# Sample Stability and Protein Composition of Saliva: Implications for Its Use as a Diagnostic Fluid

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Abstract: Saliva is an easy accessible plasma ultra-filtrate. Therefore, saliva can be an attractive alternative to blood for measurement of diagnostic protein markers. Our aim was to determine stability and protein composition of saliva. Protein stability at room temperature was examined by incubating fresh whole saliva with and without inhibitors of proteases and bacterial metabolism followed by Surface Enhanced Laser Desorption/Ionization (SELDI) analyses. Protein composition was determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) fractionation of saliva proteins followed by digestion of excised bands and identification by liquid chromatography tandem mass spectrometry (LC-MS/MS). Results show that rapid protein degradation occurs within 30 minutes after sample collection. Degradation starts already during collection. Protease inhibitors partly prevented degradation while inhibition of bacterial metabolism did not affect degradation. Three stable degradation products of 2937 Da, 3370 Da and 4132 Da were discovered which can be used as markers to monitor sample quality. Saliva proteome analyses revealed 218 proteins of which 84 can also be found in blood plasma. Based on a comparison with seven other proteomics studies on whole saliva we identified 83 new saliva proteins. We conclude that saliva is a promising diagnostic fluid when precautions are taken towards protein breakdown.

Keywords: saliva, sample stability, biomarkers, proteomics, mass spectrometry, protein breakdown

#### Introduction

Saliva is a plasma ultra-filtrate that includes specific salivary proteins produced by three major salivary glands (parotid, sub-mandibular and sub-lingual) and other smaller glands (Baum, 1993). Salivary glands produce around 750 ml of fluid each day (Chicharro, 1998). After secretion in the mouth cavity, the fluid is mixed with bacteria, lining cells, nasal secretions and bronchial secretions and is termed whole saliva (Kaufman, 2000; Kaufman, 2002). Whole saliva is easy to collect in a non-invasive way. This makes saliva an attractive alternative to blood testing (Kaufman, 2002; Lawrence, 2002). Compared to blood sampling, whole saliva collection requires no specially trained personnel, can reduce discomfort and anxiety and may simplify serial sample collection. Saliva tests are also safer than blood tests regarding the risk for hepatitis and HIV. As a diagnostic fluid, saliva has been studied in pilot experiments for several pathological conditions, such as celiac disease (Lanander-Lumikari, 2000), rheumatoid arthritis (Helenius, 2005), HIV (Holmstrom, 1990; Malamud, 1992; Matsuda, 1993; Frerichs, 1994), diabetes mellitus (Belazi, 1998; Lopez, 2003), preterm birth (Heine, 2000; Ramsey, 2003), breast cancer (Streckfus, 2005; Streckfus, 2006), sjögren's syndrome (Ryu, 2006) and for evaluation of hematopoietic stem cell transplantation (Imanguli, 2007). Saliva composition is influenced by several factors, e.g. circadian rhythms, oral health status and exercise (Dawes, 1993; Chicharro, 1998) but also micro organisms and proteases may have a considerable effect on sample stability/protein degradation. Before saliva can be used as a diagnostic fluid for protein markers in the clinic, its stability should be determined. At present there are only three studies on protein stability in saliva samples (Morris, 2002; Ng. 2003; Schipper, 2007). Two of the studies report on the stability of specific proteins i.e. IgA, Lysozyme (Ng, 2003) and IgG (Morris, 2002). One recent study determined overall protein stability of saliva samples stored on ice, at -20 °C and at -80 °C (Schipper, 2007). In the current study we evaluated in detail the overall protein stability of saliva at room temperature over the first four hours after sample

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collection since this is a critical period where protein breakdown could be expected. The effect of sample handling, inhibition of bacterial growth and inhibition of protease activity on saliva protein stability was examined by comparative profiling with Surface Enhanced Laser Desorption/Ionization Time of Flight Mass Spectrometry (SELDI-TOF-MS) (Merchant, 2000). In addition we studied whole saliva composition. Whole saliva protein composition has been studied using different proteomic strategies (Huang, 2004; Vitorino, 2004; Wilmarth, 2004; Hu, 2005; Xie, 2005; Guo, 2006; Walz, 2006). Xie et al. (Xie, 2005) identified 437 proteins in saliva using free flow electrophoreses. Guo et al. (Guo, 2006) could identify 1381 proteins employing a capillary electrophoresis approach. However, because of the complexity of whole saliva, each proteomics strategy leads to partial overlapping subsets of saliva proteins (Guo, 2006). Therefore, different proteomics strategies contribute to a comprehensive view of the whole saliva proteome. We analyzed whole saliva composition by fractionating saliva proteins on SDS-PAGE followed by LC-MS/MS analyses of digests from cut-out sections of the gel lane. This proteomics approach has not been applied to saliva before. The results of this approach are compared to previous proteomics studies on whole saliva and discussed in terms of protein origin and function.

## Materials and Methods

## Chemicals

Ammonium bicarbonate, triton X-100, azide, phenylmethylsulphonylfluoride (PMSF), EDTA, ditiothreitol (DTT), iodoacetamide,  $\alpha$ -cyano-4hydroxy cinnamic acid diethylamine salt (CHCA), formic acid (FA) and trifluoroacetic acid (TFA) were purchased from Sigma-Aldrich (Steinheim, Germany). Acetonitrile (ACN) and acetone were obtained from Biosolve (Valkenswaard, The Netherlands), leupeptin from Roche (Mannheim, Germany) and ammonium acetate and 2-propanol from Merck (Darmstadt, Germany). MES running buffer and SeeBlue Pre-Stained standard for SDS-PAGE were obtained from Invitrogen (Breda, The Netherlands). Coomassie staining (PageBlue Staining Solution) was from Fermentas (Vilnius, Lithuania). Seq. grade modified trypsin porcine was purchased from Promega (Madison, WI, U.S.A.).

## Saliva collection

Whole saliva was collected from healthy subjects, four male and three female, between 08:00 a.m. and 10:00 a.m. after overnight fasting, to minimize the influence of circadian rhythms and food debris. Subjects were asked to rinse their mouths with water and discard this before sample collection. Saliva was allowed to accumulate in the floor of the mouth. The accumulated saliva was then spit into a polypropylene test tube and this was repeated until enough saliva was collected (Navazesh, 1993). During the collection process the sample tubes were kept on ice.

### Sample pretreatment

Samples were processed according to Hu et al. (Hu, 2005). Briefly, samples were centrifuged for 5 minutes at 1300 g at 4 °C. The pellet was discarded (debris) and the supernatant was centrifuged for 15 minutes at 14000 g at 4 °C. After centrifugation, the supernatant was stored at -20 °C until analysis. Samples were analyzed the same day.

## Sample stability studies

In the first experiment, sample stability was determined in saliva obtained from seven healthy volunteers (four male, three female). Freshly collected saliva samples were either directly processed (time point 0) or left at room temperature for four hrs before processing. Aliquots of the 0 and 4 hrs time points were then analyzed by SELDI-TOF-MS in duplicate (see below).

In a second experiment a unique saliva sample freshly collected from one healthy male volunteer was divided in 3 aliquots of 1.2 ml and incubated for 0, 0.5, 1 and 4 hrs at room temperature with either a) 40  $\mu$ l of 100 mM sodium azide to inhibit bacterial activity, b) protease inhibitors: 60  $\mu$ l of 2 mg/ml PMSF in 2-propanol, 1.2  $\mu$ l of 1 mg/ml leupeptin in water, 12  $\mu$ l of 100 mM EDTA, or c) no additives (control). Water was added to a final volume of 1.273 ml for all 3 conditions. At each time point an aliquot was taken and treated as described above (sample pre-treatment section). Thereafter, samples were analyzed in triplicate by SELDI-TOF-MS for protein profiling.

CM10 weak cation exchange proteinchip arrays (Ciphergen biosystems, Fremont, CA, U.S.A.) were assembled in a 96 well bioprocessor and the spots were washed two times with 200 µl binding buffer

(100 mM NH<sub>4</sub>Ac pH 4.0, 0.05% Triton X-100) for 5 minutes with vigorous shaking. After removing the buffer from the wells, 90 µl binding buffer and  $10 \ \mu l$  saliva sample were randomly applied to the spots (in duplicate or triplicate as detailed above). Samples were allowed to incubate for 30 minutes with continuous shaking. Then, they were removed and spots were washed 3 times with 200 µl binding buffer for 5 minutes and once with 200 µl de-ionized water for 5 minutes. The chips were removed from the bioprocessor and air-dried for 15 minutes, followed by two additions (1  $\mu$ l each) of a 20% solution of CHCA prepared in 50% ACN and 0.5% TFA. Spots were analyzed using the ProteinChip Reader (model PBS II, Ciphergen Biosystems). The mass spectrometer was calibrated using the All-in-One peptide calibration kit (Ciphergen Biosystems) with a focus mass of 6000 Da. Spectra from the saliva samples were collected with the proteinchip software 3.1 (Ciphergen Biosystems) in the mass range 1–20 kDa. Laser intensity was 190, ionsource voltage 20000 V and detector voltage 2150 V. Cluster analysis was performed by Ciphergen Express 3.0 software (Ciphergen Biosystems): a) between samples collected at 0 hr and 4 hr, combining spectra of all seven volunteers measured in duplicate (28 spectra in total) and b) between different time points (0 hrs, 0.5 hrs, 1 hr and 4 hrs) for every condition (control, in presence of azide and in presence of protease inhibitors) measured in triplicate. Before cluster analyses, spectra to be compared were selected, the baseline was subtracted and profiles were normalized using total ion current. Peaks with a signal to noise ratio higher than 5 were selected and were clustered with peaks with similar masses (mass deviation 0.3%) in other profiles with signal to noise ratios higher than 2. The percentage of spectra in which a peak must appear in order to form a cluster was set to 20%. Significant differences (p < 0.05) in peak height of particular masses were calculated.

#### Saliva protein composition

A saliva sample freshly obtained from a healthy volunteer was processed immediately after collection as described in the sample pretreatment section. 10  $\mu$ l of processed saliva were mixed with NuPAGE LDS sample buffer (Invitrogen, Carlsbad, CA, U.S.A.) according to standard protocol from the manufacturer. SDS-PAGE was then performed on a NuPAGE 12% Bis-Tris gel (Invitrogen)

run at 200 V for 50 minutes with MES buffer (Invitrogen). Proteins were visualized with Coomassie staining. For protein identification, the whole lane was excised in 30 bands. Each band was cut into small pieces and stored at -20 °C until analysis. Then, they were washed in water and dehydrated in ACN. Reduction was performed by covering gel pieces with 10 mM DTT in 100 mM ammonium bicarbonate for 1 hr at 60 °C. DTT solution was then replaced by 55 mM iodoacetamide in 100 mM ammonium bicarbonate and gel pieces were incubated at room temperature in the dark for 45 minutes. After washing in water and dehydration in ACN, 0.1 µg of trypsin (in 50 mM ammonium bicarbonate) was added and gel pieces were allowed to rehydrate on ice for 20 minutes. Digestion was carried out overnight at 37 °C. Peptides were extracted by treating the gel pieces with 0.1%FA for 30 minutes with continuous shaking. Peptide mixtures were then stored at -20 °C until LC-MS/MS analysis was performed.

Separation of the resulting tryptic peptide mixtures was performed by nano-scale reversed-phase LC-MS/MS. The Agilent 1100 nanoflow/capillary LC system (Agilent, Paolo Alto, CA, U.S.A.) was equipped with a trapping column (5  $\times$  0.3 mm  $C_{18}RP$ ) (Dionex/LC Packings, Amsterdam, The Netherlands) and a nanocolumn  $(150 \times 0.075 \text{ mm})$ C<sub>18</sub>Pepmap) (Dionex/LC Packings). Peptides mixtures were injected into the trapping column at a flow rate of 10 µl/min (3%ACN/0.1%TFA). After 10 minutes the trapping column was switched into the nanoflow system and the trapped peptides were separated using the nanocolumn at a flow rate of 0.3 µl/min in a linear gradient elution from 95%A (3%ACN/0.1%TFA) to 50%B (97%ACN/ 0.1%TFA) in 70 minutes, followed by an increase up to 80%B in 5 minutes. The eluting peptides were on-line electrosprayed into the QStar XL Hybrid ESI Quadrupole time-of-flight tandem mass spectrometer, ESI-QTOF-MS/MS (Applied Biosystems, Framingham, MA; MDS Sciex, Concord, Ontario, Canada) provided with a nanospray source equipped with a New Objective ESI needle (10 µm tip diameter). Typical values for needle voltage were 2 kV in positive ion mode. The mass spectrometer was set to perform data acquisition in the positive ion mode, typically with a selected mass range of 300-1500 m/z. Peptides with +2 to +4 charge states were selected for tandem mass spectrometry, and the time of summation of MS/ MS events was set to be 2 s. The three most

abundant charged peptides above a 30 count threshold were selected for MS/MS and dynamically excluded for 60 s with 50 amu mass tolerance.

ProID software (Applied Biosystems) was used to identify proteins from the mass spectrometric datasets according to UniProt database (May 2005, 181,000 entries). Mass tolerance was set to 0.15 Da (MS) and 0.1 Da (MS/MS) and carboxamidomethylation and methionine oxidation were chosen as modifications for database search.

## Results

### Sample stability

The stability of saliva at room temperature after sample collection from four male and three female volunteers was evaluated. Freshly collected saliva samples were either directly processed (time point 0) or left at room temperature for 4 hrs and processed as described in the sample pretreatment section. Aliquots taken at the two time points were then spotted in duplicate on CM10 weak cation exchange chips and protein profiles were obtained by SELDI-TOF-MS. Representative spectra obtained from the 1 to 10 kDa range are shown in Figure 1. In this mass range degradation products of larger proteins can be expected. When comparing the protein profiles of fresh samples (0 hrs) of the seven volunteers (A-G) it is evident that there is already considerable variation, especially in the mass range of 1 to 5 kDa between the different individuals. This may be due to biological variation and/or may indicate different degrees of protein degradation between individuals. Also over the period of 4 hrs at room temperature many changes in the spectra can be observed (Fig. 1). To find common peaks that were changed over the 4 hrs period in all seven samples we performed a cluster analyses on the acquired spectra. In total 11 differences were detected and listed in Table 1 together with their fold change in peak intensity between the two conditions. Most peptides are decreased in abundance at 4 hrs, probably because they are further degraded into single amino acids during this period. However, 3 peptides with masses 2937 Da, 3370 Da and 4132 Da are increasing in time which indicates that they are relatively stable breakdown products of larger proteins. Although SELDI technology allows rapid comparison of sample composition, protein/peptide identification is troublesome



Figure 1. Sample stability at room temperature. Protein profiles of saliva samples of seven volunteers (A-G) taken at 0 and 4 hrs of incubation at room temperature are shown for the mass range of 1000 to 10000 Da. Protein profiles were generated using CM10 proteinchips and 100 mM NH<sub>4</sub>Ac pH 4.0 as binding and washing buffer. CHCA was used as matrix.

because it involves purification of each degradation product. Therefore, we attempted to identify the 2937 Da breakdown product by direct SELDI-MS/MS which is possible for peptides with masses below 3000 Da. However, the 2937 Da peptide could not be fragmented by MS/MS even with the highest energy settings and argon as collision gas. This indicates that it is very stable, possibly due to a high degree of post-translational modifications such as glycosylation which may also explain its stability in vivo. As Figure 2 indicates, the three marker peptides can already

**Table 1.** Masses with significantly different peak intensities between 0 and 4 hrs of incubation of whole saliva at room temperature.

Peak (m/z)	p-value	Fold change
2937	0.0017	6.8
3370	0.025	2.0
4132	0.047	3.0
4368	0.0017	-6.1
4928	0.0017	-17.5
5210	0.018	-3.7
5376	0.0017	-16.5
5839	0.018	-2.8
7751	0.0017	-6.1
10422	0.0088	-5.0
15495	0.0017	-4.9

Clusters were determined using S/N > 5 (first pass) and S/N > 2 (second pass). Differences were considered significant if p < 0.05.

be detected in "fresh" samples (0 hrs), although with lower intensities. This indicates that breakdown already starts during sample collection and suggests that these markers may be useful indicators of protein breakdown in saliva samples. We examined the protein degradation in saliva in detail to obtain more knowledge on the time frame of the degradation process and whether it was possible to inhibit degradation. Protein degradation could be caused by bacteria in the mouth cavity and/or by proteases present in saliva. Therefore, we studied the influence of sodium azide, an inhibitor of bacterial energy metabolism, and of a protease inhibitor cocktail consisting of



**Figure 2.** Detailed view of the SELDI profile of volunteer A (see also Fig. 1) in the mass range of 2500 to 5000 Da for saliva samples taken at 0 and 4 hrs of incubation at room temperature. The labeled peaks are discovered degradation markers. The complete list of markers is shown in Table 1.

PMSF, leupeptin (both serine and cysteine protease inhibitors) and EDTA, an inhibitor of metallo-proteases. Saliva samples were incubated for 0, 0.5, 1 and 4 hrs in the presence and absence of the above mentioned inhibitors. Subsequently, protein profiles were generated (Fig. 3) and compared for differences by cluster analyses as described above. In Figure 4 the number of significant differences is depicted for the different conditions and the different time points compared to 0 hrs (control). For saliva without inhibitors already 19 differences were observed in the first 30 minutes incubation. Thereafter, the number of differences stabilizes. This can be explained by assuming that equilibrium has been reached at this point between the formation of peptides from the breakdown of larger proteins and the degradation of these peptides into single amino acids which are in the mass range of the matrix peaks and therefore are not detected. At 4 hrs 26 differences were observed compared to 0 hrs. This indicates that protein degradation in saliva is a relatively rapid process. It is also clear from Figure 4 that protein breakdown is almost not affected by the addition of azide to the samples, indicating that bacterial metabolism is not contributing much to the protein degradation process, at least for the first hour after collection. The protease inhibitor cocktail is more effective in slowing down the degradation process (Fig. 4). At 4 hrs, 19 differences were observed in the presence of protease inhibitors compared to 26 differences in the control sample. Nevertheless, protein degradation is still substantial with the inhibitor cocktail used. Different inhibitors or combinations of inhibitors need to be evaluated to determine their effectiveness.

#### The saliva proteome

To determine the saliva composition, saliva proteins were fractionated by SDS-PAGE (Fig. 5). The whole lane was sliced into 30 bands and digested by trypsin. The digests of the bands were subjected to LC-MS/MS for protein identification, as described in detail in the Materials and Methods section. In total we identified 218 proteins, 182 with 99% confidence and 36 with 95% confidence. A complete list of identified proteins is shown in Table 2. Proteins were classified into 12 functional categories based on information from Swiss Prot, Source and Human Protein Reference Database.



Figure 3. Representative SELDI spectra of a saliva sample incubated at 0, 0.5, 1 and 4 hrs at room temperature in the absence (control) and presence of sodium azide, an inhibitor of bacterial metabolism, and a protease inhibitor cocktail.

For each protein also the functional category is listed. In Figure 6 an overview of the different categories is given. The largest category (19.2%) consists of enzymes involved in metabolism, mainly in carbohydrate metabolism (12.8%). This includes enzymes such as  $\alpha$ -amylase, lactate dehydrogenase, malate dehydrogenase and fructose-biphosphate aldolase. Another important category (17.9%) includes proteins that are involved in immune response and defense against bacteria. In this group there is a large cluster of IgG chains besides antibactericidal peptides such as dermcidin and bactericidal permeability-increasing protein. Also many proteins from bacterial origin were identified (11% of total). 10.6% of the proteins are

involved in degradation. Six proteases were identified in this group e.g. kallikrein, cathepsin D and lysozyme C. Thirteen protease inhibitors are also part of this category such as cystatins, alpha-2macroglobulin and TIMP-1. The proteases are likely to contribute to the rapid breakdown of saliva proteins that was described above. Also many structural proteins (14.7% of total) were found which are probably derived from cells lining the mouth cavity together with other intracellular proteins that were identified. The transport proteins (8.3% of total) are mainly serum-derived such as albumin, apolipoprotein A-1, transferrin, and ceruloplasmin. Minor categories of proteins are signaling (5.5%), protein modification (4.6%), cell growth and differentiation (2.3%), cell adhesion (3.7%), and proteins involved in maintaining redox status (2.3%). We also compared our results, listed in Table 2, to the HUPO plasma proteome initiative list of 3020 plasma proteins, identified with at least two peptides by LC-MS/MS (www.bioinformatics. med.umich.edu/hupo/ppp). According to the



**Figure 4.** Number of significant differences in peak intensity between the different conditions (• control, + azide and **A** protease inhibitors) and the different time points compared to 0 hrs. Differences were calculated from the spectra (Fig. 3) for the mass ranges of 1000 to 20000 Da using cluster analyses of triplicate measurements of the samples. Clusters were defined using S/N > 5 (first pass) and S/N > 2 (second pass). Differences were considered significant if p < 0.05.

 Table 2. List of proteins identified with 99% and 95% confidence in human saliva.

Protein name	Accession nr	Function	Mass (Da)
99% confidence:			
14-3-3 protein beta/alpha	P31946	Signalling	27951
14-3-3 protein zeta/delta§	P63104	Signalling	27745
6-phosphogluconate dehydrogenase,	P52209	Energy/metabolism	53009
decarboxylating			
78 kDa glucose-regulated protein	P11021	Protein Folding/Repair	72333
	D60700	Ctru seture 1/Cute alcalate	44707
Actin like protoin 3 <sup>#</sup>	P00709 D61159	Structural/Cytoskeletal	41/3/
Actin-related protein 2/3 complex	P50008	Structural/Cytoskeletal	19536
subunit 4 <sup>#</sup>	1 00000	Off detailar Oytoskeletai	10000
Adenine phosphoribosyltransferase	P07741	Energy/metabolism	19477
Adenosylhomocysteinase <sup>#</sup>	P23526	Energy/metabolism	47585
Alcohol dehydrogenase [NADP+]#	P14550	Energy/metabolism	36442
Alcohol dehydrogenase class IV	P40394	Energy/metabolism	40006
mu/sigma chain#			
Aldehyde dehydrogenase, dimeric	P30838	Energy/metabolism	50379
NADP-preferring"	000040		20004
Aldo-keto reductase family	060218	Energy/metabolism	36021
	D06733	Energy/metabolism	47038
Alpha-1-acid alvconrotein 1	P02763	Defense/Immunoresponse	23512
precursor <sup>§,#</sup>	1 02/00	Derense/immunoresponse	20012
Alpha-1-antitrypsin precursor <sup>§</sup>	P01009	Protein Degradation/Inhibitor	46737
Alpha-actinin 1§	P12814	Structural/Cytoskeletal	103058
Apolipoprotein A-I precursor§	P02647	Transport	30778
Arginase 1§	P05089	Energy/metabolism	34735
ATPase 4, plasma membrane-type <sup>#</sup>	Q9SU58	Micro organism	105718
Bactericidal permeability-increasing	P17213	Transport	53396
protein precursor <sup>#</sup>	D00700		40040
Calgranulin B <sup>3</sup>	PU0702		13242
Carboyulostoraso 2 procursor	PZ3280	Energy/metabolism	30300
Cathensin D precursor	P07339	Protein Degradation/Inhibitor	44552
Ceruloplasmin precursor <sup>§</sup>	P00450	Transport	122205
Chaperone protein dnaK <sup>#</sup>	Q7NXI3	Micro organism	69122
Chitinase 3-like protein 2 precursor#	Q15782	Cell Growth/Differentiation	43501
Chloride intracellular channel protein 1	O00299	Transport	26792
Clusterin precursor§	P10909	Cell Growth/Differentiation	52495
Cofilin, non-muscle isoform	P23528	Structural/Cytoskeletal	18371
Complement C3 precursor <sup>3</sup>	P01024	Signalling	187164
Complement C4 precursor <sup>3</sup>	P01028	Defense/Immunoresponse	192771
Complement lactor in precursors	P00003 D311/6	Structural/Cytoskeletal	139070
Cystatin A <sup>§</sup>	P01040	Protein Degradation/Inhibitor	11006
Cystatin B <sup>§</sup>	P04080	Protein Degradation/Inhibitor	11140
Cystatin C precursor <sup>§</sup>	P01034	Protein Degradation/Inhibitor	15799
Cystatin D precursor	P28325	Protein Degradation/Inhibitor	16080
Cystatin S precursor	P01036	Protein Degradation/Inhibitor	16214
Cystatin SA precursor	P09228	Protein Degradation/Inhibitor	16445
Cystatin SN precursor	P01037	Protein Degradation/Inhibitor	16362
	P81605	Detense/Immunoresponse	11284
Desmodoin 2 precursor	QU248/	Cell Adhesion/Communication	99962 107502
Diable homolog mitochondrial precursor <sup>#</sup>	L 27220		27121
Dihydroxy-acid dehydratase <sup>#</sup>		Micro organism	58965
Dipeptidyl peptidase IV <sup>§,#</sup>	P27487	Protein Degradation/Inhibitor	88279
DNA polymerase IV <sup>#</sup>	Q9JYS8	Micro organism	35966
	-	č	(Continued)

Elongation factor 1-aphna <sup>6</sup> P68104         Protein Synthesis         50141           Elongation factor 1-gamma         P2684         Protein Synthesis         49988           Ezrin <sup>1,4</sup> P15311         Cell GrowthOlfferentiation         69288           Ezrin <sup>1,4</sup> P47766         Structural/Cytoskeletal         31219           Famesyl pyrophosphate synthetase <sup>4</sup> P14324         Energy/metabolism         15033           Flörinogen gamma chain precursor <sup>4</sup> P02679         Protein Modification/Polymerization         51512           Fix Crotein <sup>4</sup> P04075         Energy/metabolism         39289           Fructose-bisphosphate aldolase A <sup>5</sup> P04075         Energy/metabolism         39289           Fructose-bisphosphate aldolase C         P09972         Energy/metabolism         39289           Galectin-5 lunding protein precursor <sup>4</sup> P06396         Structural/Cytoskeletal         86888           Galectin-5 lunding protein precursor <sup>4</sup> P06396         Structural/Cytoskeletal         86898           Glucase-6, phosphate isomerase <sup>5</sup> P06744         Energy/metabolism         3016           Glucase-6, phosphate         P04406         Energy/metabolism         3016           Glutatione S-transferase P         P09511         Signaling </th <th>Protein name</th> <th>Accession nr</th> <th>Function</th> <th>Mass (Da)</th>	Protein name	Accession nr	Function	Mass (Da)
Elongation factor 1-gamma         P26641         Protein Synthesis         49988           Fractin capping protein beta subunit         P47756         Structural/Cytoskeletal         31219           Framesyl prophosphate subunit         P47756         Structural/Cytoskeletal         31219           Fatty acid-binding protein, epidemal         Q01469         Energy/metabolism         40532           Fix/C protein*         P02679         Protein Modification/Polymeitzation         51512           Fix/C protein*         Q0239(9         Micro organism         46687           Fructose-bisphosphate aldolase A*         P04075         Energy/metabolism         392289           Fructose-bisphosphate aldolase C         P09972         Energy/metabolism         39325           Galectin-7*         P47929         Cell Adhesion/Communication         14944           Gelsoin precursor*         P06368         Structural/Cytoskeletal         86688           Glutamini-(HANA synthetase*         Q085262         Micro organism         64103           Glutamini-(HANA synthetase*         Q085262         Micro organism         64103           Glutamini-(HANA synthetase*         Q08541         Transport         45205           Heat shock Cogante 71 kDa protein*         P090738         Transport         51676	Elongation factor 1-alpha§	P68104	Protein Synthesis	50141
Eziñs <sup>3,4</sup> P15311         Cell Growth/Differentiation         69268           Factin capping protein beta subunit         P47756         Structural/Cytoskeletal         31219           Famesyl pyrophosphate synthetase <sup>4</sup> P14324         Energy/metabolism         15033           Flbringen gamma chain precursor <sup>3</sup> P02679         Protein Modification/Polymerization         51512           Flbringen gamma chain precursor <sup>3</sup> P02679         Protein Modification/Polymerization         51512           Flbringen gamma chain precursor <sup>4</sup> P04075         Energy/metabolism         39289           Fructose-bisphosphate aldolase A <sup>5</sup> P04075         Energy/metabolism         39325           Galectin-3 binding protein precursor <sup>4</sup> P06386         Structural/Cytoskeletal         86698           Genome polyprotein <sup>4</sup> P1753         Micro organism         63016           Glutase-G-phosphate isomerase <sup>8</sup> P06744         Energy/metabolism         63016           Glutastino-S-transferase P         P90921         Signaling         23225           Glyceraldehyde-3-phosphate         P04406         Energy/metabolism         33922           Glutastino-S-transferase P         P90211         Signaling         23225           Glyceraldehyde-3-phosphate         P04406<	Elongation factor 1-gamma	P26641	Protein Synthesis	49988
F-actin capping protein beta subunit P47756 Structural/Cytoskeletal 31219 Famesy lyrophosphate synthetase* P14324 Energy/metabolism 40532 Fatty acid-binding protein, epidermal Q01469 Energy/metabolism 15033 Fitz Sprotein* Q829(9 Protein Modification/Polymerization 51512 FixC protein* Q829(9 Protein Modification/Polymerization 39325 Fructose-bisphosphate aldolase C P09972 Energy/metabolism 39325 Galectin-7 <sup>8</sup> P06390 Cell Adhesion/Communication 14944 Gelsolin procursor* P06734 Energy/metabolism 255497 Glucose-6-phosphate isomerase* P06744 Energy/metabolism 63016 Glutaminy-HRAN synthetase* Q8EC26 Micro organism 64103 Glutaminy-HRAN synthetase* Q8EC26 Micro organism 64103 Glutaminy-HRAN synthetase* P04711 Signalling 23225 Glyceraldehydrogenase 1 P04709 Protein Folding/Repair 70052 Heat shock Cognate 71 KB protein * P00738 Transport 45205 Heat shock Cognate 71 KB protein* P1112 Protein Folding/Repair 70058 Hemoglobin alpha chain P69905 Transport 51676 Hyothetical 84.6 KD protein* P04746 Defense/Immunoresponse 36508 Ig apma-2 chain C region* P0178 Defense/Immunoresponse 36508 Ig apma-2 chain C region* P01877 Defense/Immunoresponse 36508 Ig agmma-2 chain C region* P01877 Defense/Immunoresponse 12751 Ig heavy chain V-III region ROCK 474* P01768 Defense/Immunoresponse 12751 Ig heavy chain V-III region ROCK 474* P01768 Defense/Immunoresponse 12751 Ig heavy chain V-III region ROK 474* P01768 Defense/Immunoresponse 12561 Ig heavy chain V-III region ROK 474* P01768 Defense/Immunoresponse 12751 Ig heavy chain V-III region ROK 474* P01761 Defense/Immunoresponse 12561 Ig heavy chain V-III region ROK 474* P01761 Defense/Immunoresponse 12561 Ig heavy chain V-III region ROK 474* P01761 Defense/Immunoresponse 12561 Ig heavy chain V-III region ROK 474* P01761 Defense/Immunoresponse 11	Ezrin <sup>§,#</sup>	P15311	Cell Growth/Differentiation	69268
Farnesyl pyrophosphate synthetase*P14324Energy/metabolism40532Flohrogen gamma chain precursor*P02679Protein Modification/Polymerization51612Flohrogen gamma chain precursor*Q02679Protein Modification/Polymerization51612Fluctore-bisphosphate aldolase A*P04075Energy/metabolism39285Galectin-3 binding protein precursor*Q08390Cell Adhesion/Communication65331Galectin-7*P05396Structural/Cytoskeletal85687Galectin-7*P05396Structural/Cytoskeletal85688Glucese-5-phosphate isomerase*Q082626Micro organism255497Glucese-6-phosphate isomerase*Q082626Micro organism64103Glutathinols - Stransferase PP09211Signaling23225Glyceraldehyde-3-phosphateP04406Energy/metabolism35922Glyceraldehyde-3-phosphateP04406Energy/metabolism35922Heat shock Cognate 71 kDa protein*P11142Protein Folding/Repair70052Heat shock Cognate 71 kDa protein*P002738Transport15126Hemoglobin beta chainQ9UK54Transport15126Hemoglobin alpha chainQ9UK54Transport15126Hemoglobin alpha chainQ9UK54Transport15126Hemoglobin alpha chainQ9UK54Transport15126Hemoglobin Cregion*P01876Defense/Immunoresponse37655Ig alpha-2 chain C region*P01876Defense/Immunoresponse37655Ig alpha-2 chain	F-actin capping protein beta subunit	P47756	Structural/Cytoskeletal	31219
Fatty acid-binding protein, epidermalQ01469Energy/metabolism1503Floriogen gamma chain precursor <sup>8</sup> P02679Protein Modification/Polymerization51512FixC, protein <sup>8</sup> Ca829K9Micro organism45687Fructose-bisphosphate aldolase A <sup>8</sup> P04075Energy/metabolism39325Galectin-7 <sup>8</sup> P4729Cell Adhesion/Communication65331Galectin-7 <sup>8</sup> P06386Structural/Cytoskeletal85688Genome polyprotein*P17593Micro organism255497Glucse-6-phosphate isomerase <sup>6</sup> P06744Energy/metabolism63016Glutamini-HRNA synthetase*Q&EG26Micro organism64103Glutamini-HRNA synthetase*Q&EG26Micro organism64103Glutamini-HRNA synthetase*P06744Energy/metabolism35922dehydrogenase 1P17593Transport45205Heat shock C0 RobateP00773Transport70828Hernoglobin alpha chainP69905Transport15126Hernoglobin alpha chainQ9U/K84Transport15126Hernoglobin alpha chainQ9U/K84Transport15126Hernoglobin alpha chainQ9U/K84Micro organism84602g alpha 2 chain C region <sup>6</sup> P01876Defense/Immunoresponse37655g alpha 2 chain C region <sup>6</sup> P01876Defense/Immunoresponse37655g alpha 2 chain C region <sup>6</sup> P01876Defense/Immunoresponse12790g hapy chain V-H liegion MDPC 47A*P01761Defense/Immunoresponse	Farnesyl pyrophosphate synthetase <sup>#</sup>	P14324	Energy/metabolism	40532
Fibrinogen gamma chain precursor <sup>8</sup> P02679         Protein Modification/Polymerization         51512           FixC protein <sup>4</sup> Q82940         Micro organism         39285           Fructose-bisphosphate aldolase C         P00975         Energy/metabolism         39285           Galactin-3 binding protein precursor <sup>5</sup> Q08380         Cell Adhesion/Communication         64331           Galectin-75         P47929         Cell Adhesion/Communication         65331           Galectin-75         P06396         Structural/Cytoskeletal         65698           Genome polyprotein <sup>#</sup> P17593         Micro organism         63016           Glucsose-5-phosphate isomerase <sup>5</sup> P06744         Energy/metabolism         63016           Glutathinos E-transferase P         P09211         Signaling         23225           Glyceraldehyde-3-phosphate         P04406         Energy/metabolism         35922           Haptoglobin precursor         P00738         Transport         45055           Heat shock cognate 71 KDa protein <sup>5</sup> P11142         Protein Folding/Repair         70052           Hemaglobin alpha chain         P69905         Transport         51676           Hurpin         Q92790         Transport         51676           Hurpin <td>Fatty acid-binding protein, epidermal</td> <td>Q01469</td> <td>Energy/metabolism</td> <td>15033</td>	Fatty acid-binding protein, epidermal	Q01469	Energy/metabolism	15033
FixC protein <sup>4</sup> (Constant) (Cons	Fibrinogen gamma chain precursor <sup>§</sup>	P02679	Protein Modification/Polymerization	า 51512
Fructose-bisphosphate aldolase Δ <sup>§</sup> P04075         Energy/metabolism         39229           Galectin-3 binding protein precursor <sup>§</sup> Q08380         Cell Adhesion/Communication         65331           Galectin-7 <sup>§</sup> P06396         Structural/Cytoskeletal         85698           Gelsolin precursor <sup>§</sup> P06396         Structural/Cytoskeletal         85698           Gelsonin precursor <sup>§</sup> P06396         Structural/Cytoskeletal         85698           Glucase-6-phosphate isomerase <sup>§</sup> P06744         Energy/metabolism         63016           Glutathino S-transferase P         P09211         Signalling         23222           Glyceraldehyde-3-phosphate         P04406         Energy/metabolism         35922           Glyceraldehyde-3-phosphate         P00738         Transport         45205           Heat shock Cognate 71 kDa protein <sup>§</sup> P11142         Protein Folding/Repair         70898           Hemoglobin alpha chain         Q9UK54         Transport         15126           Hemoglobin alpha chain         Q9UK54         Transport         61676           Hurpin         Q04283         Micro organism         84602           g alpha-1 chain C region <sup>§</sup> P01877         Defense/Immunoresponse         36508 <td< td=""><td>FixC protein<sup>#</sup></td><td>Q8Z9K9</td><td>Micro organism</td><td>45687</td></td<>	FixC protein <sup>#</sup>	Q8Z9K9	Micro organism	45687
Fructose-bisphosphate aldolase C P09972 Energy/metabolism 39325 Galectin-3 <sup>6</sup> UR380 Cell Adhesion/Communication 14944 Gelsolin precursor <sup>4</sup> P7593 Micro organism 255497 Glucase-6-phosphate isomerase <sup>6</sup> P17593 Micro organism 63016 Glutaminyl-tRNA synthetase <sup>4</sup> QBEC26 Micro organism 64103 Glutaminyl-tRNA synthetase <sup>4</sup> QBEC26 Micro organism 64103 Glutaminyl-tRNA synthetase <sup>4</sup> P06744 Energy/metabolism 35922 dehydrogenase 1 Haptoglobin precursor P00738 Transport 45205 Heat shock 70 kDa protein <sup>5</sup> P08107 Protein Folding/Repair 70052 Heat shock 70 kDa protein <sup>5</sup> P08107 Protein Folding/Repair 70858 Heat shock 70 kDa protein <sup>5</sup> P02790 Transport 15126 Hemoglobin lapta chain P69905 Transport 15126 Hemoglobin lapta chain P69905 Transport 15126 Hemoglobin labta chain P69905 Transport 15126 Hemoglobin Vergion MOPC 47A <sup>47</sup> P01787 Defense/Immunoresponse 37655 Ig alpha-2 chain C region <sup>5</sup> P01877 Defense/Immunoresponse 37655 Ig alpha-2 chain C region <sup>5</sup> P01877 Defense/Immunoresponse 386108 Ig gamma-1 chain C region <sup>5</sup> P01877 Defense/Immunoresponse 12975 Ig heavy chain V-III region NEVM <sup>4#</sup> P0178 Defense/Immunoresponse 12975 Ig heavy chain V-III region NEVM <sup>4#</sup> P0171 Defense/Immunoresponse 12975 Ig heavy chain V-III region KEM <sup>4#</sup> P0176 Defense/Immunoresponse 12431 Ig heavy chain V-III region KEM <sup>4#</sup> P0179 Defense/Immunoresponse 12431 Ig heavy chain V-III region KEM <sup>4#</sup> P0179 Defense/Immunoresponse 12431 Ig heavy chain V-III region KEÅ <sup>4#</sup> P01764 Defense/Immunoresponse 11608 Ig kappa chain V-I region CAR <sup>5</sup> P01837 Defense/Immunoresponse 11636 Ig kappa chain V-II region KEÅ <sup>4#</sup> P01764 Defense/Immunoresponse 11734 Ig heavy chain V-III region KEÅ <sup>4#</sup> P01764 Defense/Immunoresponse 11736 Ig heavy chain V-III region KEÅ <sup>4#</sup> P01764 Defense/Immunoresponse 11636 Ig	Fructose-bisphosphate aldolase A§	P04075	Energy/metabolism	39289
Galectin-3 binding protein precursor <sup>8</sup> Q08380Cell Adhesion/Communication65331Galectin-7 sP47929Cell Adhesion/Communication14944Gelsolin precursor <sup>8</sup> P06396Structural/Cytoskeletal85698Glucose-6-phosphate isomerase <sup>5</sup> P06744Energy/ metabolism63016Glutathino S-transferase PP09211Signalling23225Glyceraldehyde-3-phosphateP04406Energy/metabolism35922dehydrogenase 1P00738Transport45205Haptoglobin precursorP00738Transport45205Heat shock 70 kDa protein 1 <sup>5</sup> P08107Protein Folding/Repair70052Heat shock 70 kDa protein 1 <sup>5</sup> P02790Transport51676HurpinQ9UK54Transport51676HurpinQ9UK54Transport51676HurpinQ9UK54Transport51676HurpinQ9UK54Transport51676HurpinQ9UK54Transport51676HurpinQ9UK54Transport51676Jagha-1 chain C region <sup>8</sup> P01877Defense/Immunoresponse36508Jg galma-2 chain C region <sup>8</sup> P01877Defense/Immunoresponse36850Jg haavy chain V-Hi region NEVM*P01780Defense/Immunoresponse12975Jg haavy chain V-Hi region RAL**P01771Defense/Immunoresponse12975Jg haavy chain V-Hi region RAL**P01786Defense/Immunoresponse12975Jg haavy chain V-Hi region RAL**P01780Defense/Immunoresponse <td>Fructose-bisphosphate aldolase C</td> <td>P09972</td> <td>Energy/metabolism</td> <td>39325</td>	Fructose-bisphosphate aldolase C	P09972	Energy/metabolism	39325
Galectin-75P47929Cell Adhesion/Communication14944Gelsolin precursor <sup>5</sup> P06396Structural/Cyloskeletal85698Genome polyprotein <sup>4</sup> P17593Micro organism63016Glucase-6-phosphate isomerase <sup>5</sup> P06744Energy/ metabolism63016Glutarninyl-IRNA synthetase <sup>4</sup> Q8EG26Micro organism64103Glutarninyl-IRNA synthetase <sup>4</sup> P0811Signalling23225dehydrogenase 1Energy/metabolism35922dehydrogenase 1P00738Transport45205Heat shock 70 kDa protein 1 <sup>6</sup> P018107Protein Folding/Repair70898Hemoglobin precursorP01738Transport15126Hemoglobin beta chainP2905Transport15126Hemoglobin beta chainP042790Transport151676HurpinQ9UK54Transport151676Hypothetical 84.6 kDa protein <sup>#</sup> Q9UK84Transport51676g alpha-1 chain C region <sup>5</sup> P01877Defense/Immunoresponse36508g garma-2 chain C region <sup>5</sup> P01877Defense/Immunoresponse35825g heavy chain V-III region MOPC 47A <sup>#</sup> P01786Defense/Immunoresponse12975g heavy chain V-III region NEWM <sup>#</sup> P01825Defense/Immunoresponse12975g heavy chain V-III region MDC4P01781Defense/Immunoresponse12781g heavy chain V-III region MEA <sup>§,#</sup> P01780Defense/Immunoresponse12582precursor <sup>#</sup> P01847Defense/Immunoresponse12682g hea	Galectin-3 binding protein precursor <sup>§</sup>	Q08380	Cell Adhesion/Communication	65331
Gelsolin precursor*P06396Structural/Cytoskeletal85698Genome polyprotein*P17593Micro organism255497Glucase-6-phosphate isomerase*P06744Energy/ metabolism63016Glutathione S-transferase PP09211Signalling23225Glyceraldehyde-3-phosphateP04406Energy/metabolism35922Ghyceraldehyde-3-phosphateP04406Energy/metabolism35922Haptoglobin precursorP00738Transport45205Heat shock cognate 71 kDa protein*P11142Protein Folding/Repair70898Hemoglobin alpha chainQ9UK54Transport15126Hemoglobin alpha chainQ9UK54Transport51676HurpinQ9UIV8Protein Degradation/Inhibitor44276Hypothetical 84.6 kDa protein*Q04263Micro organism84602Ig alpha-2 chain C region*P01876Defense/Immunoresponse366168Ig gamma-1 chain C region*P01877Defense/Immunoresponse32885Ig heavy chain V-III region GAL3*P01771Defense/Immunoresponse12970Ig heavy chain V-III region GAL3*P01781Defense/Immunoresponse12875Ig heavy chain V-III region GAL3*P01785Defense/Immunoresponse12875Ig heavy chain V-III region GAL3*P01781Defense/Immunoresponse12731Ig heavy chain V-III region CHR*P01784Defense/Immunoresponse12731Ig heavy chain V-III region GL4*P01760Defense/Immunoresponse12731Ig abpa cha	Galectin-7 <sup>§</sup>	P47929	Cell Adhesion/Communication	14944
Genome polyprotein <sup>#</sup> P17593         Micro organism         255497           Glucose-6-phosphate isomerase <sup>8</sup> Q&EG26         Micro organism         631016           Glutaminyl-tRNA synthetase <sup>#</sup> Q&EG26         Micro organism         64103           Glutathione S-transport         P09211         Signalling         23225           dehydrogenase 1         Energy/metabolism         35922           Heat shock 70 kDa protein 1 <sup>6</sup> P08107         Protein Folding/Repair         70052           Heat shock 70 kDa protein 1 <sup>6</sup> P08107         Protein Folding/Repair         70898           Hemoglobin beta chain         P69905         Transport         15126           Hemoglobin beta chain         Q9UK54         Transport         15176           Hypothetical 84.6 kDa protein <sup>#</sup> Q4U263         Micro organism         84602           Ig alpha-1 chain C region <sup>5</sup> P01876         Defense/Immunoresponse         36508           Ig gamma-1 chain C region <sup>5</sup> P01876         Defense/Immunoresponse         32845           Ig heavy chain V-II region RAL <sup>3#</sup> P01771         Defense/Immunoresponse         12975           Ig heavy chain V-II region TAR <sup>5#</sup> P01780         Defense/Immunoresponse         12730           Ig hea	Gelsolin precursor <sup>§</sup>	P06396	Structural/Cytoskeletal	85698
Glucase-6-phosphate isomerase <sup>8</sup> P06744       Energy/metabolism       63016         Glutaminyl-RNA synthetase <sup>#</sup> QBEG26       Micro organism       64103         Glutaminyl-RNA synthetase <sup>#</sup> P04406       Energy/metabolism       35922         Glyceraldehyde-3-phosphate       P04406       Energy/metabolism       35922         Glyceraldehyde-3-phosphate       P00738       Transport       45205         Haptoglobin precursor       P00738       Transport       45205         Heat shock Yor RDa protein 1 <sup>5</sup> P08107       Protein Folding/Repair       70858         Hemoglobin beta chain       Q9UK54       Transport       15126         Hemoglobin beta chain       Q9UK8       Transport       51676         Hypothetical 84.6 kDa protein <sup>#</sup> Q04263       Micro organism       84602         Ig alpha-1 chain C region <sup>§</sup> P01876       Defense/Immunoresponse       36608         Ig gamma-1 chain C region <sup>§</sup> P01877       Defense/Immunoresponse       129790         Ig heavy chain V-II region MDPC 47A <sup>#</sup> P01786       Defense/Immunoresponse       129790         Ig alpha-2 chain C region <sup>§</sup> P01877       Defense/Immunoresponse       12970         Ig heavy chain V-III region NEWM <sup>#</sup> P01782       Defense/Imm	Genome polyprotein <sup>#</sup>	P17593	Micro organism	255497
Glutaminyl-IRNA synthetase*         QBEG26         Micro organism         64103           Glutathione S-transferase P         P09211         Signalling         23225           Glyceraldehyde-3-phosphate         P04406         Energy/metabolism         35922           dehydrogenase 1	Glucose-6-phosphate isomerase <sup>§</sup>	P06744	Energy/ metabolism	63016
Glutathione S-transferase P P09211 Signalling 23225 dehydrogenase 1 Signalling Signalling 23225 dehydrogenase 1 Signalling Signalling 23225 Heat shock cognate 71 kDa protein <sup>§</sup> P08107 Protein Folding/Repair 70052 Heat shock cognate 71 kDa protein <sup>§</sup> P11142 Protein Folding/Repair 70898 Hemoglobin beta chain QBUK54 Transport 15126 Hemoglobin beta chain QBUK54 Transport 15126 Hemoglobin beta chain QBUK54 Transport 15126 Hemoglobin beta chain QBUK54 Transport 15126 Hurpin QBUIV8 Protein Degradation/Inhibitor 44276 Hurpin QBUIV8 Protein Degradation/Inhibitor 44276 Hypothetical 84.6 kDa protein <sup>#</sup> QO4263 Micro organism 84602 Ig alpha-1 chain C region <sup>§</sup> P01877 Defense/Immunoresponse 36508 Ig gamma-1 chain C region <sup>§</sup> P01857 Defense/Immunoresponse 36508 Ig gamma-1 chain C region <sup>§</sup> P01857 Defense/Immunoresponse 12975 Ig heavy chain V-III region NEWM <sup>#</sup> P01825 Defense/Immunoresponse 12790 Ig heavy chain V-III region NEWM <sup>#</sup> P01825 Defense/Immunoresponse 12731 Ig heavy chain V-III region GAL <sup>##</sup> P01771 Defense/Immunoresponse 12582 precursor <sup>#</sup> Jakawa Defense/Immunoresponse 12582 precursor <sup>#</sup> Jakawa Defense/Immunoresponse 12582 precursor <sup>#</sup> P01834 Defense/Immunoresponse 12682 precursor <sup>#</sup> P01842 Defense/Immunoresponse 12682 precursor <sup>#</sup> P01842 Defense/Immunoresponse 11609 Jg kappa chain V-II region CAR <sup>§</sup> P01610 Defense/Immunoresponse 11609 Jg kappa chain V-II region S <sup>#,#</sup> P01610 Defense/Immunoresponse 11830 Jg kappa chain V-I region S <sup>#,#</sup> P01610 Defense/Immunoresponse 11830 Jg kappa chain V-I region S <sup>#,#</sup> P01619 Defense/Immunoresponse 11830 Jg kappa chain V-I region S <sup>#,#</sup> P01619 Defense/Immunoresponse 11830 Jg kappa chain V-I region NEW <sup>#,#</sup> P01741 Defense/Immunoresponse 11830 Jg kappa chain V-I region NEW <sup>#,#</sup> P01842 Defense/Immunoresponse 11830 Jg lambda chain V-I region NEW <sup>#,#</sup> P01842 Defense/Immunoresponse 11830 Jg lambda chain V-I region NEW <sup>#,</sup>	Glutaminyl-tRNA synthetase <sup>#</sup>	Q8EG26	Micro organism	64103
Glyceraldehyde-3-phosphateP04406Energy/metabolism35922dehydrogenase 1Haptoglobin precursorP00738Transport45205Heat shock 70 kDa protein 1 <sup>§</sup> P08107Protein Folding/Repair700828Heat shock cognate 71 kDa protein <sup>§</sup> P11142Protein Folding/Repair70898Hemoglobin alpha chainQ9UK54Transport13964Hemoglobin beta chainQ9UK54Transport51676HurpinQ9UK54Transport51676Hypothetical 84.6 kDa protein*Q04263Micro organism84602g alpha-1 chain C region*P01876Defense/Immunoresponse36508ig galma-1 chain C region*P01877Defense/Immunoresponse35885ig ghaz chain V region NEWM*P01857Defense/Immunoresponse12975ig heavy chain V-III region NEWM*P01771Defense/Immunoresponse12795ig heavy chain V-III region NEWM*P01771Defense/Immunoresponse12862ig heavy chain V-III region TUR**P01779Defense/Immunoresponse12882precursor*P01834Defense/Immunoresponse12882ig kappa chain V-I region GAL**P01834Defense/Immunoresponse11609ig kappa chain V-I region GAL**P01810Defense/Immunoresponse11604ig kappa chain V-I region GAL**P01810Defense/Immunoresponse11604ig kappa chain V-I region GAL**P01810Defense/Immunoresponse11609ig kappa chain V-I region GAL**P01834Defense/Immunoresponse <t< td=""><td>Glutathione S-transferase P</td><td>P09211</td><td>Signalling</td><td>23225</td></t<>	Glutathione S-transferase P	P09211	Signalling	23225
dehydrogenase 1 Haptoglobin precursor PO0738 Transport 45205 Heat shock Cognete 71 kDa protein $^{19}$ P08107 Protein Folding/Repair 70898 Hemoglobin alpha chain P69905 Transport 15126 Hemoglobin beta chain Q9UK54 Transport 51676 Hurpin Q9UIV8 Protein Degradation/Inhibitor 44276 Jenson Degradation/Inhibitor 44276 Japha-2 chain C region P01876 Defense/Immunoresponse 37655 Ig alpha-2 chain C region P01876 Defense/Immunoresponse 36508 Jg gamma-1 chain C region P01876 Defense/Immunoresponse 36508 Jg gamma-1 chain C region P01876 Defense/Immunoresponse 36508 Jg gamma-2 chain C region P01876 Defense/Immunoresponse 36508 Jg gamma-2 chain C region P01876 Defense/Immunoresponse 36508 Jg gamma-2 chain C region P01876 Defense/Immunoresponse 32505 Jg heavy chain V-III region MOPC 47A <sup>#</sup> P01786 Defense/Immunoresponse 12975 Jg heavy chain V-III region MEWM <sup>#</sup> P01825 Defense/Immunoresponse 12790 Jg heavy chain V-III region GAL <sup>§,#</sup> P01771 Defense/Immunoresponse 13566 Jg heavy chain V-III region TUR <sup>§,#</sup> P01774 Defense/Immunoresponse 13566 Jg heavy chain V-III region TUR <sup>§,#</sup> P01774 Defense/Immunoresponse 12582 precursor <sup>#</sup> J Jg kapa chain C region <sup>#</sup> P01834 Defense/Immunoresponse 12582 precursor <sup>#</sup> J Jg kapa chain V-I region WEA <sup>§,#</sup> P01764 Defense/Immunoresponse 11609 Jg kapa chain V-I region MWA <sup>§,#</sup> P01610 Defense/Immunoresponse 11704 Jg kapa chain V-I region MWA <sup>§,#</sup> P01610 Defense/Immunoresponse 11808 Jg kapa chain V-I region MWA <sup>§,#</sup> P01619 Defense/Immunoresponse 11803 Jg kapa chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11830 Jg kapa chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11830 Jg kapa chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11830 Jg kapa chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11237 Jg lambda chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11237 Jg lambda chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11237 Jg lambda chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11237 Jg lambda chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11526 Jg lamb	Glyceraldehyde-3-phosphate	P04406	Energy/metabolism	35922
Haptoglobin precursorP00738Transport45205Heat shock Cognate 71 kDa protein $\$$ P08107Protein Folding/Repair70052Heat shock cognate 71 kDa protein $\$$ P11142Protein Folding/Repair70898Hemoglobin alpha chainP69905Transport13964Hemoglobin beta chainQ9UK54Transport13964Hemopexin precursor $\$$ P02790Transport51676HurpinQ9UK64Transport51676Hypothetical 84.6 kDa protein "Q04263Micro organism84602Ig alpha-1 chain C region $\$$ P01876Defense/Immunoresponse36508Ig gamma-1 chain C region $\$$ P01877Defense/Immunoresponse36508Ig gamma-2 chain C region $\$$ P01859Defense/Immunoresponse12970Ig heavy chain V-II region NEWM#P01781Defense/Immunoresponse12790Ig heavy chain V-III region NEWM#P01771Defense/Immunoresponse12731Ig heavy chain V-III region TUR $\$$ P01779Defense/Immunoresponse12431Ig heavy chain V-III region TUR $\$$ P01764Defense/Immunoresponse12682Ig kappa chain V-I region GAR $\$$ P01696Defense/Immunoresponse11608Ig kappa chain V-I region B6 $\$$ P01696Defense/Immunoresponse11608Ig kappa chain V-I region B6 $\$$ P01610Defense/Immunoresponse11608Ig kappa chain V-I region B6 $\$$ P01625Defense/Immunoresponse11608Ig kappa chain V-I region B6 $\$$ P01626Defense/Immunorespo	dehydrogenase 1			
Heat shock 70 kDa protein $1^8$ P08107 Protein Folding/Repair 70052 Heat shock cognate 71 kDa protein $^8$ P11142 Protein Folding/Repair 70898 Hemoglobin alpha chain P69905 Transport 15126 Hemoglobin beta chain Q9UK54 Transport 131664 Hemopexin precursor P077 P07898 Hemopexin precursor P077 P07898 Hemopexin precursor P077 P07898 Hurpin Q9UV8 Protein Degradation/Inhibitor 44276 Hypothetical 84.6 kDa protein P0787 Defense/Immunoresponse 36506 Ig alpha-1 chain C region P01876 Defense/Immunoresponse 36508 Ig gama-1 chain C region P01877 Defense/Immunoresponse 36508 Ig gama-2 chain C region P01877 Defense/Immunoresponse 36508 Ig gama-2 chain C region P01877 Defense/Immunoresponse 12975 Ig heavy chain V-Iregion NEWM# P01786 Defense/Immunoresponse 12790 Ig heavy chain V-Iligion NEWM# P01786 Defense/Immunoresponse 12791 Ig heavy chain V-III region NEWM# P01781 Defense/Immunoresponse 12791 Ig heavy chain V-III region TUR <sup>5,#</sup> P01781 Defense/Immunoresponse 12731 Ig heavy chain V-III region TUR <sup>5,#</sup> P01764 Defense/Immunoresponse 12682 precursor III region TUR <sup>5,#</sup> P01764 Defense/Immunoresponse 12682 precursor III region CAR <sup>§</sup> P01834 Defense/Immunoresponse 12682 precursor III region GAL <sup>§,#</sup> P01764 Defense/Immunoresponse 11609 Ig kappa chain V-III region GAR <sup>§,#</sup> P01610 Defense/Immunoresponse 11608 Ig kappa chain V-I region GAR <sup>§,#</sup> P01611 Defense/Immunoresponse 11608 Ig kappa chain V-I region B6 <sup>§,#</sup> P01619 Defense/Immunoresponse 11608 Ig kappa chain V-I region B6 <sup>§,#</sup> P01619 Defense/Immunoresponse 11636 Ig kappa chain V-I region NEW <sup>#</sup> P01742 Defense/Immunoresponse 11636 Ig kappa chain V-I region NEW <sup>#</sup> P01842 Defense/Immunoresponse 11636 Ig kappa chain V-I region NEW <sup>#</sup> P01842 Defense/Immunoresponse 11830 Ig lambda chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11833 Ig lambda chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11835 Ig lambda chain V-I region NEW <sup>#</sup> P01714 Defense/Immunoresponse 11835 Ig lambda chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11835 Ig lambda chain V-I region NEW <sup>#</sup> P017	Haptoglobin precursor	P00738	Transport	45205
Heat shock cognate 71 kDa protein <sup>§</sup> P11142         Protein Folding/Repair         70898           Hemoglobin alpha chain         P69905         Transport         15126           Hemoglobin beta chain         Q9UK54         Transport         13964           Hemoglobin beta chain         Q9UK54         Transport         51676           Hurpin         Q9UIV8         Protein Degradation/Inhibitor         44276           Hypothetical 84.6 kDa protein <sup>#</sup> Q04263         Micro organism         84602           Ig alpha-1 chain C region         P01877         Defense/Immunoresponse         37655           Ig alpha-1 chain C region MOPC 47A <sup>#</sup> P01857         Defense/Immunoresponse         35885           Ig gamma-2 chain V region MOPC 47A <sup>#</sup> P01825         Defense/Immunoresponse         12771           Ig heavy chain V-II region NEWM <sup>#</sup> P01825         Defense/Immunoresponse         12731           Ig heavy chain V-III region THL <sup>#</sup> P01771         Defense/Immunoresponse         12366           Ig heavy chain V-III region THL <sup>#</sup> P01771         Defense/Immunoresponse         12431           Ig heavy chain V-III region THL <sup>#</sup> P01771         Defense/Immunoresponse         12682           Ig heavy chain V-III region CAR <sup>§</sup> P01610         De	Heat shock 70 kDa protein 1 <sup>§</sup>	P08107	Protein Folding/Repair	70052
Hemoglobin alpha chainP69905Transport15126Hemoglobin beta chainQ9UK54Transport13964Hemopexin precursor <sup>8</sup> P02790Transport51676HurpinQ9UIV8Protein Degradation/Inhibitor44276Hypothetical 84.6 KDa protein <sup>#</sup> Q04263Micro organism84602Ig alpha-1 chain C region <sup>8</sup> P01876Defense/Immunoresponse37655Ig alpha-2 chain C region <sup>8</sup> P01877Defense/Immunoresponse36608Ig gamma-1 chain C region <sup>8</sup> P01859Defense/Immunoresponse12975Ig heavy chain V region MOPC 47A <sup>#</sup> P01786Defense/Immunoresponse127790Ig heavy chain V-III region GAL <sup>5,#</sup> P01781Defense/Immunoresponse12771Ig heavy chain V-III region TUF <sup>8,#</sup> P01771Defense/Immunoresponse12731Ig heavy chain V-III region TUF <sup>8,#</sup> P01774Defense/Immunoresponse12582precursor <sup>#</sup> P01834Defense/Immunoresponse12582g kappa chain V-I region CAR <sup>§</sup> P01610Defense/Immunoresponse11609Ig kappa chain V-I region CAR <sup>§,#</sup> P01610Defense/Immunoresponse11604Ig kappa chain V-I region B6 <sup>§,#</sup> P01619Defense/Immunoresponse11830Ig kappa chain V-I region MEK <sup>§,#</sup> P01619Defense/Immunoresponse11830Ig kappa chain V-I region MAI <sup>§,#</sup> P01625Defense/Immunoresponse11830Ig kappa chain V-I region NEK <sup>#,#</sup> P01619Defense/Immunoresponse11830Ig kappa chain V-I region NEK <sup>#,#</sup> P	Heat shock cognate 71 kDa protein <sup>§</sup>	P11142	Protein Folding/Repair	70898
Hemoglobin beta chainQ9UK54Transport13964Hemopexin precursorsP02790Transport51676HurpinQ9UIV8Protein Degradation/Inhibitor44276Hypothetical 84.6 kDa protein#Q04263Micro organism84602Ig alpha-1 chain C regionP01876Defense/Immunoresponse37655Ig gamma-1 chain C region\$P01877Defense/Immunoresponse36508Ig gamma-2 chain C region MOPC 47A#P01859Defense/Immunoresponse32885Ig heavy chain V-II region MOPC 47A#P01825Defense/Immunoresponse12975Ig heavy chain V-II region GAL\$#P01711Defense/Immunoresponse12731Ig heavy chain V-III region HIL#P01771Defense/Immunoresponse12731Ig heavy chain V-III region TH\$#P01771Defense/Immunoresponse12661Ig heavy chain V-III region TH\$#P01764Defense/Immunoresponse12682precursor#Ig heavy chain V-III region CAR\$P01596Defense/Immunoresponse11609Ig kappa chain V-I region CAR\$P01610Defense/Immunoresponse11609Ig kappa chain V-I region CAR\$P01610Defense/Immunoresponse11840Ig kappa chain V-I region CAR\$P01619Defense/Immunoresponse11840Ig kappa chain V-I region CAR\$P01625Defense/Immunoresponse11840Ig kappa chain V-II region CAR\$P01619Defense/Immunoresponse11840Ig kappa chain V-II region CAR\$P01625Defense/Immunoresponse11840Ig kappa chain	Hemoglobin alpha chain	P69905	Transport	15126
Hemopexin precursorP02790Transport51676HurpinQ9UIV8Protein Degradation/Inhibitor44276Hypothetical 84.6 kDa proteinQ04263Micro organism84602Ig alpha-1 chain C regionP01876Defense/Immunoresponse37655Ig alpha-2 chain C regionP01876Defense/Immunoresponse36106Ig gamma-1 chain C regionP01877Defense/Immunoresponse36106Ig gamma-2 chain C regionP01857Defense/Immunoresponse35885Ig heavy chain V region MOPC 47A#P01786Defense/Immunoresponse12790Ig heavy chain V-III region ALS#P01771Defense/Immunoresponse12791Ig heavy chain V-III region GALS#P01771Defense/Immunoresponse12731Ig heavy chain V-III region TURS#P01779Defense/Immunoresponse1282precursor#P01834Defense/Immunoresponse12582precursor#P01610Defense/Immunoresponse11609Ig kappa chain V-I region WEAS#P01610Defense/Immunoresponse11609Ig kappa chain V-I region GOLSP01619Defense/Immunoresponse11636Ig kappa chain V-III region BGS#P01620Defense/Immunoresponse11840Ig kappa chain V-III region GOLSP01620Defense/Immunoresponse11636Ig kappa chain V-III region CLRS#P01620Defense/Immunoresponse11636Ig kappa chain V-III region BGS#P01620Defense/Immunoresponse11636Ig kappa chain V-III region BGS#P01620Defense/Imm	Hemoglobin beta chain	Q9UK54	Transport	13964
HurpinQ9UIV8Protein Degradation/Inhibitor44276Hypothetical 84.6 kDa protein#Q04263Micro organism84602Ig alpha-1 chain C regionP01876Defense/Immunoresponse37655Ig alpha-2 chain C region§P01877Defense/Immunoresponse38608Ig gamma-1 chain C region§P01877Defense/Immunoresponse38685Ig heavy chain V region MOPC 47A#P01786Defense/Immunoresponse12975Ig heavy chain V-II region NEWM#P01825Defense/Immunoresponse12770Ig heavy chain V-III region HIL#P01771Defense/Immunoresponse12731Ig heavy chain V-III region TUR§.#P01771Defense/Immunoresponse12821Ig heavy chain V-III region TUR§.#P01779Defense/Immunoresponse12821Ig kappa chain V-III region CAR§P01596Defense/Immunoresponse12582Ig kappa chain V-II region CAR§P01610Defense/Immunoresponse11609Ig kappa chain V-I region GOL§P04611Defense/Immunoresponse11608Ig kappa chain V-I region GOL§P0426Defense/Immunoresponse11608Ig kappa chain V-I region GOL§P04206Defense/Immunoresponse11830Ig kappa chain V-I region GOL§P04206Defense/Immunoresponse11830Ig kappa chain V-III region StåtP01625Defense/Immunoresponse11830Ig kappa chain V-III region NEV#P01720Defense/Immunoresponse11830Ig kappa chain V-III region NEV#P01625Defense/Immunoresponse11830	Hemopexin precursor <sup>®</sup>	P02790	Transport	51676
Hypothetical 84.6 kDa protein*Q04263Micro organism84602Ig alpha-1 chain C regionP01876Defense/Immunoresponse37655Ig alpha-2 chain C regionP01877Defense/Immunoresponse36508Ig gamma-2 chain C regionP01857Defense/Immunoresponse35885Ig heavy chain V region MOPC 47A#P01786Defense/Immunoresponse12975Ig heavy chain V-II region NEWM#P01825Defense/Immunoresponse12975Ig heavy chain V-III region GALP01771Defense/Immunoresponse12731Ig heavy chain V-III region TURS#P01779Defense/Immunoresponse12431Ig heavy chain V-III region TURS#P01774Defense/Immunoresponse12822Ig heavy chain V-III region TURS#P017764Defense/Immunoresponse12431Ig heavy chain V-III region CAR\$P01596Defense/Immunoresponse11609Ig kappa chain V-I region WEA\$#P01610Defense/Immunoresponse11608Ig kappa chain V-I region OKA\$#P01610Defense/Immunoresponse11840Ig kappa chain V-I region Len\$P01625Defense/Immunoresponse11830Ig kappa chain V-I region Len\$P01842Defense/Immunoresponse11837Ig lambda chain V-I region Len\$P01842Defense/Immunoresponse11830Ig kappa chain V-II region NEW#P01701Defense/Immunoresponse11830Ig kappa chain V-II region NEW#P01781Defense/Immunoresponse11830Ig kappa chain V-II region NEW#P01714Defense/Immunoresponse <td< td=""><td>Hurpin</td><td>Q9UIV8</td><td>Protein Degradation/Inhibitor</td><td>44276</td></td<>	Hurpin	Q9UIV8	Protein Degradation/Inhibitor	44276
Ig alpha-1 chain C regionP01876Defense/Immunoresponse37655Ig alpha-2 chain C regionP01877Defense/Immunoresponse36508Ig gamma-1 chain C regionP01857Defense/Immunoresponse36106Ig gamma-2 chain C regionP01857Defense/Immunoresponse38508Ig heavy chain V-II region MOPC 47A#P01786Defense/Immunoresponse12975Ig heavy chain V-III region NEWM#P01825Defense/Immunoresponse12731Ig heavy chain V-III region TUR\$#P01771Defense/Immunoresponse12731Ig heavy chain V-III region TUR\$#P01779Defense/Immunoresponse12431Ig heavy chain V-III region TUR\$#P01764Defense/Immunoresponse1282y kappa chain V-II region CAR\$P01834Defense/Immunoresponse11609Ig kappa chain V-I region GAL\$#P01610Defense/Immunoresponse11608Ig kappa chain V-I region GOL\$P01610Defense/Immunoresponse11608Ig kappa chain V-I region GOL\$P01619Defense/Immunoresponse11636Ig kappa chain V-I region GOL\$P01822Defense/Immunoresponse11636Ig kappa chain V-II region GOL\$P01826Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01826Defense/Immunoresponse11636Ig kappa chain V-II region SI*P01826Defense/Immunoresponse11636Ig kappa chain V-II region SI*P01842Defense/Immunoresponse11636Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse <td< td=""><td>Hypothetical 84.6 kDa protein*</td><td>Q04263</td><td>Micro organism</td><td>84602</td></td<>	Hypothetical 84.6 kDa protein*	Q04263	Micro organism	84602
Ig alpha-2 chain C regionsP018/7Defense/Immunoresponse36508Ig gamma-1 chain C regionsP01857Defense/Immunoresponse36106Ig gamma-2 chain C regionsP01859Defense/Immunoresponse35885Ig heavy chain V region MOPC 47A#P01786Defense/Immunoresponse12975Ig heavy chain V-II region RLS#P01771Defense/Immunoresponse12790Ig heavy chain V-III region TURS#P01771Defense/Immunoresponse12731Ig heavy chain V-III region TURS#P01779Defense/Immunoresponse12825Ig heavy chain V-III region TURS#P01764Defense/Immunoresponse12582precursor#P01834Defense/Immunoresponse11609Ig kappa chain V-I region CAR\$P01610Defense/Immunoresponse11609Ig kappa chain V-I region GAR\$P01610Defense/Immunoresponse11840Ig kappa chain V-I region GOL\$P01619Defense/Immunoresponse11840Ig kappa chain V-I region GOL\$P01625Defense/Immunoresponse11830Ig kappa chain V-I region RS*P01822Defense/Immunoresponse11237Ig lambda chain C regions#P01822Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01714Defense/Immunoresponse11237Ig lambda chain V-I region HIP01717Defense/Immunoresponse11237 <td< td=""><td>Ig alpha-1 chain C region</td><td>P01876</td><td>Defense/Immunoresponse</td><td>37655</td></td<>	Ig alpha-1 chain C region	P01876	Defense/Immunoresponse	37655
Ig gamma-1 chain C regionsP01857Defense/Immunoresponse36106Ig gamma-2 chain C regionsP01859Defense/Immunoresponse35885Ig heavy chain V-II region MOPC 47A*P01786Defense/Immunoresponse12975Ig heavy chain V-III region NEWM*P01825Defense/Immunoresponse12731Ig heavy chain V-III region TUR\$**P01771Defense/Immunoresponse13566Ig heavy chain V-III region TUR\$**P01779Defense/Immunoresponse12431Ig heavy chain V-III region TUR\$**P01764Defense/Immunoresponse12582precursor*Ig kappa chain V-I region CAR\$P01596Defense/Immunoresponse11609Ig kappa chain V-I region CAR\$P01610Defense/Immunoresponse11704Ig kappa chain V-I region GOL\$P01611Defense/Immunoresponse11840Ig kappa chain V-I region GOL\$P01619Defense/Immunoresponse11830Ig kappa chain V-I region GOL\$P01625Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01625Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01701Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01711Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01701Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01701Defense/Immunoresponse11237Ig lambda chain V-I region HI*P01771Defense/Immunoresponse11725Ig lambda chain V-I region HI*P01714 <td>Ig alpha-2 chain C region<sup>3</sup></td> <td>P01877</td> <td>Defense/Immunoresponse</td> <td>36508</td>	Ig alpha-2 chain C region <sup>3</sup>	P01877	Defense/Immunoresponse	36508
Ig gamma-2 chain C region*P01839Defense/Immunoresponse35885Ig heavy chain V-III region MOPC 47A*P01786Defense/Immunoresponse12975Ig heavy chain V-III region NEWM*P01825Defense/Immunoresponse12790Ig heavy chain V-III region GAL <sup>§,*</sup> P01771Defense/Immunoresponse12731Ig heavy chain V-III region HIL*P01771Defense/Immunoresponse12582Ig heavy chain V-III region TUR <sup>§,*</sup> P01764Defense/Immunoresponse12582precursor*Ig kappa chain C region*P01834Defense/Immunoresponse11609Ig kappa chain V-I region CAR <sup>§</sup> P01506Defense/Immunoresponse11608Ig kappa chain V-I region MEA <sup>§,**</sup> P01610Defense/Immunoresponse11608Ig kappa chain V-I region GOL <sup>§</sup> P01611Defense/Immunoresponse11840Ig kappa chain V-I region B6 <sup>§,**</sup> P01619Defense/Immunoresponse11830Ig kappa chain V-I region GOL <sup>§</sup> P01842Defense/Immunoresponse11830Ig kappa chain V-I region NEW <sup>**</sup> P01842Defense/Immunoresponse11237Ig lambda chain V-I region NEW <sup>**</sup> P01701Defense/Immunoresponse11453Ig lambda chain V-I region NEW <sup>**</sup> P01714Defense/Immunoresponse11453Ig lambda chain V-II region NHI*P01717Defense/Immunoresponse11453Ig lambda chain V-I region NEW <sup>**</sup> P01701Defense/Immunoresponse11453Ig lambda chain V-I region NEW <sup>**</sup> P01714Defense/Immunoresponse11517Ig muda chain V-	Ig gamma-1 chain C region <sup>3</sup>	P01857	Defense/Immunoresponse	36106
Ig heavy chain V-II region NIOPC 4/A* P01786 Defense/Immunoresponse 12973 Ig heavy chain V-III region NEWM# P01825 Defense/Immunoresponse 12731 Ig heavy chain V-III region GAL <sup>§,#</sup> P01771 Defense/Immunoresponse 12731 Ig heavy chain V-III region TUR <sup>§,#</sup> P01779 Defense/Immunoresponse 12431 Ig heavy chain V-III region VH26 P01764 Defense/Immunoresponse 12582 precursor <sup>#</sup> Ig kappa chain C region * P01834 Defense/Immunoresponse 11609 Ig kappa chain V-I region CAR <sup>§</sup> P01596 Defense/Immunoresponse 11608 Ig kappa chain V-I region WEA <sup>§,#</sup> P01610 Defense/Immunoresponse 11608 Ig kappa chain V-I region MEA <sup>§,#</sup> P01610 Defense/Immunoresponse 11840 Ig kappa chain V-I region B6 <sup>§,#</sup> P01610 Defense/Immunoresponse 11636 Ig kappa chain V-I region GOL <sup>§</sup> P04206 Defense/Immunoresponse 11830 Ig kappa chain V-II region GOL <sup>§</sup> P04206 Defense/Immunoresponse 11830 Ig kappa chain V-II region Len <sup>§</sup> P01625 Defense/Immunoresponse 11237 Ig lambda chain C regions <sup>#</sup> P01842 Defense/Immunoresponse 11237 Ig lambda chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11453 Ig lambda chain V-I region NEW <sup>#</sup> P01701 Defense/Immunoresponse 11453 Ig lambda chain V-I region NEW <sup>#</sup> P01714 Defense/Immunoresponse 11393 Ig lambda chain V-III region GNI <sup>§</sup> P01714 Defense/Immunoresponse 11393 Ig lambda chain V-III region HI <sup>§</sup> P01591 Defense/Immunoresponse 11393 Ig lambda chain V-III region HI <sup>§</sup> P01591 Defense/Immunoresponse 15594 Interleukin-1 receptor antagonist prec. P18510 Defense/Immunoresponse 15594 Interleukin-1 precursor P06870 Protein Degradation/Inhibitor 28890 Keratin, type I cytoskeletal 10 P13645 Structural/Cytoskeletal 46214 Keratin, type I cytoskeletal 10 P13645 Structural/Cytoskeletal 59519 Keratin, type I cytoskeletal 14 <sup>§,#</sup>	Ig gamma-2 chain C region <sup>3</sup>	P01859	Defense/Immunoresponse	35885
Id heavy chain V-III region NEW*P01025Defense/Immunoresponse12790Ig heavy chain V-III region HIL*P01781Defense/Immunoresponse12731Ig heavy chain V-III region TUR§.*P01771Defense/Immunoresponse13566Ig heavy chain V-III region TUR§.*P01764Defense/Immunoresponse12582precursor*Ig kappa chain C region*P01834Defense/Immunoresponse12682Ig kappa chain V-I region CAR§P01596Defense/Immunoresponse11609Ig kappa chain V-I region WEA§.*P01610Defense/Immunoresponse11608Ig kappa chain V-I region B6§.*P01611Defense/Immunoresponse11636Ig kappa chain V-II region B6§.*P01619Defense/Immunoresponse11636Ig kappa chain V-II region B6§.*P01625Defense/Immunoresponse11636Ig kappa chain V-II region B6§.*P01625Defense/Immunoresponse11237Ig lambda chain V-II region NEW*P01701Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01701Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01701Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01714Defense/Immunoresponse11333Ig lambda chain V-II region HIIP01777Defense/Immunoresponse11335Ig lambda chain V-I region HIIP01771Defense/Immunoresponse11335Ig lambda chain V-I region HIIP01771Defense/Immunoresponse11517Ig mucha chain V-II region HIIP01717	Ig heavy chain V region MOPC 47A"	PU1/80	Defense/Immunoresponse	12975
Ig heavy chain V-III region GAL*PO 1761Defense/Immunoresponse12751Ig heavy chain V-III region HIL*P01771Defense/Immunoresponse13566Ig heavy chain V-III region TUR§.*P01779Defense/Immunoresponse12421Ig heavy chain V-III region TUR§.*P01764Defense/Immunoresponse12582precursor*Ig kappa chain C region *P01834Defense/Immunoresponse11609Ig kappa chain C region CAR§P01596Defense/Immunoresponse11609Ig kappa chain V-I region CAR§P01610Defense/Immunoresponse11704Ig kappa chain V-I region MEA§.*P01610Defense/Immunoresponse11830Ig kappa chain V-I region B6§.*P01619Defense/Immunoresponse11830Ig kappa chain V-II region GOL§P01625Defense/Immunoresponse11237Ig lambda chain V-IV region Len§P01842Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01701Defense/Immunoresponse11237Ig lambda chain V-I region SH§P01714Defense/Immunoresponse11237Ig lambda chain V-II region Len§P01701Defense/Immunoresponse11237Ig lambda chain V-II region SH§P01714Defense/Immunoresponse11237Ig lambda chain V-II region HilP01771Defense/Immunoresponse11237Ig lambda chain V-II region SH§P01714Defense/Immunoresponse11237Ig lambda chain V-II region HilP01717Defense/Immunoresponse11333Ig lambda chain V-II region HilP01717<	Ig heavy chain V-II region NEVIVI"	PU1020	Defense/Immunoresponse	12790
Ig heavy chain V-III region TURP01771Defense/Immunoresponse12431Ig heavy chain V-III region VH26P01764Defense/Immunoresponse12431Ig kappa chain C region#P01834Defense/Immunoresponse12582precursor#If kappa chain C region CARP01596Defense/Immunoresponse11609Ig kappa chain V-I region CARP01610Defense/Immunoresponse11608Ig kappa chain V-I region WEAP01610Defense/Immunoresponse11608Ig kappa chain V-I region GOLP01611Defense/Immunoresponse11636Ig kappa chain V-I region GOLP01625Defense/Immunoresponse11636Ig kappa chain V-I region GOLP01625Defense/Immunoresponse11237Ig lambda chain V-I region LenP01842Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11237Ig lambda chain V-III region LOIP01714Defense/Immunoresponse11333Ig lambda chain V-III region LOIP01714Defense/Immunoresponse11393Ig lambda chain V-III region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse11517Ig mu chain C region HilP01717Defense/Immunoresponse11535Ig lambda chain V-III region HilP01717Defense/Immunoresponse11534Ig lambda chain V-III region HilP01714Defense/Immunoresponse	Ig heavy chain V-III region GAL <sup>or</sup>	PU1/01	Defense/Immunoresponse	12/31
Ig heavy chain V-III region VH26P01764Defense/Immunoresponse12431Ig heavy chain V-III region VH26P01764Defense/Immunoresponse12582Ig kappa chain C region#P01834Defense/Immunoresponse11609Ig kappa chain V-I region CAR§P01596Defense/Immunoresponse11608Ig kappa chain V-I region WEA§.#P01610Defense/Immunoresponse11704Ig kappa chain V-I region B6§.#P01619Defense/Immunoresponse11840Ig kappa chain V-II region GOL§P04206Defense/Immunoresponse11830Ig kappa chain V-II region GOL§P04206Defense/Immunoresponse11830Ig kappa chain V-IV region Len§P01625Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11453Ig lambda chain V-I region NEW#P04208Defense/Immunoresponse11725Ig lambda chain V-I region NEW#P04208Defense/Immunoresponse11725Ig lambda chain V-II region NEW#P01714Defense/Immunoresponse11393Ig lambda chain V-II region SI\$P01714Defense/Immunoresponse11393Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kalikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II\$#Q14525Structural/Cytoskele	Ig heavy chain V III region THP <sup>§,#</sup>	D01770	Defense/Immunoresponse	12/21
Ig havy chain V-III region V120P01704Defense/Immunoresponse12002precursor*Ig kappa chain C region*P01834Defense/Immunoresponse11609Ig kappa chain V-I region CARP01596Defense/Immunoresponse11608Ig kappa chain V-I region WEAP01610Defense/Immunoresponse11608Ig kappa chain V-I region B6P01611Defense/Immunoresponse11636Ig kappa chain V-III region B6P01619Defense/Immunoresponse11636Ig kappa chain V-III region GOLP04206Defense/Immunoresponse11636Ig kappa chain V-IV region LenP01625Defense/Immunoresponse12640Ig lambda chain C regions*P01842Defense/Immunoresponse11237Ig lambda chain V-I region NEW*P01701Defense/Immunoresponse11725Ig lambda chain V-I region LOIP80748Defense/Immunoresponse11393Ig lambda chain V-III region SHP01714Defense/Immunoresponse11393Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse11554Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse15594Keratin, type I cuticular HA3-IIP13645Structural/Cytoskeletal46214Keratin, type I cytoskeletal 14P13645Structural/Cytoskeletal51490Keratin, type I cytoskeletal 14P13645Structu	Ig heavy chain V III region V/H26	P01764	Defense/Immunoresponse	12431
In ConstantImplementationImplementationIg kappa chain C region#P01834Defense/Immunoresponse11609Ig kappa chain V-I region CAR§P01596Defense/Immunoresponse11608Ig kappa chain V-I region WEA§.#P01610Defense/Immunoresponse11704Ig kappa chain V-I region WEA§.#P01611Defense/Immunoresponse11840Ig kappa chain V-I region B6§.#P01619Defense/Immunoresponse11636Ig kappa chain V-II region GOL§P04206Defense/Immunoresponse11830Ig kappa chain V-IV region Len§P01625Defense/Immunoresponse12640Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11453Ig lambda chain V-I region LOI§P80748Defense/Immunoresponse11393Ig lambda chain V-III region SH§P01714Defense/Immunoresponse11393Ig lambda chain V-III region SH§P01714Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II§.#Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Kerati	precursor <sup>#</sup>	101704	Derense/immunoresponse	12502
InstructionInstructionInstructionInstructionIg kappa chain V-I region CARP01596Defense/Immunoresponse11608Ig kappa chain V-I regionP01610Defense/Immunoresponse11704Ig kappa chain V-I regionP01611Defense/Immunoresponse11840Ig kappa chain V-III region GOLP01619Defense/Immunoresponse11636Ig kappa chain V-III region GOLP01625Defense/Immunoresponse11830Ig kappa chain V-IV region LenP01625Defense/Immunoresponse11237Ig lambda chain C regions#P01701Defense/Immunoresponse11453Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11725Ig lambda chain V-I region LOIP80748Defense/Immunoresponse11935Ig lambda chain V-III region LOIP80748Defense/Immunoresponse11393Ig lambda chain V-III region LOIP01714Defense/Immunoresponse11393Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11517Ig muchain C regionP01871Defense/Immunoresponse11517Ig muchain C regionP01871Defense/Immunoresponse115594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse2055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-IIP13645Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal51490Keratin, typ	la kappa chain C region <sup>#</sup>	P01834	Defense/Immunoresponse	11609
Ig kappa chain V-I region WEAP01610Defense/Immunoresponse11704Ig kappa chain V-I regionP01611Defense/Immunoresponse11840Ig kappa chain V-III region B6P01611Defense/Immunoresponse11840Ig kappa chain V-III region GOLP01619Defense/Immunoresponse11830Ig kappa chain V-III region GOLP01625Defense/Immunoresponse11830Ig kappa chain V-IV region LenP01625Defense/Immunoresponse1237Ig lambda chain C regionsP01842Defense/Immunoresponse11725Ig lambda chain V-I region NEWP01701Defense/Immunoresponse11725Ig lambda chain V-III region SHP01714Defense/Immunoresponse11725Ig lambda chain V-III region SHP01714Defense/Immunoresponse11935Ig lambda chain V-III region HilP01717Defense/Immunoresponse11393Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11393Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse115594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse2055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal46214Keratin, type I cytoskeletal 14 <sup>§,#</sup> P02533Structural/Cytoskeletal51490Cordin ucrdiS1490S1490S1490S1490 <td>Ig kappa chain V-I region CAR<sup>§</sup></td> <td>P01596</td> <td>Defense/Immunoresponse</td> <td>11608</td>	Ig kappa chain V-I region CAR <sup>§</sup>	P01596	Defense/Immunoresponse	11608
Ig kappa chain V-I regionP01611Defense/Immunoresponse11840Ig kappa chain V-III region $GOL^{\$}$ P01619Defense/Immunoresponse11636Ig kappa chain V-III region $GOL^{\$}$ P04206Defense/Immunoresponse11830Ig kappa chain V-IV region Len $^{\$}$ P01625Defense/Immunoresponse1237Ig lambda chain C regions#P01701Defense/Immunoresponse11453Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11725Ig lambda chain V-I region UOI $^{\$}$ P80748Defense/Immunoresponse11393Ig lambda chain V-III region LOI $^{\$}$ P80748Defense/Immunoresponse11393Ig lambda chain V-III region SH $^{\$}$ P01714Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal46214Keratin, type I cytoskeletal 14 $^{\$,\#}$ P02533Structural/Cytoskeletal51490(Continued)StippeStippeStippeStippeStippe	la kappa chain V-l region $WEA^{\S,\#}$	P01610	Defense/Immunoresponse	11704
Ig kappa chain V-III region $B6^{\$,\#}$ P01619Defense/Immunoresponse11636Ig kappa chain V-III region $GOL^{\$}$ P04206Defense/Immunoresponse11830Ig kappa chain V-IV region Len $\$$ P01625Defense/Immunoresponse12640Ig lambda chain C regions#P01842Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11453Ig lambda chain V-I region NEW#P04208Defense/Immunoresponse11725Ig lambda chain V-I region LOI $\$$ P80748Defense/Immunoresponse11393Ig lambda chain V-III region LOI $\$$ P01714Defense/Immunoresponse11517Ig lambda chain V-III region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II $\$$ P13645Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal51490Keratin, type I cytoskeletal 14 $\$$ .#P02533Structural/Cytoskeletal51490	la kappa chain V-I region	P01611	Defense/Immunoresponse	11840
Ig kappa chain V-III region $GOL^{\$}$ P04206Defense/Immunoresponse11830Ig kappa chain V-IV region Len $\$$ P01625Defense/Immunoresponse12640Ig lambda chain C regions#P01842Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11453Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11725Ig lambda chain V-II region LOI $\$$ P80748Defense/Immunoresponse11333Ig lambda chain V-III region LOI $\$$ P80748Defense/Immunoresponse11393Ig lambda chain V-III region SH $\$$ P01714Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II $\$$ #Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal51490Keratin, type I cytoskeletal 14 $\$$ .#P02533Structural/Cytoskeletal51490	lg kappa chain V-III region B6 <sup>§,#</sup>	P01619	Defense/Immunoresponse	11636
Ig kappa chain V-IV region LenP01625Defense/Immunoresponse12640Ig lambda chain C regions#P01842Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11453Ig lambda chain V-I region WAH§.#P04208Defense/Immunoresponse11725Ig lambda chain V-III region LOI§P80748Defense/Immunoresponse11935Ig lambda chain V-III region SH§P01714Defense/Immunoresponse11393Ig lambda chain V-III region SH§P01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II§.#Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Keratin, type I cytoskeletal 14 <sup>§,#</sup> P02533Structural/Cytoskeletal51490(Continued)Structural/Cytoskeletal51490	Ig kappa chain V-III region GOL§	P04206	Defense/Immunoresponse	11830
Ig lambda chain C regions#P01842Defense/Immunoresponse11237Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11453Ig lambda chain V-I region WAH§.#P04208Defense/Immunoresponse11725Ig lambda chain V-II region LOI§P80748Defense/Immunoresponse11935Ig lambda chain V-III region SH§P01714Defense/Immunoresponse11393Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse49557Immunoglobulin J chain§P01591Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II§.#Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal51490Keratin, type I cytoskeletal 14§.#P02533Structural/Cytoskeletal51490	Ig kappa chain V-IV region Len§	P01625	Defense/Immunoresponse	12640
Ig lambda chain V-I region NEW#P01701Defense/Immunoresponse11453Ig lambda chain V-I region WAH§,#P04208Defense/Immunoresponse11725Ig lambda chain V-III region LOI§P80748Defense/Immunoresponse11935Ig lambda chain V-III region SH§P01714Defense/Immunoresponse11393Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse49557Immunoglobulin J chain§P01591Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II§,#Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal51490Keratin, type I cytoskeletal 14§,#P02533Structural/Cytoskeletal51490	Ig lambda chain C regions <sup>#</sup>	P01842	Defense/Immunoresponse	11237
Ig lambda chain V-I region WAH Ig lambda chain V-III region LOI Ig lambda chain V-III region LOI Ig lambda chain V-III region SH Ig lambda chain V-III region SH Ig lambda chain V-IV region HilP04208 P80748 P01714 P01717 Defense/ImmunoresponseDefense/Immunoresponse11725 11935Ig lambda chain V-III region SH Ig lambda chain V-IV region HilP01714 P01717Defense/Immunoresponse11393 1517Ig mu chain C region Immunoglobulin J chain Interleukin-1 receptor antagonist prec.P01871 P18510 P6870Defense/Immunoresponse Protein Degradation/Inhibitor28890 28890 2890Keratin, type I cuticular HA3-II Keratin, type I cytoskeletal 10 Keratin, type I cytoskeletal 14 §.#P13645 P02533Structural/Cytoskeletal Structural/Cytoskeletal51490 (Continued)	Ig lambda chain V-I region NEW#	P01701	Defense/Immunoresponse	11453
Ig lambda chain V-III region LOIP80748Defense/Immunoresponse11935Ig lambda chain V-III region SHP01714Defense/Immunoresponse11393Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse49557Immunoglobulin J chainP01591Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-IIP13645Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal5951490Keratin, type I cytoskeletal 14P02533Structural/Cytoskeletal51490	Ig lambda chain V-I region WAH <sup>§,#</sup>	P04208	Defense/Immunoresponse	11725
Ig lambda chain V-III region SH§P01714Defense/Immunoresponse11393Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse49557Immunoglobulin J chain§P01591Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II <sup>§,#</sup> Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Keratin, type I cytoskeletal 14 <sup>§,#</sup> P02533Structural/Cytoskeletal51490	Ig lambda chain V-III region LOI§	P80748	Defense/Immunoresponse	11935
Ig lambda chain V-IV region HilP01717Defense/Immunoresponse11517Ig mu chain C regionP01871Defense/Immunoresponse49557Immunoglobulin J chain§P01591Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II <sup>§,#</sup> Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Keratin, type I cytoskeletal 14 <sup>§,#</sup> P02533Structural/Cytoskeletal51490	Ig lambda chain V-III region SH§	P01714	Defense/Immunoresponse	11393
Ig mu chain C regionP01871Defense/Immunoresponse49557Immunoglobulin J chain§P01591Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II§.#Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Keratin, type I cytoskeletal 14§.#P02533Structural/Cytoskeletal51490	Ig lambda chain V-IV region Hil	P01717	Defense/Immunoresponse	11517
Immunoglobulin J chain§P01591Defense/Immunoresponse15594Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II§,#Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Keratin, type I cytoskeletal 14§,#P02533Structural/Cytoskeletal51490	Ig mu chain C region	P01871	Defense/Immunoresponse	49557
Interleukin-1 receptor antagonist prec.P18510Defense/Immunoresponse20055Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II <sup>§,#</sup> Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Keratin, type I cytoskeletal 14 <sup>§,#</sup> P02533Structural/Cytoskeletal51490	Immunoglobulin J chain <sup>§</sup>	P01591	Defense/Immunoresponse	15594
Kallikrein 1 precursorP06870Protein Degradation/Inhibitor28890Keratin, type I cuticular HA3-II <sup>§,#</sup> Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Keratin, type I cytoskeletal 14 <sup>§,#</sup> P02533Structural/Cytoskeletal51490	Interleukin-1 receptor antagonist prec.	P18510	Defense/Immunoresponse	20055
Keratin, type I cuticular HA3-IIS,#Q14525Structural/Cytoskeletal46214Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Keratin, type I cytoskeletal 14 <sup>§,#</sup> P02533Structural/Cytoskeletal51490	Kallikrein 1 precursor	P06870	Protein Degradation/Inhibitor	28890
Keratin, type I cytoskeletal 10P13645Structural/Cytoskeletal59519Keratin, type I cytoskeletal 14 <sup>§,#</sup> P02533Structural/Cytoskeletal51490(Continued)	Keratin, type I cuticular HA3-II <sup>§,#</sup>	Q14525	Structural/Cytoskeletal	46214
Keratin, type I cytoskeletal 14 <sup>s,#</sup> P02533 Structural/Cytoskeletal 51490	Keratin, type I cytoskeletal 10	P13645	Structural/Cytoskeletal	59519
	Keratin, type I cytoskeletal 14 <sup>8,#</sup>	P02533	Structural/Cytoskeletal	51490

Protein name	Accession nr	Function	Mass (Da)
Keratin, type I cytoskeletal 16 <sup>§</sup>	P08779	Structural/Cytoskeletal	51137
Keratin, type I cytoskeletal 9§	P35527	Structural/Cvtoskeletal	62129
Keratin, type I microfibrillar 48 kDa#	P02534	Structural/Cytoskeletal	46674
Keratin, type II cuticular HB4 <sup>#</sup>	Q9NSB2	Structural/Cytoskeletal	64895
Keratin, type II cytoskeletal 1 <sup>#</sup>	P04104	Structural/Cytoskeletal	65092
Keratin, type II cytoskeletal 1§	P04264	Structural/Cytoskeletal	65886
Keratin, type II cytoskeletal 2 epidermal <sup>§</sup>	P35908	Structural/Cytoskeletal	65865
Keratin, type II cytoskeletal 4§	P19013	Structural/Cytoskeletal	57285
Keratin, type II cytoskeletal 5§	P13647	Structural/Cytoskeletal	62447
Keratin, type II cytoskeletal 6A	P02538	Structural/Cytoskeletal	59914
Keratin, type II cytoskeletal 6D <sup>#</sup>	P48667	Structural/Cytoskeletal	42468
Keratin, type II cytoskeletal 6E	P48668	Structural/Cytoskeletal	59894
Keratin, type II microfibrillar,	P15241	Structural/Cytoskeletal	53682
component 7C <sup>#</sup>		,	
Lactoperoxidase precursor	P22079	Redox	80288
Lactotransferrin precursor§	P02788	Transport	78182
Leukotriene A-4 hydrolase	P09960	Energy/metabolism	69154
L-lactate dehydrogenase A chain§	P00338	Energy/metabolism	36558
L-lactate dehydrogenase B chain§	P07195	Energy/metabolism	36507
Long palate, lung and nasal epith.	Q8TDL5	Defense/Immunoresponse	52442
carc.ass. prot.1prec.			
L-plastin <sup>§</sup>	P13796	Structural/Cytoskeletal	70158
Lysozyme C precursor	P61626	Protein Degradation/Inhibitor	16537
Macrophage capping protein	P40121	Structural/Cytoskeletal	38518
Malate dehydrogenase, cytoplasmic	P40925	Energy/metabolism	36295
Maspin precursor	P36952	Protein Degradation/Inhibitor	42138
Matrix metalloproteinase-9 precursor§	P14780	Protein Degradation/Inhibitor	78427
Maturase K <sup>#</sup>	Q9GI85	Micro organism	61017
Metalloproteinase inhibitor 1 prec.§	P01033	Protein Degradation/Inhibitor	23171
Moesin	P26038	Structural/Cytoskeletal	67689
Monocyte differentiation antigen CD14	P08571	Defense/Immunoresponse	40076
precursor <sup>s,#</sup>			
Mucin 5B precursor	Q9HC84	Cell Adhesion/Communication	590499
Myeloperoxidase precursor	P05164	Defense/Immunoresponse	83869
Myoglobin <sup>#</sup>	P02144	Transport	17053
Myosin heavy chain, non-muscle type A <sup>s</sup>	P35579	Structural/Cytoskeletal	226401
N-acetylglucosamine kinase*	Q9UJ70	Energy/metabolism	37244
Neutrophil gelatinase-associated	P80188	Transport	22588
lipocalin prec. <sup>3</sup>	D07000	NA:	00070
Outer membrane usher protein pefC	P37868	Micro organism	86370
Deptidul probul dia trans isomoroso A	060007	Dratain Folding/Danair	17001
Pepuluyi-protyr cis-trains isomerase A	P02937	Protein Foluing/Repair	17001
Peroxiredoxin 5, milochonunai precursor	P30044	Redox	22020
Phoenbatidylothanoloming hinding protoin	P30041	Redux Protoin Dogradation/Inhibitor	24904
	F 30000	Frotein Degradation/Initibitor	20920
Phosphoglucorate kinase 1	P3007 1	Energy/metabolism	1110
Phosphoglycorate mutase 1	P19660	Energy/metabolism	22672
Phospholipid transfor protoin proc <sup>§#</sup>	P 10009	Energy/metabolism	20073
Plasminogen activator inhibitor 2 prec <sup>#</sup>	P05120	Signalling	16506
Polymeric immunoglobulin recentor	D01833	Defense/Immunoresponse	40590
precursor	101000	Derense/inimanoresponse	00014
Proactivator polypentide precursor	P07602	Protein Degradation/Inhibitor	58113
Profilin-1§	P07737	Structural/Cytoskeletal	14923
Prolactin-inducible protein precursor <sup>§</sup>	P12273	Defense/Immunoresponse	16572
Proline-rich protein 3 precursor	P02814	Unknown	8188
peptide P-B)		0	0100
Prominin 1 precursor <sup>#</sup>	O43490	Signalling	97202
	-		(Continued)

Protein-glutamine glutamyltransferase         Q08188         Energy/metabolism         76632           Purine nucleoside phosphorylase         P00491         Energy/metabolism         32118           Purine nucleoside phosphorylase         P00491         Energy/metabolism         57806           Ras-related CD botkinum toxin         P1513         Transport         21429           Substrate 2*         P52566         Signalling         20637           Solo Calcium-binding protein A7 <sup>5</sup> P31151         Cell Growth/Differentiation         11326           Salivary alpha-amylase precursor         P04745         Energy/metabolism         39200           Bike 2 precursor <sup>4</sup> P2778         Energy/metabolism         91611           Seriner/threonine-protein kinase RIPK4#         P57078         Energy/metabolism         77050           Seriner/threonine-protein kinase RIPK4#         P57078         Energy/metabolism         77011           Serine/threonine-protein kinase RIPK4#         P52707<	Protein name	Accession nr	Function	Mass (Da)
Purine nucleoside phosphorylase         P00491         Energy/metabolism         32118           Private kinase, isozymes MIM2 <sup>9</sup> P14618         Energy/metabolism         57806           Rab GDP dissociation inhibitor beta         P50395         Signalling         21429           substrate 2*         21429         21429         21429           Substrate 2*         P15153         Transport         21857           S100 calcum-eprotein kinase BR1-         O92785         Energy/metabolism         32280           Bike 2 precursor <sup>4</sup> Serine/threonine-protein kinase BR1-         O92785         Energy/metabolism         91611           Serine/threonine-protein kinase RIPK4"         P57078         Energy/metabolism         91611           Serine/threonine-protein kinase RIPK4"         P57078         Energy/metabolism         91611           Serine/threonine-protein kinase RIPK4"         P57078         Energy/metabolism         97011           Serine/threonine-protein kinase RIPK4"         P57078         Energy/metabolism         91611           Serine/threonine-protein kinase RIPK4"         P57078         Energy/metabolism         91611           Serine/threonine-protein kinase RIPK4"         P57078         Energy/metabolism         97011           Spance licarcinna antigen 1*         P29	Protein-glutamine glutamyltransferase E prec.§	Q08188	Energy/metabolism	76632
Pyruvate kinase, isozymes Mi1/M2 <sup>8</sup> P14618 Energy/metabolism 57806 Rab GPD dissociation inhibitor bata P50395 Signaling 50663 Ras-related C3 botulinum toxin P15153 Transport 21429 Rho GDP-dissociation inhibitor 2 P52566 Signalling 22857 Solivary alpha-amylase precursor P04745 Energy/metabolism 57768 Serine/threonine-protein kinase RIPK4 <sup>4</sup> P57078 Energy/metabolism 91611 Serine/threonine-protein xinase RIPK4 <sup>4</sup> P10599 Redox 11606 Transport 41855 Transpolin-2 Transport 48195 Transpolin-2 P2050 Transport 48195 Transpolin-2 P2050 Transport 48195 Transpolin-2 P37802 Structural/Cytoskeletal 22260 Transpolins 87878 P29401 Energy/metabolism 87878 Trosephosphate isomerase isomerise <sup>6</sup> P20401 Energy/metabolism 67878 Trosephosphate isomerase isomerise <sup>6</sup> P20401 Energy/metabolism 33872 Zinc-alpha-2-glycoprotein precursor <sup>8</sup> P25311 Energy/metabolism 32827 Zinc-alpha-2-glycoprotein precursor <sup>8</sup> P31947 Signalling 27774 A054 Sobosomal protein S20 <sup>4</sup> Q7V42 Micro organism 10264 GS rhosomal protein S20 <sup>4</sup> Q7V42 Micro organism 10264 GS rhosomal protein S20 <sup>4</sup> Q7V42 Micro organism 10264 GS rhosomal protein S20 <sup>4</sup> Q32 <sup>4</sup> Q7V42 Micro organism 10264 GS rhosomal protein S20 <sup>4</sup> Q32 <sup>5</sup> Ener	Purine nucleoside phosphorvlase	P00491	Energy/metabolism	32118
Råb GDP dissociation inhibitor betaP50395Signäling50683Ras-related C3 botulinum toxinP15153Transport21429substrate 2"P52566Signalling22857Rho GDP-dissociation inhibitor 2P5151Cell Growth/Differentiation11326Salivary alpha-amylase precursorP04745Energy/metabolism39280Bike 2 precursor"P04745Energy/metabolism39280Serine/threonise-protein kinase RH-K4"P57078Energy/metabolism91611Serine/threonise-protein kinase RH-K4"P57078Energy/metabolism91611Serine/threonise-protein kinase RH-K4"P57078Energy/metabolism91611Serine/threonise-protein kinase RH-K4"P57078Energy/metabolism91611Serine/threonise-protein kinase RH-K4"P57078Energy/metabolism91611Serine/threonise-protein kinase RH-K4"P57078Energy/metabolism91611Serine/threonise-protein kinase RH-K4"P57078Energy/metabolism77680Short patek, lung and nasalQ90BC9Structural/Cytoskeletal18154SPARCE/like protein 1 precursorQ14515Protein Degradation/Inhibitor75216SignalingCarconaseP37802Structural/Cytoskeletal22850TransportTransport27830Transport27830TranspolaleseP37802Structural/Cytoskeletal22250TranspolaleseP37802Structural/Cytoskeletal22250Transpolate lisomerase isomerise*P20611Energy/meta	Pvruvate kinase, isozvmes M1/M2§	P14618	Energy/metabolism	57806
Ras-related C3 botulinum toxin       P15153       Transport       21429         Rho GDP-dissociation inhibitor 2       P52566       Signalling       22857         S100 calcium-binding protein A7 <sup>6</sup> P31151       Cell Growth/Differentiation       11326         Serine/Itreonine-protein kinase BRI-1       Q92PS9       Energy/metabolism       37768         Serine/Itreonine-protein kinase BRI-4       Q92PS9       Energy/metabolism       39280         Serine/Itreonine-protein kinase BRI-4       Q92PS9       Energy/metabolism       39280         Serine/Itreonine-protein kinase BRI-4       Q92PS9       Energy/metabolism       39280         Serine/Itreonine-protein kinase BRI-4       Q92PS7       Transport       27011         Serine/Itreonine-protein kinase BRI-4       Q92BOR5       Transport       27011         Serine/Itreonine-protein kinase BRI-4       Q9UBC9       Structural/Cytoskeletal       2806         Space       Cell acrino/Inhibitor       75216       Structural/Cytoskeletal       27830         Momolog <sup>m</sup> P1599       Redox       11666       117ansabot       48195         Transport       P2061       Transport       27830       11666         Transelolase       P3787       Energy/metabolism       37540 <t< td=""><td>Rab GDP dissociation inhibitor beta</td><td>P50395</td><td>Signalling</td><td>50663</td></t<>	Rab GDP dissociation inhibitor beta	P50395	Signalling	50663
substrate 2 <sup>#</sup> Rho GDP-dissociation inhibitor 2 PG266 Signalling Pd4745 Energy/metabolism Pd474 Energy/metabolism Pd4745 Energy/metabolism Pd474 Energy/metabolism Pd474 Pd475 Energy/metabolism Pd474 Pd478 Energy/metabolism Pd474 Pd475 Energy/metabolism Pd474 Pd474 Pd474 Energy/metabolism Pd474 Pd474 Pd474 Energy/metabolism Pd474 Pd475 Energy/metabolism Pd474	Ras-related C3 botulinum toxin	P15153	Transport	21429
Price CDP-dissociation inhibitor 2P52566Signalling22857S100 calcium-binding protein AT <sup>6</sup> P31151Cell Growth/Differentiation11326Salvary alpha-amylase precursorP04745Energy/metabolism39280Berine/Itreonine-protein kinase BP1-092P59Energy/metabolism39280Berine/Itreonine-protein kinase BP14P2778Transport77050Serine/Itreonine-protein kinase BP144"P57078Energy/metabolism91611Serine/Itreonine-protein kinase BP144"P57078Energy/metabolism91611Serine/Itreonine-protein spreadQ90BC5Transport27011Short palate, lung and nasalQ90BC79Transport27031Sprace.Structural/Cytoskeletal18154Squamous cell carcinoma antigen 1 <sup>6</sup> P22508Protein Degradation/Inhibitor45665Squamous cell carcinoma antigen 1 <sup>6</sup> P20578Energy/metabolism37540TransclolaleP3737Energy/metabolism37540TransclolaleP37802Structural/Cytoskeletal22260TransportP20061Transport67878TransportP31020Structural/Cytoskeletal22260TransportP24011Energy/metabolism34532Von Ener's gland protein precursorP31025Transport19250TransportQ46543Protein Folding/Repair26538Von Ener's gland protein precursorP31047Signaling2777443-3 protein sigma <sup>5</sup> Q31947Signaling27774<	substrate 2 <sup>#</sup>	1 10100	Hanoport	21120
\$100 calcium-binding protein A7 <sup>8</sup> P31151         Cell Growth/Differentiation         11326           Salivary alpha-amylase precursor         P04745         Energy/metabolism         39280           Silvary alpha-amylase precursor <sup>8</sup> P0778         Energy/metabolism         39280           Silve 2 precursor <sup>8</sup> Serine/Threonine-protein kinase RIPK4 <sup>#</sup> P57078         Energy/metabolism         91611           Serine/Threonine-protein Nasa         Q90UBC9         Structural/Cytoskeletal         18154           Space         Qaration/Inhibitor         75216         Squamous cell carcinoma antigen 1 <sup>8</sup> P29508         Protein Degradation/Inhibitor         7540           Transobalamin I precursor         P20161         Transport         48195         Transberotial         22260           Transketolase <sup>6</sup> P29101         Energy/metabolism         67878	Rho GDP-dissociation inhibitor 2	P52566	Signalling	22857
Salivary alpha-amylase precursor       P04745       Energy/metabolism       57768         Serine/Ithreonine-protein kinase BRI1-       Q22PS9       Energy/metabolism       39280         Serine/Ithreonine-protein kinase BRIP44*       P57078       Energy/metabolism       91611         Serine/Ithreonine-protein kinase BRIP44*       P57078       Energy/metabolism       91611         Serine/Ithreonine-protein kinase BRIP44*       P57078       Transport       27011         Sprite.arc.ass.prot.2pre.       Structural/Cytoskeletal       18154         Spance.ike protein 1 precursor       Q14515       Protein Degradation/Inhibitor       75216         Squamous cell carcinoma antigen 1*       P29508       Protein Degradation/Inhibitor       44565         Sugar fermentation stimulation protein       Q97VP5       Micro organism       27830         Transcobalamin I precursor       P30502       Structural/Cytoskeletal       22220         Transketolase*       P73737       Transport       48195         Transketolase*       P23802       Structural/Cytoskeletal       22220         Transport       C48543       Protein Degradation/Inhibitor       8583         Yorosine recombinase serC       Q8U70       Kinco organism       34532         Viprosine recombinase serC       Q8U704	S100 calcium-binding protein A7 <sup>§</sup>	P31151	Cell Growth/Differentiation	11326
Sarinet Threanine-protein kinase BRI1- Q2/P59 Energy/metabolism 39280 Serinet/Threanine-protein kinase BRI1- Q2/P59 Energy/metabolism 39280 Serinet/Threanine-protein kinase RIPK4 <sup>#</sup> P57078 Energy/metabolism 91611 Serotransferrin precursor <sup>4</sup> Q40BC5 Transport 77050 Short palet, lung and nasal Q96DR5 Transport 77050 Small proline-rich protein 3 Q9UBC9 Structural/Cytoskeletal 18154 SPARC-like protein 1 precursor Q14515 Protein Degradation/Inhibitor 75216 Squamous cell carcinoma antigen 1 <sup>§</sup> P29508 Protein Degradation/Inhibitor 44565 Sugar fermentation stimulation protein Q97VP5 Micro organism 27830 homolog <sup>#</sup> Transport 27837 Energy/metabolism 37540 Transpolase P37837 Energy/metabolism 67878 Transpolase Server 20061 Transport 44195 Transpolase Server 20061 Transport 44552 Ubiquitin <sup>#</sup> Q46543 Protein Folding/Repair 26538 Von Ebner's gland protein precursor P31025 Transport 19250 Zinc-alpha-2-glycoprotein precursor P31027 Transport 10264 Zos Thosomal protein L5 <sup>#</sup> Q46739 Protein Degradation/Inhibitor 163278 Zinc-alpha-2-glycoprotein precursor <sup>8</sup> P25371 Energy/metabolism 33872 <b>25% confidence protein</b> B4339 Confidence Protein B47 Lass Protein D5gradation/Inhibitor 163278 Zinc-alpha-2-glycoprotein L5 <sup>#</sup> Q46731 Defense/Immunoresponse 76796 CartionedPhytopic antigen-related cell P06731 Defense/Immunoresponse 76796 Chabase <sup>#</sup> P11413 Energy/metabolis	Salivary alpha-amylase precursor	P04745	Energy/metabolism	57768
Canage Sector       Canage Sector       Canage Sector       Canage Sector         Serime Three on the sector       Q90 DR5       Transport       27701         Serime Three on the sector       Q90 DR5       Transport       27011         Serime Three on the sector       Q90 DR5       Transport       27011         Small proline-rich protein 3       Q90 DR5       Structural/Cytoskeletal       18154         SPARC-like protein 1 precursor       Q14515       Protein Degradation/Inhibitor       44565         Sugar fermentation stimulation protein       Q97 VP5       Micro organism       27630         Transclolase       P10599       Redox       11606       11606         Transalolase       P10599       Redox       11606       118154         Transclolase       P10599       Redox       11606       118154         Transclolase       P10599       Redox       11606       118154         Transclolase       P10590       Redox       11606       118154         Transclolase       P10590       Redox       11606       118154         Transclolase       P10590       Redox       160617       118375         Transclolase       P10502       Transport       26538       119362	Serine/threonine-protein kinase BRI1-	097PS9	Energy/metabolism	39280
Inc productP57078Energy/metabolism91611Serine/Intreonine-protein kinase RIPK4*P57078Fransport77050Serine/Intreonine-protein anasalQ90ER5Transport27011epith.carc.ass.prot.2prec.Structural/Cytoskeletal18154SPARC-like protein 1 precursorQ14515Protein Degradation/Inhibitor75216Squamous cell carcinoma antigen 1 <sup>§</sup> P29508Protein Degradation/Inhibitor44665Sugar fermentation stimulation proteinQ87VP5Micro organism27830Inoredoxin <sup>§</sup> P10599Redox11606Transpodalamin I precursorP20061Transport48195Transcobalamin I precursorP20061Transport28192Transcobalamin I precursorP20061Transport48195Transpelin-2P37802Structural/Cytoskeletal22280Transcobalamin I precursorP20401Energy/metabolism67878Troisephosphate isomerase isomerise <sup>§</sup> P60174Protein Degradation/Inhibitor8583Von Ebner's gland protein precursorP31025Transport19250Struc-alpha-2-glycoprotein precursorP31947Signalling27774305 ribosomal protein 520*Q48CRH2Micro organism10264505 ribosomal protein 520*Q47VQL2Micro organism103675Stacturage (NADPH) 1*P16152Energy/metabolism30244Alpha-2-macroglobulin precursorP01023Protein Degradation/Inhibitor163278Bact.l/permeability-increasing protein- </td <td>like 2 precursor<sup>#</sup></td> <td>QUZI UU</td> <td>Energy/metabolism</td> <td>00200</td>	like 2 precursor <sup>#</sup>	QUZI UU	Energy/metabolism	00200
Sertoransfernin precursor <sup>§</sup> P02787 Transport 77050 Short palate, lung and nasal Q96DR5 Transport 27011 pith.carc.as.prot.2prc. Small proline-rich protein 3 Q9UBC9 Structural/Cytoskeletal 18154 SpARC-like protein 1 precursor Q14515 Protein Degradation/Inhibitor 75216 Squamous cell carcinoma antigen 1 <sup>§</sup> P29508 Protein Degradation/Inhibitor 44665 Sugar fermentation stimulation protein Q87VP5 Micro organism 27830 Transcobalamin 1 precursor P20061 Transport 48195 Transcobalamin 1 precursor P37802 Structural/Cytoskeletal 22260 Transcobalamin 1 precursor P31025 Transport 84532 Ubiquitin <sup>#</sup> Von Ebner's gland protein precursor P31025 Transport 931025 Transport 925311 Energy/metabolism 33872 <b>9%</b> confidence protein s <b>14</b> -3-3 protein sigma <sup>3</sup> P31947 Signalling 27774 A3-3 protein sigma <sup>3</sup> P31947 Signalling 27774 Ala-3-3 protein Sigma <sup>3</sup> P01023 Protein Degradation/Inhibitor 163278 Acetyl-CoA acetyltransferase <sup>4</sup> P45359 Energy/metabolism 41241 Alanyl-tNA synthetas <sup>6</sup> Q871.14 Micro organism 20236 Acetyl-CoA acetyltransferase <sup>4</sup> P45359 Energy/metabolism 41241 Alanyl-tNA synthetase <sup>6</sup> P01023 Protein Degradation/Inhibitor 163278 Bact.Upermeability-increasing protein- Beta crystallin B1 (Beta-35) <sup>#</sup> P36374 Cell Growth/Differentiation 27892 Carbonyl reductase [NADPH] 1 <sup>#</sup> P16152 Energy/metabolism 30244 Carbonyl reductase P3657 Energy/metabolism 30244 Carbonyl reductase P3657 Energy/metabolism 30244 Carbonyl	Serine/threonine-protein kinase RIPK4 <sup>#</sup>	P57078	Energy/metabolism	91611
ControlationControlationControlationControlationPointCarcass.prot.2prec.Carcass.prot.2prec.Carcass.prot.2prec.Small proline-rich protein 3Q9UBC9Structural/Cytoskeletal18154SPARC-like protein 1 precursorQ14515Protein Degradation/Inhibitor75216Squamous cell carcinoma antigen 1sP29508Protein Degradation/Inhibitor44565Sugar fermentation stimulation proteinQ97VP5Micro organism27830homolog <sup>#</sup> Transpot48195Transpot48195Transpationalini 1 precursorP20061Transpot48195TranspatiolaseP37802Structural/Cytoskeletal22260Transpelin-2P37802Structural/Cytoskeletal22260Transpelin-2P37802Structural/Cytoskeletal22260Transpelin-2P37802Structural/Cytoskeletal22858Transpelin-2P37802Structural/Cytoskeletal22858Transpelin-2P37802Structural/Cytoskeletal22850Transpentine recursorP25311Energy/metabolism34532Von Eher's gland protein precursorP31947Signalling2777430S ribosomal protein S20 <sup>#</sup> Q3CRH2Micro organism1026450S ribosomal protein 52 <sup>#</sup> P4359Energy/metabolism30244Acetly-Cox Acetly transferase <sup>#</sup> P4359Patein Degradation/Inhibitor163278Bact/upermeability-increasing protein-Q8N4F0Transport49172Idea acetly transferase <sup>#</sup> P4359<	Serotransferrin precursor§	P02787	Transport	77050
Distry plate, instructExostriceTransport21011Small proline-rich protein 3Q9UBC9Structural/Cytoskeletal18154Small proline-rich protein 3Q9UBC9Structural/Cytoskeletal18154Squarnous cell carcinoma antigen 1 <sup>5</sup> P29508Protein Degradation/Inhibitor44665Sugar fermentation stimulation proteinQ97VP5Micro organism27830InomologitP10599Redox11606Transcobalamin 1 precursorP20061Transport48195Transcobalamin 1 precursorP20061Transport48195Transcobalamin 1 precursorP20061Transport48195Transephosphate isomerase isomerise <sup>5</sup> P60174Protein Folding/Repair26538Trosephosphate isomerase isomerise <sup>5</sup> P60174Protein Folding/Repair26538Von Ebner's gland protein precursorP31025Transport19250Zinc-alpha-2-glycoprotein precursorP31947Signalling2777430S ribosomal protein Sgm <sup>4</sup> P31947Signalling2777430S ribosomal protein Sgm <sup>4</sup> Q47VQL2Micro organism10264Acetyl-CoA acetyltransferase <sup>4</sup> P45359Energy/metabolism41241Alanyl-tRNA synthetase <sup>4</sup> Q971J4Micro organism20236Acetyl-CoA acetyltransferase <sup>4</sup> P45359Energy/metabolism41241Alanyl-tRNA synthetase <sup>4</sup> Q971J4Micro organism20236Carbonyl reductase [NADPH] 1 <sup>4*</sup> P16152Energy/metabolism30675Alpha-z-macroglobulin pr	Short palate lung and pasal	096DR5	Transport	27011
Small proline-rich protein 3 Q9UBC9 Structural/Cytoskeletal 18154 SPARC-like protein 1 precursor Q14515 Protein Degradation/Inhibitor 75216 Spane cell carcinoma antigen 1 <sup>s</sup> P29508 Protein Degradation/Inhibitor 44565 Sugar fermentation stimulation protein Q97VP5 Micro organism 27830 homolog <sup>#</sup> Transcobalamin 1 precursor P20061 Transport 48195 Transcobalamin 1 precursor P20061 Transport 48195 Transcobalate isomerase isomerase <sup>§</sup> P60174 Protein Folding/Repair 26538 Von Ebner's gland protein precursor P31025 Transport 19250 Zinc-alpha-2-glycoprotein precursor <sup>§</sup> P25311 Energy/metabolism 33872 Zinc-alpha-2-glycoprotein precursor <sup>§</sup> P25311 Energy/metabolism 33872 Zinc-alpha-2-glycoprotein precursor <sup>§</sup> P31947 Signalling 27774 AlonyI-RTNA synthetase <sup>#</sup> Q971J4 Micro organism 20236 Acetyl-CoA acetyltransferase <sup>#</sup> Q4539 Energy/metabolism 41241 AlonyI-RTNA synthetase <sup>#</sup> Q971J4 Micro organism 203675 Alpha-2-macroglobulin precursor <sup>§</sup> P01023 Protein Degradation/Inhibitor 163278 Bact.//permeability-increasing protein- Bate drystallin B1 (Beta-35) <sup>#</sup> P35674 Cell Growth/Differentiation 27892 Carbonyl reductase [NADPH] 1 <sup>#</sup> P16152 Energy/metabolism 3244 Carcinoembryonic antigen-related cell P06731 Defense/Immunoresponse 76796 Chaparone protein htpG P61185 Micro organism 73731 Cystatin B <sup>#</sup> Q86225 Protein Degradation/Inhibitor 11103 Dihydrolipoyllysine-residue P36957 Energy/metabolism 3244 Ferendoxin II <sup>#</sup> P41793 Micro organism 43640 Succinyltansferase <sup>#</sup> P41793 Micro organism 43640 Succinyltansferase <sup>#</sup> P41793 Micro organism 59135 dehydrogenase <sup>#</sup> P41793 Micro organism 59135 dehydrogenase <sup>#</sup> P11413 Energy/metabolism 59135 dehydrogenase <sup>#</sup> P10943 Micro organism 59135	enith carc ass prot 2prec	QUODINU	Transport	27011
Shar Dilke protein 1 precursor Q14515 Protein Degradation/Inhibitor 75216 Squamous cell carcinoma antigen 1 <sup>8</sup> P29508 Protein Degradation/Inhibitor 44565 Squar fermentation stimulation protein Q97VP5 Micro organism 27830 homolog <sup>#</sup> P10599 Redox 11606 Transcobalamin 1 precursor P20061 Transport 48195 Transcobalamin 1 precursor P31025 Transport 94532 Ubiquitin <sup>#</sup> 046543 Protein Degradation/Inhibitor 8583 Von Ebner's gland protein precursor P31025 Transport 9250 Zinc-alpha-2-glycoprotein precursor <sup>8</sup> P25311 Energy/metabolism 33872 <b>95% confidence proteins</b> 1225 Acetly-CoA acetyltransferase <sup>#</sup> P45359 Energy/metabolism 41241 Alanyl-tRNA synthetase <sup>#</sup> Q37U42 Micro organism 10264 50S ribosomal protein L5 <sup>#</sup> Q8CRH2 Micro organism 103675 Alpha-2-macroglobulin precursor <sup>\$</sup> P01023 Protein Degradation/Inhibitor 163278 Bact.//permeability-increasing protein- Beta crystallin B1 (Beta-35) <sup>#</sup> P53674 Cell Growth/Differentiation 27892 Carbonyl reductase [NADPH] 1 <sup>#</sup> P16152 Energy/metabolism 30244 Carcinoembryonic antigen-related cell P06731 Defense/Immunoresponse 76796 Chaparone protein htpG P61185 Micro organism 73731 Cystatin B <sup>#</sup> Q36255 Protein Degradation/Inhibitor 11103 Dihydrolipoyllysine-residue P36957 Energy/metabolism 48640 succinyltransferase <sup>#</sup> P41793 Micro organism 255428 Glucose-6-phosphate 1- etat acety protein #P1755 Structural/Cytoskeletal 322818 Ferredoxin II <sup>#</sup> P1754 Micro organism 2554288 Glucose-6-phosphate 1- P11413 Energy/metabolism 59135	Small proline_rich protein 3		Structural/Cytoskeletal	18154
Squamous cell carcinoma antigen 1 <sup>s</sup> Squamous cell carcinoma antigen 1 <sup>s</sup> Sigar fermentation stimulation protein Micro organism 27830 Trianscobalamin I precursor P10599 Transpelin-2 P2061 Transport 48195 Transpelin-2 P37837 Energy/metabolism 37540 Transpelin-2 P2061 Transport 48195 Transpelin-2 P37802 Structural/Cytoskeletal 22260 Transpelin-2 P37802 Structural/Cytoskeletal 22260 Transpelin-2 P37802 Structural/Cytoskeletal 22260 Transpelin-2 P37802 Structural/Cytoskeletal 22260 Transpelin-2 P37802 Structural/Cytoskeletal 22260 Transport 48195 Transport 9260 Transport 92610 Station-2014 Station 2014 Station 2014 Statio	SPARC-like protein 1 precursor	014515	Protein Degradation/Inhibitor	75216
Sugar fermentation stimulation protein log7VP5P25300Frotein Degration Micro organismP4503 P7630homolog* Transcobalamin I precursorP10599Redox11606Transcobalamin I precursorP20061Transport48195Transcobalamin I precursorP20061Transport48195Transpelin-2P37802Structural/Cytoskeletal22260Transpelin-2P37802Structural/Cytoskeletal22638Triosephosphate isomerase isomerise*P60174Protein Folding/Repair26538Tyrosine recombinase xerCQ8UC70Micro organism34532Ubiquitin*O46543Protein Degradation/Inhibitor8583Von Ebner's gland protein precursorP31025Transport19250Zinc-alpha-2-glycoprotein precursor*P25311Energy/metabolism33872 <b>95% confidence proteins97</b> 947Signalling2777430S ribosomal protein S20*Q7VQL2Micro organism1026450S ribosomal protein L5*Q87VL2Micro organism103675Alpha-2-anzorglobulin precursor*P01023Protein Degradation/Inhibitor163278Bact.l/permeability-increasing protein-Q8N4F0Transport49172Ike 1 prec.Bata systallin B1 (Beta-35)*P53674Cell Growth/Differentiation27892Carbonyl reductase [NADPH] 1*P16152Energy/metabolism30244Carcinoembryonic antigen-related cellP06731Defense/Immunoresponse76796Chah. mol. Sprec. <sup>§,#</sup> P24929Ce	Squamous cell carcinoma antigen 1§	D20508	Protein Degradation/Inhibitor	11565
OrganCarlow	Sugar fermentation stimulation protein	007\/D5	Micro organism	27830
Thioredoxin <sup>§</sup> P10599 Redox 11606 Transcobalamin   precursor P37837 Energy/metabolism 37540 Transcobalamin   precursor P20061 Transport 48195 Transgelin-2 P37802 Structural/Cytoskeletal 22260 Transketolase <sup>§</sup> P29401 Energy/metabolism 67878 Triosephosphate isomerase isomerise <sup>§</sup> P60174 Protein Folding/Repair 26538 Tyrosine recombinase xerC Q8UC70 Micro organism 34532 Ubiquitin <sup>#</sup> O46543 Protein Degradation/Inhibitor 8583 Yon Ebner's gland protein precursor P31025 Transport 19250 Zinc-alpha-2-glycoprotein precursor <sup>§</sup> P25311 Energy/metabolism 33872 <b>95% confidence proteins</b> 925311 Energy/metabolism 20236 So ribosomal protein L5 <sup>#</sup> Q8CRH2 Micro organism 10264 505 ribosomal protein L5 <sup>#</sup> Q971J4 Micro organism 20236 Acetyl-CoA acetyltransferase <sup>#</sup> P45359 Energy/metabolism 103675 Alpha-2-macroglobulin precursor <sup>§</sup> P10123 Protein Degradation/Inhibitor 163278 Bact./permeability-increasing protein- Beta crystallin B1 (Beta-35) <sup>#</sup> P53674 Cell Growth/Differentiation 27892 Carbonyl reductase [NADPH] 1 <sup>#</sup> P16152 Energy/metabolism 30244 Carcinoembryonic antigen-related cell P06731 Defense/Immunoresponse 76796 adh. mol.5prec. <sup>§,#</sup> Q8625 Protein Degradation/Inhibitor 11103 Dihydrolipoyllysine-residue P36957 Energy/metabolism 48840 Succinyltransferase <sup>#</sup> P41793 Micro organism 73731 Cystatin B <sup>#</sup> Q86252 Protein Degradation/Inhibitor 11103 Dihydrolipoyllysine-residue P36957 Energy/metabolism 48840 Succinyltransferase <sup>#</sup> P41793 Micro organism 9962 Genome protein htpG P61185 Micro organism 9962 Genome polyrotein alpha-2 subunit <sup>#</sup> P41793 Micro organism 9962 Genome polyrotein alpha-2 subunit <sup>#</sup> P41793 Micro organism 9962 Genome polyrotein in BP9-beta <sup>#</sup> P41793 Micro organism 9962 Genome polyrotein f <sup>#</sup> P40237 Micro organism 9962 Genome polyrotein f <sup>#</sup> P40548 Protein Folding/Repair 83133 Hut operon positive regulatory protein <sup>#</sup> P40943 Micro organism 9135	bomolog <sup>#</sup>	QUIVED	Micro organism	27030
Transaldolase 1743 Transacbalamin I precursor P20061 Transport 48195 Transgelin-2 P37837 Energy/metabolism 37540 Transcobalamin I precursor P20061 Transport 48195 Transgelin-2 P37802 Structural/Cytoskeletal 22260 Transketolase <sup>5</sup> P60174 Protein Folding/Repair 26538 Tyrosine recombinase xerC Q8UC70 Micro organism 34532 Ubiquitin <sup>#</sup> 046543 Protein Degradation/Inhibitor 8583 Yon Ebner's gland protein precursor P31025 Transport 19250 Sinc-alpha-2-glycoprotein precursor P31025 Transport 19250 Sinc-alpha-2-glycoprotein precursor P31027 Transport 10264 505 ribosomal protein S20 <sup>#</sup> Q7VQL2 Micro organism 10264 505 ribosomal protein S20 <sup>#</sup> Q8CRH2 Micro organism 10264 505 ribosomal protein L5 <sup>#</sup> Q8CRH2 Micro organism 10264 505 ribosomal protein L5 <sup>#</sup> Q8CRH2 Micro organism 103675 Alpha-2-macroglobulin precursor <sup>8</sup> P01023 Protein Degradation/Inhibitor 163278 Bact.//permeability-increasing protein- Q8N4F0 Transport 49172 Like 1 prec. Beta crystallin B1 (Beta-35) <sup>#</sup> P3674 Cell Growth/Differentiation 27892 Carbonyl reductase [NADPH] 1 <sup>#</sup> P16152 Energy/metabolism 30244 Carcinoembryonic antigen-related cell P06731 Defense/Immunoresponse 76796 adh. mol.5prec. <sup>§,#</sup> Catalase <sup>§</sup> P0400 Redox 59625 CD9 antigen (p24) <sup>#</sup> P21926 Cell Adhesion/Communication 25285 Chaperone protein htpG P61185 Micro organism 49174 F-actin capping protein alpha-2 subunit <sup>#</sup> P41793 Micro organism 49174 F-actin capping protein alpha-2 subunit <sup>#</sup> P41793 Micro organism 59135 dehydrogenase <sup>#</sup> Feredoxin II <sup>#</sup> P0623 Protein Degradation/Inhibitor 11103 Dihydrolipoyllysine-residue P36957 Energy/metabolism 49174 F-actin capping protein alpha-2 subunit <sup>#</sup> P41793 Micro organism 59135 dehydrogenase <sup>#</sup> Feredoxin II <sup>#</sup> P0623 Protein Folding/Repair 83133 Hut operon positive regulatory protein <sup>#</sup> P08238 Protein Folding/Repair 83133 Hut operon positive regulatory protein <sup>#</sup> P10943 Micro organism 59135	Thioredoxin <sup>§</sup>	P10500	Peday	11606
Transcobalamin I precursor P20061 Transport 48195 Transcobalamin I precursor P20061 Transport 48195 Transcobalamin I precursor P20061 Transport 48195 Transpelin-2 P37802 Structural/Cytoskeletal 22260 Transketolase <sup>§</sup> P60174 Protein Folding/Repair 26538 Tyrosine recombinase xerC Q8UC70 Micro organism 34532 Ubiquitin <sup>#</sup> 046543 Protein Degradation/Inhibitor 8583 Von Ebner's gland protein precursor P31025 Transport 19250 Zinc-alpha-2-glycoprotein precursor <sup>§</sup> P25311 Energy/metabolism 33872 <b>95% confidence proteins</b> 207774 A1-3-3 protein sigma <sup>§</sup> P31947 Signalling 27774 305 ribosomal protein S20 <sup>#</sup> Q7VQL2 Micro organism 10264 50S ribosomal protein S20 <sup>#</sup> Q8CRH2 Micro organism 20236 Acetyl-CoA acetyltransferase <sup>#</sup> P45359 Energy/metabolism 41241 Alanyl-tRNA synthetase <sup>#</sup> Q97114 Micro organism 103675 Alpha-2-macroglobulin precursor <sup>§</sup> P01023 Protein Degradation/Inhibitor 163278 Bact.Upermeability-increasing protein- Q8N4F0 Transport 27892 Carbonyl reductase [NADPH] 1 <sup>#</sup> P16152 Energy/metabolism 30244 Carcinoembryonic antigen-related cell P06731 Defense/Immunoresponse 76796 adh. m0.5prec. <sup>§,#</sup> Catalase <sup>§</sup> P04040 Redox 59625 CD9 antigen (p24) <sup>#</sup> P21926 Cell Adhesion/Communication 27892 Catalase <sup>§</sup> P04040 Redox 59625 Chaperone protein htpG P61185 Micro organism 48640 succinyltransferase <sup>#</sup> P41793 Micro organism 49174 F-actin capping protein alpha-2 subunit <sup>#</sup> P41793 Micro organism 9962 Genome polyprotein <sup>#</sup> P17594 Micro organism 9962 Genome polyprotein <sup>#</sup> P17594 Micro organism 59135 dehydrogenase <sup>#</sup> P10943 Micro organism 59135	Transaldolaso	P 10099	Eporav/motobolism	37540
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Transketolase <sup>§</sup> P29401 Energy/metabolism 67878 Triansketolase <sup>§</sup> P60174 Protein Folding/Repair 26538 Tyrosine recombinase xerC Q8UC70 Micro organism 34532 Ubiquitin <sup>#</sup> O46543 Protein Degradation/Inhibitor 8883 Von Ebner's gland protein precursor P31025 Transport 19250 Zinc-alpha-2-glycoprotein precursor <sup>§</sup> P25311 Energy/metabolism 33872 <b>95% confidence proteins</b> 14-3-3 protein sigma <sup>§</sup> P31947 Signalling 27774 305 ribosomal protein L5 <sup>#</sup> Q7VQL2 Micro organism 20236 Acetyl-CoA acetyltransferase <sup>#</sup> P45359 Energy/metabolism 41241 Alanyl-tRNA synthetase <sup>#</sup> Q971.14 Micro organism 103675 Alpha-2-macroglobulin precursor <sup>§</sup> P01023 Protein Degradation/Inhibitor 163278 Bact.l/permeability-increasing protein- Q8N4F0 Transport 49172 like 1 prec. Beta crystallin B1 (Beta-35) <sup>#</sup> P53674 Cell Growth/Differentiation 27892 Carbonyl reductase [NADPH] 1 <sup>#</sup> P16152 Energy/metabolism 30244 Carcinoembryonic antigen-related cell P06731 Defense/Immunoresponse 76796 chaperone protein htpG P61185 Micro organism 73731 Cystatin B <sup>#</sup> Q86225 Protein Degradation/Inhibitor 1103 Chapter (p24) <sup>#</sup> P21926 Cell Adhesion/Communication 25285 Chaperone protein htpG P61185 Micro organism 73731 Cystatin B <sup>#</sup> P41793 Micro organism 49174 F-actin capping protein alpha-2 subunit <sup>#</sup> P41793 Micro organism 2962 Genome polyprotein <sup>#</sup> P17594 Micro organism 2962 Genome polyprotein <sup>#</sup> P17594 Micro organism 59135 dehydrogenase <sup>#</sup> P141413 Energy/metabolism 59135 dehydrogenase <sup>#</sup> P10943 Micro organism 4174 F-actin capping protein HSP 90-beta <sup>#</sup> P08238 Protein Folding/Repair 83133 Hut operon positive regulatory protein <sup>#</sup> P10943 Micro organism 1064	Tranagolin 2	F 2000 I	Structural/Cytookolotal	40195
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	nut operon positive regulatory protein"	P10943	wicro organism	(Continued)

Protein name	Accession nr	Function	Mass (Da)
Hypothetical protein ynaA <sup>#</sup>	P77658	Micro organism	37060
Hypothetical UPF0135 protein CPn0137 <sup>#</sup>	Q9Z946	Micro organism	27236
Ig heavy chain V region UPC10 <sup>§,#</sup>	P01811	Defense/Immunoresponse	13001
Ig kappa chain V-II region TEW§	P01617	Defense/Immunoresponse	12316
Ig kappa chain V-III region NG9 precursor <sup>§,#</sup>	P01621	Defense/Immunoresponse	10729
Myeloblastin precursor	P24158	Protein Degradation/Inhibitor	27807
Potential phospholipid-transporting ATPase VA <sup>#</sup>	O60312	Energy/metabolism	167688
Probable Na(+)/H(+) antiporter nhx-9	P35449	Micro organism	75281
Probable serine/threonine-protein kinase#	P28966	Micro organism	65248
Pyruvate kinase, isozymes R/L <sup>#</sup>	P30613	Energy/metabolism	61830
Rho GDP-dissociation inhibitor 1	P52565	Signalling	23076
Serum albumin precursor§	P02768	Transport	69367
Vinculin <sup>#</sup>	P18206	Cell adhesion/Communication	123668
Zinc finger protein 446 <sup>#</sup>	Q9NWS9	Signalling	48957

<sup>§</sup>Proteins that are also found in plasma according to the HUPO Plasma Proteome Initiative list of plasma proteins (www.bioinformatics. med.umich.edu/app/hupo/ppp/).

\*Novel saliva proteins identified in this study compared to seven previous studies (see Fig. 7).

HUPO list, 84 proteins (38.5%) identified in the current study and indicated in Table 2 are also found in plasma. To determine the relevance of the identified proteins, we compared our results to seven other proteomics studies (Huang, 2004;

**Figure 5.** SDS-PAGE of saliva proteins. Lane 1 represents the molecular weight markers. Lane 2 represents proteins present in 10  $\mu$ I of processed saliva. This lane was cut into 30 bands for further identification by LC-MS/MS.

Wilmarth, 2004; Vitorino, 2004; Hu, 2005; Xie, 2005; Walz, 2006; Guo, 2006) on whole saliva composition. Figure 7 shows that there is only partial overlap with our study. Based on this analyses 83 new saliva proteins were identified in our study which are indicated in Table 2.

#### Discussion

There is growing interest in using saliva as a diagnostic fluid because of its relatively simple and non-invasive collection procedures. A prerequisite for measuring diagnostic protein markers in saliva is that these proteins are stable in saliva. In this study we show that relatively rapid protein degradation occurs in whole saliva samples at room temperature. We developed a SELDI-based assay to quickly monitor sample integrity. With this assav we show that protein degradation in saliva at room temperature is rapid and starts already during sample collection and handling. Three degradation products with masses of 2937 Da, 3370 Da and 4132 Da were discovered that can be used to monitor the degradation process and to determine the quality of a saliva sample before protein analyses. These markers increase 2 to 7-fold over a period of 4 hrs storage at room temperature, suggesting they are stable breakdown products of larger proteins. The proteome analyses indicates that there are at least six proteases present in saliva (see Table 2) which are probably involved in the observed protein degradation. However, also 13



Figure 6. Functional categories of identified proteins, based on information from Swiss Prot, Source and Human Protein Reference Database.

protease inhibitor proteins were identified which may counteract protease activity. Nevertheless, the overall balance is clearly in favour of degradation. Protein breakdown in saliva could be partly inhibited by a protease inhibitor cocktail targeting serine, cysteine and metallo-proteases. Also in another study, that investigated storage of saliva samples at different temperatures, only partially prevention of degradation was observed with a different inhibitor cocktail (Schipper, 2007). More research is clearly needed to find more effective protease inhibitor cocktails to prevent degradation. A complicating factor in such studies will be that many protease inhibitors are peptides themselves or covalently bind to proteins thereby changing their masses. Both will interfere with proteomics measurements in biomarker discovery studies but may



Figure 7. Venn diagrams comparing the proteome results obtained with this study (A) versus those achieved by Xie et al. (Xie, 2005) (B), Hu et al. (Hu, 2005) (C), Vitorino et al. (Vitorino, 2004) (D), Walz et al. (Walz, 2006) (E), Huang et al. (Huang, 2004) (F), Wilmarth et al. (Wilmarth, 2004) (G), Guo et al. (Guo, 2006) (H). Only part of the data of the study by Guo et al. is publicly available and was used in this comparison.

not interfere with ELISA-based measurements of individual proteins. Based on the results of our study we recommend to freeze samples immediately after collection, e.g. in liquid nitrogen, to minimize protein breakdown. Sample processing at 4 °C as well as the use of protease inhibitors can help to reduce degradation. Based on a study by Schipper et al. (Schipper, 2007) long time storage at -80 °C is recommended.

Several different strategies have been employed to analyze the saliva proteome such as 2 D gel (Huang, 2004; Wilmarth, 2004; Vitorino, 2004; Hu, 2005; Walz, 2006), capillary iso-electric focusing (Guo, 2006), and free flow electrophoresis (Xie, 2005). Our approach was to fractionate saliva proteins by SDS-PAGE followed by LC-MS/MS for protein identification. Overall 218 proteins were identified by this proteomics strategy, not applied to saliva before. From the identified proteins we deduced the main functions. These are: carbohydrate-breakdown, immune response/ defence against bacteria, and protein degradation. By comparing our results with seven previous proteomics studies (Fig. 7) on whole saliva composition we find only partial overlap with our study. 83 new saliva proteins from our study which were not previously identified are indicated in Table 2. These results show that with each proteomics strategy, partial overlapping subsets of saliva proteins are identified. Therefore, different proteomic approaches will contribute to a more comprehensive view of the saliva proteome. Many of the identified proteins are also found in plasma. Comparison with the HUPO plasma proteome database learned that 38.5% of the identified proteins can also be found in plasma. This relatively high percentage of plasma proteins in saliva illustrate the possibilities for use of saliva as an alternative to blood for diagnosis and biomarker

discovery. However, protein breakdown in saliva samples poses a serious problem for quantitative measurements. We conclude that saliva can be a promising diagnostic fluid when precautions are taken towards protein breakdown.

### Acknowledgements

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