1 Research Article

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Urinary proteome of dogs with kidney injury during babesiosis

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22 Abstract

23 This study aimed to identify proteins found in the urine of dogs with renal dysfunction 24 leading to acute injury during the natural course of babesiosis (n=10) and to compare them 25 with proteins of a control group (n=10) to reveal any potential biomarkers of renal damage. 26 Pooled urine samples of both groups were separated by 2D electrophoresis (two dimensional 27 electrophoresis), followed by the identification of all proteins using MALDI-TOF mass 28 spectrometry (matrix assisted laser desorption ionization-time of flight). In total, 176 proteins 29 were identified in the urine samples from healthy dogs, and 403 proteins were identified in the 30 urine samples from dogs with babesiosis. Of the 176 proteins, 146 were assigned exclusively 31 to healthy dogs, and 373 of the 403 proteins were assigned exclusively to dogs with 32 babesiosis; 30 proteins were common to both groups. Characteristic analysis of the 373 33 proteins found in dogs with babesiosis led to the isolation of 8 proteins associated with 10 34 metabolic pathways that were attributed to immune and inflammatory response development. 35 Furthermore, it was hypothesized that the epithelial-mesenchymal transition might play an 36 important role in mechanisms underlying pathological renal tissue changes during babesiosis, 37 as indicated by a causal relationship network built by combining 5 of the 10 selected 38 metabolic pathways and 4 of the 8 proteins associated with these pathways. These included 39 cadherins, gonadotropin releasing hormone receptors, inflammatory responses mediated by 40 chemokine and cytokine signalling pathways, integrins, interleukin and TGF-β (transforming 41 growth factor β) pathways. These pathways were linked by interleukin-13, bone 42 morphogenetic protein 7, $\alpha 2(1)$ collagen, and FER tyrosine kinase, which are potential 43 damage biomarkers during babesiosis in dogs that might be assigned to early renal injury. 44

45 Keywords: Acute kidney injury; Babesiosis; Dog; Proteomics; Urine

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46 Introduction

47 After heart failure, kidney disease is the most frequent cause of lowering the quality and shortening the life of people and dogs. Kidney injuries, which take one of two forms, 48 49 acute kidney injury (AKI) and chronic kidney disease (CKD), are caused by various factors. 50 In humans, 7.8% of patients with AKI also develop CKD, and 4.9% of patients reach end-51 stage renal disease [1]. Most AKI cases in medicine and veterinary science are diagnosed 52 based on the serum or plasma concentrations of non-protein nitrogenous creatinine (Cr) and 53 urea compounds. The sensitivity of this method is small and not suitable for early AKI 54 detection [2], and seeking markers and methods adequate for the early detection of glomeruli 55 and/or tubule injury before the decreased glomerular filtration rate (GFR) is signalled by 56 increased Cr concentrations is thus necessary [3–6]. One such method is proteomic analysis, 57 which compares the protein profiles of normal urine with those typical for a given disease to 58 select potential diagnostic, therapeutic and prognostic biomarkers [7,8]. With decreased 59 GMRs and subsequent azotemia and urea, AKI is among the most frequently occurring 60 complications of babesiosis in dogs and may provide a natural model for identifying early and 61 specific markers of kidney injury in this species [9,10]. Moreover, during babesiosis occurring 62 naturally in dogs, AKI potentially provides a good model for selected studies on AKI in 63 humans. This is indicated by comparative analysis of the urine proteomes in humans and 64 dogs, as many proteins related to human diseases, including kidney diseases, have been 65 identified in canine urine [11,12]. In addition, domestic dogs (*Canis lupus familiaris*) are increasingly perceived as an excellent animal model for studying complex human diseases 66 67 [13]. Because they have a fully described genome and share a habitat with humans, dogs may 68 be used for epidemiological studies on diseases shared between the two species. Canine DNA 69 and protein sequences are much closer to humans than those of mice, suggesting that dogs are 70 also more similar to many aspects of human biology than mice [14–16]. This study aimed to

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- identify proteins found in the urine of dogs with renal dysfunction leading to acute injury
 during the natural course of babesiosis and compare them with proteins of the control group to
 reveal any potential biomarkers of renal injury.
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75 Materials and methods

76 Animals and sample collection

77 Dogs were enrolled during routine admission to Faculty of Veterinary Medicine 78 clinics at the University of Life Sciences in Lublin. Informed consent was obtained from the owners prior to the clinical investigations and sample collections. The studies were reviewed 79 80 and approved by the Ethics Committee of the University of Life Sciences in Lublin (Poland) 81 No 70/2018. The study involved 20 mixed-breed dogs (10 males, 10 females) weighing 5-8 82 kg (median 6.2 kg) and aged 2–7 years (median 4.35 years), divided into two groups. All dogs 83 underwent individual clinical and laboratory tests to determine their health status, and in 84 particular in diseased group to show signs of kidney damage. Group 1 (study group, n=10; five males and five females), consisted of dogs naturally infected with *B. canis*, while group 2 85 86 (control group, n=10; five males and five females) consisted of healthy [17]. All dogs in the 87 first group showed symptoms of babesiosis (apathy, anorexia, changes in urine colour, pale 88 mucous membranes), and haematology analysis revealed thrombocytopenia (platelets $12-88 \times$ 89 10^{9} /l) and anaemia (erythrocytes $3.5-5.3 \times 10^{12}$ /l.) All dogs were nonazotemic, serum 90 creatinine concentration remained within the reference range. All dogs in this group had 91 Babesia-positive blood smears, which were additionally confirmed by PCR, performed 92 according to the protocol described by Adaszek and Winiarczyk [9]. Possible co-infections 93 (borreliosis, anaplasmosis, ehrlichiosis) were excluded in all dogs based on PCR and ELISA 94 results [18]. All dogs of the first group were successfully treated with imidocarb (5 mg/kg 95 s.c.). Dogs of group 2 were clinically healthy and were referred to the clinic for vaccination

96 purposes. Blood smear analysis and PCR for B. canis gave negative results for all animals of 97 this group. Voided midstream urine samples were collected in the morning, and each sample 98 was centrifuged on the day of collection at $500 \times g$ for 10 minutes at 4°C. The supernatants 99 were removed, and protease inhibitors were added (Protease Inhibitor Cocktail, Roche 100 Diagnostic Corp.). Urine protein (low proteinuria denoted by "+", moderate proteinuria denoted by "++", and severe proteinuria denoted by "+++") and Cr concentrations were 101 102 measured by the enzymatic colorimetric method (BS-130 analyser, Mindray), and basic 103 urinalysis with microscopic sediment analysis was performed on the fresh urine samples. Urine specific gravity (USG) was measured using a refractometer. The remaining urine was 104 105 frozen at -80°C for further analysis. Macroscopic evaluation of urine in group 1 showed 106 yellow to dark brown sample colours, while all group 2 samples were yellow. Urine protein 107 analysis revealed proteinuria in eight of the 10 group 1 dogs, and eight dogs of this group also 108 had urine protein/Cr ratios > 0.5. Urine dipstick analysis showed haemoglobinuria in seven of 109 the 10 group 1 dogs, which was severe (+++) in two dogs. Urine specific gravity decreased in all diseased dogs and amounted to 1.015 on average. None of the control group dogs had 110 111 proteinuria or haemoglobinuria. Statistically higher concentrations of urinary biomarkers 112 (uIgG/uCr, uTHP/uCr, and uRBP/uCr) were found in the urine samples of all dogs with 113 babesiosis compared to those in the control animals (p < 0.05), indicating dysfunctional 114 glomerular and tubular kidney regions [17]. For proteomic analysis, 10 individual urine 115 samples (0.5 ml each) from groups 1 and 2 were collected and pooled from affected and 116 healthy dogs, respectively. Each pooled urine sample was subjected to desaltation on the filter 117 to enable quick ultrafiltration with a high-density coefficient (Amicon Ultra Merck). Protein 118 concentrations were measured with a microlitre spectrophotometer (NANO), and the urine 119 samples were then prepared and subjected to 2D electrophoresis. Each individual gel spot was

then analysed by mass spectrometry with the MALDI-TOF (matrix-assisted laser desorption
ionization – time of flight) technique.

122

123 2D electrophoresis

124 Two-dimensional electrophoresis was used to separate the proteins contained in the 125 tested urine samples [19]. Preliminary tests have shown that the optimum amount of protein 126 for 2D electrophoresis is 85 µg; thus, this amount of protein was broken down via a 127 precipitation and purification kit (ReadyPrep[™] 2-D Cleanup Kit, Bio-Rad, Warsaw, Poland). 128 The obtained protein pellets were then dissolved in a rehydration buffer, and the resulting 129 solutions were applied to a rehydration plate and covered with 17-cm immobilized pH 130 gradient (IPG-immobilized pH gradient) strips for isoelectric focusing (pH 3-10, Bio-Rad). 131 To soak the gel present on the strips with the protein sample, the strips were removed after a 132 12-hour rehydration period and then subjected to the first electrophoresis dimension (IEF-100 133 Hoefer; 250 V/30 min; 10 000 V/3 hrs; 60 kV/hr, with a current limit of 50 µA/strip hrs). 134 Under the influence of the electric field, proteins contained in the strips were subjected to 135 migration by siting in a location corresponding to the isoelectric point of the given protein. 136 After separation, the IPG strips were prepared for the second electrophoresis dimension to 137 separate the proteins by molecular mass. Vertical electrophoretic separation utilized 12.5% 138 polyacrylamide gels and the following current parameters: 600 V/30 mA/100 W in an 139 electrophoretic chamber (PROTEAN® II xi, Bio-Rad). The obtained gels were subjected to a 140 standard colouring procedure with silver in the presence of formaldehyde as a regulator. The 141 protein spots were cut out of the gels, decolourised, reduced and alkylated using dithiothreitol 142 and iodoacetamide [20]. Gel fragments containing proteins were subjected to digestion to 143 obtain shorter peptide fragments. Trypsin digestion occurred in 50 mM ammonium 144 bicarbonate buffer at 37°C for 12 hours (Promega, Trypsin Gold, Mass Spectrometry Grade,

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145	Technical Bulletin) [21]. The obtained peptides were subsequently eluted from the gel with a
146	water/acetonitrile/TFA solution (v:v 450:500:50). The extracted peptides were purified using
147	C18 Zip-TIP pipette tips according to the manufacturer's instructions (Merck Chemicals,
148	Billerica, MA, USA, PR 02358, Technical Note) and applied to the MTP AnchorChip 384
149	plate (Bruker, Bremen, Germany).
150	
151	Mass spectrometry
152	After the protein samples were dried on the MPT AnchorChip 384 plate, their surfaces
153	were covered with a super-saturated solution of α -cyano4-hydroxycinnamic acid (HCCA,
154	Bruker), functioning as a matrix mediating the transmission of energy to the sample.
155	Simultaneously, 0.5 μ l of a peptide standard was applied to the calibration fields (Peptide
156	Calibration Standard II, Bruker), which were also covered with the matrix solution.
157	Spectrometric analysis was performed using the Ultraflextreme III MALDI TOF/TOF
158	(Bruker), and flexControl 3.3 (Bruker) software was applied for mass spectra collection. The
159	obtained peptides were subjected to mild ionization using the MALDI-TOF instrument in the
160	linear mode within the 900-4000 Da mass scope in the reflectron mode. The obtained mass
161	spectra were analysed with flexAnalysis 3.4 (Bruker) software as follows: smoothing
162	(Savitsky-Golay method), baseline subtraction (Top Hat baseline algorithm), and peak
163	geometry (Stanford Network Analysis Platform (SNAP) algorithm). All peaks with signal to
164	noise ratios > 3 were qualified for further analysis. Experimental data were analysed using the
165	abovementioned software to exclude peaks originating from trypsin or environmental
166	pollution. To ensure correct identification, selecting possible post-translation modifications
167	using BioTools 3.2 (Bruker) software was essential. Post-translation modifications were
168	derived from both the methodology used as well as the metabolic processes of the patients.
169	The obtained spectra were compared to the Swiss-Prot database restricted to "bony

- 170 vertebrate" taxa using Mascot 2.2 software with a maximum error of 0.3 Da. If the obtained
- 171 result was not statistically significant, the original peptide ions were subjected to
- 172 fragmentation in the tandem spectrometry mode [22,23].
- 173
- 174 **Results**

Based on the clinicopathological variables all dogs with babesiosis met the criteria for early phase of AKI. They had proteinuria with UPC>0.5, decreased urine specific gravity amounted to 1.015 on average and significantly elevated value of uIgG/uCr, uTHP/uCr, and uRBP/uCr that indicated glomerular and tubular damage.

179 In this study, 176 proteins were identified in pooled urine samples collected from 180 healthy dogs, and 403 proteins were identified in pooled urine samples collected from dogs 181 with babesiosis. Tables 1 and 2 contain lists of the proteins, along with their names, scores, 182 molecular weights, number of matches, UniProt base accession numbers and hyperlinks. With 183 the Venna programme (http://bioinfogp.cnb.csic.es), 146 of the 176 proteins were assigned 184 exclusively to healthy dogs, and 373 of the 403 proteins were exclusively assigned to dogs 185 with babesiosis; 30 proteins were common to both groups (Fig. 1). To further evaluate the 373 186 proteins found in only the dogs with babesiosis, the Panther programme 187 (http://www.pantherdb.org) was used to isolate 21 proteins from the *Canis familiaris* species, 188 which were used to form a collection of potential diagnostic and pathophysiological 189 biomarkers for this disease (Table 3). Further analysis of these 21 proteins led to the isolation 190 of 8 proteins associated with 10 metabolic pathways that were attributed to immune and 191 inflammatory response development (Table 4). These results showed that the epithelial-192 mesenchymal transition (EMT) might play an important role in the mechanisms underlying 193 pathological changes in renal tissues during the course of babesiosis, as indicated by the 194 causal relationship network built by combining 5 of the 10 selected metabolic pathways and 4

195 of the 8 proteins for which the pathways were associated. These included cadherins, 196 gonadotropin releasing hormone receptors, inflammatory responses mediated by chemokine 197 and cytokine signalling pathways, integrins, and TGF- β pathways. These pathways were 198 linked by interleukin (IL)-13, bone morphogenetic protein 7, α 2(1) collagen, and FER 199 tyrosine kinase.

200

201 **Discussion**

202 Non-specific immune responses are activated to limit the initial phase of parasitic invasion or infection by pathogenic micro-organisms. Parasitic invasion initiates type Th2 203 204 immune responses, characterised by the activation of Th2 lymphocytes, eosinophilia, 205 basophilia, mast cells, and alternatively, activated macrophages (AAM). This process is 206 accompanied by the secretion of IgE antibodies and numerous cytokines, such as IL-3, IL-4, 207 IL-5, IL-9 IL-10, IL-13 and TGF-β. IL-13 plays a key role in regulating the anti-parasitic 208 response [24], and is a primary factor inducing fibrosis processes in many chronic contagious 209 and autoimmune diseases [25]. IL-13 increases the concentration of TGF- β , which leads to 210 collagen deposition in lung and kidney tissues [26], by stimulating macrophages to produce 211 TGF- β via the IL-13R α 2 receptor. Inhibition of IL-13R α 2 expression reduces TGF- β 212 secretion and decreases collagen deposition in the tissues. Therefore, IL-13R α 2 is considered 213 a feasible target molecule for therapies aimed at preventing fibrosis processes involving TGF-214 β [27,28]. Fibrosis is considered the final stage in the development of CKD regardless of the 215 primary cause, and the effector cells of this process include myofibroblasts developed from 216 tubule epithelial cells transformed during the EMT process [29,30]. During this transition, 217 cells lose polarity, loosening their communication abilities and degrading the basement 218 membrane. Adhesive molecules that bond both epithelial cells and the basement membrane, 219 such as E-cadherin and integrins, are replaced by mesenchymal cell markers, such as N-

220 cadherin, unstriated muscle α -actin, vimentin, fibronectin and collagen I. In an inflammatory 221 environment, the EMT maintains tissue homoeostasis by inducing structural regeneration and 222 reconstruction after harmful stress. Extinction of the inflammatory reaction results in 223 termination of the EMT and a return to the original state. Long-term support of the EMT 224 process leads to fibrous degeneration as well as structural and functional tissue and organ 225 disorders [31,32]. Pleiotropic TGF-β molecules and bone morphogenetic proteins (BMPs), 226 belonging to the transforming growth factor- β (TGF- β SF) superfamily, participate in one of 227 the most well-known signalling pathways in the ETM process [33–35]. TGF-β plays a 228 significant role in kidney diseases by functioning in fibrosis, inflammatory responses, 229 apoptosis, and cell growth and diversification. Increased TGF-B levels lead to loss of the 230 epithelial phenotype, acquisition of the mesenchymal phenotype and collagen accumulation. 231 On the other hand, BMP-7 inhibits fibrosis, exerts anti-inflammatory effects and stimulates 232 the regeneration of damaged kidney tissues. During ontogeny, BMP-7 has a decisive impact 233 on the number of nephrons and the size of the organ [36]. Serine-threonine kinase receptors 234 and cytoplasmic proteins (Smads) participate in transferring TGF-β/BMP pathway signals. By 235 bonding with its TBRII receptor on the cell surface, TGF-B activates the TBRI receptor, which 236 passes the signal via the phosphorylation of Smad2 and Smad3. Similarly, BMP-7 bonds its 237 surface receptors BAMPRI and BAMPRII and phosphorylates the Smad proteins 1, 5, and 8. 238 The phosphorylated proteins (Smads) complex with the Smad4 protein, which permeates the 239 kernel and induces the transcription of effector genes. Smad3, induced by TGF-B stimulation, 240 can combine with the Col1A2 gene promoter to activate the expression of type $1\alpha^2$ collagen, 241 which may accumulate in interstitial tissue and contribute to extracellular matrix (ECM) 242 accumulation, leading to fibrous degeneration of the organ. Alternatively, TGF- β and BMP-7 243 expression can be controlled by extracellular signal-regulated kinases (ERKs) or mitogen-244 activated protein kinases (MAPKs) [37]. In experimental systems, BMP-7 recombinant

245 protein expression or BMP-7 overexpression inhibits fibrosis during diabetic nephropathy or 246 AKI, TGF-B-initiated EMT and E-cadherin suppression. BMP-7 manifests as a protective 247 agent against kidney diseases by exerting an anti-inflammatory effect, reflected by the 248 inhibition of neutrophil, monocyte and macrophage infiltration and activity as well as by 249 repression of the expression of the proinflammatory cytokines IL-6 and IL-1 β and the 250 proinflammatory chemokines MCP1 and IL-8 [38]. BMP-7 showed anti-apoptotic activity in 251 experiments on tubular epithelial cell (TEC) lines. The presence of α -1 antitrypsin abolishes 252 the TGF-β/Smad3 signalling pathway and inhibits fibrosis, which indicates its therapeutic 253 potential [39]. The BMP-7 mRNA expression in kidney bioptats of dogs with innate portal-254 collateral fusion was higher than that in healthy dogs. Attempts are being made to establish the causality between increased BMP-7 expression and kidney disturbances accompanying 255 256 this disease, manifesting as kidney enlargement, increased glomerular filtration, polyuria and 257 polydipsia. After pathological vessels are surgically corrected, it is important that the kidneys 258 return to normal functioning, and the properties of BMP-7 associated with fibrosis inhibition, 259 apoptosis and anti-inflammatory effects may be useful for accomplishing this goal, aiding in 260 the conservative treatment of this disease [40]. Among the current concepts involving the 261 therapeutic use of BMP-7 in kidney diseases, attention is drawn to the widespread BMP-7 262 receptors in various organs and the risks of side effects. Therefore, antagonists that selectively 263 stimulate receptors associated with renal tissues are sought, and those that are present in bone 264 tissues, for example, must be omitted[37].

265

266 Conclusion

In summary, to the best of our knowledge, this is the first study to comprehensively analyse the urinary proteome of dogs with babesiosis, demonstrating the association of the identified proteins with the disease and indirectly confirming the occurrence of Th2 immune

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270	responses to Babesia canis infection. Urine Interleukin-13, bone morphogenetic protein 7,
271	$\alpha 2(1)$ collagen and FER tyrosine kinase are potential biomarkers of kidney damage during
272	babesiosis in dogs that might be assigned to early renal injury; however, verifying their
273	significance in the diagnosis and prognosis of the disease requires further study.
274	
275	Declarations of interest
276	The authors have declared that no competing interests exist.
277	Acknowledgements
278	We thank Dorota Pietras-Ozga, PhD for technical assistance with the electrophoresis
279	procedurę.
280	
281	Funding
282	This work was partly supported by the Polish National Science Centre (NCN) [grant
283	numbers UMO-2016/23/N/NZ5/02576; UMO-2017/25/N/NZ5/01875]
284	
285	Role of the funding source
286	None to declare
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- 395
- 396 Tables
- **397 Table 1**

398 Peptides identified in the urine of healthy dogs.

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Protein name	Score	Mass	Matches	Access no.	Hyperlink
Endophilin-A2	64	41.7	9	Q2KJA1	http://www.uniprot.org/uniprot/Q2KJA1
BTB/POZ domain- containing protein KCTD1	66	29.7	7	Q719H9	http://www.uniprot.org/uniprot/Q719H9
Prolyl 3-hydroxylase 3	52	82.6	11	Q8IVL6	http://www.uniprot.org/uniprot/Q8IVL6
Essential MCU regulator	54	11.5	4	Q2M2S2	http://www.uniprot.org/uniprot/Q2M2S2
C-X-C motif chemokine 3	43	11.3	4	Q10746	http://www.uniprot.org/uniprot/Q10746
Desmin	65	53.3	10	Q5XFN2	http://www.uniprot.org/uniprot/Q5XFN2
Uromodulin	65	72.9	13	Q862Z3	http://www.uniprot.org/uniprot/Q862Z3
Heat shock factor-binding protein 1	51	8.5	4	O75506	http://www.uniprot.org/uniprot/O75506
Phosphoglucomutase-2	45	69.9	11	Q7TSV4	http://www.uniprot.org/uniprot/Q7TSV4
Methylmalonyl-CoA mutase, mitochondrial	50	83.6	12	Q9GK13	http://www.uniprot.org/uniprot/Q9GK13
Histone H1t	51	22.1	6	P40286	http://www.uniprot.org/uniprot/P40286
General transcription factor II-I	50	110.6	8	A7MB80	http://www.uniprot.org/uniprot/A7MB80
Zinc finger protein 106	68	210.8	19	O88466	http://www.uniprot.org/uniprot/O88466
Protein CutA	76	19.2	6	O60888	http://www.uniprot.org/uniprot/O60888
Protein Lines homolog 1	58	87.5	11	Q8NG48	http://www.uniprot.org/uniprot/Q8NG48
Dihydropyrimidinase- related protein 1	48	62.5	9	Q14194	http://www.uniprot.org/uniprot/Q14194
Interleukin-22	43	20.3	4	Q9GZX6	http://www.uniprot.org/uniprot/Q9GZX6
BTB/POZ domain- containing protein KCTD1	46	29.7	4	Q719H9	http://www.uniprot.org/uniprot/Q719H9
Ribosome-binding protein 1	48	164.8	9	Q28298	http://www.uniprot.org/uniprot/Q28298
Glycogen debranching enzyme	43	176.9	12	Q2PQH8	http://www.uniprot.org/uniprot/Q2PQH8
6-phosphofructo-2- kinase/fructose-2,6- bisphosphatase 3	67	54.2	9	Q28901	http://www.uniprot.org/uniprot/Q28901
60S ribosomal protein L37	58	11.3	8	P79244	http://www.uniprot.org/uniprot/P79244
Interleukin-11	46	21.6	6	P47873	http://www.uniprot.org/uniprot/P47873
Vascular cell adhesion protein 1	63	82.3	13	P19320	http://www.uniprot.org/uniprot/P19320
Ig heavy chain V region AC38 205.12	66	13	4	P06330	http://www.uniprot.org/uniprot/P06330
Collagen alpha-1(XXV) chain	88	65.1	13	Q9BXS0	http://www.uniprot.org/uniprot/Q9BXS0
Sphingosine 1-phosphate receptor 3	51	43	8	Q99500	http://www.uniprot.org/uniprot/Q99500
Vascular cell adhesion protein 1	51	82.3	11	P19320	http://www.uniprot.org/uniprot/P19320
Vacuolar protein sorting- associated protein 4B	41	49.6	6	P46467	http://www.uniprot.org/uniprot/P46467
SPRY domain-containing protein 7	51	22.2	5	Q2T9X3	http://www.uniprot.org/uniprot/Q2T9X3

Myoglobin	48	17.3	7	P02185	http://www.uniprot.org/uniprot/P02185
Retinol-binding protein 2	43	15.8	5	Q08652	http://www.uniprot.org/uniprot/Q08652
Mesenteric estrogen- dependent adipogenesis protein	53	34.6	6	A4IFN2	http://www.uniprot.org/uniprot/A4IFN2
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	49	40.9	6	Q0MQB6	http://www.uniprot.org/uniprot/Q0MQB6
Nucleoside diphosphate kinase A	51	17.3	5	Q05982	http://www.uniprot.org/uniprot/Q05982
PR domain zinc finger protein 12	49	40.7	6	A2AJ77	http://www.uniprot.org/uniprot/A2AJ77
Gastric inhibitory polypeptide receptor	53	54	8	P48546	http://www.uniprot.org/uniprot/P48546
Carbohydrate sulfotransferase 1	54	47.5	9	Q9EQC0	http://www.uniprot.org/uniprot/Q9EQC0
Ras-specific guanine nucleotide-releasing factor 1	50	146.3	13	Q13972	http://www.uniprot.org/uniprot/Q13972
Coiled-coil domain- containing protein 184	39	20.7	3	Q52MB2	http://www.uniprot.org/uniprot/Q52MB2
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4-like 2	42	10.1	3	Q9NRX3	http://www.uniprot.org/uniprot/Q9NRX3
Elongation factor 1-beta	59	25	7	Q5E983	http://www.uniprot.org/uniprot/Q5E983
Uncharacterized protein C12orf60 homolog	52	28.3	10	Q810N5	http://www.uniprot.org/uniprot/Q810N5
Serum albumin	44	70.6	10	P49822	http://www.uniprot.org/uniprot/P49822
DNA-binding protein RFX5	52	65.7	11	P48382	http://www.uniprot.org/uniprot/P48382
C2 domain-containing protein 3	50	262.6	15	Q4AC94	http://www.uniprot.org/uniprot/Q4AC94
Protein deglycase DJ-1	55	20.1	6	Q95L19	http://www.uniprot.org/uniprot/Q95LI9
Calmodulin-regulated spectrin-associated protein 1	54	179.9	12	D3Z8E6	http://www.uniprot.org/uniprot/D3Z8E6
Zinc finger protein 101	49	51.9	7	Q8IZC7	http://www.uniprot.org/uniprot/Q8IZC7
Mini-chromosome maintenance complex- binding protein	51	73.8	7	Q9BTE3	http://www.uniprot.org/uniprot/Q9BTE3
Protein SOX-16 (fragment)	46	6.9	5	Q62247	http://www.uniprot.org/uniprot/Q62247
Essential MCU regulator, mitochondrial	45	11.5	4	Q2M2S2	http://www.uniprot.org/uniprot/Q2M2S2
G protein-coupled receptor kinase 7	52	62.6	7	Q9Z2G7	http://www.uniprot.org/uniprot/Q9Z2G7
Golgi SNAP receptor complex member 1	49	28.6	11	Q2TBU3	http://www.uniprot.org/uniprot/Q2TBU3
Metaxin-2	52	30.1	5	O88441	http://www.uniprot.org/uniprot/O88441
Glutathione S-transferase Mu 1	52	26.1	7	P10649	http://www.uniprot.org/uniprot/P10649
Calpain-2 catalytic subunit	58	80.7	9	Q27971	http://www.uniprot.org/uniprot/Q27971
Pleckstrin homology domain-containing family G member 4B	56	141.6	15	Q96PX9	http://www.uniprot.org/uniprot/Q96PX9
Profilin-4	52	14.6	6	Q9D6I3	http://www.uniprot.org/uniprot/Q9D6I3
EH domain-containing protein 4	52	61.4	12	Q9H223	http://www.uniprot.org/uniprot/Q9H223

Hepcidin	59	9.3	5	Q8MJ80	http://www.uniprot.org/uniprot/Q8MJ80
Glycine receptor subunit beta	52	56.8	7	P48167	http://www.uniprot.org/uniprot/P48167
Sulfotransferase 4A1	51	33.4	8	P63046	http://www.uniprot.org/uniprot/P63046
Unconventional myosin-Id	59	116.9	10	O94832	http://www.uniprot.org/uniprot/O94832
Actin-related protein 2/3 complex subunit 3	48	20.8	6	Q3T035	http://www.uniprot.org/uniprot/Q3T035
Actin-related protein 2/3 complex subunit 3	48	20.8	6	Q3T035	http://www.uniprot.org/uniprot/Q3T035
Autophagy-related protein 16-1	49	68.9	7	Q676U5	http://www.uniprot.org/uniprot/Q676U5
Carbonic anhydrase 5B, mitochondrial	61	36.8	5	Q9Y2D0	http://www.uniprot.org/uniprot/Q9Y2D0
Putative olfactory receptor 2B3	50	36.2	4	O76000	http://www.uniprot.org/uniprot/O76000
Zinc finger protein 75D	51	60.2	10	P51815	http://www.uniprot.org/uniprot/P51815
Trafficking protein particle complex subunit 1	57	16.9	6	Q17QI1	http://www.uniprot.org/uniprot/Q17QI1
Golgi SNAP receptor complex member 1	52	28.6	9	Q2TBU3	http://www.uniprot.org/uniprot/Q2TBU3
Zinc finger protein 491	50	52.9	9	Q8N8L2	http://www.uniprot.org/uniprot/Q8N8L2
Cytoskeleton-associated protein 2-like	61	83.4	12	A5PK21	http://www.uniprot.org/uniprot/A5PK21
Retinoic acid receptor RXR-beta (Fragment)	52	49.8	9	P49743	http://www.uniprot.org/uniprot/P49743
Apolipoprotein A-II	54	11.3	4	E2RAK7	http://www.uniprot.org/uniprot/E2RAK7
Tubulin polymerization- promoting protein family member 2	50	18.5	6	Q4R3A0	http://www.uniprot.org/uniprot/Q4R3A0
Bcl-2-like protein 2	49	20.9	6	Q1RMX3	http://www.uniprot.org/uniprot/Q1RMX3
Mini-chromosome maintenance complex- binding protein	52	73.8	16	A5PJM5	http://www.uniprot.org/uniprot/A5PJM5
Alpha-2,8-sialyltransferase 8F	55	45.4	8	P61647	http://www.uniprot.org/uniprot/P61647
H-2 class I histocompatibility antigen, K-B alpha chain	62	41.7	11	P01901	http://www.uniprot.org/uniprot/P01901
Fibroleukin	53	50.8	9	Q14314	http://www.uniprot.org/uniprot/Q14314
Phosphatidylethanolamine- binding protein 2	52	21.7	6	Q8VIN1	http://www.uniprot.org/uniprot/Q8VIN1
Zinc finger and SCAN domain-containing protein 5A	63	56.9	8	Q9BUG6	http://www.uniprot.org/uniprot/Q9BUG6
Fructose-1,6-bisphosphatase 1	54	37	5	Q3SZB7	http://www.uniprot.org/uniprot/Q3SZB7
Beta-defensin 107A	51	7.9	3	A4H217	http://www.uniprot.org/uniprot/A4H217
Golgi SNAP receptor complex member 1	62	28.6	10	Q62931	http://www.uniprot.org/uniprot/Q62931
Zinc finger protein 624	63	102.5	13	Q9P2J8	http://www.uniprot.org/uniprot/Q9P2J8
Prelamin-A/C	62	74.6	12	P48679	http://www.uniprot.org/uniprot/P48679
Aspartate-tRNA ligase, cytoplasmic	51	57.5	18	P15178	http://www.uniprot.org/uniprot/P15178
Beta-lactoglobulin	69	20.6	6	Q29146	http://www.uniprot.org/uniprot/Q29146
ATP synthase subunit alpha, mitochondrial	63	59.8	16	P25705	http://www.uniprot.org/uniprot/P25705
RUN and FYVE domain- containing protein 2	55	70.8	18	Q8R4C2	http://www.uniprot.org/uniprot/Q8R4C2

Pyridine nucleotide- disulfide oxidoreductase	57	63.5	10	Q3U4I7	http://www.uniprot.org/uniprot/Q3U4I7
domain-containing protein 2 Profilin-3	51	15	7	Q8R4C2	http://www.uniprot.org/uniprot/Q9DAD6
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Prolyl 3-hydroxylase 3	62	82.6	10	Q8IVL6	http://www.uniprot.org/uniprot/Q8IVL6
Tumor susceptibility gene 101 protein	56	44.1	7	Q99816	http://www.uniprot.org/uniprot/Q99816
Vascular cell adhesion protein 1	51	82.4	10	P29533	http://www.uniprot.org/uniprot/P29533
Ataxin-7	53	93.8	8	Q8R4I1	http://www.uniprot.org/uniprot/Q8R4I1
Gamma-aminobutyric acid receptor subunit alpha-1	53	52.1	6	P08219	http://www.uniprot.org/uniprot/P08219
43 kDa receptor-associated protein of the synapse	63	47.6	10	P12672	http://www.uniprot.org/uniprot/P12672
Protein-arginine deiminase type-2	57	76	9	P20717	http://www.uniprot.org/uniprot/P20717
Heat shock factor-binding protein 1	53	8.6	6	Q9CQZ1	http://www.uniprot.org/uniprot/Q9CQZ1
Non-homologous end- joining factor 1	55	34.1	7	Q6AYI4	http://www.uniprot.org/uniprot/Q6AYI4
Microtubule-associated protein RP/EB family member 1	51	30.1	10	Q5R7Z5	http://www.uniprot.org/uniprot/Q5R7Z5
Protein kish-A	56	8.4	6	Q9CR64	http://www.uniprot.org/uniprot/Q9CR64
Ubiquitin carboxyl- terminal hydrolase 14	56	56.3	9	P40826	http://www.uniprot.org/uniprot/P40826
Cap-specific mRNA (nucleoside-2'-O-)- methyltransferase 1	64	96.6	12	Q9DBC3	http://www.uniprot.org/uniprot/Q9DBC3
DNA dC->dU-editing enzyme APOBEC-3G	65	45.9	8	Q694B9	http://www.uniprot.org/uniprot/Q694B9
Annexin A10	63	37.8	8	Q9UJ72	http://www.uniprot.org/uniprot/Q9UJ72
Cysteine and glycine-rich protein 2	57	21.8	6	P97314	http://www.uniprot.org/uniprot/P97314
Calmodulin-regulated spectrin-associated protein 1	50	179.9	15	D3Z8E6	http://www.uniprot.org/uniprot/D3Z8E6
Tyrosine-protein phosphatase non-receptor type 12	58	87.2	7	P35831	http://www.uniprot.org/uniprot/P35831
Dual specificity phosphatase DUPD1	55	24.3	6	P0C595	http://www.uniprot.org/uniprot/P0C595
Protein cereblon	53	50.1	10	Q5R6Y2	http://www.uniprot.org/uniprot/Q5R6Y2
Testis-expressed sequence 33 protein	53	30.8	5	O43247	http://www.uniprot.org/uniprot/O43247
Complexin-3	51	17.6	7	Q8WVH0	http://www.uniprot.org/uniprot/Q8WVH0
Plasmalemma vesicle-	61	50.6	12	Q9WV78	http://www.uniprot.org/uniprot/Q9WV78
associated protein Calcium/calmodulin- dependent protein kinase II inhibitor 1	53	8.6	4	A7MBG3	http://www.uniprot.org/uniprot/A7MBG3
BTB/POZ domain- containing protein KCTD1	56	29.7	6	Q719H9	http://www.uniprot.org/uniprot/Q719H9
Threonine synthase-like 2	62	54.8	6	Q86YJ6	http://www.uniprot.org/uniprot/Q86YJ6
Probable tRNA pseudouridine synthase 1	65	36.6	7	Q5M934	http://www.uniprot.org/uniprot/Q5M934

Ras-related protein Rab-7a	51	23.8	8	P51149	http://www.uniprot.org/uniprot/P51149
Essential MCU regulator,	52	11.5	4	Q2M2S2	http://www.uniprot.org/uniprot/Q2M2S2
mitochondrial Golgi SNAP receptor	51	28.6	5	088630	http://www.uniprot.org/uniprot/O88630
complex member 1 Dual specificity	54	25.5	8	Q68J44	http://www.uniprot.org/uniprot/Q68J44
phosphatase DUPD1	_		_	-	
GTP-binding protein Rheb Radical S-adenosyl	53	20.5	5	Q921J2	http://www.uniprot.org/uniprot/Q921J2
methionine domain- containing protein 2	60	42.4	10	Q9MZU4	http://www.uniprot.org/uniprot/Q9MZU4
Zinc finger protein 624	50	102.5	11	Q9P2J8	http://www.uniprot.org/uniprot/Q9P2J8
Neurofibromin	56	320.5	16	P97526	http://www.uniprot.org/uniprot/P97526
Protein FAM184B	54	121.9	13	Q9ULE4	http://www.uniprot.org/uniprot/Q9ULE4
Phosphomannomutase 2	58	28.4	6	Q3SZJ9	http://www.uniprot.org/uniprot/Q3SZJ9
Isocitrate dehydrogenase [NADP] cytoplasmic	53	47	6	P41562	http://www.uniprot.org/uniprot/P41562
Beta-1,3- galactosyltransferase 4	44	42.9	7	Q5TJE8	http://www.uniprot.org/uniprot/Q5TJE8
Transmembrane protein 238	51	18.1	4	C9JI98	http://www.uniprot.org/uniprot/C9JI98
Protein FAM3C	51	25.0	7	Q810F4	http://www.uniprot.org/uniprot/Q810F4
Coiled-coil domain- containing protein 136	51	133.7	9	Q3TVA9	http://www.uniprot.org/uniprot/Q3TVA9
Protein KHNYN	50	75.1	9	Q80U38	http://www.uniprot.org/uniprot/Q80U38
Retinol-binding protein 2	50	15.8	4	Q08652	http://www.uniprot.org/uniprot/Q08652
Tetratricopeptide repeat protein 36	72	20.7	7	Q3SZV0	http://www.uniprot.org/uniprot/Q3SZV0
E3 ubiquitin-protein ligase RNF152	62	23.1	6	D2H6Z0	http://www.uniprot.org/uniprot/D2H6Z0
Protein RCC2	50	56.8	10	Q9P258	http://www.uniprot.org/uniprot/Q9P258
Signal peptidase complex subunit 2	54	25.3	6	Q5RAY6	http://www.uniprot.org/uniprot/Q5RAY6
Protein myomaker	50	25.1	4	A6NI61	http://www.uniprot.org/uniprot/A6NI61
Apoptosis-enhancing nuclease	57	37.6	9	Q9CZI9	http://www.uniprot.org/uniprot/Q9CZI9
Short-chain specific acyl- CoA dehydrogenase, mitochondrial	53	44.6	9	P16219	http://www.uniprot.org/uniprot/P16219
Fanconi anemia group B protein	61	99.4	12	Q8NB91	http://www.uniprot.org/uniprot/Q8NB91
Dual-specificity phosphatase 28	70	18.7	6	Q4G0W2	http://www.uniprot.org/uniprot/Q4G0W2
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	65	50.3	12	Q4R517	http://www.uniprot.org/uniprot/Q4R517
Zinc finger and SCAN domain-containing protein 5A	51	56.9	9	Q9BUG6	http://www.uniprot.org/uniprot/Q9BUG6
Eukaryotic translation initiation factor 4E-binding protein 1	50	12.7	5	Q0P5A7	http://www.uniprot.org/uniprot/Q0P5A7
39S ribosomal protein L30, mitochondrial	57	18.7	6	Q58DV5	http://www.uniprot.org/uniprot/Q58DV5
WAP four-disulfide core domain protein 12	57	12.7	4	A4K2P0	http://www.uniprot.org/uniprot/A4K2P0
UV-stimulated scaffold	55	82.6	12	Q9D479	http://www.uniprot.org/uniprot/Q9D479

protein A					
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	52	17.1	4	Q9U109	http://www.uniprot.org/uniprot/Q9UI09
Tektin-4	59	51.3	8	Q8WW24	http://www.uniprot.org/uniprot/Q8WW24
Heterochromatin protein 1- binding protein 3	65	61.5	12	Q5SSJ5	http://www.uniprot.org/uniprot/Q5SSJ5
Natriuretic peptides B	37	15.1	4	P16859	http://www.uniprot.org/uniprot/P16859
Zinc finger protein 624	59	102.5	12	Q9P2J8	http://www.uniprot.org/uniprot/Q9P2J8
G kinase-anchoring protein 1	55	42.2	5	Q5XIG5	http://www.uniprot.org/uniprot/Q5XIG5
OTU domain-containing protein 6B	59	34	8	Q8N6M0	http://www.uniprot.org/uniprot/Q8N6M0
Tetratricopeptide repeat protein 36	64	20.7	9	Q3SZV0	http://www.uniprot.org/uniprot/Q3SZV0
Leucine-rich repeat and coiled-coil domain- containing protein 1	61	120.6	12	Q69ZB0	http://www.uniprot.org/uniprot/Q69ZB0
Poly [ADP-ribose] polymerase 12	61	80.5	12	Q9H0J9	http://www.uniprot.org/uniprot/Q9H0J9
Cortexin-2	53	9.1	6	P0C2S0	http://www.uniprot.org/uniprot/P0C2S0
Luc7-like protein 3	51	51.9	11	Q3SX41	http://www.uniprot.org/uniprot/Q3SX41
Putative uncharacterized protein encoded by CRHR1-IT1	52	17.2	9	Q96LR1	http://www.uniprot.org/uniprot/Q96LR1
DNA replication licensing factor MCM4	56	97.1	11	P33991	http://www.uniprot.org/uniprot/P33991
Acyl-CoA synthetase family member 2, mitochondrial	63	69	9	Q17QJ1	http://www.uniprot.org/uniprot/Q17QJ1
Transthyretin	45	16.4	3	P49143	http://www.uniprot.org/uniprot/P49143]
Putative uncharacterized protein DKFZp434L187	62	15.1	8	Q9UFV3	http://www.uniprot.org/uniprot/Q9UFV3
Protein AAR2 homolog	52	43.9	10	Q08DJ7	http://www.uniprot.org/uniprot/Q08DJ7
Annexin A5	55	36	5	P08758	http://www.uniprot.org/uniprot/P08758
Apolipoprotein A-II	53	11.3	5	P0DN36	http://www.uniprot.org/uniprot/P0DN36
Retinol-binding protein 4	44	23.4	6	P27485	http://www.uniprot.org/uniprot/P27485
BTB/POZ domain- containing protein KCTD1	49	29.7	6	Q719H9	http://www.uniprot.org/uniprot/Q719H9
Collagen alpha-2(I) chain	45	80.9	11	С0НЈР6	http://www.uniprot.org/uniprot/C0HJP6
L-gulonolactone oxidase	55	51	13	Q8HXW0	http://www.uniprot.org/uniprot/Q8HXW0
Zinc finger protein 624	58	102.5	12	Q9P2J8	http://www.uniprot.org/uniprot/Q9P2J8
Cilia- and flagella- associated protein 52	57	69.2	11	Q8N1V2	http://www.uniprot.org/uniprot/Q8N1V2
Autophagy-related protein 16-1	53	68.9	12	Q676U5	http://www.uniprot.org/uniprot/Q676U5
IQ domain-containing protein D	55	51.8	13	Q17QH9	http://www.uniprot.org/uniprot/Q17QH9
Fibroblast growth factor 12	55	27.6	6	P61328	http://www.uniprot.org/uniprot/P61328
Interferon-induced protein with tetratricopeptide repeats 1	52	52.8	12	Q4R5F5	http://www.uniprot.org/uniprot/Q4R5F5
Fanconi anemia group B protein	50	99.4	13	Q8NB91	http://www.uniprot.org/uniprot/Q8NB91
Protein TMEM155	55	14.4	5	Q5R4Y3	http://www.uniprot.org/uniprot/Q5R4Y3

Transmembrane protein 225	58	26.3	5	Q6GV28	http://www.uniprot.org/uniprot/Q6GV28
Telomerase reverse transcriptase	65	128.6	10	O14746	http://www.uniprot.org/uniprot/O14746
Tetratricopeptide repeat protein 36	64	20.7	9	Q3SZV0	http://www.uniprot.org/uniprot/Q3SZV0
Arginine/serine-rich protein 1	52	33.7	8	Q9BUV0	http://www.uniprot.org/uniprot/Q9BUV0
V-set and transmembrane domain-containing protein 2B	61	30.4	6	A6NLU5	http://www.uniprot.org/uniprot/A6NLU5
Ninein	52	245.2	20	Q8N4C6	http://www.uniprot.org/uniprot/Q8N4C6
Electron transfer flavoprotein subunit beta	51	27.9	7	Q68FU3	http://www.uniprot.org/uniprot/Q68FU3
Coiled-coil domain- containing protein 25	53	24.6	6	Q86WR0	http://www.uniprot.org/uniprot/Q86WR0
Protein-arginine deiminase type-2	49	76	8	P20717	http://www.uniprot.org/uniprot/P20717
Radical S-adenosyl methionine domain- containing protein 2	55	42.4	8	Q9MZU4	http://www.uniprot.org/uniprot/Q9MZU4
Golgi SNAP receptor complex member 1	61	28.6	7	O88630	http://www.uniprot.org/uniprot/O88630
BTB/POZ domain- containing protein KCTD1	55	29.7	5	Q719H9	http://www.uniprot.org/uniprot/Q719H9
Zinc finger and SCAN domain-containing protein 5A	57	56.9	9	Q9BUG6	http://www.uniprot.org/uniprot/Q9BUG6
Calcium-binding mitochondrial carrier protein SCaMC-3	51	52.7	9	Q6GQS1	http://www.uniprot.org/uniprot/Q6GQS1

401 **Table 2**

402 Peptides identified in the urine of dogs with babesiosis.

403

Protein name	Score	Mass	Matches	Access no.	Hyperlink
Lipase member N	54	45.7	8	Q5VXI9	http://www.uniprot.org/uniprot/Q5VXI9
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	57	50.3	9	Q4R517	http://www.uniprot.org/uniprot/Q4R517
TATA box-binding protein-like protein 2	51	39.3	5	Q6SJ95	http://www.uniprot.org/uniprot/Q6SJ95
Interferon gamma	53	18.1	5	P01581	http://www.uniprot.org/uniprot/P01581
m7GpppX diphosphatase	57	38.8	9	Q96C86	http://www.uniprot.org/uniprot/Q96C86
Peptidyl-prolyl cis-trans isomerase F, mitochondrial	52	22.	6	P30404	http://www.uniprot.org/uniprot/P30404
Mast cell carboxypeptidase A	52	48.9	6	P15088	http://www.uniprot.org/uniprot/P15088
SprT-like domain- containing protein Spartan	54	56.1	14	G3X912	http://www.uniprot.org/uniprot/G3X912
39S ribosomal protein L50, mitochondrial	54	18.3	9	Q8VDT9	http://www.uniprot.org/uniprot/Q8VDT9
Trafficking protein particle complex subunit 1	55	17	6	Q5NCF2	http://www.uniprot.org/uniprot/Q5NCF2
Desmin	36	53.3	9	Q5XFN2	http://www.uniprot.org/uniprot/Q5XFN2
Dysferlin	57	240	17	Q9ESD7	http://www.uniprot.org/uniprot/Q9ESD7
Leucine-rich repeat- containing protein 14 O	54	55.7	6	A5PJJ5	http://www.uniprot.org/uniprot/A5PJJ5
Coenzyme Q-binding protein COQ10 homolog B, mitochondrial	58	28	10	Q51019	http://www.uniprot.org/uniprot/Q5I0I9
Bactericidal permeability- increasing protein (fragment)	54	49	6	Q28739	http://www.uniprot.org/uniprot/Q28739
G protein-activated inward rectifier potassium channel 4	51	48.3	6	P48548	http://www.uniprot.org/uniprot/P48548
Gamma-aminobutyric acid receptor subunit beta-2	56	59.3	11	P47870	http://www.uniprot.org/uniprot/P47870
Ankyrin repeat domain- containing protein 42	53	43.6	7	Q8N9B4	http://www.uniprot.org/uniprot/Q8N9B4
Protein FAM83B	62	115.2	9	Q5T0W9	http://www.uniprot.org/uniprot/Q5T0W9
Gamma-aminobutyric acid receptor subunit alpha-4	62	61.3	8	Q9D6F4	http://www.uniprot.org/uniprot/Q9D6F4
Zinc finger protein 624	61	102.5	14	Q9P2J8	http://www.uniprot.org/uniprot/Q9P2J8
Hyaluronan and proteoglycan link protein 2	54	38.6	8	Q9ESM3	http://www.uniprot.org/uniprot/Q9ESM3
HAUS augmin-like complex subunit 2	55	23.4	4	Q5RE16	http://www.uniprot.org/uniprot/Q5RE16
Thromboxane-A synthase	54	60.7	10	P49430	http://www.uniprot.org/uniprot/P49430
Vimentin	54	53.7	12	P20152	http://www.uniprot.org/uniprot/P20152
TD and POZ domain-	51	42.2	10	Q717B2	http://www.uniprot.org/uniprot/Q717B2

containing protein 2					
Kinase suppressor of Ras 2	62	110	22	Q3UVC0	http://www.uniprot.org/uniprot/Q3UVC0
Cortexin-2	55	9.2	8	Q3URE8	http://www.uniprot.org/uniprot/Q3URE8
Transmembrane protein 240	53	20.3	5	Q5SV17	http://www.uniprot.org/uniprot/Q5SV17
Protein FAM71C	50	27.9	11	Q8NEG0	http://www.uniprot.org/uniprot/Q8NEG0
Carboxylesterase 1E	58	61.8	13	Q64176	http://www.uniprot.org/uniprot/Q64176
Cytochrome P450 3A31	67	58	13	070537	http://www.uniprot.org/uniprot/O70537
Leucine-rich repeat- containing protein 14	61	55.3	6	Q15048	http://www.uniprot.org/uniprot/Q15048
Protein phosphatase Slingshot homolog 1	66	116.5	15	Q8WYL5	http://www.uniprot.org/uniprot/Q8WYL5
Twinkle protein, mitochondrial	53	77.6	8	Q96RR1	http://www.uniprot.org/uniprot/Q96RR1
Ubiquitin-conjugating enzyme E2 N	53	17.2	4	Q0P5K3	http://www.uniprot.org/uniprot/Q0P5K3
Delta-1-pyrroline-5- carboxylate synthase	55	87.8	7	Q9Z110	http://www.uniprot.org/uniprot/Q9Z110
40S ribosomal protein S11	35	18.6	3	Q9XSU4	http://www.uniprot.org/uniprot/Q9XSU4
Synaptic vesicle membrane protein VAT-1 homolog- like	61	46.2	8	Q9HCJ6	http://www.uniprot.org/uniprot/Q9HCJ6
Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	40	18	6	E2RK33	http://www.uniprot.org/uniprot/E2RK33
Trafficking protein particle complex subunit 1	63	17	7	Q5NCF2	http://www.uniprot.org/uniprot/Q5NCF2
Rab GDP dissociation inhibitor beta	44	50.8	8	097556	http://www.uniprot.org/uniprot/O97556
Parvalbumin alpha	54	12.1	10	P20472	http://www.uniprot.org/uniprot/P20472
B-cell lymphoma 6 protein homolog	52	58.8	11	P41183	http://www.uniprot.org/uniprot/P41183
Probable tubulin polyglutamylase TTLL1	53	49.5	9	Q5PPI9	http://www.uniprot.org/uniprot/Q5PPI9
Neurofilament medium polypeptide	50	95.8	7	P12839	http://www.uniprot.org/uniprot/P12839
Suppressor of tumorigenicity 7 protein	55	67.7	9	Q07E08	http://www.uniprot.org/uniprot/Q07E08
Vesicle transport protein USE1	67	30.8	7	Q9CQ56	http://www.uniprot.org/uniprot/Q9CQ56
Protein C12orf4 homolog	67	54.3	8	D4A770	http://www.uniprot.org/uniprot/D4A770
Cell death activator CIDE-A	67	24.8	6	O70302	http://www.uniprot.org/uniprot/O70302
Tryptophan 5-hydroxylase 2	58	56.8	9	Q2HZ26	http://www.uniprot.org/uniprot/Q2HZ26
Kelch-like protein	57	70.2	8	Q2T9Z7	http://www.uniprot.org/uniprot/Q2T9Z7
Ubiquitin carboxyl- terminal hydrolase 37	63	111	12	Q86T82	http://www.uniprot.org/uniprot/Q86T82
Coatomer subunit beta'	60	103.2	6	P35605	http://www.uniprot.org/uniprot/P35605
Centrosomal protein of 170 kDa protein B	61	171.2	11	Q80U49	http://www.uniprot.org/uniprot/Q80U49
Eukaryotic translation initiation factor 4 gamma 2	68	102.6	15	Q62448	http://www.uniprot.org/uniprot/Q62448
Trifunctional enzyme subunit alpha, mitochondrial	51	83.3	6	Q64428	http://www.uniprot.org/uniprot/Q64428
Isovaleryl-CoA dehydrogenase, mitochondrial	55	46.9	6	P12007	http://www.uniprot.org/uniprot/P12007

Pericentrin	60	380.6	32	O95613	http://www.uniprot.org/uniprot/O95613
Hydroxysteroid dehydrogenase-like protein 2	54	45.5	5	A4FUZ6	http://www.uniprot.org/uniprot/A4FUZ6
Ras-related protein Rab- 34, isoform NARR	53	21.1	4	P0D183	http://www.uniprot.org/uniprot/P0DI83
Interferon-induced protein with tetratricopeptide repeats 1	70	55.8	11	Q4R5F5	http://www.uniprot.org/uniprot/Q4R5F5
CysteinetRNA ligase, mitochondrial	62	62	12	Q2KIF8	http://www.uniprot.org/uniprot/Q2KIF8
Ubiquitin carboxyl- terminal hydrolase 37	63	111.2	13	F1N5V1	http://www.uniprot.org/uniprot/F1N5V1
Interferon regulatory factor 2-binding protein 1	67	62.6	8	Q8IU81	http://www.uniprot.org/uniprot/Q8IU81
Ubiquitin carboxyl- terminal hydrolase 37	84	111.2	14	F1N5V1	http://www.uniprot.org/uniprot/F1N5V1
Centrosomal protein of 152 kDa	55	197.9	12	O94986	http://www.uniprot.org/uniprot/O94986
E3 SUMO-protein ligase PIAS2	57	64.3	9	Q6AZ28	http://www.uniprot.org/uniprot/Q6AZ28
ATR-interacting protein	61	72.4	11	Q9N077	http://www.uniprot.org/uniprot/Q9N077
T-cell surface glycoprotein CD3 epsilon chain	54	23	4	P27597	http://www.uniprot.org/uniprot/P27597
Rab GDP dissociation inhibitor beta	55	50.8	10	O97556	http://www.uniprot.org/uniprot/O97556
Elongation factor Tu GTP- binding domain-containing protein 1	64	127.1	16	Q8C0D5	http://www.uniprot.org/uniprot/Q8C0D5
HIV Tat-specific factor 1 homolog	57	86.6	12	Q8BGC0	http://www.uniprot.org/uniprot/Q8BGC0
Peptidyl-prolyl cis-trans isomerase A	58	18.1	5	Q9TTC6	http://www.uniprot.org/uniprot/Q9TTC6
Tektin-4	58	51.3	7	Q8WW24	http://www.uniprot.org/uniprot/Q8WW24
Sp110 nuclear body protein	58	79.6	9	Q9HB58	http://www.uniprot.org/uniprot/Q9HB58
Rab11 family-interacting protein 5	57	69.9	10	Q8R361	http://www.uniprot.org/uniprot/Q8R361
Alkyldihydroxyacetonepho sphate synthase, peroxisomal	53	73.7	8	O00116	http://www.uniprot.org/uniprot/O00116
Fibroblast growth factor 9	57	23.5	4	P31371	http://www.uniprot.org/uniprot/P31371
Lysozyme C	52	16.9	5	Q659U0	http://www.uniprot.org/uniprot/Q659U0
Phosphoribosyl pyrophosphate synthase- associated protein 2	55	41.2	7	O08618	http://www.uniprot.org/uniprot/O08618
Zona pellucida sperm- binding protein 3	60	47.1	6	P42098	http://www.uniprot.org/uniprot/P42098
Galactoside 2-alpha-L- fucosyltransferase 2	62	39.1	8	077485	http://www.uniprot.org/uniprot/O77485
39S ribosomal protein L30, mitochondrial	56	18.7	7	Q58DV5	http://www.uniprot.org/uniprot/Q58DV5
Desmin	47	53.3	6	Q5XFN2	http://www.uniprot.org/uniprot/Q5XFN2
Dipeptidyl peptidase 1 (fragment)	43	50.1	4	097578	http://www.uniprot.org/uniprot/O97578
Vimentin	50	53.7	8	P20152	http://www.uniprot.org/uniprot/P20152
Serine/threonine-protein kinase 3	53	57.1	9	Q9JI10	http://www.uniprot.org/uniprot/Q9JI10
Neurofilament medium polypeptide	62	95.8	12	P12839	http://www.uniprot.org/uniprot/P12839

Rab GDP dissociation					
inhibitor beta	62	50.8	8	O97556	http://www.uniprot.org/uniprot/O97556
Zinc finger protein 624	65	102.5	10	Q9P2J8	http://www.uniprot.org/uniprot/Q9P2J8
Uncharacterized protein KIAA1683 homolog	64	87	6	Q8WNU4	http://www.uniprot.org/uniprot/Q8WNU4
Phosphatidylserine decarboxylase proenzyme	56	47.7	5	Q58DH2	http://www.uniprot.org/uniprot/Q58DH2
Probable tubulin polyglutamylase TTLL1	66	49.4	9	Q0VC71	http://www.uniprot.org/uniprot/Q0VC71
ATP synthase subunit d, mitochondrial	63	18.7	5	P13620	http://www.uniprot.org/uniprot/P13620
Breast cancer anti-estrogen resistance protein 3	61	93.5	8	Q58DL5	http://www.uniprot.org/uniprot/Q58DL5
Sperm surface protein Sp17	61	17.4	4	Q15506	http://www.uniprot.org/uniprot/Q15506
Actin-related protein T1	55	42.1	6	Q4R821	http://www.uniprot.org/uniprot/Q4R821
Inhibitor of nuclear factor kappa-B kinase subunit beta	54	87.8	7	O88351	http://www.uniprot.org/uniprot/O88351
Glucosamine-6-phosphate isomerase 2	53	31.3	5	Q9CRC9	http://www.uniprot.org/uniprot/Q9CRC9
E3 ubiquitin-protein ligase TRIM32	55	73.5	9	Q13049	http://www.uniprot.org/uniprot/Q13049
Protein FAM98B	56	45.9	6	Q80VD1	http://www.uniprot.org/uniprot/Q80VD1
DNA topoisomerase 2- alpha	56	173.5	11	Q01320	http://www.uniprot.org/uniprot/Q01320
Interferon alpha-1/13	50	22.1	4	P01562	http://www.uniprot.org/uniprot/P01562
Bone morphogenetic protein 7	56	21.5	6	P34819	http://www.uniprot.org/uniprot/P34819
Protein phosphatase Slingshot homolog 1	60	116.5	16	Q8WYL5	http://www.uniprot.org/uniprot/Q8WYL5
Serum albumin	42	70.6	14	P49822	http://www.uniprot.org/uniprot/P49822
Peroxiredoxin-1	61	22.3	9	Q6B4U9	http://www.uniprot.org/uniprot/Q6B4U9
Zinc finger BED domain- containing protein 5	48	80.2	11	A4Z944	http://www.uniprot.org/uniprot/A4Z944
Zinc finger and SCAN domain-containing protein 9	57	47	9	015535	http://www.uniprot.org/uniprot/O15535
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	69	11.1	7	Q4R5E2	http://www.uniprot.org/uniprot/Q4R5E2
Tektin-4	67	51.3	11	Q8WW24	http://www.uniprot.org/uniprot/Q8WW24
Elongation factor Tu GTP- binding domain-containing protein 1	70	127.1	16	Q8C0D5	http://www.uniprot.org/uniprot/Q8C0D5
DCC-interacting protein 13-beta	68	75	7	Q8NEU8	http://www.uniprot.org/uniprot/Q8NEU8
Ras-related protein Rab-28	55	25	5	Q3SWY9	http://www.uniprot.org/uniprot/Q3SWY9
Translation initiation factor eIF-2B subunit delta	55	58.4	8	Q63186	http://www.uniprot.org/uniprot/Q63186
D-beta-hydroxybutyrate dehydrogenase, mitochondrial	62	15.2	7	P86198	http://www.uniprot.org/uniprot/P86198
Gap junction alpha-8 protein	69	49.9	12	Q8K4Q9	http://www.uniprot.org/uniprot/Q8K4Q9
Dual-specificity phosphatase 28	54	18.7	7	Q4G0W2	http://www.uniprot.org/uniprot/Q4G0W2
39S ribosomal protein L30,	53	18.7	7	Q58DV5	http://www.uniprot.org/uniprot/Q58DV5

mitochondrial					
Ras-related protein Rab-36	61	36.8	12	O95755	http://www.uniprot.org/uniprot/O95755
tRNA-dihydrouridine(20) synthase [NAD(P)+]-like	50	55.8	10	Q9NX74	http://www.uniprot.org/uniprot/Q9NX74
AP-3 complex subunit mu-2	55	47.2	5	P53677	http://www.uniprot.org/uniprot/P53677
OTU domain-containing protein 6B	52	34	7	Q8N6M0	http://www.uniprot.org/uniprot/Q8N6M0
A-kinase anchor protein 10, mitochondrial	57	74.1	10	O88845	http://www.uniprot.org/uniprot/O88845
Hemoglobin subunit beta	56	16.3	6	P02073	http://www.uniprot.org/uniprot/P02073
Single-pass membrane and coiled-coil domain- containing protein 2	55	34.1	8	Q95JR4	http://www.uniprot.org/uniprot/Q95JR4
Myotrophin	56	13.1	5	Q3T0F7	http://www.uniprot.org/uniprot/Q3T0F7
Zinc finger protein 622	77	54.8	17	Q96983	http://www.uniprot.org/uniprot/Q969S3
Protein POF1B	63	68.9	10	Q8WVV4	http://www.uniprot.org/uniprot/Q8WVV4
HORMA domain-	57	45.4	8	D3ZWE7	http://www.uniprot.org/uniprot/D3ZWE7
containing protein 1 Sperm surface protein Sp17	58	17.4	7	Q15506	http://www.uniprot.org/uniprot/Q15506
Tyrosine-protein kinase BAZ1B	56	172.2	14	Q9Z277	http://www.uniprot.org/uniprot/Q9Z277
Nicolin-1	43	24.6	8	Q861Y6	http://www.uniprot.org/uniprot/Q861Y6
Parvalbumin alpha	63	12.1	11	P20472	http://www.uniprot.org/uniprot/P20472
Vimentin (fragment)	58	51.9	12	P48670	http://www.uniprot.org/uniprot/P48670
Protein FAM3C	52	24.9	7	Q92520	http://www.uniprot.org/uniprot/Q92520
Uncharacterized aarF domain-containing protein kinase 5	53	66.3	8	Q3MIX3	http://www.uniprot.org/uniprot/Q3MIX3
Interferon-induced protein with tetratricopeptide repeats 1	51	55.8	9	P09914	http://www.uniprot.org/uniprot/P09914
Oxidoreductase HTATIP2	50	27.4	10	A2T7G9	http://www.uniprot.org/uniprot/A2T7G9
Glutathione S-transferase alpha M14	52	25.4	10	GSTA1_PIG	http://www.uniprot.org/uniprot/P51781
Sperm acrosome membrane-associated protein 3	50	18.8	8	B6VH75	http://www.uniprot.org/uniprot/B6VH75
Protein FAM204A	53	27.1	6	Q8C6C7	http://www.uniprot.org/uniprot/Q8C6C7
Ras-related protein Rab-36	55	36.8	8	O95755	http://www.uniprot.org/uniprot/O95755
Neurofibromin	50	323.1	24	Q04690	http://www.uniprot.org/uniprot/Q04690
Oxidoreductase HTATIP2	52	27.4	6	A2T7G9	http://www.uniprot.org/uniprot/A2T7G9
Transmembrane emp24 domain-containing protein 9	61	27.5	6	Q3T133	http://www.uniprot.org/uniprot/Q3T133
Centromere protein H	61	28	8	Q3T0L1	http://www.uniprot.org/uniprot/Q3T0L1
Centrosomal protein of 104 kDa	72	105	14	Q80V31	http://www.uniprot.org/uniprot/Q80V31
Nicolin-1	55	24.5	6	Q9BSH3	http://www.uniprot.org/uniprot/Q9BSH3
Acylphosphatase-2	57	10.9	5	P35745	http://www.uniprot.org/uniprot/P35745
Mitofusin-1	58	84.5	9	Q811U4	http://www.uniprot.org/uniprot/Q811U4
Ras-related protein Rab-36	54	36.8	9	O95755	http://www.uniprot.org/uniprot/O95755
Hippocalcin-like protein 1	51	22.4	7	P62748	http://www.uniprot.org/uniprot/P62748

Stanniocalcin-2	47	34.1	9	Q5RAT2	http://www.uniprot.org/uniprot/Q5RAT2
Major vault protein	51	96.2	14	Q9EQK5	http://www.uniprot.org/uniprot/Q9EQK5
Peptidyl-prolyl cis-trans isomerase FKBP1A	59	12	4	Q62658	http://www.uniprot.org/uniprot/Q62658
Tyrosine-protein phosphatase non-receptor type 12	54	87.2	17	P35831	http://www.uniprot.org/uniprot/P35831
Kinase suppressor of Ras 2	52	108.9	16	Q6VAB6	http://www.uniprot.org/uniprot/Q6VAB6
Putative ATP-dependent RNA helicase DHX30	54	136.9	10	Q2NKY8	http://www.uniprot.org/uniprot/Q2NKY8
U3 small nucleolar RNA- associated protein 14 homolog A	53	88.2	10	Q3T0Q8	http://www.uniprot.org/uniprot/Q3T0Q8
39S ribosomal protein L30, mitochondrial	64	18.7	7	Q58DV5	http://www.uniprot.org/uniprot/Q58DV5
Growth arrest and DNA damage-inducible proteins- interacting protein 1	63	25.9	8	Q9CR59	http://www.uniprot.org/uniprot/Q9CR59
Protein FAM57B	66	31.2	7	Q71RH2	http://www.uniprot.org/uniprot/Q71RH2
Ras-related protein Rab- 9A	35	23.1	4	P24408	http://www.uniprot.org/uniprot/P24408
Probable tubulin polyglutamylase TTLL1	53	49.5	6	Q5PPI9	http://www.uniprot.org/uniprot/Q5PPI9
Adenylyl cyclase- associated protein 2	51	53.1	8	Q9CYT6	http://www.uniprot.org/uniprot/Q9CYT6
Collagen alpha-1(I) chain (fragments)	55	75.2	12	C0HJP1	http://www.uniprot.org/uniprot/C0HJP1
NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	54	51.4	8	Q0MQI4	http://www.uniprot.org/uniprot/Q0MQI4
Rho GTPase-activating protein 18	54	75.2	9	Q8N392	http://www.uniprot.org/uniprot/Q8N392
Rho GTPase-activating protein 39	65	122.2	11	Q9C0H5	http://www.uniprot.org/uniprot/Q9C0H5
Unconventional myosin-Ie	71	127.4	13	Q63356	http://www.uniprot.org/uniprot/Q63356
Zinc finger and SCAN domain-containing protein 25	55	62.6	8	Q6NSZ9	http://www.uniprot.org/uniprot/Q6NSZ9
Four and a half LIM domains protein 2	55	34.1	5	035115	http://www.uniprot.org/uniprot/O35115
Putative uncharacterized protein MYH16	59	128,4	16	Q9H6N6	http://www.uniprot.org/uniprot/Q9H6N6
EGF domain-specific O- linked N- acetylglucosamine transferase	61	62.6	12	A0JND3	http://www.uniprot.org/uniprot/A0JND3
Annexin A10	55	37.8	6	Q9UJ72	http://www.uniprot.org/uniprot/Q9UJ72
Beta-crystallin B2	51	37.8	4	P02522	http://www.uniprot.org/uniprot/P02522
Tripartite motif-containing protein 42	51	85.7	8	Q8IWZ5	http://www.uniprot.org/uniprot/Q8IWZ5
Syndecan-4	53	21.5	4	O35988	http://www.uniprot.org/uniprot/O35988
OTU domain-containing protein 6B	53	34	7	Q8N6M0	http://www.uniprot.org/uniprot/Q8N6M0
Desmin	65	53.6	7	O62654	http://www.uniprot.org/uniprot/O62654
Cytospin-A	50	125	10	Q2KNA0	http://www.uniprot.org/uniprot/Q2KNA0
OTU domain-containing protein 6B	53	34	7	Q8N6M0	http://www.uniprot.org/uniprot/Q8N6M0
Glutathione S-transferase alpha M14	66	25.4	6	P51781	http://www.uniprot.org/uniprot/P51781

Ribosome-binding protein 1	53	164.8	13	Q28298	http://www.uniprot.org/uniprot/Q28298
Zinc finger protein castor homolog 1	56	193.3	18	Q86V15	http://www.uniprot.org/uniprot/Q86V15
Sorting nexin-3	53	18.8	6	Q1RMH8	http://www.uniprot.org/uniprot/Q1RMH8
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	61	32.6	6	Q9CQA3	http://www.uniprot.org/uniprot/Q9CQA3
Coiled-coil domain- containing protein 122	60	32.4	7	Q5T0U0	http://www.uniprot.org/uniprot/Q5T0U0
Zinc finger C2HC domain- containing protein 1C	58	61.1	15	Q9BGW4	http://www.uniprot.org/uniprot/Q9BGW4
Ceramide synthase 3	58	61.1	8	Q8IU89	http://www.uniprot.org/uniprot/Q8IU89
Tetratricopeptide repeat protein 36	55	20.7	8	Q3SZV0	http://www.uniprot.org/uniprot/Q3SZV0
Ras-related protein Rab-17	51	23.7	9	Q9H0T7	http://www.uniprot.org/uniprot/Q9H0T7
Transmembrane and coiled-coil domain- containing protein 5A	52	34.5	5	Q8N6Q1	http://www.uniprot.org/uniprot/Q8N6Q1
Inosine triphosphate pyrophosphatase	56	21.8	6	Q9BY32	http://www.uniprot.org/uniprot/Q9BY32
Vacuolar protein sorting- associated protein 29	51	20.7	6	Q9UBQ0	http://www.uniprot.org/uniprot/Q9UBQ0
AP-3 complex subunit mu-2	66	47.2	8	P53677	http://www.uniprot.org/uniprot/P53677
Ras and EF-hand domain- containing protein homolog	60	71.3	10	Q5RI75	http://www.uniprot.org/uniprot/Q5RI75
Protein C19orf12 homolog	65	15.1	6	Q8WUR0	http://www.uniprot.org/uniprot/Q8WUR0
Serine palmitoyltransferase 2	54	63.6	9	015270	http://www.uniprot.org/uniprot/O15270
Thioredoxin, mitochondrial	53	18.4	4	P97493	http://www.uniprot.org/uniprot/P97493
Vesicle transport protein USE1	57	30.8	9	Q9CQ56	http://www.uniprot.org/uniprot/Q9CQ56
Far upstream element- binding protein 3 O	55	61.9	7	Q96I24	http://www.uniprot.org/uniprot/Q96I24
Nesprin-3	51	112.3	20	Q4FZC9	http://www.uniprot.org/uniprot/Q4FZC9
Zinc finger protein 532	50	112.2	15	Q6NXK2	http://www.uniprot.org/uniprot/Q6NXK2
Hemoglobin subunit epsilon (fragment)	50	15.6	6	O13071	http://www.uniprot.org/uniprot/O13071
Vimentin	60	53.7	15	P20152	http://www.uniprot.org/uniprot/P20152
Centromere protein H	61	28	7	Q3T0L1	http://www.uniprot.org/uniprot/Q3T0L1
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1	60	93.4	11	Q9MZS1	http://www.uniprot.org/uniprot/Q9MZS1
Pleckstrin homology-like domain family A member 3	59	13.9	5	Q9WV95	http://www.uniprot.org/uniprot/Q9WV95
Zinc finger and SCAN domain-containing protein 5A	71	56.9	11	Q9BUG6	http://www.uniprot.org/uniprot/Q9BUG6
Signal recognition particle receptor subunit beta	55	29.7	7	Q4FZX7	http://www.uniprot.org/uniprot/Q4FZX7
Tetratricopeptide repeat protein 6	53	60	8	Q86TZ1	http://www.uniprot.org/uniprot/Q86TZ1
Protein phosphatase 1 regulatory subunit 36	53	47.7	8	D3Z0R2	http://www.uniprot.org/uniprot/D3Z0R2
Oculomedin	53	5.3	4	Q9Y5M6	http://www.uniprot.org/uniprot/Q9Y5M6

Interleukin-2	57	17.8	6	Q95KP3	http://www.uniprot.org/uniprot/Q95KP3
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	54	11	5	O43678	http://www.uniprot.org/uniprot/O43678
Ras-related protein Rab-36	57	36.8	7	O95755	http://www.uniprot.org/uniprot/O95755
ATP-dependent 6- phosphofructokinase, liver type	51	58.8	10	P17858	http://www.uniprot.org/uniprot/P17858
AarF domain-containing protein kinase 4	52	59.6	6	Q6AY19	http://www.uniprot.org/uniprot/Q6AY19
Fidgetin-like protein 1	61	74.8	12	Q6PIW4	http://www.uniprot.org/uniprot/Q6PIW4
Neutrophil cytosol factor 4	61	39.1	8	Q15080	http://www.uniprot.org/uniprot/Q15080
Glycine amidinotransferase, mitochondrial	61	48.8	4	Q9D964	http://www.uniprot.org/uniprot/Q9D964
Uncharacterized protein C1orf168 homolog	62	82.8	9	A2A995	http://www.uniprot.org/uniprot/A2A995
Haptoglobin	51	36.9	5	P19006	http://www.uniprot.org/uniprot/P19006
F-box/LRR-repeat protein 8	53	41.4	5	Q96CD0	http://www.uniprot.org/uniprot/Q96CD0
Desmin	45	53.3	9	Q5XFN2	http://www.uniprot.org/uniprot/Q5XFN2
Torsin-4A	52	47.3	6	Q9NXH8	http://www.uniprot.org/uniprot/Q9NXH8
OTU domain-containing protein 6B	61	34	6	Q8N6M0	http://www.uniprot.org/uniprot/Q8N6M0
39S ribosomal protein L2, mitochondrial	63	33.5	9	Q2TA12	http://www.uniprot.org/uniprot/Q2TA12
Telomerase reverse transcriptase	61	128.6	8	O14746	http://www.uniprot.org/uniprot/O14746
Solute carrier family 15 member 1	48	79.3	5	Q8WMX5	http://www.uniprot.org/uniprot/Q8WMX5
Tripartite motif-containing protein 75	59	54.4	7	Q3UWZ0	http://www.uniprot.org/uniprot/Q3UWZ0
Probable ATP-dependent RNA helicase DDX28	59	59.8	6	Q9NUL7	http://www.uniprot.org/uniprot/Q9NUL7
Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	57	17.6	4	E2RK33	http://www.uniprot.org/uniprot/E2RK33
Cap-specific mRNA (nucleoside-2'-O-)- methyltransferase 1	59	96.6	12	Q9DBC3	http://www.uniprot.org/uniprot/Q9DBC3
Protein MB21D2	65	49	8	Q8C525	http://www.uniprot.org/uniprot/Q8C525
Desmin	29	53.3	3	Q5XFN2	http://www.uniprot.org/uniprot/Q5XFN2
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	60	11	5	O43678	http://www.uniprot.org/uniprot/O43678
Oculomedin	46	5.3	4	Q9Y5M6	http://www.uniprot.org/uniprot/Q9Y5M6
Glycogen phosphorylase, brain form	52	96.9	12	Q5MIB6	http://www.uniprot.org/uniprot/Q5MIB6
V-set and transmembrane domain-containing protein 2B	62	30.3	5	Q9JME9	http://www.uniprot.org/uniprot/Q9JME9
Microsomal triglyceride transfer protein large subunit	65	99.6	11	P55156	http://www.uniprot.org/uniprot/P55156
E3 ubiquitin-protein ligase ARIH2	56	59.3	8	Q9Z1K6	http://www.uniprot.org/uniprot/Q9Z1K6
Ubiquitin carboxyl- terminal hydrolase 37	58	111	6	Q86T82	http://www.uniprot.org/uniprot/Q86T82
Putative homeodomain	53	88	9	Q9UMS5	http://www.uniprot.org/uniprot/Q9UMS5

transcription factor 1					
Junction plakoglobin	53	82.4	6	P14923	http://www.uniprot.org/uniprot/P14923
Pericentriolar material 1 protein	52	230	10	Q15154	http://www.uniprot.org/uniprot/Q15154
43 kDa receptor-associated protein of the synapse	60	47.6	13	P12672	http://www.uniprot.org/uniprot/P12672
Desmin	45	53.3	6	Q5XFN2	http://www.uniprot.org/uniprot/Q5XFN2
Probable tubulin polyglutamylase TTLL1	63	49.4	10	095922	http://www.uniprot.org/uniprot/O95922
Ubiquitin carboxyl- terminal hydrolase 48	61	121.1	8	Q86UV5	http://www.uniprot.org/uniprot/Q86UV5
Parvalbumin alpha	62	12.1	7	P20472	http://www.uniprot.org/uniprot/P20472
Putative fatty acid-binding protein 5-like protein 3	51	11.5	6	A8MUU1	http://www.uniprot.org/uniprot/A8MUU1
Tyrosine-protein phosphatase non-receptor type 6	49	70	11	P81718	http://www.uniprot.org/uniprot/P81718
Zinc finger protein 624	65	102.5	13	Q9P2J8	http://www.uniprot.org/uniprot/Q9P2J8
Zinc finger and SCAN domain-containing protein 5A	65	56.9	11	Q9BUG6	http://www.uniprot.org/uniprot/Q9BUG6
Actin-related protein 2/3 complex subunit 3	51	20.8	7	Q3T035	http://www.uniprot.org/uniprot/Q3T035
FSD1-like protein	56	60.2	9	Q9BXM9	http://www.uniprot.org/uniprot/Q9BXM9
UPF0585 protein C16orf13	54	22.8	7	Q96S19	http://www.uniprot.org/uniprot/Q96S19
HAUS augmin-like complex subunit 6	60	109.6	12	Q7Z4H7	http://www.uniprot.org/uniprot/Q7Z4H7
FSD1-like protein	62	60.2	9	Q9BXM9	http://www.uniprot.org/uniprot/Q9BXM9
Protocadherin alpha-C2	62	110	8	Q9Y5I4	http://www.uniprot.org/uniprot/Q9Y5I4
Ral guanine nucleotide dissociation stimulator-like 2	63	84.5	7	Q5TJE5	http://www.uniprot.org/uniprot/Q5TJE5
Cilia- and flagella- associated protein 99	57	52.5	7	D6REC4	http://www.uniprot.org/uniprot/D6REC4
Ras-related protein Rab-39A	51	25.4	5	Q14964	http://www.uniprot.org/uniprot/Q14964
Protein FAM229B	63	8.9	5	Q4G0N7	http://www.uniprot.org/uniprot/Q4G0N7
Zinc finger protein ZFP69B	55	62.8	6	Q9UJL9	http://www.uniprot.org/uniprot/Q9UJL9
NAD-dependent protein deacetylase sirtuin-7	53	45.7	7	B2RZ55	http://www.uniprot.org/uniprot/B2RZ55
Zona pellucida sperm- binding protein 2	44	81.1	8	P47983	http://www.uniprot.org/uniprot/P47983
Peroxiredoxin-1	61	22.3	7	Q06830	http://www.uniprot.org/uniprot/Q06830
Transcriptional repressor NF-X1	54	130	10	Q12986	http://www.uniprot.org/uniprot/Q12986
Phosphatidylinositol 4- phosphate 5-kinase type-1 alpha	62	60.8	12	P70182	http://www.uniprot.org/uniprot/P70182
Transcriptional repressor NF-X1	53	130	10	P70182	http://www.uniprot.org/uniprot/P70182
Tyrosine-protein kinase receptor TYRO3	52	97.2	8	P55144	http://www.uniprot.org/uniprot/P55144
Ras-related protein Rab-17	53	23.7	5	Q9H0T7	http://www.uniprot.org/uniprot/Q9H0T7
Thiamine-triphosphatase	54	25.7	9	Q9BU02	http://www.uniprot.org/uniprot/Q9BU02
Dual-specificity phosphatase 28	52	18.7	7	Q4G0W2	http://www.uniprot.org/uniprot/Q4G0W2
Peptidyl-prolyl cis-trans	57	41.1	8	Q9CR16	http://www.uniprot.org/uniprot/Q9CR16

isomerase D					
Artemin	51	24.2	6	Q6AYE8	http://www.uniprot.org/uniprot/Q6AYE8
Zinc finger and SCAN domain-containing protein 5A	77	56.9	7	Q9BUG6	http://www.uniprot.org/uniprot/Q9BUG6
SLAIN motif-containing protein 2	50	62.6	7	Q8CI08	http://www.uniprot.org/uniprot/Q8CI08
Adenylyl cyclase- associated protein 2	52	53.2	7	P52481	http://www.uniprot.org/uniprot/P52481
Acylphosphatase-2	51	11.2	6	P00818	http://www.uniprot.org/uniprot/P00818
Centriolar coiled-coil protein of 110 kDa	51	11.9	14	Q7TSH4	http://www.uniprot.org/uniprot/Q7TSH4
Zinc finger and SCAN domain-containing protein 5A	51	56.9	8	Q9BUG6	http://www.uniprot.org/uniprot/Q9BUG6
Fibronectin type 3 and ankyrin repeat domains protein 1	54	38.6	6	Q6B858	http://www.uniprot.org/uniprot/Q6B858
Hemoglobin subunit beta	60	16.3	8	Q6B858	http://www.uniprot.org/uniprot/Q6B858
Ankyrin repeat and death domain-containing protein 1A	51	57.9	10	Q495B1	http://www.uniprot.org/uniprot/Q495B1
Protein-arginine deiminase type-4	63	75.1	11	Q9Z183	http://www.uniprot.org/uniprot/Q9Z183
Actin-binding Rho- activating protein	60	43	10	Q8BUZ1	http://www.uniprot.org/uniprot/Q8BUZ1
Myotrophin	51	13.1	6	Q3T0F7	http://www.uniprot.org/uniprot/Q3T0F7
Ras GTPase-activating protein 2	52	97.8	9	P58069	http://www.uniprot.org/uniprot/P58069
Cleavage and polyadenylation specificity factor subunit 1	54	162.4	9	Q10569	http://www.uniprot.org/uniprot/Q10569
Cholecystokinin	55	12.9	5	P41520	http://www.uniprot.org/uniprot/P41520
Cortexin-2	55	9.2	4	Q3URE8	http://www.uniprot.org/uniprot/Q3URE8
Uncharacterized protein C12orf60	53	27.7	7	Q5U649	http://www.uniprot.org/uniprot/Q5U649
Tetratricopeptide repeat protein 36	66	20.7	9	Q3SZV0	http://www.uniprot.org/uniprot/Q3SZV0
Coiled-coil domain- containing protein 81	64	76.8	18	Q6ZN84	http://www.uniprot.org/uniprot/Q6ZN84
Tyrosine-protein kinase Fer	63	95.1	23	Q9TTY2	http://www.uniprot.org/uniprot/Q9TTY2
Tetratricopeptide repeat protein 36	59	20.7	8	Q3SZV0	http://www.uniprot.org/uniprot/Q3SZV0
Ras-related protein Rab-36	64	36.8	10	O 95755	http://www.uniprot.org/uniprot/O95755
Rab GDP dissociation inhibitor beta	66	50.8	8	097556	http://www.uniprot.org/uniprot/O97556
Centromere/kinetochore protein zw10 homolog	63	89.6	15	O43264	http://www.uniprot.org/uniprot/O43264
Parvalbumin alpha	62	12.1	10	P20472	http://www.uniprot.org/uniprot/P20472
Complement C1q subcomponent subunit B	62	26.6	8	Q2KIV9	http://www.uniprot.org/uniprot/Q2KIV9
Double-stranded RNA- binding protein Staufen homolog 2	68	62.8	10	Q9NUL3	http://www.uniprot.org/uniprot/Q9NUL3
CD209 antigen-like protein B	66	37.7	7	Q8CJ91	http://www.uniprot.org/uniprot/Q8CJ91
SRC kinase signaling inhibitor 1	66	112.7	11	Q9C0H9	http://www.uniprot.org/uniprot/Q9C0H9
Oxidoreductase HTATIP2	72	27.4	7	A2T7G9	http://www.uniprot.org/uniprot/A2T7G9

TyrosinetRNA ligase, cytoplasmic	51	59.4	12	Q4KM49	http://www.uniprot.org/uniprot/Q4KM49
Zinc finger protein 101	50	51.9	10	Q8IZC7	http://www.uniprot.org/uniprot/Q8IZC7
60S ribosomal protein L37	53	11.3	7	P79244	http://www.uniprot.org/uniprot/P79244
Zinc finger protein 621	52	50.2	6	Q6ZSS3	http://www.uniprot.org/uniprot/Q6ZSS3
E3 ubiquitin-protein ligase RNF152	50	23.1	5	D2H6Z0	http://www.uniprot.org/uniprot/D2H6Z0
Ras-related protein Rab-36	68	36.8	9	O95755	http://www.uniprot.org/uniprot/O95755
Prolactin	64	26.1	7	Q9QZL1	http://www.uniprot.org/uniprot/Q9QZL1
Vacuolar ATPase assembly integral membrane protein Vma21	50	44.4	4	Q78T54	http://www.uniprot.org/uniprot/Q78T54
Hemoglobin subunit beta	69	16.3	10	P02073	http://www.uniprot.org/uniprot/P02073
Sterile alpha and TIR motif-containing protein 1	60	80.8	12	I3L5V6	http://www.uniprot.org/uniprot/I3L5V6
39S ribosomal protein L50, mitochondrial	62	18.3	6	Q8VDT9	http://www.uniprot.org/uniprot/Q8VDT9
Interferon regulatory factor 2-binding protein 1	66	62.6	14	Q8IU81	http://www.uniprot.org/uniprot/Q8IU81
FUN14 domain-containing protein 2	50	16.6	5	Q9D6K8	http://www.uniprot.org/uniprot/Q9D6K8
Potassium voltage-gated channel subfamily B member 1	62	96.7	13	Q14721	http://www.uniprot.org/uniprot/Q14721
Collagen alpha-2(I) chain	64	129.8	9	O46392	http://www.uniprot.org/uniprot/O46392
Protein AAR2 homolog	61	43.9	9	Q08DJ7	http://www.uniprot.org/uniprot/Q08DJ7
Aurora kinase C	65	35.9	13	Q9UQB9	http://www.uniprot.org/uniprot/Q9UQB9
NAD-dependent protein deacetylase sirtuin-7	58	45.7	14	Q8BKJ9	http://www.uniprot.org/uniprot/Q8BKJ9
Peroxiredoxin-1	56	22.3	9	Q06830	http://www.uniprot.org/uniprot/Q06830
Perilipin-3	52	47.1	7	Q5RAV8	http://www.uniprot.org/uniprot/Q5RAV8
Protein kish-A	52	8.3	4	Q148I3	http://www.uniprot.org/uniprot/Q148I3
Ras-related protein Rab-36	50	36.8	6	O95755	http://www.uniprot.org/uniprot/O95755
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	62	50.3	12	Q4R517	http://www.uniprot.org/uniprot/Q4R517
Glycogen phosphorylase, liver form	51	97.9	12	P09811	http://www.uniprot.org/uniprot/P09811
Integrin alpha-11	50	134.1	13	P61622	http://www.uniprot.org/uniprot/P61622
Neuropathy target esterase	63	150.9	17	Q3TRM4	http://www.uniprot.org/uniprot/Q3TRM4
Oncostatin-M	61	28.8	9	P13725	http://www.uniprot.org/uniprot/P13725
Vesicle transport protein USE1	63	30.8	9	Q9CQ56	http://www.uniprot.org/uniprot/Q9CQ56
Testicular haploid expressed gene protein	50	43.8	8	Q5XHX8	http://www.uniprot.org/uniprot/Q5XHX8
Serine/threonine-protein phosphatase 6 catalytic subunit	55	35.8	7	O00743	http://www.uniprot.org/uniprot/O00743
E3 ubiquitin-protein ligase MARCH8	53	33.7	5	Q0VD59	http://www.uniprot.org/uniprot/Q0VD59
Phospholipase A2	25	17.0	3	P06596	http://www.uniprot.org/uniprot/P06596
Protein polyglycylase TTLL10	55	80.2	13	A4Q9F3	http://www.uniprot.org/uniprot/A4Q9F3
T-complex protein 1 subunit gamma	58	61.1	13	Q3T0K2	http://www.uniprot.org/uniprot/Q3T0K2

Vimentin (fragment)	57	51.9	14	P48670	http://www.uniprot.org/uniprot/P48670
Ras-related protein Rab-36	61	36.8	9	O 95755	http://www.uniprot.org/uniprot/O95755
Interferon-induced protein with tetratricopeptide repeats 1	54	55.8	10	Q4R5F5	http://www.uniprot.org/uniprot/Q4R5F5
Uncharacterized protein C1orf186	52	19.6	4	Q6ZWK4	http://www.uniprot.org/uniprot/Q6ZWK4
Isocitrate dehydrogenase [NADP] cytoplasmic	51	47.1	7	Q9XSG3	http://www.uniprot.org/uniprot/Q9XSG3
Dual-specificity phosphatase	51	18.7	5	Q4G0W2	http://www.uniprot.org/uniprot/Q4G0W2
Methylmalonic aciduria type A protein, mitochondrial	50	46.9	6	Q8IVH4	http://www.uniprot.org/uniprot/Q8IVH4
Rab GDP dissociation inhibitor beta	47	50.8	8	O97556	http://www.uniprot.org/uniprot/O97556
Vacuolar protein sorting- associated protein 4B	62	49.5	14	Q5R658	http://www.uniprot.org/uniprot/Q5R658
C-type natriuretic peptide	66	13.5	9	P56283	http://www.uniprot.org/uniprot/P56283
T-complex protein 1 subunit alpha	64	60.8	14	P18279	http://www.uniprot.org/uniprot/P18279
Carboxylesterase 1E	67	61.8	11	Q64176	http://www.uniprot.org/uniprot/Q64176
Stefin-2	52	11.9	6	P35174	http://www.uniprot.org/uniprot/P35174
Ras-related protein Rab-2B	55	24.5	6	P59279	http://www.uniprot.org/uniprot/P59279
Hemoglobin subunit epsilon (fragment)	53	15.6	5	O13071	http://www.uniprot.org/uniprot/O13071
Adenylosuccinate synthetase lisozyme 1	53	50.5	8	Q8N142	http://www.uniprot.org/uniprot/Q8N142
Fragile X mental retardation protein 1 homolog	52	67.3	7	Q5R9B4	http://www.uniprot.org/uniprot/Q5R9B4
Calponin-1	50	33.4	8	Q2HJ38	http://www.uniprot.org/uniprot/Q2HJ38
Calponin-1	84	33.4	10	Q9GK38	http://www.uniprot.org/uniprot/Q9GK38
Tyrosine-tRNA ligase, cytoplasmic	58	59.5	9	Q5R8T5	http://www.uniprot.org/uniprot/Q5R8T5
14 kDa phosphohistidine phosphatase	50	14	4	Q9NRX4	http://www.uniprot.org/uniprot/Q9NRX4
N-acetylgalactosamine-6- sulfatase	45	58.4	4	Q32KH5	http://www.uniprot.org/uniprot/Q32KH5
Norrin	58	15.6	6	Q2KI78	http://www.uniprot.org/uniprot/Q2KI78
Ribosome biogenesis protein BOP1	50	83.2	8	P97452	http://www.uniprot.org/uniprot/P97452
Sp110 nuclear body protein	51	79.6	7	Q9HB58	http://www.uniprot.org/uniprot/Q9HB58
Endophilin-A2	52	41.7	7	Q62419	http://www.uniprot.org/uniprot/Q62419
Ras-related protein Rab-36	54	36.8	5	095755	http://www.uniprot.org/uniprot/O95755
Putative uncharacterized protein C6orf50	53	12.6	5	Q9HD87	http://www.uniprot.org/uniprot/Q9HD87
Cytochrome P450 2C23	52	57	8	P24470	http://www.uniprot.org/uniprot/P24470
Protein MB21D2	52	49	9	Q8C525	http://www.uniprot.org/uniprot/Q8C525
Heat shock 70 kDa protein 4L (fragments)	52	23.8	9	P86265	http://www.uniprot.org/uniprot/P86265
Oxidoreductase HTATIP2	53	27.4	6	A2T7G9	http://www.uniprot.org/uniprot/A2T7G9
Ras-related protein Rab-36	56	36.8	6	095755	http://www.uniprot.org/uniprot/O95755
OTU domain-containing protein 6B	54	34	7	Q8N6M0	http://www.uniprot.org/uniprot/Q8N6M0

Suppressor of IKBKE 1	53	23.7	8	Q9CPR7	http://www.uniprot.org/uniprot/Q9CPR7
Myb/SANT-like DNA-					
binding domain-containing protein 3	64	32.7	8	Q0III0	http://www.uniprot.org/uniprot/Q0III0
Ras-related protein Rab-36	52	36.8	8	095755	http://www.uniprot.org/uniprot/O95755
Calpastatin	50	77.6	11	P27321	http://www.uniprot.org/uniprot/P27321
NACHT, LRR and PYD domains-containing protein 5	62	123.4	21	Q647I9	http://www.uniprot.org/uniprot/Q647I9
Mitochondrial uncoupling protein 3	38	34.6	5	Q9N2I9	http://www.uniprot.org/uniprot/Q9N2I9
Hemoglobin subunit beta	62	16.3	8	P02073	http://www.uniprot.org/uniprot/P02073
Diacylglycerol kinase theta	50	104	11	Q6P5E8	http://www.uniprot.org/uniprot/Q6P5E8
C-type natriuretic peptide	65	13.5	8	P56283	http://www.uniprot.org/uniprot/P56283
Interleukin-12 receptor subunit beta-2	55	98.5	17	Q99665	http://www.uniprot.org/uniprot/Q99665
Tumor necrosis factor receptor superfamily member 5	58	33.4	7	P27512	http://www.uniprot.org/uniprot/P27512
Tetratricopeptide repeat protein 34	53	61.8	10	A8MYJ7	http://www.uniprot.org/uniprot/A8MYJ7
TATA box-binding protein-associated factor RNA polymerase I subunit D	52	33	4	Q5M948	http://www.uniprot.org/uniprot/Q5M948
Tetratricopeptide repeat protein 36	65	20.7	9	Q3SZV0	http://www.uniprot.org/uniprot/Q3SZV0
Nicolin-1	62	24.5	9	Q9BSH3	http://www.uniprot.org/uniprot/Q9BSH3
Gamma-tubulin complex	51	103.8	22	Q921G8	http://www.uniprot.org/uniprot/Q921G8
component 2 Calcium/calmodulin- dependent protein kinase II inhibitor 1	52	8.6	6	A7MBG3	http://www.uniprot.org/uniprot/A7MBG3
Tropomodulin-4	53	39.5	7	Q0VC48	http://www.uniprot.org/uniprot/Q0VC48
Protein THEM6	51	24	6	Q5XIE1	http://www.uniprot.org/uniprot/Q5XIE1
F-box/SPRY domain- containing protein 1	55	31.1	7	Q8K3B1	http://www.uniprot.org/uniprot/Q8K3B1
Actin-like protein 7B	52	45.9	9	Q9Y614	http://www.uniprot.org/uniprot/Q9Y614
Kinase suppressor of Ras 2	56	110	20	Q3UVC0	http://www.uniprot.org/uniprot/Q3UVC0
Cytospin-A	50	125	17	Q2KNA0	http://www.uniprot.org/uniprot/Q2KNA0
Uridine 5'-monophosphate synthase	51	52.6	8	P11172	http://www.uniprot.org/uniprot/P11172
Coiled-coil domain- containing protein 25	50	24.6	8	Q78PG9	http://www.uniprot.org/uniprot/Q78PG9
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	64	17.1	6	Q9U109	http://www.uniprot.org/uniprot/Q9UI09
Ras-related protein Rab-36	62	36.8	9	095755	http://www.uniprot.org/uniprot/O95755
Epididymal-specific lipocalin-5	65	20.8	8	P06911	http://www.uniprot.org/uniprot/P06911
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	57	11.1	7	Q4R5E2	http://www.uniprot.org/uniprot/Q4R5E2
Zinc finger protein castor homolog 1	72	193.3	15	Q86V15	http://www.uniprot.org/uniprot/Q86V15
Hippocalcin-like protein 1	62	22.4	6	P62748	http://www.uniprot.org/uniprot/P62748

Uncharacterized protein	56	27.7	10	Q5U649	http://www.uniprot.org/uniprot/Q5U649
C12orf60		27.7	10	230047	
Mini-chromosome maintenance complex- binding protein	56	73.6	10	Q8R3C0	http://www.uniprot.org/uniprot/Q8R3C0
Transmembrane protein 132C	59	122.6	8	Q8N3T6	http://www.uniprot.org/uniprot/Q8N3T6
Ubiquitin carboxyl- terminal hydrolase isozyme L1	56	25.2	5	P50103	http://www.uniprot.org/uniprot/P50103
Apolipoprotein A-II	54	11.2	4	P0DM93	http://www.uniprot.org/uniprot/P0DM93
Kinesin light chain 2	52	69.3	10	Q9H0B6	http://www.uniprot.org/uniprot/Q9H0B6
Glutathione peroxidase 3	50	25.6	6	P23764	http://www.uniprot.org/uniprot/P23764
Prolactin	55	26.6	5	P12420	http://www.uniprot.org/uniprot/P12420
Arginine/serine-rich protein 1	51	33.7	5	Q9BUV0	http://www.uniprot.org/uniprot/Q9BUV0
Amyloid beta A4 protein (fragment)	58	6.2	4	Q29149	http://www.uniprot.org/uniprot/Q29149
Leucine-rich repeat- containing protein 49	61	79.4	7	Q91YK0	http://www.uniprot.org/uniprot/Q91YK0
PH and SEC7 domain- containing protein 3	50	115.3	11	Q2PFD7	http://www.uniprot.org/uniprot/Q2PFD7
Insulin	54	12.5	5	P01321	http://www.uniprot.org/uniprot/P01321
Dual-specificity phosphatase 28	54	18.7	6	Q4G0W2	http://www.uniprot.org/uniprot/Q4G0W2
Calpain-2 catalytic subunit	50	80.8	8	P17655	http://www.uniprot.org/uniprot/P17655
Peroxiredoxin-1	52	22.3	6	Q06830	http://www.uniprot.org/uniprot/Q06830
Ras-related protein Rab-25	53	23.5	6	P46629	http://www.uniprot.org/uniprot/P46629
tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like	53	72.4	9	Q91XI1	http://www.uniprot.org/uniprot/Q91XI1
AarF domain-containing protein kinase 4	56	59.6	8	Q6AY19	http://www.uniprot.org/uniprot/Q6AY19
RING finger protein 10	52	90.7	7	Q08E13	http://www.uniprot.org/uniprot/Q08E13
E3 ubiquitin-protein ligase RNF152	60	23.1	5	D2H6Z0	http://www.uniprot.org/uniprot/D2H6Z0
Protein-arginine deiminase type-3	53	76.3	7	Q9Z184	http://www.uniprot.org/uniprot/Q9Z184
Sentan	65	16.6	5	A6NMZ2	http://www.uniprot.org/uniprot/A6NMZ2
Plakophilin-4	53	132.3	8	Q68FH0	http://www.uniprot.org/uniprot/Q68FH0
Urotensin-2B	65	13.0	8	Q765I1	http://www.uniprot.org/uniprot/Q76511
Signal peptidase complex subunit 2	53	25.3	8	Q15005	http://www.uniprot.org/uniprot/Q15005
Tektin-4	54	51.3	12	Q8WW24	http://www.uniprot.org/uniprot/Q8WW24
Cytochrome P450 2J3	53	58.4	10	P51590	http://www.uniprot.org/uniprot/P51590
Ras-related protein Rab-36	64	36.8	9	095755	http://www.uniprot.org/uniprot/O95755
Isocitrate dehydrogenase [NADP] cytoplasmic	50	47.2	6	Q6XUZ5	http://www.uniprot.org/uniprot/Q6XUZ5
E3 ubiquitin-protein ligase RNF169	55	77.1	8	E9Q7F2	http://www.uniprot.org/uniprot/E9Q7F2
Class E basic helix-loop- helix protein 40	51	45.9	6	014503	http://www.uniprot.org/uniprot/O14503
Interleukin-13	55	15.5	6	Q9N0W9	http://www.uniprot.org/uniprot/Q9N0W9
Rab GDP dissociation inhibitor beta	67	50.8	7	097556	http://www.uniprot.org/uniprot/O97556
Isocitrate dehydrogenase	60	51.3	8	P54071	http://www.uniprot.org/uniprot/P54071

[NADP], mitochondrial					
Stanniocalcin-2	63	34.1	8	O97561	http://www.uniprot.org/uniprot/O97561
Ephrin type-B receptor 4	50	110.3	11	P54761	http://www.uniprot.org/uniprot/P54761
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	60	17.1	7	Q9UI09	http://www.uniprot.org/uniprot/Q9UI09
Dual-specificity phosphatase 28	54	18.7	7	Q4G0W2	http://www.uniprot.org/uniprot/Q4G0W2
Parafibromin	54	60.7	13	Q6P1J9	http://www.uniprot.org/uniprot/Q6P1J9
Bactericidal permeability- increasing protein	59	54	10	Q6AXU0	http://www.uniprot.org/uniprot/Q6AXU0
Zinc finger protein castor homolog 1	61	193.3	17	Q86V15	http://www.uniprot.org/uniprot/Q86V15
Calcitonin receptor- stimulating peptide 2	44	14.3	7	Q75V93	http://www.uniprot.org/uniprot/Q75V93
Corticoliberin	58	20.8	9	Q95MI6	http://www.uniprot.org/uniprot/Q95MI6
Urotensin-2B	50	13	6	Q765I1	http://www.uniprot.org/uniprot/Q76511
Pumilio homolog 3	53	73.9	16	Q15397	http://www.uniprot.org/uniprot/Q15397
Protein FAM162B	55	18.1	9	A6QPI4	http://www.uniprot.org/uniprot/A6QPI4
Cytochrome c oxidase subunit 6C	55	8.6	7	Q7YRK2	http://www.uniprot.org/uniprot/Q7YRK2
Aromatase	56	58.6	13	P46194	http://www.uniprot.org/uniprot/P46194
Zinc finger protein 101	50	51.9	9	Q8IZC7	http://www.uniprot.org/uniprot/Q8IZC7
Phosphatidylethanolamine- binding protein 1	52	21.2	5	Q8MK67	http://www.uniprot.org/uniprot/Q8MK67
Leucine-tRNA ligase, cytoplasmic	57	135.7	11	Q5R614	http://www.uniprot.org/uniprot/Q5R614
NACHT, LRR and PYD domains-containing protein 10	76	77.3	14	Q8CCN1	http://www.uniprot.org/uniprot/Q8CCN1
Urotensin-2B	70	13	7	Q765I1	http://www.uniprot.org/uniprot/Q765I1
Mortality factor 4-like protein 2	82	32.2	8	Q9R0Q4	http://www.uniprot.org/uniprot/Q9R0Q4
Nucleolar pre-ribosomal- associated protein 1	59	256.5	15	O60287	http://www.uniprot.org/uniprot/O60287
Serine/threonine-protein phosphatase 6 catalytic subunit	74	35.8	10	O00743	http://www.uniprot.org/uniprot/O00743
Hemopexin	63	52	7	Q91X72	http://www.uniprot.org/uniprot/Q91X72
Rab GDP dissociation inhibitor beta	52	51	8	P50397	http://www.uniprot.org/uniprot/P50397
Sperm surface protein Sp17	55	17.3	5	Q62252	http://www.uniprot.org/uniprot/Q62252
Natriuretic peptides B	46	15.1	4	P16859	http://www.uniprot.org/uniprot/P16859
Iron-responsive element- binding protein 2	55	106.1	8	B3VKQ2	http://www.uniprot.org/uniprot/B3VKQ2
STE20-related kinase adapter protein alpha	53	41.9	5	Q5E9J9	http://www.uniprot.org/uniprot/Q5E9J9
E3 ubiquitin-protein ligase RNF169	50	77.1	9	E9Q7F2	http://www.uniprot.org/uniprot/E9Q7F2
Acyl-coenzyme A synthetase ACSM2B, mitochondrial	57	64.8	8	Q68CK6	http://www.uniprot.org/uniprot/Q68CK6
Survival motor neuron protein	63	32.2	9	Q4R4F8	http://www.uniprot.org/uniprot/Q4R4F8
Tektin-4	54	51.3	8	Q8WW24	http://www.uniprot.org/uniprot/Q8WW24

Anonhaga promoting					
Anaphase-promoting complex subunit CDC26	61	9.8	4	Q3SZT7	http://www.uniprot.org/uniprot/Q3SZT7
39S ribosomal protein L30, mitochondrial	71	18.7	5	Q58DV5	http://www.uniprot.org/uniprot/Q58DV5
Interleukin-4	64	15.5	6	P55030	http://www.uniprot.org/uniprot/P55030
39S ribosomal protein L10, mitochondrial	51	29.6	8	Q3TBW2	http://www.uniprot.org/uniprot/Q3TBW2
39S ribosomal protein L30, mitochondrial	50	18.7	5	Q58DV5	http://www.uniprot.org/uniprot/Q58DV5
Acylphosphatase-2	61	11.1	7	P35744	http://www.uniprot.org/uniprot/P35744
Tektin-4	51	51.3	8	Q8WW24	http://www.uniprot.org/uniprot/Q8WW24
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2	68	95.7	17	Q9JKA9	http://www.uniprot.org/uniprot/Q9JKA9
Dual-specificity phosphatase 28	50	18.7	6	Q4G0W2	http://www.uniprot.org/uniprot/Q4G0W2
Hydroxysteroid dehydrogenase-like protein 2	63	45.5	10	A4FUZ6	http://www.uniprot.org/uniprot/A4FUZ6
Islet amyloid polypeptide	52	10	5	P17716	http://www.uniprot.org/uniprot/P17716
G-protein coupled receptor-associated sorting protein 1	51	152.8	13	Q5U4C1	http://www.uniprot.org/uniprot/Q5U4C1
Growth/differentiation factor 2	52	47.9	7	Q9UK05	http://www.uniprot.org/uniprot/Q9UK05
Cytosolic purine 5'- nucleotidase	52	65.3	10	O46411	http://www.uniprot.org/uniprot/O46411
Vesicle transport protein USE1	59	30.8	16	Q9CQ56	http://www.uniprot.org/uniprot/Q9CQ56
Putative zinc finger protein 137	61	24.7	8	P52743	http://www.uniprot.org/uniprot/P52743
Elongation factor 1-beta	52	25	5	Q5E983	http://www.uniprot.org/uniprot/Q5E983
Tektin-4	64	51.3	12	Q8WW24	http://www.uniprot.org/uniprot/Q8WW24
Parathyroid hormone/parathyroid hormone-related peptide receptor	67	66.7	9	Q1LZF7	http://www.uniprot.org/uniprot/Q1LZF7
Chorionic somatomammotropin hormone 2	50	28.2	6	P19159	http://www.uniprot.org/uniprot/P19159
Probable tubulin polyglutamylase TTLL1	51	49.5	8	Q5PPI9	http://www.uniprot.org/uniprot/Q5PPI9
Collagen alpha-1(XI) chain (fragment)	62	89.3	10	Q28083	http://www.uniprot.org/uniprot/Q28083
G kinase-anchoring protein 1	68	42.2	10	Q5XIG5	http://www.uniprot.org/uniprot/Q5XIG5
Protein phosphatase Slingshot homolog 1	67	116.5	14	Q8WYL5	http://www.uniprot.org/uniprot/Q8WYL5
Arginine/serine-rich protein 1	58	33.7	8	Q9BUV0	http://www.uniprot.org/uniprot/Q9BUV0
Sorting and assembly machinery component 50 homolog	50	52.2	6	Q8BGH2	http://www.uniprot.org/uniprot/Q8BGH2
Cystatin-B	57	11.2	4	P25417	http://www.uniprot.org/uniprot/P25417
Desmin	61	53.6	13	P17661	http://www.uniprot.org/uniprot/P17661
Transmembrane inner ear expressed protein	52	53.6	6	Q8K467	http://www.uniprot.org/uniprot/Q8K467
Putative uncharacterized protein encoded by CRHR1-IT1	50	17.2	6	Q96LR1	http://www.uniprot.org/uniprot/Q96LR1

Oculomedin	58	5.3	5	Q9Y5M6	http://www.uniprot.org/uniprot/Q9Y5M6
Protein kish-A	62	8.3	5	Q148I3	http://www.uniprot.org/uniprot/Q148I3
Rab GDP dissociation inhibitor beta	51	50.8	6	O97556	http://www.uniprot.org/uniprot/O97556
Glutathione S-transferase Mu 6	52	25.8	8	O35660	http://www.uniprot.org/uniprot/O35660
Hemoglobin subunit beta	68	16.3	8	P02073	http://www.uniprot.org/uniprot/P02073
Zinc finger and SCAN domain-containing protein 5A	62	56.9	11	Q9BUG6	http://www.uniprot.org/uniprot/Q9BUG6
Ras-related protein Rab-36	53	36.8	7	O 95755	http://www.uniprot.org/uniprot/O95755
39S ribosomal protein L50, mitochondrial	54	18.3	9	Q8VDT9	http://www.uniprot.org/uniprot/Q8VDT9
NAD-dependent protein deacetylase sirtuin-7	51	45.7	9	Q8BKJ9	http://www.uniprot.org/uniprot/Q8BKJ9
Ras-related protein Rab-36	57	36.8	12	O95755	http://www.uniprot.org/uniprot/O95755
Putative uncharacterized protein encoded by LINC01546	62	7.3	5	A6NGU7	http://www.uniprot.org/uniprot/A6NGU7
Hemoglobin subunit beta	51	16.3	7	P02073	http://www.uniprot.org/uniprot/P02073
3-oxo-5-beta-steroid 4- dehydrogenase	50	37.7	8	P51857	http://www.uniprot.org/uniprot/P51857
Synaptosomal-associated protein 29	56	29.1	7	Q9Z2P6	http://www.uniprot.org/uniprot/Q9Z2P6
Zinc finger protein 624	52	102.5	10	Q9P2J8	http://www.uniprot.org/uniprot/Q9P2J8
Ubiquitin carboxyl- terminal hydrolase 48	51	120.7	11	Q76LT8	http://www.uniprot.org/uniprot/Q76LT8
Cholecystokinin	56	12.7	4	P23362	http://www.uniprot.org/uniprot/P23362

- 405 **Table 3**
- 406 List of Canis familiaris proteins identified in the urine of dogs with babesiosis by MALDI-
- 407 TOF/TOF.
- 408

Nr	Accession ^a	Protein name	GO molecular function
1	P06596	Phospholipase A2	phospholipase
2	A4Z944	Zinc finger BED domain-containing protein 5	transcription factor
3	O46392	Collagen alpha-2(I) chain	extracellular matrix structural constituent
4	Q9XSU4	40S ribosomal protein S11	structural constituent of ribosome
5	O97556	Rab GDP dissociation inhibitor beta	G-protein modulator acyltransferase
6	Q9TTY2	Tyrosine-protein kinase Fer	tyrosine kinese activity
7	P19006	Haptoglobin	hemoglobin binding
8	Q75V93	Calcitonin receptor-stimulating peptide 2	peptide hormone
9	Q2KNA0	Cytospin-A	structural component
10	P01321	Insulin	hormone
12	Q9N2I9	Mitochondrial uncoupling protein 3	oxidative phosphorylation
11	E2RK33	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	ligase
12	Q32KH5	N-acetylgalactosamine-6-sulfatase	hydrolase
13	P27597	T-cell surface glycoprotein CD3 epsilon chain	transmembrane signalling receptor
14	P24408	Ras-related protein Rab-9A	GTPase
15	P34819	Bone morphogenetic protein 7 (fragment)	growth factor
16	Q5TJE5	Ral guanine nucleotide dissociation stimulator-like 2	guanyl-nucleotide exchange factor
17	Q9N0W9	Interleukin-13	cytokine
18	Q8WMX5	Solute carrier family 15 member 1	transporter
19	O97578	Dipeptidyl peptidase 1 (fragment)	endopeptidase
20	Q861Y6	Nicolin-1	structural component
21	P17716	Islet amyloid polypeptide	hormone

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410 a. in UniProt database (http://www.uniprot.org)

411

412 **Table 4**

413 List of 10 metabolic pathways and 8 associated proteins in the urine of dogs with babesiosis.

414

Nr	Pathway	Protein	
1	CCKR signalling map	Calcitonin receptor-stimulating peptide 2	
2	Cadherin signalling pathway	Tyrosine-protein kinase Fer	
3	Gonadotropin-releasing hormone receptor pathway	Insulin/Bone morphogenetic protein 7 (fragment)	
4	Inflammation response mediated by chemokines and cytokines	Interleukin 13	
5	Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade	Insulin/insulin-like growth factor	
6	Insulin/IGF pathway-protein kinase B signaling cascade	Insulin/insulin-like growth factor	
7	Integrin signalling pathway	Collagen alpha-2(I) chain	
8	Ras pathway	Ral guanine nucleotide dissociation stimulator-like 2	
9	T cell activation	T cell surface glycoprotein CD3 epsilon chain	
10	TGF-beta signaling pathway	Bone morphogenetic protein 7 (fragment)	

415