]	6.99	14.13	1	3	3	3	4.822E4	276	31.6	5.59	TRUE	402
P05387	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 - [RLA2_HUMAN]	6.94	45.22	1	0	2	2	2.184E4	115	11.7	4.54	TRUE	402
P42899	60S acidic ribosomal protein P2 OS=Bos taurus GN=RPLP2 PE=3 SV=1 - [RLA2_BOVIN]	6.94	45.22	1	0	2	2	2.184E4	115	11.7	4.61	TRUE	402
Q8IYT1	Protein FAM71A OS=Homo sapiens GN=FAM71A PE=2 SV=2 - [FA71A_HUMAN]	6.89	5.39	1	2	2	4	7.643E4	594	63.1	9.64	FALSE	161
O43805	Sjoegren syndrome nuclear autoantigen 1 OS=Homo sapiens GN=SSNA1 PE=1 SV=2 - [SSNA1_HUMAN]	6.86	20.17	1	1	2	3	8.416E3	119	13.6	5.38	TRUE	402
Q8NHS0	DnaJ homolog subfamily B member 8 OS=Homo sapiens GN=DNAJB8 PE=1 SV=1 - [DNJB8_HUMAN]	6.86	9.91	1	1	2	3	2.497E3	232	25.7	6.42	TRUE	402
Q3MI00	DnaJ homolog subfamily B member 1 OS=Bos taurus GN=DNAJB1 PE=2 SV=3 - [DNJB1_BOVIN]	6.65	6.76	1	0	2	3	6.780E4	340	38.2	8.63	FALSE	161
Q96QV6	Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3 - [H2A1A_HUMAN]	6.65	24.43	1	0	2	3	5.395E4	131	14.2	10.86	FALSE	161
Q2YDI9	Ferritin, mitochondrial OS=Bos taurus GN=FTMT PE=2 SV=1 - [FTMT_BOVIN]	6.63	5.37	1	0	1	3	8.235E4	242	27.3	7.33	TRUE	402
A2A3N6	Putative PIP5K1A and PSMD4-like protein OS=Homo sapiens GN=PIPSL PE=5 SV=1 - [PIPSL_HUMAN]	6.54	1.97	1	0	1	2	9.150E4	862	95.0	5.71	TRUE	402

P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 - [PSMD4_HUMAN]	6.54	4.51	1	0	1	2	9.150E4	377	40.7	4.79	TRUE	402
Q58DA0	26S proteasome non-ATPase regulatory subunit 4 OS=Bos taurus GN=PSMD4 PE=2 SV=1 - [PSMD4_BOVIN]	6.54	4.45	1	0	1	2	9.150E4	382	41.4	4.79	TRUE	402
Q96EP5	DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=1 - [DAZP1_HUMAN]	6.51	3.93	1	1	1	2	4.636E4	407	43.4	8.56	FALSE	161
Q8IZP2	Putative protein FAM10A4 OS=Homo sapiens GN=ST13P4 PE=5 SV=1 - [ST134_HUMAN]	6.48	17.08	1	0	3	4	1.505E5	240	27.4	5.08	TRUE	402
P55084	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_HUMAN]	6.43	6.12	1	1	3	3	6.108E3	474	51.3	9.41	FALSE	161
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	6.33	5.48	1	2	2	3	2.953E4	456	50.2	6.42	TRUE	402
O15173	Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1 - [PGRMC2_HUMAN]	6.29	8.52	1	1	1	2	5.591E4	223	23.8	4.88	TRUE	402
P68103	Elongation factor 1-alpha 1 OS=Bos taurus GN=EEF1A1 PE=1 SV=1 - [EF1A1_BOVIN]	6.29	9.31	1	0	3	3	2.247E5	462	50.1	9.01	FALSE	161
Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1 - [EF1A3_HUMAN]	6.29	9.31	1	0	3	3	2.247E5	462	50.2	9.07	FALSE	161
Q9BS86	Zona pellucida-binding protein 1 OS=Homo sapiens GN=ZPBP PE=2 SV=1 - [ZPBP1_HUMAN]	6.26	9.69	1	3	3	4	5.802E4	351	40.1	9.28	FALSE	161
P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [SDHB_HUMAN]	6.25	12.50	1	1	3	3	1.768E4	280	31.6	8.76	FALSE	161
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4 - [PIMT_HUMAN]	6.25	19.82	1	1	3	3	9.113E3	227	24.6	7.21	TRUE	402
P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens	6.19	3.09	1	0	1	2	1.155E5	453	48.7	8.95	FALSE	161

	GN=DLST PE=1 SV=4 - [ODO2_HUMAN]												
P11179	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Bos taurus GN=DLST PE=1 SV=2 - [ODO2_BOVIN]	6.19	3.08	1	0	1	2	1.155E5	455	48.9	8.95	FALSE	161
POC7P4	Putative cytochrome b-c1 complex subunit Rieske-like protein 1 OS=Homo sapiens GN=UQCRFS1P1 PE=5 SV=1 - [UCRIL_HUMAN]	6.18	9.19	1	0	1	2	1.182E5	283	30.8	8.87	FALSE	161
P47985	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRFS1 PE=1 SV=2 - [UCRI_HUMAN]	6.18	9.49	1	0	1	2	1.182E5	274	29.6	8.32	FALSE	161
Q56K14	60S acidic ribosomal protein P1 OS=Bos taurus GN=RPLP1 PE=3 SV=1 - [RLA1_BOVIN]	6.14	14.04	1	1	1	3	4.839E4	114	11.5	4.32	TRUE	402
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2 - [DHAK_HUMAN]	6.14	5.04	1	2	2	3	3.369E4	575	58.9	7.49	TRUE	402
P10096	Glyceraldehyde-3-phosphate dehydrogenase OS=Bos taurus GN=GAPDH PE=1 SV=4 - [G3P_BOVIN]	6.08	6.31	1	0	1	2		333	35.8	8.35	FALSE	161
Q8TAD1	Sperm protein associated with the nucleus on the X chromosome E OS=Homo sapiens GN=SPANXE PE=2 SV=1 - [SPNXE_HUMAN]	6.08	11.34	1	0	1	2		97	11.0	5.26	TRUE	402
Q9BXN6	Sperm protein associated with the nucleus on the X chromosome D OS=Homo sapiens GN=SPANXD PE=2 SV=1 - [SPNXD_HUMAN]	6.08	11.34	1	0	1	2		97	11.0	6.11	TRUE	402
Q9NS25	Sperm protein associated with the nucleus on the X chromosome B/F OS=Homo sapiens GN=SPANXB1 PE=2 SV=1 - [SPNXB_HUMAN]	6.08	10.68	1	0	1	2		103	11.8	6.15	TRUE	402
Q9NS26	Sperm protein associated with the nucleus on the X chromosome A OS=Homo sapiens GN=SPANXA1 PE=2 SV=1 - [SPNXA_HUMAN]	6.08	11.34	1	0	1	2		97	11.0	5.10	TRUE	402
Q9NY87	Sperm protein associated with the nucleus on the X chromosome C OS=Homo sapiens GN=SPANXC PE=2 SV=1 - [SPNXC_HUMAN]	6.08	11.34	1	0	1	2		97	11.0	5.10	TRUE	402
P02743	Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2 -	6.03	9.42	1	2	2	3	3.826E4	223	25.4	6.54	TRUE	402

	[SAMP_HUMAN]												
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2 - [KAP2_HUMAN]	6.00	7.18	1	1	2	2	4.202E4	404	45.5	5.07	TRUE	402
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	5.96	11.61	1	2	2	3		224	25.0	6.38	TRUE	402
P29803	Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial OS=Homo sapiens GN=PDHA2 PE=1 SV=1 - [ODPAT_HUMAN]	5.96	10.05	1	2	4	4	1.129E4	388	42.9	8.46	FALSE	161
Q3ZBD7	Glucose-6-phosphate isomerase OS=Bos taurus GN=GPI PE=2 SV=4 - [G6PI_BOVIN]	5.96	5.39	1	0	2	2	1.316E5	557	62.8	7.71	TRUE	402
Q5EAC6	Hsp90 co-chaperone Cdc37 OS=Bos taurus GN=CDC37 PE=2 SV=1 - [CDC37_BOVIN]	5.95	5.53	1	0	1	2	7.339E4	380	44.6	5.17	TRUE	402
O43247	Testis-expressed sequence 33 protein OS=Homo sapiens GN=TEX33 PE=2 SV=2 - [TEX33_HUMAN]	5.92	6.07	1	1	1	2		280	30.7	7.99	TRUE	402
Q7Z6W1	Transmembrane and coiled-coil domain-containing protein 2 OS=Homo sapiens GN=TMCO2 PE=2 SV=1 - [TMCO2_HUMAN]	5.89	8.79	1	1	1	2	1.100E5	182	20.1	8.68	FALSE	161
P0CG47	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1 - [UBB_HUMAN]	5.89	20.96	1	0	1	2	1.686E4	229	25.7	7.43	TRUE	402
P62992	Ubiquitin-40S ribosomal protein S27a OS=Bos taurus GN=RPS27A PE=1 SV=2 - [RS27A_BOVIN]	5.89	10.26	1	0	1	2	1.686E4	156	18.0	9.64	FALSE	161
P63048	Ubiquitin-60S ribosomal protein L40 OS=Bos taurus GN=UBA52 PE=1 SV=2 - [RL40_BOVIN]	5.89	12.50	1	0	1	2	1.686E4	128	14.7	9.83	FALSE	161
P0CG48	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]	5.89	21.02	1	0	1	2	1.686E4	685	77.0	7.66	TRUE	402
P0CG53	Polyubiquitin-B OS=Bos taurus GN=UBB PE=1 SV=1 - [UBB_BOVIN]	5.89	20.98	1	0	1	2	1.686E4	305	34.3	7.47	TRUE	402
P0CH28	Polyubiquitin-C OS=Bos taurus GN=UBC PE=1 SV=1 - [UBC_BOVIN]	5.89	20.87	1	0	1	2	1.686E4	690	77.5	7.66	TRUE	402
P26436	Acrosomal protein SP-10 OS=Homo sapiens GN=ACRV1 PE=1 SV=2 - [ASPX_HUMAN]	5.84	6.04	1	1	1	2	3.546E4	265	28.1	4.69	TRUE	402
P31930	Cytochrome b-c1 complex subunit 1,	5.80	4.58	1	2	2	3	5.024E	480	52.6	6.37	TRUE	402

	mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 - [QCR1_HUMAN]							4					
P23434	Glycine cleavage system H protein, mitochondrial OS=Homo sapiens GN=GCSH PE=1 SV=2 - [GCSH_HUMAN]	5.68	11.56	1	1	1	2	2.053E 4	173	18.9	4.88	TRUE	402
Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]	5.61	9.04	1	1	2	2	4.672E 4	376	42.0	5.59	TRUE	402
P02751	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4 - [FINC_HUMAN]	5.61	0.63	1	1	1	2		238 6	262. 5	5.71	TRUE	402
P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	5.60	7.60	1	0	2	2	8.964E 5	434	47.0	7.71	TRUE	402
P09104	Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3 - [ENOG_HUMAN]	5.60	7.60	1	0	2	2	8.964E 5	434	47.2	5.03	TRUE	402
Q3ZC09	Beta-enolase OS=Bos taurus GN=ENO3 PE=2 SV=1 - [ENOB_BOVIN]	5.60	7.60	1	0	2	2	8.964E 5	434	47.1	7.72	TRUE	402
P62739	Actin, aortic smooth muscle OS=Bos taurus GN=ACTA2 PE=1 SV=1 - [ACTA_BOVIN]	5.55	6.90	1	0	2	2	2.463E 4	377	42.0	5.39	TRUE	402
Q5E9B5	Actin, gamma-enteric smooth muscle OS=Bos taurus GN=ACTG2 PE=2 SV=1 - [ACTH_BOVIN]	5.55	6.91	1	0	2	2	2.463E 4	376	41.8	5.48	TRUE	402
Q3ZC07	Actin, alpha cardiac muscle 1 OS=Bos taurus GN=ACTC1 PE=2 SV=1 - [ACTC_BOVIN]	5.55	6.90	1	0	2	2	2.463E 4	377	42.0	5.39	TRUE	402
P68138	Actin, alpha skeletal muscle OS=Bos taurus GN=ACTA1 PE=1 SV=1 - [ACTS_BOVIN]	5.55	6.90	1	0	2	2	2.463E 4	377	42.0	5.39	TRUE	402
P41222	Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=1 SV=1 - [PTGDS_HUMAN]	5.50	17.37	1	2	2	2		190	21.0	7.80	TRUE	402
Q92526	T-complex protein 1 subunit zeta-2 OS=Homo sapiens GN=CCT6B PE=1 SV=5 - [TCPW_HUMAN]	5.47	6.98	1	2	2	3	7.760E 4	530	57.8	7.24	TRUE	402
Q58FG1	Putative heat shock protein HSP 90-alpha A4 OS=Homo sapiens GN=HSP90AA4P PE=5 SV=1 - [HS904_HUMAN]	5.31	3.11	1	0	1	2		418	47.7	5.19	TRUE	402
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 - [1433G_HUMAN]	5.21	9.72	1	0	2	2	1.536E 5	247	28.3	4.89	TRUE	402
P68252	14-3-3 protein gamma OS=Bos taurus GN=YWHAG PE=1 SV=2 - [1433G_BOVIN]	5.21	9.72	1	0	2	2	1.536E 5	247	28.2	4.89	TRUE	402

P62333	26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1 - [PRS10_HUMAN]	5.18	6.43	1	1	2	2	7.092E 4	389	44.1	7.49	TRUE	402
O95292	Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3 - [VAPB_HUMAN]	5.11	9.47	1	0	2	2	2.466E 5	243	27.2	7.30	TRUE	402
A2VDZ9	Vesicle-associated membrane protein-associated protein B OS=Bos taurus GN=VAPB PE=2 SV=1 - [VAPB_BOVIN]	5.11	9.47	1	0	2	2	2.466E 5	243	27.1	7.30	TRUE	402
P10515	Dihydropyridyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLAT PE=1 SV=3 - [ODP2_HUMAN]	5.08	2.63	1	1	1	2		647	69.0	7.84	TRUE	402
P52789	Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 - [HXX2_HUMAN]	5.06	1.20	1	0	1	2	3.519E 4	917	102. 3	6.05	TRUE	402
Q2YDE4	Proteasome subunit alpha type-6 OS=Bos taurus GN=PSMA6 PE=1 SV=1 - [PSA6_BOVIN]	5.03	8.94	1	2	2	3	4.957E 4	246	27.4	6.76	TRUE	402
O75071	EF-hand calcium-binding domain-containing protein 14 OS=Homo sapiens GN=EFCAB14 PE=2 SV=1 - [EFC14_HUMAN]	5.03	6.06	1	2	2	2	5.973E 4	495	55.0	6.32	TRUE	402
P62491	Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RB11A_HUMAN]	5.00	10.19	1	0	2	2	1.122E 4	216	24.4	6.57	TRUE	402
Q3MHP2	Ras-related protein Rab-11B OS=Bos taurus GN=RAB11B PE=2 SV=3 - [RB11B_BOVIN]	5.00	10.09	1	0	2	2	1.122E 4	218	24.5	5.94	TRUE	402
Q2TA29	Ras-related protein Rab-11A OS=Bos taurus GN=RAB11A PE=2 SV=3 - [RB11A_BOVIN]	5.00	10.19	1	0	2	2	1.122E 4	216	24.5	6.57	TRUE	402
Q5E9C3	Sjoegren syndrome nuclear autoantigen 1 homolog OS=Bos taurus GN=SSNA1 PE=3 SV=1 - [SSNA1_BOVIN]	4.99	10.92	1	0	1	2		119	13.6	5.68	TRUE	402
Q9BSF0	Small membrane A-kinase anchor protein OS=Homo sapiens GN=C2orf88 PE=1 SV=2 - [SMAKA_HUMAN]	4.95	32.63	1	2	2	2	1.078E 4	95	11.0	4.87	TRUE	402
Q9UFH2	Dynein heavy chain 17, axonemal OS=Homo sapiens GN=DNAH17 PE=1 SV=2 - [DYH17_HUMAN]	4.94	0.58	1	2	2	2	2.658E 4	448 5	511. 5	5.77	TRUE	402
P29692	Elongation factor 1-delta OS=Homo sapiens	4.90	8.54	1	1	2	2		281	31.1	5.01	TRUE	402

	GN=EEF1D PE=1 SV=5 - [EF1D_HUMAN]												
Q5E9F9	26S protease regulatory subunit 7 OS=Bos taurus GN=PSMC2 PE=2 SV=3 - [PRS7_BOVIN]	4.89	11.09	1	3	3	3	5.850E4	433	48.6	5.95	TRUE	402
P25325	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3 - [THTM_HUMAN]	4.88	13.47	1	2	2	2	8.313E3	297	33.2	6.60	TRUE	402
Q8TAA3	Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3 - [PSA7L_HUMAN]	4.81	5.86	1	1	1	2	2.465E4	256	28.5	8.98	FALSE	161
Q9BYZ2	L-lactate dehydrogenase A-like 6B OS=Homo sapiens GN=LDHAL6B PE=1 SV=3 - [LDH6B_HUMAN]	4.81	6.82	1	2	2	2	3.755E4	381	41.9	8.65	FALSE	161
Q9UI46	Dynein intermediate chain 1, axonemal OS=Homo sapiens GN=DNAI1 PE=1 SV=1 - [DNAI1_HUMAN]	4.63	5.29	1	2	2	2	3.027E4	699	79.2	6.87	TRUE	402
Q9H0B3	Uncharacterized protein KIAA1683 OS=Homo sapiens GN=KIAA1683 PE=2 SV=1 - [K1683_HUMAN]	4.61	2.88	1	2	2	2	2.628E4	1180	127.6	10.23	FALSE	161
Q8N0Y7	Probable phosphoglycerate mutase 4 OS=Homo sapiens GN=PGAM4 PE=2 SV=1 - [PGAM4_HUMAN]	4.54	9.45	1	0	2	2		254	28.8	6.65	TRUE	402
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 - [PDIA4_HUMAN]	4.51	4.19	1	1	2	2	7.127E4	645	72.9	5.07	TRUE	402
P59910	DnaJ homolog subfamily B member 13 OS=Homo sapiens GN=DNAJB13 PE=2 SV=1 - [DJB13_HUMAN]	4.44	7.91	1	2	2	2	6.217E4	316	36.1	7.87	TRUE	402
P04179	Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2 - [SODM_HUMAN]	4.35	12.61	1	1	2	2	1.236E4	222	24.7	8.25	FALSE	161
P06394	Keratin, type I cytoskeletal 10 OS=Bos taurus GN=KRT10 PE=3 SV=1 - [K1C10_BOVIN]	4.31	6.27	1	0	3	3	5.391E4	526	54.8	5.11	TRUE	402
Q9H4B7	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1 - [TBB1_HUMAN]	4.25	2.22	1	0	1	2	4.979E4	451	50.3	5.17	TRUE	402
Q3T189	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Bos taurus	4.21	6.79	1	0	2	2	1.848E4	280	31.5	8.60	FALSE	161

	GN=SDHB PE=2 SV=1 - [SDHB_BOVIN]												
O46629	Trifunctional enzyme subunit beta, mitochondrial OS=Bos taurus GN=HADHB PE=2 SV=1 - [ECHB_BOVIN]	4.17	4.21	1	0	2	2	8.652E3	475	51.3	9.32	FALSE	161
P55145	Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens GN=MANF PE=1 SV=3 - [MANF_HUMAN]	4.16	13.74	1	1	2	2	3.829E4	182	20.7	8.69	FALSE	161
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3 - [EF1G_HUMAN]	4.11	5.49	1	2	2	2	1.115E5	437	50.1	6.67	TRUE	402
P00727	Cytosol aminopeptidase OS=Bos taurus GN=LAP3 PE=1 SV=3 - [AMPL_BOVIN]	4.09	4.62	1	0	2	2	8.444E4	519	56.3	6.48	TRUE	402
Q5SRN2	Uncharacterized protein C6orf10 OS=Homo sapiens GN=C6orf10 PE=2 SV=3 - [CF010_HUMAN]	4.03	4.26	1	2	2	2	4.425E4	563	61.6	9.25	FALSE	161
Q32PH8	Elongation factor 1-alpha 2 OS=Bos taurus GN=EEF1A2 PE=2 SV=1 - [EF1A2_BOVIN]	4.01	4.10	1	0	2	2	8.604E4	463	50.4	9.03	FALSE	161
Q6UWQ5	Lysozyme-like protein 1 OS=Homo sapiens GN=LYZL1 PE=2 SV=2 - [LYZL1_HUMAN]	3.97	8.11	1	0	1	2		148	16.6	8.05	FALSE	161
Q7Z4W2	Lysozyme-like protein 2 OS=Homo sapiens GN=LYZL2 PE=2 SV=2 - [LYZL2_HUMAN]	3.97	8.11	1	0	1	2		148	16.6	7.84	TRUE	402
P62194	26S protease regulatory subunit 8 OS=Bos taurus GN=PSMC5 PE=2 SV=1 - [PRS8_BOVIN]	3.95	4.43	1	1	1	1	6.132E4	406	45.6	7.55	TRUE	402
P42126	Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1 - [ECI1_HUMAN]	3.92	4.97	1	1	1	2	7.706E4	302	32.8	8.54	FALSE	161
Q9UNN5	FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2 - [FAF1_HUMAN]	3.91	1.69	1	1	1	2		650	73.9	4.88	TRUE	402
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	3.88	13.08	1	3	3	3	9.047E4	260	29.2	7.40	TRUE	402
P49773	Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2 - [HINT1_HUMAN]	3.82	15.87	1	1	1	2		126	13.8	6.95	TRUE	402
P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]	3.80	3.81	1	0	2	2		472	51.5	5.16	TRUE	402
P08779	Keratin, type I cytoskeletal 16 OS=Homo	3.80	3.81	1	0	2	2		473	51.2	5.05	TRUE	402

	sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN]												
P0CG38	POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 - [POTEI_HUMAN]	3.79	1.58	1	0	2	2	6.149E3	1075	121.2	6.21	TRUE	402
P0CG39	POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 - [POTEJ_HUMAN]	3.79	1.64	1	0	2	2	6.149E3	1038	117.3	5.97	TRUE	402
P00515	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Bos taurus GN=PRKAR2A PE=1 SV=2 - [KAP2_BOVIN]	3.76	4.24	1	0	1	1	4.202E4	401	45.1	4.93	TRUE	402
Q8SQ21	Histidine triad nucleotide-binding protein 2, mitochondrial OS=Bos taurus GN=HINT2 PE=2 SV=1 - [HINT2_BOVIN]	3.61	26.99	1	0	3	3	2.521E5	163	17.1	7.50	TRUE	402
Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2 - [VAT1_HUMAN]	3.47	4.33	1	1	1	2	1.754E4	393	41.9	6.29	TRUE	402
P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	3.46	4.28	1	1	1	1	4.903E4	421	46.6	8.37	FALSE	161
Q9NQ60	Equatorin OS=Homo sapiens GN=EQTN PE=2 SV=2 - [EQTN_HUMAN]	3.41	8.50	1	2	2	2	9.178E3	294	32.8	5.00	TRUE	402
Q9BYX7	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 - [ACTBM_HUMAN]	3.40	4.27	1	0	1	1	4.049E4	375	42.0	6.33	TRUE	402
P15246	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Bos taurus GN=PCMT1 PE=1 SV=2 - [PIMT_BOVIN]	3.37	14.98	1	0	2	2	9.113E3	227	24.5	7.58	TRUE	402
Q0P565	HD domain-containing protein 2 OS=Bos taurus GN=HDDC2 PE=2 SV=1 - [HDDC2_BOVIN]	3.32	8.78	1	0	1	1	3.816E4	205	23.3	5.16	TRUE	402
Q5THR3	EF-hand calcium-binding domain-containing protein 6 OS=Homo sapiens GN=EFCAB6 PE=1 SV=1 - [EFCAB6_HUMAN]	3.17	1.33	1	1	1	1	4.724E4	1501	172.8	8.40	FALSE	161
Q7Z794	Keratin, type II cytoskeletal 1b OS=Homo	3.17	2.08	1	0	1	1	5.205E	578	61.9	5.99	TRUE	402

	sapiens GN=KRT77 PE=2 SV=3 - [K2C1B_HUMAN]							3					
Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3 - [TRAP1_HUMAN]	3.13	1.99	1	0	1	1	1.660E5	704	80.1	8.21	FALSE	161
Q2TBI4	Heat shock protein 75 kDa, mitochondrial OS=Bos taurus GN=TRAP1 PE=2 SV=1 - [TRAP1_BOVIN]	3.13	1.99	1	0	1	1	1.660E5	703	79.3	7.14	TRUE	402
Q2T9X2	T-complex protein 1 subunit delta OS=Bos taurus GN=CCT4 PE=1 SV=3 - [TCPD_BOVIN]	3.11	7.38	1	0	2	2	9.300E4	542	58.2	7.33	TRUE	402
Q9H4B8	Dipeptidase 3 OS=Homo sapiens GN=DPEP3 PE=2 SV=2 - [DPEP3_HUMAN]	3.05	3.89	1	1	1	1	5.382E4	488	53.7	7.96	TRUE	402
Q9UBS4	DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1 - [DJB11_HUMAN]	2.97	4.47	1	0	1	1		358	40.5	6.18	TRUE	402
Q3ZBA6	DnaJ homolog subfamily B member 11 OS=Bos taurus GN=DNAJB11 PE=2 SV=1 - [DJB11_BOVIN]	2.97	4.47	1	0	1	1		358	40.5	6.32	TRUE	402
O95473	Synaptogyrin-4 OS=Homo sapiens GN=SYNGR4 PE=2 SV=2 - [SNG4_HUMAN]	2.96	6.41	1	1	1	1	2.075E4	234	25.8	7.75	TRUE	402
Q8TF09	Dynein light chain roadblock-type 2 OS=Homo sapiens GN=DYNLRB2 PE=1 SV=1 - [DLRB2_HUMAN]	2.94	16.67	1	0	1	1	1.707E5	96	10.8	7.50	TRUE	402
Q32P85	Dynein light chain roadblock-type 2 OS=Bos taurus GN=DYNLRB2 PE=3 SV=1 - [DLRB2_BOVIN]	2.94	16.67	1	0	1	1	1.707E5	96	10.8	7.44	TRUE	402
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	2.92	2.80	1	0	1	1	6.702E3	858	95.3	6.83	TRUE	402
Q3SYU2	Elongation factor 2 OS=Bos taurus GN=EEF2 PE=2 SV=3 - [EF2_BOVIN]	2.92	2.80	1	0	1	1	6.702E3	858	95.3	6.83	TRUE	402
Q8TDM5	Sperm acrosome membrane-associated protein 4 OS=Homo sapiens GN=SPACA4 PE=1 SV=1 - [SACA4_HUMAN]	2.90	10.48	1	1	1	1		124	13.0	5.80	TRUE	402
Q9NR28	Diablo homolog, mitochondrial OS=Homo sapiens GN=DIABLO PE=1 SV=1 - [DBLOH_HUMAN]	2.88	4.18	1	1	1	1	7.327E4	239	27.1	5.90	TRUE	402

P00442	Superoxide dismutase [Cu-Zn] OS=Bos taurus GN=SOD1 PE=1 SV=2 - [SODC_BOVIN]	2.81	7.89	1	0	1	1		152	15.7	6.32	TRUE	402
Q3SZ14	14-3-3 protein theta OS=Bos taurus GN=YWHAQ PE=2 SV=1 - [1433T_BOVIN]	2.78	7.76	1	0	2	2	1.524E 5	245	27.7	4.78	TRUE	402
P31946	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 - [1433B_HUMAN]	2.78	7.72	1	0	2	2	1.524E 5	246	28.1	4.83	TRUE	402
P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	2.78	4.03	1	0	1	1	2.972E 5	248	27.8	4.74	TRUE	402
P62261	14-3-3 protein epsilon OS=Bos taurus GN=YWHAE PE=2 SV=1 - [1433E_BOVIN]	2.78	3.92	1	0	1	1	2.972E 5	255	29.2	4.74	TRUE	402
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	2.78	4.07	1	0	1	1	2.972E 5	246	28.2	4.84	TRUE	402
P68509	14-3-3 protein eta OS=Bos taurus GN=YWHAH PE=1 SV=2 - [1433F_BOVIN]	2.78	4.07	1	0	1	1	2.972E 5	246	28.2	4.89	TRUE	402
P68250	14-3-3 protein beta/alpha OS=Bos taurus GN=YWHAB PE=1 SV=2 - [1433B_BOVIN]	2.78	7.72	1	0	2	2	1.524E 5	246	28.1	4.87	TRUE	402
Q0VC36	14-3-3 protein sigma OS=Bos taurus GN=SFN PE=2 SV=1 - [1433S_BOVIN]	2.78	4.03	1	0	1	1	2.972E 5	248	27.8	4.72	TRUE	402
Q2KIW6	26S protease regulatory subunit 10B OS=Bos taurus GN=PSMC6 PE=2 SV=1 - [PRS10_BOVIN]	2.74	3.60	1	0	1	1	1.355E 5	389	44.0	7.20	TRUE	402
A1A4R1	Histone H2A type 2-C OS=Bos taurus GN=HIST2H2AC PE=2 SV=1 - [H2A2C_BOVIN]	2.72	21.71	1	0	2	3	1.514E 5	129	14.0	10.9 0	FALSE	161
Q6FI13	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3 - [H2A2A_HUMAN]	2.72	21.54	1	0	2	3	1.514E 5	130	14.1	10.9 0	FALSE	161
Q96C74	Ropporin-1-like protein OS=Homo sapiens GN=ROPN1L PE=1 SV=2 - [ROP1L_HUMAN]	2.71	7.83	1	1	1	1	3.536E 4	230	26.1	7.72	TRUE	402
Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDH_HUMAN]	2.68	3.03	1	1	1	1	2.048E 5	429	47.1	9.14	FALSE	161
Q8N427	Thioredoxin domain-containing protein 3 OS=Homo sapiens GN=NME8 PE=1 SV=2 - [TXND3_HUMAN]	2.66	2.89	1	1	1	1	5.120E 4	588	67.2	4.97	TRUE	402
Q9BVL2	Nucleoporin p58/p45 OS=Homo sapiens GN=NUPL1 PE=1 SV=1 - [NUPL1_HUMAN]	2.62	2.84	1	1	1	1		599	60.9	9.33	FALSE	161
Q9H0C2	ADP/ATP translocase 4 OS=Homo sapiens	2.58	4.13	1	0	1	1		315	35.0	9.89	FALSE	161

	GN=SLC25A31 PE=2 SV=1 - [ADT4_HUMAN]												
Q2YDD9	ADP/ATP translocase 4 OS=Bos taurus GN=SLC25A31 PE=2 SV=1 - [ADT4_BOVIN]	2.58	4.02	1	0	1	1		323	35.7	9.55	FALSE	161
P09622	Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 - [DLDH_HUMAN]	2.56	2.55	1	1	1	1		509	54.1	7.85	TRUE	402
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1 - [LETM1_HUMAN]	2.55	5.28	1	1	2	2	4.061E 4	739	83.3	6.70	TRUE	402
Q0VCA3	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Bos taurus GN=LETM1 PE=2 SV=1 - [LETM1_BOVIN]	2.55	1.64	1	0	1	1	2.802E 4	732	81.8	6.73	TRUE	402
Q9BY14	Testis-expressed sequence 101 protein OS=Homo sapiens GN=TEX101 PE=2 SV=2 - [TX101_HUMAN]	2.53	5.62	1	1	1	1	1.136E 5	249	26.6	4.94	TRUE	402
Q3T064	Ropporin-1 OS=Bos taurus GN=ROPN1 PE=2 SV=1 - [ROP1_BOVIN]	2.51	4.25	1	0	1	1		212	24.0	5.27	TRUE	402
P13646	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4 - [K1C13_HUMAN]	2.51	2.40	1	0	1	1	5.819E 4	458	49.6	4.96	TRUE	402
Q2M2I5	Keratin, type I cytoskeletal 24 OS=Homo sapiens GN=KRT24 PE=1 SV=1 - [K1C24_HUMAN]	2.51	2.10	1	0	1	1	5.819E 4	525	55.1	4.96	TRUE	402
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN]	2.51	6.96	1	0	1	1		230	26.2	4.92	TRUE	402
Q2TBG8	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Bos taurus GN=UCHL3 PE=2 SV=1 - [UCHL3_BOVIN]	2.51	6.96	1	0	1	1		230	26.2	4.92	TRUE	402
Q96HR9	Receptor expression-enhancing protein 6 OS=Homo sapiens GN=REEP6 PE=1 SV=1 - [REEP6_HUMAN]	2.50	7.07	1	1	1	1		184	20.7	8.56	FALSE	161
P15104	Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4 - [GLNA_HUMAN]	2.50	4.56	1	1	1	1		373	42.0	6.89	TRUE	402
O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 -	2.50	3.05	1	1	1	1	2.038E 5	394	43.6	9.00	FALSE	161

	[ECI2_HUMAN]												
Q58FF3	Putative endoplasmin-like protein OS=Homo sapiens GN=HSP90B2P PE=5 SV=1 - [ENPLL_HUMAN]	2.50	2.51	1	0	1	2	9.379E3	399	45.8	5.26	TRUE	402
Q8N1F7	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 - [NUP93_HUMAN]	2.49	3.17	1	0	1	1	5.712E4	819	93.4	5.72	TRUE	402
A5PJZ5	Nuclear pore complex protein Nup93 OS=Bos taurus GN=NUP93 PE=2 SV=1 - [NUP93_BOVIN]	2.49	3.17	1	0	1	1	5.712E4	819	93.4	5.72	TRUE	402
P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]	2.48	1.77	1	0	1	1	3.295E4	564	60.0	8.00	FALSE	161
P42785	Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE=1 SV=1 - [PCP_HUMAN]	2.48	2.82	1	1	1	1		496	55.8	7.21	TRUE	402
P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3 - [AATM_HUMAN]	2.47	3.26	1	1	1	1	6.630E4	430	47.5	9.01	FALSE	161
O60884	DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1 - [DNJA2_HUMAN]	2.46	6.55	1	0	2	2	9.562E4	412	45.7	6.48	TRUE	402
Q2HJ94	DnaJ homolog subfamily A member 2 OS=Bos taurus GN=DNAJA2 PE=2 SV=1 - [DNJA2_BOVIN]	2.46	6.55	1	0	2	2	9.562E4	412	45.7	6.48	TRUE	402
Q6P2I3	Fumarylacetoacetate hydrolase domain-containing protein 2B OS=Homo sapiens GN=FAHD2B PE=2 SV=1 - [FAH2B_HUMAN]	2.46	5.41	1	0	1	1	9.859E4	314	34.6	7.75	TRUE	402
Q96GK7	Fumarylacetoacetate hydrolase domain-containing protein 2A OS=Homo sapiens GN=FAHD2A PE=1 SV=1 - [FAH2A_HUMAN]	2.46	5.41	1	0	1	1	9.859E4	314	34.6	8.24	FALSE	161
Q96LK8	Spermatogenesis-associated protein 32 OS=Homo sapiens GN=SPATA32 PE=1 SV=3 - [SPT32_HUMAN]	2.45	4.95	1	1	1	1	8.276E4	384	42.3	4.77	TRUE	402
Q9BG11	Peroxiredoxin-5, mitochondrial OS=Bos taurus GN=PRDX5 PE=2 SV=2 - [PRDX5_BOVIN]	2.44	3.65	1	0	1	1	9.084E4	219	23.2	8.07	FALSE	161
P55854	Small ubiquitin-related modifier 3 OS=Homo	2.43	11.65	1	0	1	1		103	11.6	5.49	TRUE	402

	sapiens GN=SUMO3 PE=1 SV=2 - [SUMO3_HUMAN]												
P61955	Small ubiquitin-related modifier 2 OS=Bos taurus GN=SUMO2 PE=3 SV=1 - [SUMO2_BOVIN]	2.43	12.63	1	0	1	1		95	10.9	5.50	TRUE	402
Q6EEV6	Small ubiquitin-related modifier 4 OS=Homo sapiens GN=SUMO4 PE=1 SV=2 - [SUMO4_HUMAN]	2.43	12.63	1	0	1	1		95	10.7	7.18	TRUE	402
Q17QV3	Small ubiquitin-related modifier 3 OS=Bos taurus GN=SUMO3 PE=3 SV=1 - [SUMO3_BOVIN]	2.43	11.54	1	0	1	1		104	11.7	5.95	TRUE	402
P41976	Superoxide dismutase [Mn], mitochondrial OS=Bos taurus GN=SOD2 PE=2 SV=1 - [SODM_BOVIN]	2.42	6.31	1	0	1	1		222	24.6	8.54	FALSE	161
Q5VZ72	Izumo sperm-egg fusion protein 3 OS=Homo sapiens GN=IZUMO3 PE=2 SV=4 - [IZUM3_HUMAN]	2.41	3.77	1	1	1	1	1.325E4	239	27.7	8.29	FALSE	161
Q32LE5	Isoaspartyl peptidase/L-asparaginase OS=Bos taurus GN=ASRGL1 PE=2 SV=1 - [ASGL1_BOVIN]	2.40	3.90	1	0	1	1		308	32.0	7.40	TRUE	402
Q86VQ3	Thioredoxin domain-containing protein 2 OS=Homo sapiens GN=TXNDC2 PE=1 SV=4 - [TXND2_HUMAN]	2.39	8.14	1	2	2	2		553	60.4	4.87	TRUE	402
Q9HAE3	EF-hand calcium-binding domain-containing protein 1 OS=Homo sapiens GN=EFCAB1 PE=2 SV=1 - [EFCB1_HUMAN]	2.36	5.21	1	1	1	1	3.218E4	211	24.5	5.06	TRUE	402
Q96BH3	Epididymal sperm-binding protein 1 OS=Homo sapiens GN=ELSPBP1 PE=1 SV=2 - [ESPB1_HUMAN]	2.34	5.83	1	1	1	1		223	26.1	6.62	TRUE	402
P20674	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2 - [COX5A_HUMAN]	2.34	6.00	1	1	1	1	1.770E4	150	16.8	6.79	TRUE	402
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3 - [GANAB_HUMAN]	2.34	1.59	1	1	1	1	5.476E4	944	106.8	6.14	TRUE	402
P56597	Nucleoside diphosphate kinase homolog 5	2.33	8.49	1	1	1	1		212	24.2	6.29	TRUE	402

	OS=Homo sapiens GN=NME5 PE=2 SV=1 - [NDK5_HUMAN]												
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 - [PSB4_HUMAN]	2.32	3.79	1	0	1	1		264	29.2	5.97	TRUE	402
Q3T108	Proteasome subunit beta type-4 OS=Bos taurus GN=PSMB4 PE=1 SV=1 - [PSB4_BOVIN]	2.32	3.79	1	0	1	1		264	29.0	5.67	TRUE	402
Q96GG9	DCN1-like protein 1 OS=Homo sapiens GN=DCUN1D1 PE=1 SV=1 - [DCNL1_HUMAN]	2.32	6.56	1	1	1	1	7.175E3	259	30.1	5.34	TRUE	402
P09496	Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1 - [CLCA_HUMAN]	2.32	3.63	1	0	1	1	2.940E3	248	27.1	4.51	TRUE	402
P04973	Clathrin light chain A OS=Bos taurus GN=CLTA PE=1 SV=1 - [CLCA_BOVIN]	2.32	3.70	1	0	1	1	2.940E3	243	26.7	4.51	TRUE	402
P02769	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4 - [ALBU_BOVIN]	2.31	2.47	1	0	1	1	4.697E4	607	69.2	6.18	TRUE	402
Q16563	Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 PE=1 SV=1 - [SYPL1_HUMAN]	2.29	4.25	1	1	1	1		259	28.5	8.43	FALSE	161
P36542	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 - [ATPG_HUMAN]	2.27	4.03	1	1	1	1	4.119E4	298	33.0	9.22	FALSE	161
Q99417	C-Myc-binding protein OS=Homo sapiens GN=MYCBP PE=1 SV=3 - [MYCBP_HUMAN]	2.25	25.24	1	0	2	2		103	12.0	5.91	TRUE	402
Q2TBP7	C-Myc-binding protein OS=Bos taurus GN=MYCBP PE=3 SV=3 - [MYCBP_BOVIN]	2.25	25.24	1	0	2	2		103	12.0	5.91	TRUE	402
O14645	Axonemal dynein light intermediate polypeptide 1 OS=Homo sapiens GN=DNALI1 PE=1 SV=2 - [IDL1_HUMAN]	2.24	6.59	1	1	1	2	7.518E4	258	29.6	8.50	FALSE	161
Q5EA85	Semaphorin-4A OS=Bos taurus GN=SEMA4A PE=2 SV=1 - [SEM4A_BOVIN]	2.23	2.36	1	1	1	1		762	83.6	6.54	TRUE	402
Q58FF6	Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4 PE=5 SV=1 - [H90B4_HUMAN]	2.23	3.76	1	0	2	2	2.628E5	505	58.2	4.73	TRUE	402
P52565	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1 PE=1 SV=3 - [GDIR1_HUMAN]	2.21	7.35	1	1	1	1	2.587E4	204	23.2	5.11	TRUE	402

P30046	D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3 - [DOPD_HUMAN]	2.19	9.32	1	1	1	1	4.206E4	118	12.7	7.30	TRUE	402
P34949	Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=2 - [MPI_HUMAN]	2.18	3.78	1	1	1	1		423	46.6	5.95	TRUE	402
Q9Y4F5	Centrosomal protein of 170 kDa protein B OS=Homo sapiens GN=CEP170B PE=1 SV=4 - [C170B_HUMAN]	2.17	0.69	1	1	1	1	1.316E5	1589	171.6	6.84	TRUE	402
A5D989	Elongation factor 1-delta OS=Bos taurus GN=EEF1D PE=2 SV=2 - [EF1D_BOVIN]	2.17	4.29	1	0	1	1		280	31.1	5.06	TRUE	402
P54725	UV excision repair protein RAD23 homolog A OS=Homo sapiens GN=RAD23A PE=1 SV=1 - [RD23A_HUMAN]	2.17	2.20	1	0	1	1	2.971E4	363	39.6	4.58	TRUE	402
A3KMV2	UV excision repair protein RAD23 homolog A OS=Bos taurus GN=RAD23A PE=2 SV=1 - [RD23A_BOVIN]	2.17	2.21	1	0	1	1	2.971E4	362	39.6	4.58	TRUE	402
Q9BVM2	Protein DPCD OS=Homo sapiens GN=DPCD PE=1 SV=2 - [DPCD_HUMAN]	2.16	4.93	1	1	1	1	2.046E4	203	23.2	9.03	FALSE	161
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4 - [TPP2_HUMAN]	2.15	0.88	1	1	1	1		1249	138.3	6.32	TRUE	402
Q9NQC3	Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2 - [RTN4_HUMAN]	2.11	0.92	1	1	1	1	5.728E3	1192	129.9	4.50	TRUE	402
Q2NKG6	Protein dpy-30 homolog OS=Bos taurus GN=DPY30 PE=3 SV=1 - [DPY30_BOVIN]	2.10	9.09	1	1	1	1		99	11.2	4.88	TRUE	402
P24539	ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 - [AT5F1_HUMAN]	2.10	4.69	1	1	1	1	1.218E4	256	28.9	9.36	FALSE	161
P02545	Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 - [LMNA_HUMAN]	2.09	1.36	1	1	1	1	8.717E3	664	74.1	7.02	TRUE	402
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1 - [PSA1_HUMAN]	2.09	5.70	1	0	1	1		263	29.5	6.61	TRUE	402
Q3T0X5	Proteasome subunit alpha type-1 OS=Bos taurus GN=PSMA1 PE=1 SV=1 - [PSA1_BOVIN]	2.09	5.70	1	0	1	1		263	29.6	6.61	TRUE	402
P35968	Vascular endothelial growth factor receptor 2 OS=Homo sapiens GN=KDR PE=1 SV=2 - [VGFR2_HUMAN]	2.09	0.66	1	1	1	1		1356	151.4	5.85	TRUE	402

P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	2.09	2.03	1	1	1	1	1.845E4	592	67.5	4.60	TRUE	402
Q15435	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1 - [PP1R7_HUMAN]	2.08	5.28	1	1	2	2	2.950E4	360	41.5	4.91	TRUE	402
O75951	Lysozyme-like protein 6 OS=Homo sapiens GN=LYZL6 PE=2 SV=1 - [LYZL6_HUMAN]	2.06	6.08	1	1	1	1	5.879E4	148	16.9	6.14	TRUE	402
Q29RV1	Protein disulfide-isomerase A4 OS=Bos taurus GN=PDIA4 PE=2 SV=1 - [PDIA4_BOVIN]	2.04	2.33	1	0	1	1	1.023E5	643	72.5	5.12	TRUE	402
Q9H1X1	Radial spoke head protein 9 homolog OS=Homo sapiens GN=RSPH9 PE=1 SV=1 - [RSPH9_HUMAN]	2.04	11.23	1	2	2	2	3.263E4	276	31.3	5.43	TRUE	402
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN]	2.03	4.88	1	0	1	1		205	22.8	6.40	TRUE	402
Q3T149	Heat shock protein beta-1 OS=Bos taurus GN=HSPB1 PE=2 SV=1 - [HSPB1_BOVIN]	2.03	4.98	1	0	1	1		201	22.4	6.40	TRUE	402
Q9H853	Putative tubulin-like protein alpha-4B OS=Homo sapiens GN=TUBA4B PE=5 SV=2 - [TBA4B_HUMAN]	2.01	5.81	1	0	1	1	3.616E4	241	27.5	7.83	TRUE	402
O00330	Pyruvate dehydrogenase protein X component, mitochondrial OS=Homo sapiens GN=PDHX PE=1 SV=3 - [ODPX_HUMAN]	2.00	3.39	1	0	1	1	4.838E4	501	54.1	8.66	FALSE	161
P22439	Pyruvate dehydrogenase protein X component OS=Bos taurus GN=PDHX PE=1 SV=3 - [ODPX_BOVIN]	2.00	3.39	1	0	1	1	4.838E4	501	53.9	8.44	FALSE	161
Q9Y2B0	Protein canopy homolog 2 OS=Homo sapiens GN=CNPY2 PE=1 SV=1 - [CNPY2_HUMAN]	2.00	8.79	1	1	1	1	4.430E4	182	20.6	4.92	TRUE	402
Q7Z3Y7	Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2 - [K1C28_HUMAN]	1.99	1.94	1	0	1	1		464	50.5	5.47	TRUE	402
Q7Z3Y8	Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2 - [K1C27_HUMAN]	1.99	1.96	1	0	1	1		459	49.8	5.05	TRUE	402
Q7Z3Y9	Keratin, type I cytoskeletal 26 OS=Homo sapiens GN=KRT26 PE=1 SV=2 - [K1C26_HUMAN]	1.99	1.92	1	0	1	1		468	51.9	4.92	TRUE	402

Q7Z3Z0	Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1 - [K1C25_HUMAN]	1.99	2.00	1	0	1	1		450	49.3	5.08	TRUE	402
Q0P5J4	Keratin, type I cytoskeletal 25 OS=Bos taurus GN=KRT25 PE=2 SV=1 - [K1C25_BOVIN]	1.99	2.00	1	0	1	1		450	49.3	5.03	TRUE	402
Q0P5J6	Keratin, type I cytoskeletal 27 OS=Bos taurus GN=KRT27 PE=2 SV=1 - [K1C27_BOVIN]	1.99	1.96	1	0	1	1		460	49.9	5.10	TRUE	402
Q148H6	Keratin, type I cytoskeletal 28 OS=Bos taurus GN=KRT28 PE=2 SV=1 - [K1C28_BOVIN]	1.99	1.94	1	0	1	1		464	50.7	5.30	TRUE	402
O77797	A-kinase anchor protein 3 OS=Bos taurus GN=AKAP3 PE=2 SV=2 - [AKAP3_BOVIN]	1.97	1.17	1	0	1	1	1.760E4	858	94.6	6.71	TRUE	402
Q9BUR5	Apolipoprotein O OS=Homo sapiens GN=APOO PE=1 SV=1 - [APOO_HUMAN]	1.95	5.56	1	1	1	1	5.789E4	198	22.3	9.13	FALSE	161
O75190	DnaJ homolog subfamily B member 6 OS=Homo sapiens GN=DNAJB6 PE=1 SV=2 - [DNJB6_HUMAN]	1.95	3.07	1	0	1	1	2.497E3	326	36.1	9.16	FALSE	161
P25686	DnaJ homolog subfamily B member 2 OS=Homo sapiens GN=DNAJB2 PE=1 SV=3 - [DNJB2_HUMAN]	1.95	3.09	1	0	1	1	2.497E3	324	35.6	5.95	TRUE	402
Q0III6	DnaJ homolog subfamily B member 6 OS=Bos taurus GN=DNAJB6 PE=2 SV=1 - [DNJB6_BOVIN]	1.95	4.13	1	0	1	1	2.497E3	242	26.9	7.61	TRUE	402
Q96RQ9	L-amino-acid oxidase OS=Homo sapiens GN=IL4I1 PE=1 SV=1 - [OXLA_HUMAN]	1.94	1.76	1	1	1	1	6.345E4	567	62.8	8.68	FALSE	161
Q8TE73	Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3 - [DYH5_HUMAN]	1.93	0.17	1	1	1	1		4624	528.7	6.10	TRUE	402
Q8N387	Mucin-15 OS=Homo sapiens GN=MUC15 PE=2 SV=2 - [MUC15_HUMAN]	1.93	2.99	1	1	1	1		334	36.3	5.08	TRUE	402
Q14203	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3 - [DCTN1_HUMAN]	1.92	0.94	1	1	1	1		1278	141.6	5.81	TRUE	402
O43242	26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2 - [PSMD3_HUMAN]	1.92	2.06	1	0	1	1		534	60.9	8.44	FALSE	161
Q2KJ46	26S proteasome non-ATPase regulatory subunit 3 OS=Bos taurus GN=PSMD3 PE=2	1.92	2.06	1	0	1	1		534	60.9	8.60	FALSE	161

	SV=1 - [PSMD3_BOVIN]												
P27482	Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2 - [CALL3_HUMAN]	1.91	5.37	1	0	1	1	4.226E 5	149	16.9	4.42	TRUE	402
Q8IYS0	GRAM domain-containing protein 1C OS=Homo sapiens GN=GRAMD1C PE=2 SV=2 - [GRM1C_HUMAN]	1.88	1.21	1	1	1	1	4.697E 3	662	76.0	7.24	TRUE	402
P46379	Large proline-rich protein BAG6 OS=Homo sapiens GN=BAG6 PE=1 SV=2 - [BAG6_HUMAN]	1.88	2.03	1	2	2	2	1.105E 5	113 2	119. 3	5.60	TRUE	402
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4 - [PSB6_HUMAN]	1.88	4.60	1	1	1	1	2.213E 4	239	25.3	4.92	TRUE	402
Q6UXV1	Izumo sperm-egg fusion protein 2 OS=Homo sapiens GN=IZUMO2 PE=2 SV=1 - [IZUM2_HUMAN]	1.86	6.33	1	1	1	1	3.072E 4	221	24.8	8.79	FALSE	161
A5PKW4	PH and SEC7 domain-containing protein 1 OS=Homo sapiens GN=PSD PE=1 SV=2 - [PSD1_HUMAN]	1.86	1.07	1	1	1	1	3.813E 4	102 4	109. 5	6.87	TRUE	402
P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	1.81	2.25	1	0	1	1		400	44.1	5.14	TRUE	402
P19012	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3 - [K1C15_HUMAN]	1.81	1.97	1	0	1	1		456	49.2	4.77	TRUE	402
Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2 - [K1C17_HUMAN]	1.81	2.08	1	0	1	1		432	48.1	5.02	TRUE	402
A1L595	Keratin, type I cytoskeletal 17 OS=Bos taurus GN=KRT17 PE=2 SV=1 - [K1C17_BOVIN]	1.81	2.04	1	0	1	1		441	48.7	5.15	TRUE	402
P08728	Keratin, type I cytoskeletal 19 OS=Bos taurus GN=KRT19 PE=2 SV=1 - [K1C19_BOVIN]	1.81	2.26	1	0	1	1		399	43.9	5.01	TRUE	402
Q6J272	Protein FAM166A OS=Homo sapiens GN=FAM166A PE=2 SV=1 - [F166A_HUMAN]	1.81	3.79	1	1	1	1	2.195E 4	317	36.1	7.81	TRUE	402
Q9BQP9	BPI fold-containing family A member 3 OS=Homo sapiens GN=BPIFA3 PE=2 SV=3 - [BPIA3_HUMAN]	1.81	3.54	1	1	1	1		254	28.4	6.65	TRUE	402

P48047	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 - [ATPO_HUMAN]	1.80	5.63	1	1	1	1		213	23.3	9.96	FALSE	161
Q92896	Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2 - [GSLG1_HUMAN]	1.79	1.10	1	1	1	1		117 9	134. 5	6.90	TRUE	402
P07107	Acyl-CoA-binding protein OS=Bos taurus GN=DBI PE=1 SV=2 - [ACBP_BOVIN]	1.78	9.20	1	0	1	1	2.045E 5	87	10.0	6.57	TRUE	402
P13696	Phosphatidylethanolamine-binding protein 1 OS=Bos taurus GN=PEBP1 PE=1 SV=2 - [PEBP1_BOVIN]	1.77	7.49	1	0	1	1	1.209E 5	187	21.0	7.49	TRUE	402
P14174	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4 - [MIF_HUMAN]	1.75	7.83	1	1	1	1	2.094E 5	115	12.5	7.88	TRUE	402
Q5JVL4	EF-hand domain-containing protein 1 OS=Homo sapiens GN=EFHC1 PE=1 SV=1 - [EFHC1_HUMAN]	1.74	1.25	1	1	1	1	2.528E 4	640	73.9	6.16	TRUE	402
Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	1.72	2.01	1	1	1	1		597	68.0	6.35	TRUE	402
Q15631	Translin OS=Homo sapiens GN=TSN PE=1 SV=1 - [TSN_HUMAN]	1.71	4.39	1	0	1	1	5.379E 3	228	26.2	6.44	TRUE	402
Q08DM8	Translin OS=Bos taurus GN=TSN PE=2 SV=1 - [TSN_BOVIN]	1.71	4.39	1	0	1	1	5.379E 3	228	26.2	6.44	TRUE	402
O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
P06899	Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3 - [H2B1J_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
P23527	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3 - [H2B1O_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
P33778	Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2 - [H2B1B_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
P57053	Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2 - [H2BFS_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 7	FALSE	161
P58876	Histone H2B type 1-D OS=Homo sapiens GN=HIST1H2BD PE=1 SV=2 - [H2B1D_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
P62807	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4 -	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161

	[H2B1C_HUMAN]												
Q16778	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3 - [H2B2E_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
Q5QNW 6	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3 - [H2B2F_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
Q8N257	Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3 - [H2B3B_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
Q93079	Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3 - [H2B1H_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
Q96A08	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3 - [H2B1A_HUMAN]	1.66	8.66	1	0	1	3	1.930E 4	127	14.2	10.3 2	FALSE	161
Q99877	Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3 - [H2B1N_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
Q99879	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3 - [H2B1M_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	14.0	10.3 2	FALSE	161
Q99880	Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3 - [H2B1L_HUMAN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
Q2M2T1	Histone H2B type 1-K OS=Bos taurus GN=HIST1H2BK PE=1 SV=3 - [H2B1K_BOVIN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.2 9	FALSE	161
Q32L48	Histone H2B type 1-N OS=Bos taurus GN=HIST1H2BN PE=1 SV=3 - [H2B1N_BOVIN]	1.66	8.73	1	0	1	3	1.930E 4	126	13.9	10.3 2	FALSE	161
Q99490	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=AGAP2 PE=1 SV=2 - [AGAP2_HUMAN]	1.65	0.67	1	0	1	1		119 2	124. 6	9.89	FALSE	161
O94905	Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1 - [ERLN2_HUMAN]	1.64	3.54	1	1	1	1	7.960E 3	339	37.8	5.62	TRUE	402
P80513	Mesencephalic astrocyte-derived neurotrophic factor OS=Bos taurus GN=MANF PE=1 SV=2 - [MANF_BOVIN]	1.63	5.59	1	0	1	1		179	20.3	8.54	FALSE	161
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2 - [LDHA_HUMAN]	1.62	6.02	1	1	1	1	2.796E 3	332	36.7	8.27	FALSE	161
A7YWG4	Gamma-glutamyl hydrolase OS=Bos taurus GN=GGH PE=2 SV=1 - [GGH_BOVIN]	1.62	3.14	1	0	1	1		318	35.7	9.06	FALSE	161

P55052	Fatty acid-binding protein, epidermal OS=Bos taurus GN=FABP5 PE=1 SV=4 - [FABP5_BOVIN]	1.61	6.67	1	0	1	1		135	15.1	7.69	TRUE	402
B2RXF5	Zinc finger and BTB domain-containing protein 42 OS=Homo sapiens GN=ZBTB42 PE=1 SV=2 - [ZBT42_HUMAN]	0.00	3.08	1	1	1	1	6.901E3	422	46.5	8.47	FALSE	161
O60232	Sjogren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1 - [SSA27_HUMAN]	0.00	4.02	1	1	1	1	2.285E4	199	21.5	5.24	TRUE	402
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 - [HPRT_HUMAN]	0.00	4.59	1	1	1	1	2.227E4	218	24.6	6.68	TRUE	402
P0C0S4	Histone H2A.Z OS=Bos taurus GN=H2AFZ PE=1 SV=2 - [H2AZ_BOVIN]	0.00	7.03	1	0	1	1		128	13.5	10.58	FALSE	161
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1 - [GTR3_HUMAN]	0.00	1.81	1	0	1	1		496	53.9	7.20	TRUE	402
P18754	Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1 - [RCC1_HUMAN]	0.00	3.56	1	1	1	1	5.592E4	421	44.9	7.52	TRUE	402
P20810	Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4 - [ICAL_HUMAN]	0.00	2.40	1	1	1	1	4.461E4	708	76.5	5.07	TRUE	402
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	0.00	1.82	1	0	1	1	1.942E4	658	73.7	8.18	FALSE	161
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN]	0.00	4.56	1	1	1	1	7.885E3	263	28.5	6.92	TRUE	402
P29218	Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1 PE=1 SV=1 - [IMPA1_HUMAN]	0.00	7.94	1	2	2	2	2.115E4	277	30.2	5.26	TRUE	402
P45880	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 - [VDAC2_HUMAN]	0.00	3.40	1	0	1	1		294	31.5	7.56	TRUE	402
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1 - [ACADV_HUMAN]	0.00	2.90	1	1	1	1	3.976E4	655	70.3	8.75	FALSE	161

P53597	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4 - [SUCA_HUMAN]	0.00	4.34	1	1	1	1		346	36.2	8.79	FALSE	161
P54107	Cysteine-rich secretory protein 1 OS=Homo sapiens GN=CRISP1 PE=1 SV=1 - [CRIS1_HUMAN]	0.00	8.03	1	1	1	1	6.720E4	249	28.5	5.91	TRUE	402
Q15785	Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TOMM34 PE=1 SV=2 - [TOM34_HUMAN]	0.00	2.91	1	1	1	1	1.556E4	309	34.5	8.98	FALSE	161
Q32LA7	Histone H2A.V OS=Bos taurus GN=H2AFV PE=2 SV=3 - [H2AV_BOVIN]	0.00	7.03	1	0	1	1		128	13.5	10.58	FALSE	161
A7MBJ5	Cullin-associated NEDD8-dissociated protein 1 OS=Bos taurus GN=CAND1 PE=2 SV=1 - [CAND1_BOVIN]	0.00	1.06	1	1	1	1	1.109E5	1230	136.3	5.78	TRUE	402
Q8NAM6	Zinc finger and SCAN domain-containing protein 4 OS=Homo sapiens GN=ZSCAN4 PE=2 SV=1 - [ZSCA4_HUMAN]	0.00	2.08	1	1	1	1		433	48.9	6.95	TRUE	402
Q8TDB8	Solute carrier family 2, facilitated glucose transporter member 14 OS=Homo sapiens GN=SLC2A14 PE=2 SV=1 - [GTR14_HUMAN]	0.00	1.73	1	0	1	1		520	56.3	7.83	TRUE	402
Q96E40	Uncharacterized protein C9orf9 OS=Homo sapiens GN=C9orf9 PE=2 SV=1 - [CI009_HUMAN]	0.00	10.36	1	2	2	2		222	25.1	9.13	FALSE	161
Q96KW9	Protein SPACA7 OS=Homo sapiens GN=SPACA7 PE=2 SV=2 - [SPAC7_HUMAN]	0.00	5.13	1	1	1	1	3.939E3	195	21.5	4.78	TRUE	402
Q9BYC2	Succinyl-CoA:3-ketoacid coenzyme A transferase 2, mitochondrial OS=Homo sapiens GN=OXCT2 PE=2 SV=2 - [SCOT2_HUMAN]	0.00	5.22	1	1	1	1	6.651E4	517	56.1	7.14	TRUE	402
Q9C0H9	SRC kinase signaling inhibitor 1 OS=Homo sapiens GN=SRCIN1 PE=1 SV=3 - [SRCN1_HUMAN]	0.00	1.42	1	1	1	1		1055	112.4	9.29	FALSE	161
Q9H0K4	Radial spoke head protein 6 homolog A OS=Homo sapiens GN=RSPH6A PE=2 SV=1 - [RSH6A_HUMAN]	0.00	1.81	1	1	1	1	1.168E4	717	80.9	4.39	TRUE	402
Q9NVE4	Coiled-coil domain-containing protein 87	0.00	0.82	1	1	1	1		849	96.3	8.59	FALSE	161

	OS=Homo sapiens GN=CCDC87 PE=2 SV=2 - [CCD87_HUMAN]												
Q9P1Z2	Calcium-binding and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=CALCOCO1 PE=1 SV=2 - [CACO1_HUMAN]	0.00	1.01	1	0	1	1		691	77.3	4.82	TRUE	402
Q9UJ68	Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens GN=MSRA PE=1 SV=1 - [MSRA_HUMAN]	0.00	6.38	1	1	1	1	2.974E4	235	26.1	8.09	FALSE	161
Q9UNZ2	NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2 - [NSF1C_HUMAN]	0.00	3.24	1	0	1	1		370	40.5	5.10	TRUE	402
P13620	ATP synthase subunit d, mitochondrial OS=Bos taurus GN=ATP5H PE=1 SV=2 - [ATP5H_BOVIN]	0.00	5.59	1	0	1	1	7.300E4	161	18.7	6.24	TRUE	402
P58352	Solute carrier family 2, facilitated glucose transporter member 3 OS=Bos taurus GN=SLC2A3 PE=2 SV=1 - [GTR3_BOVIN]	0.00	1.82	1	0	1	1		494	54.0	5.60	TRUE	402
P68002	Voltage-dependent anion-selective channel protein 2 OS=Bos taurus GN=VDAC2 PE=2 SV=2 - [VDAC2_BOVIN]	0.00	3.40	1	0	1	1		294	31.6	7.55	TRUE	402
Q2KIL1	Uncharacterized protein C1orf141 homolog OS=Bos taurus PE=2 SV=1 - [CA141_BOVIN]	0.00	3.95	1	1	1	1		430	49.7	9.73	FALSE	161
Q2KJ21	Calcium-binding and coiled-coil domain-containing protein 1 OS=Bos taurus GN=CALCOCO1 PE=2 SV=1 - [CACO1_BOVIN]	0.00	1.03	1	0	1	1		680	75.6	4.93	TRUE	402
Q2KJB7	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Bos taurus GN=CPT2 PE=2 SV=1 - [CPT2_BOVIN]	0.00	1.82	1	0	1	1	1.942E4	658	74.4	8.13	FALSE	161
Q3SZC4	NSFL1 cofactor p47 OS=Bos taurus GN=NSFL1C PE=2 SV=1 - [NSF1C_BOVIN]	0.00	3.24	1	0	1	1		370	40.6	5.19	TRUE	402
Q3TOW4	Protein phosphatase 1 regulatory subunit 7 OS=Bos taurus GN=PPP1R7 PE=1 SV=1 - [PP1R7_BOVIN]	0.00	2.78	1	0	1	1		360	41.4	4.96	TRUE	402

Suppl Table 5

UniProt/SwissProt Accession	Description	Uniprot Gene Name	Potential HA-binding domain (N)
O14645	dynein axonemal light intermediate chain 1	DNALI1	BX7B (1)
O15173	progesterone receptor membrane component 2	PGRMC2	BX7B (1)
O43805	SS nuclear autoantigen 1	SSNA1	N/D
O60664	perilipin 3	PLIN3	N/D
O75071	EF-hand calcium binding domain 14	EFCAB14	N/D
O75521	enoyl-CoA delta isomerase 2	ECI2	BX7B (3)
O75947	ATP synthase, H <sup>+</sup> transporting, mitochondrial Fo complex subunit D	ATP5H	N/D
O75951	lysozyme like 6	LYZL6	N/D
O95202	leucine zipper and EF-hand containing transmembrane protein 1	LETM1	N/D
O95757	heat shock protein family A (Hsp70) member 4 like	HSPA4L	BX7B (1)
P00441	superoxide dismutase 1, soluble	SOD1	N/D
P02751	fibronectin 1	FN1	BX7B (4)
P07108	diazepam binding inhibitor, acyl-CoA binding protein	DBI	N/D
P10515	dihydrolipoamide S-acetyltransferase	DLAT	N/D
P10809	heat shock protein family D (Hsp60) member 1	HSPD1	N/D
P12273	prolactin induced protein	PIP	N/D
P12821	angiotensin I converting enzyme	ACE	N/D

P13639	eukaryotic translation elongation factor 2	EEF2	N/D
P13861	protein kinase cAMP-dependent type II regulatory subunit alpha	PRKAR2A	N/D
P14174	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	MIF	N/D
P14314	protein kinase C substrate 80K-H	PRKCSH	N/D
P14927	ubiquinol-cytochrome c reductase binding protein	UQCRB	N/D
P15289	arylsulfatase A	ARSA	N/D
P17174	glutamic-oxaloacetic transaminase 1	GOT1	N/D
P18859	ATP synthase, H <sup>+</sup> transporting, mitochondrial Fo complex subunit F6	ATP5J	N/D
P20674	cytochrome c oxidase subunit 5A	COX5A	N/D
P20810	calpastatin	CAST	BX7B (2)
P22695	ubiquinol-cytochrome c reductase core protein II	UQCRC2	N/D
P25325	mercaptopyruvate sulfurtransferase	MPST	N/D
P27797	calreticulin	CALR	BX7B (1)
P27824	calnexin	CANX	BX7B (1)
P29692	eukaryotic translation elongation factor 1 delta	EEF1D	N/D
P30044	peroxiredoxin 5	PRDX5	N/D
P30086	phosphatidylethanolamine binding protein 1	PEBP1	BX7B (1)
P31930	ubiquinol-cytochrome c reductase core protein I	UQCRC1	N/D
P31937	3-hydroxyisobutyrate dehydrogenase	HIBADH	N/D
P37198	nucleoporin 62	NUP62	N/D

P46379	BCL2 associated athanogene 6	BAG6	BX7B (2)
P48047	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, O subunit	ATP5O	BX7B (1)
P48643	chaperonin containing TCP1 subunit 5	CCT5	N/D
P50991	chaperonin containing TCP1 subunit 4	CCT4	BX7B (1)
P54709	ATPase Na <sup>+</sup> /K <sup>+</sup> transporting subunit beta 3	ATP1B3	BX7B (3)
P54727	RAD23 homolog B, nucleotide excision repair protein	RAD23B	N/D
P59282	tubulin polymerization promoting protein family member 2	TPPP2	N/D
P62491	RAB11A, member RAS oncogene family	RAB11A	N/D
Q04837	single stranded DNA binding protein 1	SSBP1	N/D
Q13561	dynactin subunit 2	DCTN2	N/D
Q14203	dynactin subunit 1	DCTN1	BX7B (3)
Q14697	glucosidase II alpha subunit	GANAB	N/D
Q15506	sperm autoantigenic protein 17 [Source:HGNC Symbol;Acc:HGNC:11210]	SPA17	N/D
Q16543	cell division cycle 37	CDC37	BX7B (1)
Q16563	synaptophysin like 1	SYPL1	N/D
Q3LXA3	triokinase and FMN cyclase	TKFC	N/D
Q5VZ72	IZUMO family member 3	IZUMO3	BX7B (1)
Q6BCY4	cytochrome b5 reductase 2	CYB5R2	N/D
Q7L266	asparaginase like 1	ASRGL1	N/D
Q7Z6W1	transmembrane and coiled-coil domains 2	TMCO2	BX7B (1)

Q86VQ3	thioredoxin domain containing 2	TXNDC2	N/D
Q86Y82	syntaxin 12	STX12	N/D
Q8IXA5	sperm acrosome associated 3	SPACA3	N/D
Q8IYT1	family with sequence similarity 71 member A	FAM71A	BX7B (3)
Q8N4E7	ferritin mitochondrial	FTMT	BX7B (1)
Q8NHS0	DnaJ heat shock protein family (Hsp40) member B8	DNAJB8	BX7B (1)
Q8TC56	family with sequence similarity 71 member B	FAM71B	BX7B (2)
Q8TDM5	sperm acrosome associated 4	SPACA4	N/D
Q8WW22	DnaJ heat shock protein family (Hsp40) member A4	DNAJA4	N/D
Q8WYR4	radial spoke head 1 homolog	RSPH1	BX7B (2)
Q96C74	rhophilin associated tail protein 1 like	ROPN1L	N/D
Q96JQ2	calmin	CLMN	BX7B (3)
Q96KW9	sperm acrosome associated 7 [Source:HGNC Symbol;Acc:HGNC:29575]	SPACA7	N/D
Q9BSF0	chromosome 2 open reading frame 88	C2orf88	N/D
Q9BVL2	nucleoporin 58	NUP58	BX7B (1)
Q9BX68	histidine triad nucleotide binding protein 2	HINT2	N/D
Q9BY14	testis expressed 101	TEX101	N/D
Q9H3G5	carboxypeptidase, vitellogenic like	CPVL	N/D
Q9H4B8	dipeptidase 3	DPEP3	BX7B (1)
Q9NQ60	equatorin	EQTN	N/D

Q9UBX1	cathepsin F	CTSF	BX7B (2)
Q9Y2B0	canopy FGF signaling regulator 2	CNPY2	N/D
Q9Y4L1	hypoxia up-regulated 1	HYOU1	BX7B (3)
Q8IZP2	Putative protein FAM10A4	ST13P4	BX7B (1)

N/D: Not-detected.

For Review Only

Suppl Table 6

Annotation Cluster 1	Enrichment Score: 1.93											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferro ni	Benjami ni	FDR
UP_KEYWORDS	Secreted	10	35.71	6.16E-04	P21741, Q16568, P20155, P03973, Q6UWM5, Q96KX0, P05109, Q96QH8, Q6X784, A4D1T9	28	1965	20581	3.74064	0.049262	0.049262	0.655983
UP_SEQ_FEATURE	signal peptide	11	39.28	0.006566	P21741, Q16568, Q6P4A8, Q8WZ59, P20155, P03973, Q6UWM5, Q96KX0, Q96QH8, Q6X784, Q8TC27	27	3346	20063	2.442862	0.549394	0.549394	7.294336
UP_KEYWORDS	Signal	12	42.85	0.01183	P21741, Q16568, Q6P4A8, Q8WZ59, P20155,	28	4160	20581	2.120295	0.62312	0.386094	11.93837

					P03973, Q6UWM5, Q96KX0, Q96QH8, Q6X784, Q8TC27, A4D1T9							
UP_KEYWORDS	Disulfide bond	10	35.71	0.026459	P21741, Q16568, Q6P4A8, Q8WZ59, P20155, P03973, Q96KX0, Q96QH8, Q8TC27, A4D1T9	28	3434	20581	2.140465	0.889074	0.519518	24.90958
UP_SEQ_FEATURE	disulfide bond	7	25	0.166538	P21741, Q16568, P20155, P03973, Q96KX0, Q96QH8, Q8TC27	27	2917	20063	1.783174	1	0.999984	87.68431
Annotation Cluster 2	Enrichment Score: 0.7449193210512107											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferro ni	Benjami ni	FDR
UP_KEYWORDS	Mitochondrion	5	17.85	0.056326	P99999, Q9NPJ3, Q00796, Q9UII2,	28	1119	20581	3.284342	0.991382	0.695313	46.17043

					Q16836							
KEGG_PATHWAY	hsa01100:Metabolic pathways	3	10.71	0.217781	P99999, Q00796, Q16836	6	1228	6910	2.813518	0.999764	0.999764	88.46748
UP_KEYWORDS	Acetylation	6	21.42	0.474806	P99999, Q9BVA1, Q9NPJ3, Q00796, Q13618, Q16836	28	3424	20581	1.28803	1	0.982787	99.89717
Annotation Cluster 3 Enrichment Score: 0.5024513212592925												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferro ni	Benjami ni	FDR
UP_KEYWORDS	Isopeptide bond	4	14.28	0.183541	P62987, Q9BVA1, P13647, Q13618	28	1132	20581	2.597299	1	0.907023	88.54006
UP_KEYWORDS	Ubl conjugation	4	14.28	0.389801	P62987, Q9BVA1, P13647, Q13618	28	1705	20581	1.724424	1	0.974835	99.48931
UP_KEYWORDS	Disease mutation	5	17.85	0.434581	P99999, Q9BVA1, P13647, Q13618, Q16836	28	2550	20581	1.441246	1	0.979683	99.77378
Annotation Cluster 4 Enrichment Score: 0.004126007188424786												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferro ni	Benjami ni	FDR

UP_KEYWORDS	Membrane	6	21.42857	0.987437	Q9BWH2, Q8WZ59, Q00796, Q6NUT2, P05109, Q8TC27	28	7494	20581	0.588499	1	1	100
UP_KEYWORDS	Transmembrane helix	4	14.28571	0.989198	Q9BWH2, Q8WZ59, Q6NUT2, Q8TC27	28	5634	20581	0.521857	1	1	100
UP_KEYWORDS	Transmembrane	4	14.28571	0.989446	Q9BWH2, Q8WZ59, Q6NUT2, Q8TC27	28	5651	20581	0.520287	1	1	100
GOTERM_CC_DIRECTORY	GO:0016021~integral component of membrane	4	14.28571	0.991776	Q9BWH2, Q8WZ59, Q6NUT2, Q8TC27	28	5163	18224	0.504247	1	1	100
UP_SEQ_FEATURE	transmembrane region	3	10.71429	0.994882	Q8WZ59, Q6NUT2, Q8TC27	27	5056	20063	0.440906	1	1	100

Suppl Table 7

Annotation Cluster	Enrichment Score: 7.263306394290177											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferro ni	Benjami ni	FDR
UP_KEYWORDS	Chaperone	11	13.58025	5.74E-09	Q16543, Q8NHS0, P27824, P46379, O95757, P10809, P48643, P27797, Q8WW22, P50991, Q9Y4L1	81	201	20581	13.90523	9.98E-07	4.99E-07	7.02E-06
GOTERM_BP_DIRECT	GO:0006457~protein folding	10	12.34568	7.29E-08	Q16543, P27824, P14314, O95757, Q14697, P48643, P27797, Q86VQ3, Q8WW22, P50991	73	180	16792	12.7793	3.78E-05	3.78E-05	1.05E-04
GOTERM_MF_DIRECT	GO:0051082~unfolded protein binding	8	9.876543	3.88E-07	Q16543, Q8NHS0,	72	110	16881	17.05152	7.57E-05	7.57E-05	4.85E-04

					P27824, P10809, P48643, P27797, Q8WW2 2, P50991							
Annotation Cluster 2	Enrichment Score: 5.760055409435151											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferro ni	Benjami ni	FDR
UP_SEQ_FEATURE	transit peptide:Mitochondrion	14	17.2839 5	5.50E- 08	O75521, P10515, O95202, P20674, Q04837, P30044, P31930, P31937, P10809, P48047, Q8N4E7, P18859, Q9BX68, P22695	81	482	2006 3	7.194355	1.77E-05	1.77E-05	7.43E- 05
UP_KEYWORDS	Transit peptide	14	17.2839 5	1.40E- 07	O75521, P10515, O95202, P20674, Q04837, P30044,	81	536	2058 1	6.636586	2.44E-05	8.14E-06	1.72E- 04

					P31930, P31937, P10809, P48047, Q8N4E7, P18859, Q9BX68, P22695							
UP_KEYWORDS	Mitochondrion	18	22.2222 2	1.10E- 06	P25325, O75521, P00441, P14927, P10515, O95202, P20674, Q04837, P30044, P31930, P31937, P10809, P48047, Q8N4E7, P18859, O75947, Q9BX68, P22695	81	111 9	2058 1	4.087181	1.92E-04	4.80E-05	0.00135 1
GOTERM_CC_DIRECT	GO:0005739~mitochondrion	20	24.6913 6	2.90E- 06	P25325, O75521, P00441, P17174, Q86VQ3, P10515, O95202,	80	133 1	1822 4	3.42299	4.70E-04	1.57E-04	0.00351

					P62491, Q04837, P30044, P31930, P31937, P10809, P48047, Q8N4E7, P18859, O75947, Q9BX68, P22695, Q6BCY4							
GOTERM_CC_DIRECT	GO:0005743~mitochondrial inner membrane	9	11.1111	6.41E-04	P31930, P10809, P48047, P14927, P18859, O95202, P20674, O75947, P22695	80	441	18224	4.64898	0.098684	0.017167	0.773065
Annotation Cluster 3	Enrichment Score: 3.0122017771459957											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferro ni	Benjami ni	FDR
KEGG_PATHWAY	hsa05016:Huntington's disease	11	13.58025	1.47E-07	P31930, P48047, Q13561, Q14203, P00441,	43	192	6910	9.206638	1.22E-05	1.22E-05	1.58E-04

					P14927, P18859, P20674, O75947, O14645, P22695							
UP_KEYWORDS	Mitochondrion	18	22.2222 2	1.10E- 06	P25325, O75521, P00441, P14927, P10515, O95202, P20674, Q04837, P30044, P31930, P31937, P10809, P48047, Q8N4E7, P18859, O75947, Q9BX68, P22695	81	111 9	2058 1	4.087181	1.92E-04	4.80E-05	0.00135 1
UP_KEYWORDS	Mitochondrion inner membrane	8	9.87654 3	8.69E- 05	P31930, P48047, P14927, P18859, O95202, P20674, O75947, P22695	81	270	2058 1	7.528487	0.015004	0.00301 9	0.10635 7
KEGG_PATHWAY	hsa00190:Oxidative	7	8.64197	1.35E-	P31930,	43	133	6910	8.457772	0.01113	0.00558	0.1443

	phosphorylation		5	04	P48047, P14927, P18859, P20674, O75947, P22695						1	
KEGG_PATHWAY	hsa05012:Parkinson's disease	7	8.641975	1.93E-04	P31930, P48047, P14927, P18859, P20674, O75947, P22695	43	142	6910	7.921716	0.015911	0.005332	0.206722
KEGG_PATHWAY	hsa05010:Alzheimer's disease	7	8.641975	4.79E-04	P31930, P48047, P14927, P18859, P20674, O75947, P22695	43	168	6910	6.695736	0.039018	0.0099	0.512174
GOTERM_CC_DIRECT	GO:0005743~mitochondrial inner membrane	9	11.11111	6.41E-04	P31930, P10809, P48047, P14927, P18859, O95202, P20674, O75947, P22695	80	441	18224	4.64898	0.098684	0.017167	0.773065
KEGG_PATHWAY	hsa04260:Cardiac muscle contraction	5	6.17284	0.001049	P31930, P14927, P54709, P20674,	43	75	6910	10.71318	0.083405	0.01441	1.117337

					P22695							
GOTERM_BP_DIRE CT	GO:0006119~oxidative phosphorylation	3	3.70370 4	0.00137 2	P31930, P14927, P22695	73	13	1679 2	53.08325	0.509512	0.13278 7	1.96728 4
GOTERM_CC_DIRE CT	GO:0005750~mitochondrial respiratory chain complex III	3	3.70370 4	0.00140 3	P31930, P14927, P22695	80	13	1822 4	52.56923	0.203451	0.02803 3	1.68469 3
GOTERM_BP_DIRE CT	GO:0006122~mitochondrial electron transport, ubiquinol to cytochrome c	3	3.70370 4	0.00183 6	P31930, P14927, P22695	73	15	1679 2	46.00548	0.614747	0.14698 3	2.62540 7
GOTERM_BP_DIRE CT	GO:0009060~aerobic respiration	3	3.70370 4	0.00878 5	P31930, P14927, P22695	73	33	1679 2	20.91158	0.989741	0.27899 9	11.9912 7
UP_KEYWORDS	Respiratory chain	3	3.70370 4	0.02500 7	P31930, P14927, P22695	81	63	2058 1	12.09935	0.987802	0.35638	26.6676 3
GOTERM_BP_DIRE CT	GO:1902600~hydrogen ion transmembrane transport	3	3.70370 4	0.02819 6	P31930, P14927, P20674	73	61	1679 2	11.31282	1	0.54217	33.9015 7
KEGG_PATHWAY	hsa01100:Metabolic pathways	13	16.0493 8	0.05705 9	P25325, P31930, P31937, Q3LXA3, Q14697, P48047, P14927, P17174, P10515, P18859, P20674, O75947, P22695	43	122 8	6910	1.701197	0.992375	0.45640 4	46.6956

KEGG_PATHWAY	hsa04932:Non-alcoholic fatty liver disease (NAFLD)	4	4.938272	0.063235	P31930, P14927, P20674, P22695	43	151	6910	4.256892	0.995581	0.452514	50.31744
UP_KEYWORDS	Electron transport	3	3.703704	0.066202	P31930, P14927, P22695	81	108	20581	7.057956	0.999993	0.548213	56.7819
Annotation Cluster 4	Enrichment Score: 2.6207276427566537											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferro ni	Benjami ni	FDR
GOTERM_MF_DIRECT	GO:0051082~unfolded protein binding	8	9.876543	3.88E-07	Q16543, Q8NHS0, P27824, P10809, P48643, P27797, Q8WW22, P50991	72	110	16881	17.05152	7.57E-05	7.57E-05	4.85E-04
GOTERM_BP_DIRECT	GO:0050821~protein stabilization	8	9.876543	1.86E-06	Q16543, P46379, P10809, P48643, P27797, Q86Y82, P54709, P50991	73	136	16792	13.53102	9.65E-04	4.83E-04	0.002693
INTERPRO	IPR017998:Chaperone tailless complex polypeptide 1 (TCP-1)	3	3.703704	9.82E-04	P10809, P48643, P50991	74	12	18559	62.69932	0.173511	0.173511	1.217609

INTERPRO	IPR027413:GroEL-like equatorial domain	3	3.70370 4	0.00155	P10809, P48643, P50991	74	15	1855 9	50.15946	0.259889	0.13970 3	1.91612
INTERPRO	IPR027409:GroEL-like apical domain	3	3.70370 4	0.00176 7	P10809, P48643, P50991	74	16	1855 9	47.02449	0.290442	0.10807 3	2.18157 5
INTERPRO	IPR002423:Chaperonin Cpn60/TCP-1	3	3.70370 4	0.00176 7	P10809, P48643, P50991	74	16	1855 9	47.02449	0.290442	0.10807 3	2.18157 5
UP_KEYWORDS	Stress response	3	3.70370 4	0.05784	O95757, P10809, Q9Y4L1	81	100	2058 1	7.622593	0.999969	0.52312 4	51.7958 2
UP_KEYWORDS	Nucleotide-binding	11	13.5802 5	0.15456 3	O95757, P13639, Q3LXA3, P10809, P48643, P50991, P30086, Q9BX68, Q9Y4L1, P62491, P13861	81	178 8	2058 1	1.563171	1	0.76793 7	87.2088 6
GOTERM_MF_DIRECTORY	GO:0005524~ATP binding	8	9.87654 3	0.44196 6	O95757, Q3LXA3, P10809, P48643, Q8WW2 2, P50991, P30086, Q9Y4L1	72	149 5	1688 1	1.254627	1	0.99555 8	99.9311 6
UP_KEYWORDS	ATP-binding	7	8.64197	0.45761	O95757,	81	139	2058	1.278652	1	0.95632	99.9443

			5	9	Q3LXA3, P10809, P48643, P50991, P30086, Q9Y4L1		1	1			2	

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