PROTEOMIC ANALYSIS OF AGE-RELATED CHANGES IN OVINE CEREBROSPINAL FLUID

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ABSTRACT

Cerebrospinal fluid (CSF) circulates through the brain and has a unique composition reflecting the biological processes of the brain. Identifying ageing CSF biomarkers can aid in understanding the ageing process and interpreting CSF protein changes in neurodegenerative diseases. In this study, ovine CSF proteins from young (1-2 year old), middle aged (3-6 year old) and old (7-10 year old) sheep were systemically studied. CSF proteins were labelled with iTRAQ tagging reagents and fractionated by 2-dimensional high performance, liquid chromatography. Tryptic peptides were identified using MS/MS fragmentation ions for sequencing and quantified from iTRAQ reporter ion intensities at m/z 114, 115, 116 and 117. Two hundred thirty one peptides were detected, from which 143 proteins were identified. There were 52 proteins with >25% increase in concentrations in the old sheep compared to the young. 33 of them increased >25% but <50%, 13 increased >50% but <1 fold, 6 increased >1 fold [i.e. haptoglobin (Hp), haemoglobin, neuroendocrine protein 7B2, IgM, fibrous sheath interacting protein 1, vimentin]. There were 18 proteins with >25% decrease in concentrations in the old sheep compared to the young. 17 of them decreased >25% but <50%, and histone deacetylase 7 (HDAC7) was gradually decreased for over 80%. Glutathione S-transferase was decreased in middle aged CSF compared to both young and old CSF. The differential expressions of 3 proteins (Hp, neuroendocrine protein 7B2, IgM) were confirmed by immunoassays. These data expand our current knowledge regarding ovine CSF proteins, supply the necessary information to understand the ageing process in the brain and provide a basis for diagnosis of neurodegenerative diseases.

Highlights

- CSF protein changes during normal ageing process
- Seventy proteins were changed in concentration among different aged sheep CSF
- A common ageing CSF biomarker identified to date is immunoproteins
- Identifying ageing CSF biomarker help understand the ageing process in the brain

Key words: ageing, CSF, biomarkers, proteomics, choroid plexus, neurodegenerative disease

1. INTRODUCTION

Cerebrospinal fluid (CSF) is a clear, colourless bodily fluid that circulates through the brain and communicates freely with the brain extracellular fluid. In adult humans, about two-thirds of CSF is secreted by the choroid plexus (CP) at the rate of about 0.35-0.4 ml / min or 500-600 ml / day, while the remainder is from the extrachoroidal sources [1]. CSF has a unique composition that is different from the plasma, due to the presence of blood-brain barrier (BBB) and blood-CSF barrier (BCSFB), the active secretion at the CP and specific transport systems for moving substances between blood and CSF. In comparison to plasma ultrafiltrate, CSF contains higher concentrations of sodium, chloride, and magnesium and lower concentrations of glucose, proteins, amino acids, uric acid, potassium, bicarbonate, calcium and phosphate [2]. The CSF is in direct contact with the brain interstitial fluid, and the composition of the CSF therefore reflects biological processes occurring in the brain [3]. This understanding has led to an interest in the potential for discovering biomarkers within the CSF, which can be used to monitor brain function and aid in diagnosis of neurological diseases.

During ageing, several structural, chemical, and functional changes occur in the brain. The weight and volume of both cerebral cortex and hippocampus reduce, and the ventricular system expands to fill the space vacated by the brain parenchyma [4]. In contrast, the CP in the lateral ventricles doubles in weight, leading to significant increase of the ratio of the CP and the brain in weight [5,6]. The CSF secretion by the CP is decreased, leading to a decreased overall turnover of CSF which can affect its protein composition.

There are few studies on the CSF biology during ageing in absence of any neurological diseases, and the drastically incomplete knowledge hinders us from understanding the ageing process in the brain. In this study, we systemically characterized age-related protein changes in ovine CSF using a gel free proteomic mass spectrometry (MS) approach with isobaric labelled samples (iTRAQ) techniques. The advantage of using sheep in this study is that adequate CSF samples of all age groups can be obtained, with facile control over gender selection and environmental factors. Furthermore, we have previous characterized the age-related changes in the CP structure and function in the sheep, and found that the secretion rate of the CP is decreased thus slowed overall CSF turnover, which contributed to the increased protein concentrations within the CSF with increasing age [6-10].

2. METHODS

2.1. Sample collection

Clun Forest strain adult female sheep aged between 1 and 10 year old were divided into 3 groups: young (aged 1-2 years); middle-aged (3-6 years) and old (7-10 years). Each group comprises 7 sheep. Sheep were anaesthetized with *i.v.* thiopentone sodium (20 $mg.kg^{-1}$) and heparinised (20,000 IU heparin kg^{-1}). CSF samples were collected from the cisterna magna by needle puncture [11]. Samples were spun at 10 000 g for 10 min at 4 °C. CSF samples with any blood contamination determined by the presence of erythrocytes in the solution or precipitation were discarded. Supernatants were immediately stored at -80 °C until being analysed. All procedures were within the Home Office Scientific procedures Act, 1986 (HMSO, London, UK), and were approved by King's College London research ethics committee.

2.2. Sample preparation for MS analysis

Equal volumes of CSF samples from seven individuals within each group were pooled to give a final volume of 80 μl per age group. An internal standard (IS) was prepared by pooling equal amount of each sample from the analysis set. The pooled samples were then digested with sequencing grade porcine trypsin (Promega, Fitchburg, Wisconsin, USA) overnight at 37 °C, followed by reduction and alkylation steps performed according to the instructions outlined in the iTRAQ labelling kit (AB Sciex, Framingham, MA, USA). Following this, the digests were then dried down in a vacuum centrifuge and iTRAQ labelling carried out also according to instructions in the iTRAQ labelling kit. Each iTRAQ tag was assigned as follows: iTRAQ reagent 114 for Young, 115 for Middle-age, 116 for Old and 117 for the IS.

Both MS and MS/MS analysis was performed on the fractionated peptides using an Applied Biosystems 4800 MALDI TOF/TOF mass spectrometer. The mass spectrometer was operated under control of 4000 Series Explorer v3.5.2 software (Applied Biosystems, Waltham, Massachusetts, USA). A total of 1000 shots per MS spectrum (no stop conditions) and 2500 shots per MS/MS spectrum (no stop conditions) were acquired. The following MS/MS acquisition settings were used: 2KV operating mode with CID on and precursor mass window resolution set to 300.00 (FWHM). Peak lists of MS and MS/MS spectra were generated using 4000 Series Explorer v3.5.2 software and the following parameters were used after selective labelling of monoisotopic mass peaks: MS peak lists: S/N threshold 10, Savitzky Golay smoothing (3 points across peak (FWHM)), no baseline correction, MS/MS peak lists: S/N threshold 14; smoothing algorithm: Savitzky Golay, smoothing (7 points across peak (FWHM)).

2.3. Quantitative MS analysis

Liquid chromatography fractionation and subsequent MS analysis was conducted as described before [12]. Briefly, labelled tryptic peptides obtained from protein digestion were pooled and dissolved in 2.4 ml of SCX buffer A (10 mM phosphate, 20% acetonitrile) and centrifuged at 15,000 × *g* for 5 min to remove any insoluble debris. The peptide mixture was loaded onto a Polysulphoethyl A column (4.6 mm × 100 mm, 5 μm, 300 Å, PolyLC Inc.) using a flow rate of 800 μl / min. The bound sample was washed using SCX buffer A for approximately 20 min, until non-binding mixture components were removed (as determined by the UV traces returning to baseline levels). Peptides were then eluted at 400 μl / min using a gradient of SCX buffer B (SCX A containing 1 M potassium chloride) of 0–30% over 30 min. Fractions were collected manually at 60 s intervals. SCX fractions containing peptides were dried to completeness and dissolved in 30 µl of RP buffer A (2% acetonitrile) before separating further using an Ultimate 3000 chromatography system connected to a Probot fraction collector (Dionex, Sunnyvale, CA, USA). Samples were randomised and loaded onto a C18 trapping column before eluting onto a 75 µm internal diameter C18 PepMap column. Peptides were washed for 15 min in RP buffer A before eluting with a 2–50% gradient of acetonitrile over 120 min, followed by further elution with 90% acetonitrile for 15 min. Eluted peptide fractions were spotted onto a MALDI-MS target plate every 10 s with 3 mg/ml α-cyano-2-hydroxy cinnamic acid at a flow rate of 1.2 µl/min. A blank injection was performed between peptide runs to minimise sample carry-over.

Peptides were analysed using an Applied Biosystems 4800 Proteomics Analyser with close external standards to calibrate the instrument. Survey spectra were collected from the range 900 to 4000 Da, with a focus mass of 2500 Da. Fifty shots were fired per sub-spectrum, with 1000 total shots per spectrum without stop conditions. All sub-spectra were accepted, and laser intensity was set to 3750. For product ion analysis, a maximum of 10 precursor ions per spot were selected automatically with a minimum signal-to-noise ratio of 40. Lowest-intensity precursors were acquired first.

An automated database search was run using GPS Explorer v3.6 (AB Sciex, Framingham, MA, USA). MASCOT was used as the search engine to search the NCBI non-redundant database version Oct 04, 2011, using the following search parameters: species = mammals; precursor ion mass tolerance of 150 ppm; MS/MS fragment ion mass tolerance of 0.3 Da; iTRAQ fragment ion mass tolerance of 0.2 Da. Oxidation of methionine residues were allowed as variable modifications, and N-term (iTRAQ), lysine (iTRAQ) and MMTS modification of cysteine residues were set as fixed modifications. Protein were identified on the basis of having at least one peptide with an ion score above 95% confidence. All identified CSF proteins were subjected to functional analyses using PubMed search (https://www.ncbi.nlm.nih.gov/pubmed/) and the PANTHER classification system (http://www.pantherdb.org/genes/batchIdSearch.jsp) [13]. Only peptides unique for a given protein was considered for relative quantification. iTRAQ Ratios were normalized using the following formula: iTRAQ Ratio = Ratio/(median iTRAQ Ratio of all found pairs) that was applied in GPS Explorer software.

2.4. Enzyme-linked immunosorbent assay (ELISA)

Experiments were performed using commercially available ovine protein ELISA kits: sheep haptoglobin (HP), sheep neuroendocrine protein 7B2 (MyBioscience, San Diego, CA, USA), according to the manufactory instructions. The target protein concentrations in CSF were determined according to the standard curve with known concentrations of the target proteins.

2.5. Western Immunoblotting

CSF samples (15 μl) were mixed with equal amount of 2x Laemmli sample buffer (Sigma-Aldrich, St. Louis, Missouri, USA). The samples were loaded onto precast 10% SDS–polyacrylamide gel (Bio-Rad Laboratories, Hercules, CA, USA) and were electrophoresed at 60 mV constant voltage until the dye front reached the bottom of the gel. The electrophoresed protein was transferred onto a 0.45 μm thick nitrocellulose membrane, which was saturated for 1 h with 5% (w/v) milk powder in tris-buffered saline (TBS) containing 0.05% Tween 20 (TBS-T). Membranes were then incubated with the primary antibodies rabbit anti-sheep mu chain (1:500)(Sigma-Aldrich, St. Louis, Missouri, USA), anti-sheep IgG (1:500)(Zymed-Thermo Fisher Scientific, Waltham, Massachusetts, USA); or anti-human haemoglobin β/γ/δ (H-76) (1:200)(Santa Cruz Biotechnology, Santa Cruz, CA, USA) overnight at 4 °C. Thereafter the membranes were washed and incubated with horseradish peroxidase-conjugated goat anti-rabbit IgG (1:1000)(Dako-Agilent technologies, Santa Clara, California, USA). After final wash, the immunostained proteins were developed using a Pierce ECL developing kit (Thermo Fisher Scientific, Waltham, Massachusetts, USA), and were detected by a Fluorchem M image system (ProteinSimple, San Jose, California, USA). A CSF sample was used as an internal standard for each Western blotting experiment. The Western bolts images were analysed using Image studio lite version 5.2 software (LI-COR Biosciences, Lincoln, Nebraska, USA). Each band was analysed by manually selecting them to obtain the density measurement. The ratios of the sample density to the internal reference were used and compared among age groups.

2.6. Data Analysis

All values were expressed as mean ± SEM. One way ANOVA with Tukey post-hoc study was used to analyse comparisons among the 3 age groups. SPSS version 19 (SPSS INC., Chicago, USA) was used for the analysis. Values of $P < 0.05$ were considered statistically significant, and values of $P < 0.01$ were considered statistically highly significant.

3. RESULTS

3.1. Identification of proteins in CSF

The total protein concentration in the CSF increased with advancing age, as these sheep showed age-related reduction in CSF secretion / turnover [10]. We therefore applied equal amount volume of CSF in the analysis instead of using equal amount of CSF proteins. Two hundred and thirty one peptides were detected from the pooled CSF samples. All but 5 of the peptides were named. From these peptides, 143 proteins were identified. Of these proteins, 78 were identified with at least two peptides while the reminder was identified with a single peptide (Supplement 1 and 2). These proteins included not only relatively abundant proteins, such as albumin, IgG, transthyretin, transferrin, haptoglobin, complements, and various apolipoproteins, but also lower abundance peptides such as neuropeptide Y (see Supplement 1 and 2). The functional classification of the 143 identified proteins was listed in Table 1.

3.2. Quantitative analysis of CSF proteins in different age groups

iTRAQ not only identifies CSF proteins but also enable us to quantitatively compare the proteins with different labels [14]. Although the protein profile in each iTRAQ experiment may vary when complex protein mixture are analysed, quantitative comparison is valid when the same peptide is detected in samples at the same time. We therefore compared the ratios of an individual age group to the pooled CSF group. Our results demonstrated that there were substantial quantitative differences in many proteins between the three groups. We separated these proteins into 2 main groups: whose levels have increased (Table 2) or decreased (Table 3) greater than 25%. There were 52 proteins with >25% increase in concentrations in the old sheep compared to the young (Table 2). 33 of them increased >25% but <50% [e.g. insulin like growth factor binding proteins (IGFBPs), Complements], 13 increased >50% but <1 fold [e.g. transthyretin (TTR), apolipoprotein C-III), 6 increased >1 fold [i.e. haptoglobin (Hp), haemoglobin (HGB), neuroendocrine protein 7B2, immunoglobin M (IgM), fibrous sheath interacting protein 1, vimentin] (Table 2). There were 18 proteins with >25% decrease in concentrations in the old sheep compared to the young. 17 of them decreased >25% but <50% (e.g. fibrinogen, transferrin), and histone deacetylase 7 (HDAC7) was gradually decreased for over 80% (Table 3). Glutathione S-transferase was decreased in middle aged CSF compared to both young and old CSF.

3.3. Validation of proteins associated with ageing process

To confirm peptide-based protein identifications and variant proteins as suggested by tandem MS, ELISA and Western Immunoblotting were performed on the CSF samples. As the first step towards verifying these ageing biomarkers in Table 2, that displayed more than 1 fold among the 3 age groups, all commercially available antibodies and ELISA kits for the sheep proteins were purchased for further analysis. These were sheep Hp ELISA kit, sheep neuroendocrine protein 7B2 ELISA kit, anti-sheep mu chain and sheep IgG antibodies. In addition, an antibody for human haemoglobin β/γ/δ (H-76) was bought as there were no specific antibodies for sheep haemoglobin. Specific ovine protein ELISA kits indicated there were significant increase of Hp and neuroendocrine protein 7B2 in the old CSF (Fig 1). Western blots of sheep mu chain showed significant increase in IgM in old CSF, in contrast, there were no changes in IgG among age groups (Fig 2). There were no bands on Western immunoblots with the anti-human haemoglobin β/γ/δ antibody on the ovine CSF samples (data not shown).

4. DISCUSSION

In this study, we studied ovine CSF proteome and compared CSF protein levels between different ages. We identified 143 different ovine CSF proteins using MS/MS fragmentation ions for sequencing, and generated the most complete characterization of ovine CSF proteome to date according to our knowledge. The number of proteins detected in ovine CSF was similar with in bovine CSF [15], but was lower compared to human CSF proteome [16], probably because both the ovine and bovine protein database are far less than completed than the human [17]. A large percentage of ovine CSF proteins (21.7%) are binding proteins, including the major CNS apolipoproteins (e.g. A, C, D, E), consistent with CSF “sink action” [1]. We did not find the apolipoprotein B, the major apolipoprotein in the blood that is not present in CSF, indicating the minimal blood contamination in our CSF samples [18,19]. To maximize efficient use of the MS, 7 ovine CSF samples with same age were pooled into a group, similar to our previous studies [12]. This approach will ensure adequate materials to identify low abundant proteins and minimized inter-subject variability, which was kept in minimum as the sheep was carefully controlled over their age, gender, disease states, season *etc*. The variability can be further addressed by performing careful follow-on / validation of aliquot from each individual animal.

Using iTRAQ reporter ion intensities at m/z114, 115, 116, 117, 52 proteins were found to be increased for more than 25% between ages, and 6 of them (neuroendrocrine protein 7B2, IgM, fibrous sheath interacting protein 1, Hp, HGB, vimentin) were gradually increased for more than one fold with age. There were 18 proteins with >25% decrease in concentrations between ages, and the HDAC7 gradually decreased in concentrations for more than 80%. GST decreased in middle aged CSF samples compared to both young and old CSF samples.

While high throughput proteomic analysis of CSF proteins selects candidate proteins for further study, candidate proteins identified by this approach need to be validated before their biological roles are pursued extensively. As the first step towards developing candidate ageing markers, we sought to use commercially available antibodies against the candidate proteins on individual ovine CSF samples. We used as much as possible of commercially available sheep protein diagnosis kits/antibodies, and validated 3 candidate proteins: Hp, neuroendocrine secretory protein 7B2 and IgM.

Hp is an acute-phase protein that scavenges HGB in the event of haemolysis, but also can be induced by inflammation [20, 21]. Human CSF Hp has a role in the protection of the CNS against autoimmune inflammatory responses after aneurysmal subarachnoid haemorrhage [22]. Increased human CSF Hp concentration were found in a number of neurological diseases, e.g. idiopathic normal pressure hydrocephalus, traumatic brain injury, Gullain-Barre syndrome and neuromyelitis optica [23, 24]. Chamoun et al. [25] reported there was an increased likelihood of detecting Hp in human CSF with age and suggested Hp was a marker of BCSFB dysfunction.

Neuroendocrine secretory protein 7B2 resides in the secretory granules of neuroendocrine cells and functions as a specific chaperone for the proprotein convertase 2 [26] as well as an anti-aggregation secretory chaperone associated with neurodegenerative diseases [27]. The normal concentration of 7B2 in human CSF is

10-100 folds greater than in plasma [26, 28], suggesting 7B2 is originated from the brain.

The brain has historically been considered an ‘immune privileged region’, as it is separated from peripheral circulation by BBB and BCSFB. However, the brain also contains microglia, the counterpart to macrophages which actively surveys the brain [29]. A recent study suggests that brain immune surveillance communicates with the immune system and can generate adaptive immune responses [30]. In our study, 13.3% identified CSF proteins were immunoproteins, which are proteins with immunological activities, e.g. immunoglubins and complements. Among them, IgM significant was increased in the old ovine CSF. IgM plays an important role in cytolytic reactions and agglutination [31], and is strongly related with a fatal neurodegenerative disease called prion disease [32]. There was a correlation between CSF IgM and CSF apolipoproteins in patients with neurological diseases [33]. In contrast, IgG levels in the CSF were not different between different age groups. IgM is the largest antibody and moves out of the brain only with CSF clearance, while IgG is the most abundant but the smallest antibody and moves out of the brain via additional efflux system [34]. The increase of IgM in the old CSF could be caused by either the old sheep were subjected to some infections that the young sheep were not, and / or the old sheep had slower CSF turnover rates compared to the young ones - [10].

The HGB expression in vertebrates was previously thought to be restricted to red blood cells, however the expression of HGB was found in both rat and human neurons [35, 36] and HGB was detected in the CSF of normal human controls [37]. HGB was involved in neuronal mitochondrial energetics with epigenetic changes to histones and may provide neuroprotection in multiple sclerosis by supporting neuronal metabolism [38]. Although the sequence homology of haemoglobin β in *ovis aries* vs. human is 83% homology, Western blots with an anti-human haemoglobin β/γ/δ (H-76) antibody showed no reaction with the ovine CSF samples.

To our best knowledge, there are only 2 studies on ageing CSF biomarkers in human. Utilising a shotgun proteomics strategy in conjunction with ICAT (isotope-coded affinity tags), Zhang *et al.* [18] identified 312 different CSF proteins, of which 187 were identified with at least two peptides while the reminder was identified with a single peptide. The authors discovered 6 proteins that were changed more than one fold between the young and old human CSF, i.e. agrin, bromodomain, splice isoform γ-2 of P36873, protein phosphatase, hypothetical protein, serine/threonine protein phosphatase, ubiquinol-cytochrome *c* reductase. An important issue in Zhang's study is that the changes in the relative amount of proteins were measured with pooled CSF samples. The variability between humans is more than between sheep. The study could not define if the age-related difference found were due to difference in some individuals or being distributed over all participants. Although follow up immunoassays can partially address this problem, this approach is limited by availability of sufficiently sensitive antibodies. Another study on age-related changes in human CSF proteome was conducted by Baird et al. [19] using the Slow off-rate modified Aptamer Array technique. Baird et al. identified 82 proteins that were changed over age 28-82, most of which are associated with immune system activation or response to injury. These biomarkers overlap with our discovery in immunoproteins, indicating a role for inflammatory process in CNS ageing. A recent study found in healthy ageing human CSF, there was a three-fold increase of soluble triggering receptor expressed on myeloid cell 2 (TREM 2), which functions in immune response and may be involved in chronic inflammation [39].

Ageing is associated with chronic inflammation. Inflammageing describes the close relationship between low-grade chronic inflammation and ageing in various organs, including the brain [40]. A number of theories have been developed to define the inflammageing, such as redox stress, mitochondrial damage, immunosenescence, endocrinosenescence, epigenetic modification etc [41]. The age-related changes in the brain including the inflammageing may provide a substrate for developing neurodegenerative disease. Indeed, inflammation has long been associated with neurodegenerative diseases [42]. Future studies on neurodegenerative diseases should consider the ageing factor. An important precondition for discovering CSF biomarkers in neurodegenerative diseases is an understanding of the dynamic nature of the CSF proteome during normal ageing process.

A number of Alzheimer's disease (AD) biomarkers, such as amyloid beta, tau, neurofilament light, were detected in ovine CSF. Total tau and neurofilament light levels were comparable with human levels [43]. We also found a few of AD related proteins in the ovine CSF, e.g. Apolipoprotein E, Amyloid beta A4 protein isoform b precursor, amyloid precursor-like protein 1, and they were not significantly different in concentrations among the age groups. Sheep are not known to develop AD naturally, probably due to their shorter lifespan compared to humans and being culled once past their useful lifespan for the farmers [43].

In conclusion, this study has generated detail knowledge of the ovine proteome and presented a number of suitable candidate proteins for further study in terms of their physiological variation in CSF during ageing. It would be important to validate the results of this study in CSF from humans in future and to conduct further experiments to understand their roles in healthy ageing and neurodegerative diseases. Changes in the CSF proteins during ageing without disease may be small and heterogeneous between individuals. Thus a combination of a number of studies on CSF ageing biomarkers would provide a full picture of ageing related changes in CSF proteome. A common ageing CSF biomarker identified to date is immunoproteins indicating a role of the immune response and inflammation in normal ageing process in the brain. MS analysis usually serves to identify candidates, functional and follow up studies will be needed for understanding the physiology of brain ageing as well as for recognizing neurodegenerative disease-associated changes in CSF proteome patterns.

COMPETING FINANCIAL INTERESTS

There is no conflict of interest.

AUTHOR CONTRIBUTIONS

This project was conceived by R.C. and J.E.P. The *in vivo* experiments in this paper were performed by C.P.C. and R.C., while the quantitative mass spectrometry experiment was conducted by H.R.F. Data were analysed and interpreted by R.C., H.R.F., and S.Z. The manuscript was prepared by R.C., S.Z., H.R.F., C.P.C, and D.G.A.M. All authors have read and approved the final copy.

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Table 1. Functional classification of ovine CSF proteins

Protein function group	**Protein number**	**Percentage (%**
Binding proteins	31	21.7
Peptide hormones	14	9.8
Enzymes for metabolism/signalling	36	25.2
Structural molecules	23	16.1
Immunoproteins	19	13.3
Coagulation proteins	9	6.3
Unknown	11	7.7
Total	143	100

Table 2: A list of proteins showing more than 25% age-related increase in ovine CSF

Protein name	Accession number	Peptide count	Average iTRAQ ratio young/IS	Average iTRAQ ratio middle-age/IS	Average iTRAQ ratio old/IS	% increase
Haptoglobin	gi|258499	3	0.57 [3]	0.51 [3]	1.56 [3]	Age-related increase >1 fold
	gi|998960	1	0.43 [1]	0.39 [1]	1.44 [1]	
Haemoglobin	gi|122686 beta subunit	3	0.49 [3]	1.06 [3]	1.90 [3]	
	gi|1787 alpha subunit	1	0.95 [1]	1.56 [1]	1.88 [1]	
Vimentin	gi|21757045	2	0.47 [2]	0.44 [2]	1.06 [2]	
IgM (Ig mu chain)	gi|165945	2	0.56 [2]	0.61 [2]	1.21 [2]	
Neuroendrocrine protein 7B2 isoform 1	gi|221139785	1	1.17 [1]	1.83 [1]	2.50 [1]	
Fibrous sheath interacting protein 1	gil28175039	1	0.23 [1]	0.34 [1]	0.78 [1]	
Transthyretin	gil57526651	7	0.63 [11]	0.73 [11]	1.09 [11]	Age-related increase >50% but <1 fold
Serpin A3-1	gil31340900	4	0.73 [5]	0.63 [5]	1.28 [5]	
Apolipoprotein C-III	gil47564119	3	0.74 [3]	1.09 [3]	1.22 [3]	
Inter-alpha-trypsin inhibitor	gil59857769	2	0.95 [2]	1.16 [2]	1.57 [2]	
	gil48374067	2	0.82 [2]	1.12 [2]	1.68 [2]	
Actin	gil929752	1	0.78 [1]	0.82 [1]	1.55 [1]	
Calcium uniporter channel	gil833995	1	1.28 [1]	0.88 [1]	2.36 [1]	
Thyroxine-binding globulin	gil155369640	1	0.66 [1]	0.62 [1]	1.07 [1]	
Beta-actin-like protein 2-like	gil57043600	1	0.78 [1]	0.82 [1]	1.55 [1]	
Retinoic acid receptor responder protein 2	gil346716116	1	0.58 [1]	0.97 [1]	0.91 [1]	
Neuropeptide Y	gil30923117	1	0.78 [1]	1.4 [1]	1.54 [1]	
Pyruvate kinase isozymes m1/m2 isoform	gil33286418	1	1.05 [1]	0.59 [1]	1.61 [1]	
Serum paroxonase/arylesterase 1	gil126722853	1	0.99 [1]	0.91 [1]	2.18 [1]	
Complement C1r-B	gil164518925	1	0.91 [1]	0.91 [1]	1.44 [1]	
Ceruloplasmin	gil57617174	14	0.85 [17]	0.84 [17]	1.15 [17]	Age-related increase >25% but <50%
Clusterin	gil27806907	7	0.81 [9]	0.93 [9]	1.10 [9]	
IGF-2	gil57164331	2	0.83 [2]	1.43 [2]	1.20 [2]	
IGFBP-2	gil57164237	7	0.90 [7]	1.14 [7]	1.25 [7]	
IGFBP-4	gil27807009	1	0.59 [1]	0.82 [1]	0.76 [1]	
IGFBP-5	gil263306	1	1.69 [1]	1.32 [1]	2.19 [1]	
IGFBP-6	gil56849568	1	0.39 [1]	0.72 [1]	0.82 [1]	
	gil5705897	1	0.79 [1]	1.13 [1]	0.96 [1]	
IGFBP-7	gil4504619	3	0.75 [3]	0.61 [3]	1.01 [3]	
Beta 2-microglubin	gil57164311	4	0.91 [4]	0.99 [4]	1.17 [4]	

Primary amine oxidase	gil30794300	3	0.75 [3]	0.91 [3]	1.06 [3]	
Complement C4	gil1227	7	0.84 [7]	0.96 [7]	1.06 [7]	
	gil1235	5	0.76 [5]	0.91 [5]	1.06 [5]	
	gil50567362	4	0.87 [4]	1.08 [4]	1.14 [4]	
	gil1314244	1	0.96 [1]	1.52 [1]	1.64 [1]	
Complement C3	gil4093220	1	0.76 [1]	0.96 [1]	1.03 [1]	
Complement C6	gil47115536	1	0.76 [1]	1.20 [1]	0.98 [1]	
Complement C8	gil841248	1	0.61 [1]	0.73 [1]	0.78 [1]	
Chromogranin B	gil12644006	2	1.00 [2]	1.28 [2]	1.32 [2]	
Alpha-macroglubin	gil290543549	2	0.78 [2]	0.92 [2]	1.17 [2]	
Beta-2 glycoprotein 1	gil54792721	2	0.79 [3]	1.01 [3]	1.06 [3]	
	gil57528174	2	0.65 [2]	0.81 [2]	1.14 [2]	
Plasminogen	gil833995	2	0.89 [2]	0.87 [2]	1.12 [2]	
	gil51702791	1	0.83 [1]	0.99 [1]	1.12 [1]	
Proactivator polypeptide	gil27806447	2	0.60 [2]	0.76 [2]	0.83 [2]	
Apolipoprotein D	gil348582766	1	0.71 [1]	0.99 [1]	0.90 [1]	
Brain-type ribonuclease	gil2381819	1	0.82 [1]	1.37 [1]	1.22 [1]	
Extracellular superoxide dismutase	gil130508829	1	0.54 [1]	0.85 [1]	0.72 [1]	
Phosphatidylcholine sterol acyltransferase	gil21542351	1	1.10 [1]	0.90 [1]	1.62 [1]	
Eukephalin	gil223387	1	0.86 [1]	1.07 [1]	1.10 [1]	
Neuroserpin	gil18158628	1	0.43 [1]	0.66 [1]	0.58 [1]	
Alpha-2 antiplasmin	gil27807209	1	0.58 [1]	0.72 [1]	0.82 [1]	
Niemann-pick C2 protein	gil28373999	1	0.74 [1]	0.71 [1]	0.94 [1]	
Rheumatoid factor Fab	gil3659940	1	1.07 [1]	1.42 [1]	1.60 [1]	
Neuroblastoma suppressor	gil13928832	1	1.04 [1]	1.07 [1]	1.35 [1]	
Malate dehydrogenase	gil5174539	1	0.75 [1]	0.72 [1]	0.99 [1]	
Alpha-1 antiproteinase	gil461443	1	0.28 [1]	0.28 [1]	0.40 [1]	
Kininogen-1	gil57109938	1	0.74 [1]	0.97 [1]	1.11 [1]	
Fibromodalin	gil453157	1	0.78 [1]	0.84 [1]	0.91 [1]	

Column headings refer to the following: accession number is the reference for each protein in the NCBInr database; peptide count refers to the number of unique peptides with MS/MS ion scores used for protein identification; the average iTRAQ ratios are shown after data normalisation followed by the number of peptides used for quantification in square brackets. IS = internal standard.

Table 3: A list of proteins showing more than 25% age-related decrease in ovine CSF

Protein name	**Accession number**	**Peptide count**	**Average iTRAQ ratio young/IS**	**Average iTRAQ ratio middle-age/IS**	**Average iTRAQ ratio old/IS**	**% decrease**
Histon deacetylase 7	gi|30913010	1	3.85 [1]	1.39 [1]	0.76 [1]	Age-related decrease >80%
Fibrinogen	gil1346006	3	1.25 [3]	1.40 [3]	0.74 [3]	Age-related decrease >25% but <50%
	gil3789962	3	1.03 [3]	1.15 [3]	0.87 [3]	
	gil6980816	2	1.23 [2]	1.42 [2]	0.92 [2]	
Neurosecretory protein VGF	gil17136078	2	1.39 [2]	1.04 [2]	0.99 [2]	
Beta-1,3-N-actyl glucosamingl transferase 6	gil61553937	2	1.64 [2]	1.38 [2]	1.17 [2]	
Tetranectin	gil37409	2	1.23 [2]	1.37 [2]	0.83 [2]	
Transferrin	gil2318026	2	1.40 [2]	1.09 [2]	0.98 [2]	
Calreticulin	gil545920	2	0.95 [2]	1.11 [2]	0.64 [2]	
	gil237420	1	0.91 [1]	0.99 [1]	0.55 [1]	
Contactin-2	gil4827022	2	1.25 [2]	0.73 [2]	0.77 [2]	
V-set and transmembrane domain protein 2A	gil20306326	1	1.12 [2]	0.81 [2]	0.59 [2]	
Cadherin-15	gil4826669	1	1.39 [1]	0.89 [1]	0.72 [1]	
Chain A, Divalent cation tolerant protein cuta	gil56554578	1	1.37 [1]	1.04 [1]	1.00 [1]	
Cell adhesion molecule 4	gil21686977	1	1.11 [1]	0.50 [1]	0.77 [1]	
Adipsin / complement factor D	gil773265	1	1.50 [1]	1.27 [1]	1.09 [1]	
Nidogen-2	gil2791962	1	1.35 [1]	1.22 [1]	0.70 [1]	
Protein C	gil163487	1	0.93 [1]	0.68 [1]	0.69 [1]	
Neurocan core protein	gil77681353	1	1.11 [1]	0.71 [1]	0.61 [1]	
Protein kinase C-binding protein NELL-2	gil2494290	1	1.81 [1]	1.40 [1]	1.00 [1]	
Nuclear factor of activated T cells cytoplasmic isoform 2	gil27886541	1	0.96 [1]	1.56 [1]	0.38 [1]	

Column headings refer to the following: accession number is the reference for each protein in the NCBInr database; peptide count refers to the number of unique peptides with MS/MS ion scores used for protein identification; the average iTRAQ ratios are shown after data normalisation followed by the number of peptides used for quantification in square brackets. IS = internal standard.

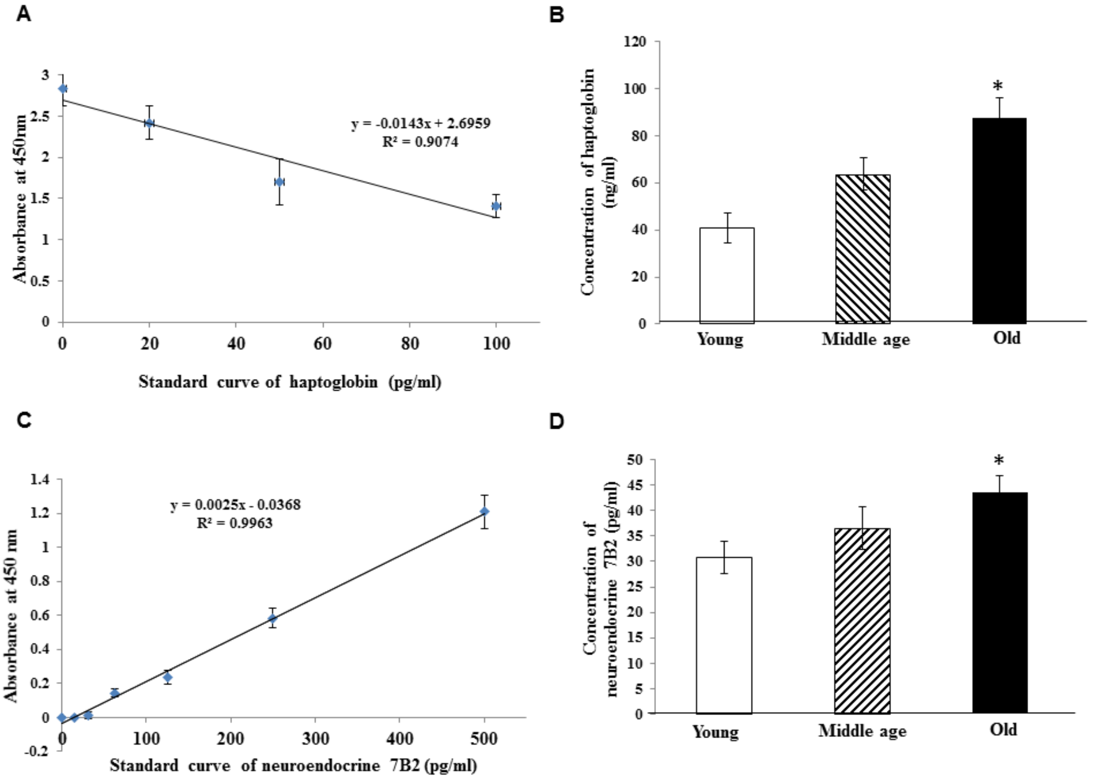

Figure 1. Concentration of haptoglobin (HP) and neuroendocrine protein 7B2 in CSF of young, middle age, and old groups by ELISA assay. A, C are standard curves of Hp (A) and neuroendocrine 7B2 (C); B and D summarized the concentrations of Hp (B) and neuroendocrine 7B2 (D) in CSF from different age groups, n = 7. *compared to young group, P<0.01.

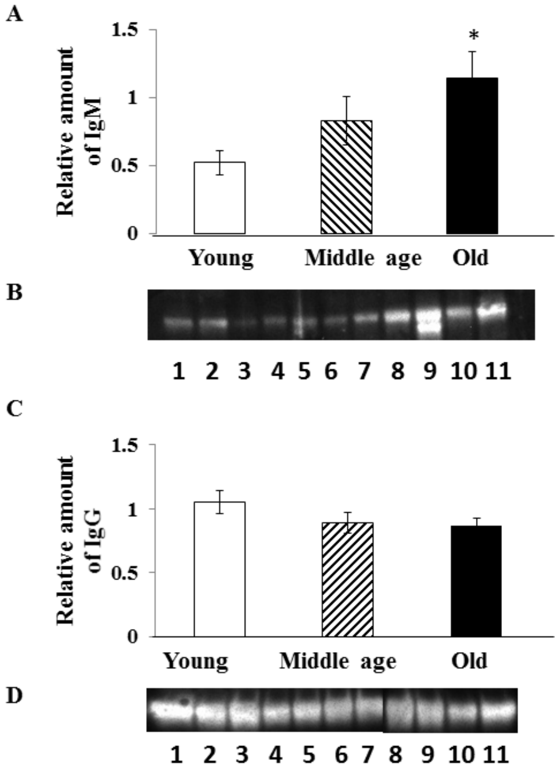

Figure 2. Relative amount of IgM (A) and IgG (C) in CSF between different ages, which was based on their band density of *Western* immunoblotting image of IgM (B) and IgG (D) respectively. In image B or D, lanes 1-4: young CSF; lanes 5-7: middle aged CSF; lanes 8-10: old CSF; lane 11: molecular size marker. *compared to young group, $P<0.01$

Supplement 1. Total peptides (231) were identified from the ovine CSF samples

	Protein		Peptide count	Total ion score	Average iTRAQ ratio			iTRAQ Standard Deviation			iTRAQ Peptides		
Protein common name	**MW**	**PI**			**114/117**	**115/117**	**116/117**	**114/117**	**115/117**	**116/117**	**114/117**	**115/117**	**116/117**
Serum albumin precursor	79687	6	43	2879	1	2	1.1	0.6	0.7	0.3	147	147	147
Serotransferrin; Transferrin; Beta-1 metal-binding globulin;	88817	7	20	1321	1	1	1.1	0.5	0.6	0.4	36	36	36
Serum albumin;	79648	6	18	1217	1	2	1.1	0.7	0.7	0.4	70	70	70
Angiotensinogen;	54004	7	15	1182	1	1	1.1	0.6	0.6	0.3	19	19	19
Apolipoprotein A-I, apoA-1	31729	6	15	1043	1	1	1.2	0.5	0.4	0.3	27	27	27
Ceruloplasmin precursor	129919	6	14	1038	1	1	1.4	0.4	1.0	0.5	17	17	17
Complement C3	205367	6	15	969	1	1	1.1	0.4	0.4	0.2	23	23	23
Alpha-1-antiproteinase precursor	50699	6	13	804	1	1	1.3	0.6	0.5	0.4	19	19	19
Apolipoprotein E;	38112	6	10	687	1	1	1.3	0.4	0.3	0.2	16	16	16
Complement component	43395	6	10	576	1	1	1.2	0.6	0.4	0.3	10	10	10
Preprocomplement component C3	205042	6	9	570	1	1	1.1	0.3	0.3	0.2	16	16	16
Transferrin	86771	7	7	549	1	1	1.0	0.4	0.4	0.3	16	16	16
Alpha-2-HS-glycoprotein precursor	41651	5	6	534	1	1	1.0	0.4	0.6	0.3	8	8	8
Immunoglobulin lambda light chain constant region segment 1	13045	8	5	525	1	1	1.3	0.5	0.6	0.3	15	15	15
Keratin 1	70200	8	8	504	3	5	1.8	1.1	1.6	0.6	10	10	10
Alpha-1-antiproteinase precursor	51106	6	9	502	1	1	1.3	0.6	0.6	0.4	13	13	13
Ig lambda chain C region - sheep (fragment)	13172	8	4	495	1	1	1.3	0.5	0.5	0.2	15	15	15
Complement C3 preproprotein	204039	6	8	483	1	1	1.1	0.3	0.4	0.2	14	14	14
Contactin-1 precursor	122263	6	6	481	2	2	1.4	1.0	1.2	0.5	7	7	7
Transthyretin precursor	17582	6	7	464	1	1	1.3	0.4	0.7	0.4	11	11	11
Complement component C4	15520	5	7	463	1	1	1.3	0.4	0.5	0.3	7	7	7
Complement C4	108118	6	9	458	1	2	1.3	0.5	0.5	0.4	9	9	9
Clusterin preproprotein	55864	6	7	455	1	1	1.3	0.4	0.4	0.2	9	9	9
Albumin	79319	6	7	442	1	2	1.1	1.3	1.8	0.7	21	21	21
Fibronectin	95323	9	6	421	2	1	1.2	0.9	1.1	0.4	7	7	7
Keratin, type I cytoskeletal 9	66102	5	4	411	2	4	1.7	1.6	3.5	0.8	4	4	4

Immunoglobulin gamma-1 chain	55492	6	6	399	1	1	1.1	0.5	0.4	0.2	14	14	14
Antithrombin-III precursor	57635	6	7	397	1	2	1.2	0.3	0.2	0.2	7	7	7
Insulin-like growth factor-binding protein 2 precursor	37202	7	7	394	1	2	1.5	0.4	0.7	0.3	7	7	7
Pigment epithelium-derived factor precursor	50039	7	5	388	2	2	1.6	1.1	1.7	0.3	5	5	5
Gelsolin Actin-depolymerizing factor;	91483	6	6	371	1	2	1.2	0.4	0.5	0.3	6	6	6
Prostaglandin-H2 D-isomerase	22795	6	4	343	1	2	1.2	0.5	0.5	0.3	8	8	8
Beta-2-microglobulin precursor	14845	6	4	340	1	1	1.4	0.4	0.6	0.2	4	4	4
Plasminogen	41059	8	4	322	1	2	1.4	0.3	0.5	0.2	4	4	4
Ectonucleotide pyrophosphatase/phosphodiesterase family member 2	111363	7	7	316	1	2	1.4	0.6	0.8	0.4	7	7	7
Complement component C4	15731	6	5	287	1	1	1.3	0.4	0.4	0.3	5	5	5
Chain A, crystal structure of the first active autolysate form of the porcine alpha trypsin	14234	8	3	286	1	1	1.1	0.4	0.4	0.1	5	5	5
Chain E, leech-derived tryptase inhibitortrypsin complex	25594	8	3	286	1	1	1.1	0.4	0.4	0.1	5	5	5
Serpin A3-1 precursor	49726	6	4	278	1	1	1.5	0.4	0.5	0.4	5	5	5
Amyloid beta A4 protein isoform b precursor	91357	5	4	276	1	1	1.1	0.4	0.4	0.3	5	5	5
72 kda type IV collagenase precursor	81088	5	5	275	1	1	1.2	0.8	0.3	0.3	5	5	5
Phospholipid transfer protein	59170	6	3	256	1	2	1.1	0.5	0.7	0.3	4	4	4
Insulin-like growth factor-binding protein 7	32245	8	3	253	1	1	1.2	0.9	0.4	0.4	3	3	3
Keratin, type II cytoskeletal 2 epidermal	70811	8	3	243	2	2	1.2	0.1	0.3	0.2	3	3	3
Brevican core protein	103281	5	3	241	2	2	1.5	0.3	0.4	0.3	3	3	3
Fibrinogen beta chain; Fibrinopeptide B	59432	8	3	239	1	2	0.9	0.2	0.0	0.1	3	3	3
Apolipoprotein A-I	33204	5	3	232	1	1	1.1	0.3	0.4	0.3	5	5	5
Chain A, crystal structure of bovine holo-rbp at ph 4.0	22019	5	4	230	1	2	1.3	0.3	0.4	0.1	6	6	6
Complement component 4, gene 2	205543	7	4	228	1	2	1.4	0.3	0.5	0.4	4	4	4

Hypothetical protein	263095	6	3	227	1	1	1.0	0.4	0.3	0.2	3	3	3
Keratin 10	62434	5	3	221	2	2	1.2	0.8	0.6	0.3	3	3	3
Hemoglobin subunit beta; Beta-globin	17983	7	3	219	1	2	2.3	0.1	0.2	0.2	3	3	3
Inter-alpha-trypsin inhibitor heavy chain H2 precursor	114147	7	4	217	1	2	1.2	0.6	0.6	0.3	4	4	4
Neurosecretory protein VGF precursor	69569	5	2	203	2	2	1.2	0.3	0.5	0.3	2	2	2
Fibronectin	69908	8	2	199	2	1	1.3	0.2	0.5	0.0	2	2	2
Prothrombin	76294	6	4	196	1	1	1.2	0.1	0.3	0.7	4	4	4
Pigment epithelium-derived factor	50486	6	3	196	2	2	1.6	0.3	0.4	0.2	3	3	3
Factor xiia inhibitor precursor	55333	6	3	193	1	2	1.5	0.3	0.2	0.3	3	3	3
Apolipoprotein C-III precursor	11982	5	3	186	1	2	1.4	0.0	0.1	0.1	3	3	3
Primary amine oxidase, lung isozyme	87835	6	3	184	1	1	1.3	0.1	0.1	0.2	3	3	3
Sex hormone-binding globulin	41550	5	2	172	2	2	1.4	0.4	0.9	0.1	2	2	2
Apolipoprotein A-IV precursor	48023	6	3	171	1	1	1.1	0.5	0.4	0.1	4	4	4
Complement C3 alpha chain	90597	5	2	168	1	2	1.2	0.5	0.1	0.2	3	3	3
Beta-1,3-N-acetylglucosaminyltransferase bgnt-6	45814	6	2	164	2	2	1.4	0.4	0.4	0.1	2	2	2
Serum albumin	78092	6	4	162	1	2	1.1	0.4	0.7	0.2	6	6	6
DKFZP459P137 protein	58526	5	3	162	1	1	1.4	0.2	0.3	0.3	3	3	3
Collagen alpha-1(XII) chain long isoform precursor	356530	5	2	159	1	1	1.1	0.0	0.1	0.2	2	2	2
Pigment epithelium-derived factor	49797	6	2	157	2	2	1.5	0.1	0.3	0.2	2	2	2
Transcription factor AEBP1	85223	5	3	155	1	1	1.4	0.1	0.6	0.3	3	3	3
Fibrinogen A-alpha chain	46124	6	3	155	1	2	1.0	0.2	0.1	0.2	3	3	3
Haptoglobin heavy chain, hph chain	30384	6	3	153	1	1	1.9	0.2	0.2	0.3	3	3	3
Chromogranin B	79125	5	2	151	1	2	1.6	0.1	0.1	0.0	2	2	2
Metalloproteinase inhibitor 2	25216	7	2	149	1	1	1.1	0.2	0.1	0.1	2	2	2
Chitinase-3-like protein 1	46169	9	3	148	1	1	1.5	0.2	0.3	0.3	3	3	3
Tetranectin	25324	6	2	145	1	2	1.0	0.2	0.1	0.6	2	2	2
Vitamin D-binding protein	28956	5	3	140	1	1	1.2	0.4	0.3	0.4	4	4	4
Transferrin	7637	8	2	137	2	2	1.2	0.3	0.1	0.0	2	2	2

Limbic system-associated membrane protein precursor	40309	6	2	136	1	1	1.0	0.1	0.2	0.1	2	2	2
Fibrinogen alpha chain	1991	4	1	136	1	1	1.7	0.0	0.0	0.0	1	1	1
Insulin-like growth factor II preproprotein	20980	9	2	134	1	2	1.4	0.1	0.0	0.0	2	2	2
Complement component C7 precursor	103502	7	2	130	1	1	1.0	0.2	0.0	0.1	2	2	2
Unnamed protein product	55266	5	2	130	1	2	1.1	0.1	0.3	0.0	2	2	2
Dickkopf-related protein 3 precursor	40484	5	2	129	1	1	0.9	0.5	0.2	0.2	3	3	3
Beta-2-glycoprotein 1 precursor	43614	9	2	129	1	1	1.3	0.4	0.7	0.1	3	3	3
WAP, kazal, immunoglobulin, kunitz and NTR domain-containing protein 2 precursor	68543	6	2	128	1	1	1.1	0.2	0.1	0.0	2	2	2
Inter-alpha (globulin) inhibitor H4	108789	6	2	125	1	2	1.9	0.0	0.1	0.2	2	2	2
Calcium uniporter channel component [cattle, heart, Peptide Mitochondrial Partial, 18 aa, segment 3	2470	5	1	123	2	1	2.8	0.0	0.0	0.0	1	1	1
Plasminogen precursor	101001	8	2	121	1	1	1.3	0.1	0.2	0.1	2	2	2
Calreticulin	52543	4	2	119	1	2	0.8	0.1	0.2	0.1	2	2	2
Amyloid precursor-like protein 1	74871	6	2	117	1	1	0.9	0.4	0.7	0.2	2	2	2
Unnamed protein product	55767	5	2	116	1	1	1.3	0.1	0.1	0.1	2	2	2
Immunoglobulin kappa light chain constant region	13396	6	2	114	2	2	1.1	0.4	0.1	0.1	3	3	3
Insulin-like growth factor-binding protein 7	32027	8	2	113	1	1	1.4	0.1	0.0	0.3	2	2	2
Beta-2-glycoprotein 1	43957	9	2	109	1	1	1.3	0.2	0.4	0.2	2	2	2
Superoxide dismutase [Cu-Zn]	17556	6	2	106	1	1	1.1	0.1	0.1	0.1	2	2	2
Immunoglobulin lambda-6c light chain variable region	12870	5	1	106	2	1	1.5	0.0	0.0	0.0	1	1	1
Alpha-macroglobulin	178259	6	2	104	1	1	1.4	0.4	0.4	0.2	2	2	2
Igg1 heavy chain constant region	39259	6	2	101	1	1	1.2	0.8	0.7	0.3	7	7	7
Myocilin; Trabecular meshwork-induced glucocorticoid response protein;	58155	5	2	99	2	2	1.2	0.3	0.4	0.5	2	2	2
Immunoglobulin mu chain	57811	5	2	99	1	1	1.4	0.0	0.1	0.0	2	2	2

Chain c, the crystal structure of modified bovine fibrinogen	51472	5	2	98	1	2	1.1	0.1	0.1	0.0	2	2	2
Proactivator polypeptide	64672	5	2	97	1	1	1.0	0.1	0.4	0.1	2	2	2
Apolipoprotein D, apod	31277	5	1	95	2	2	1.4	0.0	0.0	0.0	1	1	1
Insulin-like growth factor-binding protein 6	14741	11	1	93	1	2	1.1	0.0	0.0	0.0	1	1	1
Hepatocarcinogenesis-specific protein/hemopexin homolog	33129	9	2	93	2	2	1.6	0.4	0.4	0.3	3	3	3
Inter-alpha-trypsin inhibitor heavy chain H4	108849	6	2	90	1	2	2.0	0.1	0.2	0.0	2	2	2
Phospholipid transfer protein	57667	7	2	89	1	1	1.0	0.2	0.4	0.2	2	2	2
Inhibitor of carbonic anhydrase precursor	85724	6	2	89	1	1	1.1	0.0	0.2	0.3	2	2	2
Unnamed protein product	12782	5	2	89	1	1	1.4	0.0	0.2	0.3	2	2	2
Collagen type I alpha 1	10249	5	1	87	2	3	1.3	0.0	0.0	0.0	1	1	1
Contactin-2 precursor	119638	8	2	87	2	1	0.9	0.1	0.1	0.0	2	2	2
Fibulin-1	70865	5	2	85	1	2	1.2	0.7	0.3	0.4	2	2	2
Cadherin-15 preproprotein	91489	5	1	84	2	1	0.9	0.0	0.0	0.0	1	1	1
Vitamin K-dependent protein S precursor	83178	5	2	83	1	1	0.7	0.4	0.2	0.1	2	2	2
Apolipoprotein D-like	23365	5	1	83	1	1	1.1	0.0	0.0	0.0	1	1	1
Unnamed protein product	75687	6	2	81	2	2	1.3	0.5	0.2	0.2	2	2	2
Glutaminyl cyclase	28410	7	1	80	3	2	2.4	0.0	0.0	0.0	1	1	1
Chain a, divalent cation tolerant protein cuta	16967	6	1	79	2	2	1.2	0.0	0.0	0.0	1	1	1
Vitronectin precursor	57941	6	1	79	1	1	1.4	0.0	0.0	0.0	1	1	1
V-type proton atpase subunit S1 precursor	53615	5	1	77	1	1	0.9	0.0	0.0	0.0	1	1	1
Calreticulin	52957	4	1	76	1	1	0.6	0.0	0.0	0.0	1	1	1
Brain-type ribonuclease	20326	10	1	75	1	2	1.4	0.0	0.0	0.0	1	1	1
Similar to pro alpha 1(I) collagen	14422	9	1	73	1	1	1.3	0.0	0.0	0.0	1	1	1
Alpha 1 (I) chain propeptide	105492	6	1	73	1	1	1.3	0.0	0.0	0.0	1	1	1
Type I collagen alpha 1 chain	37821	5	1	73	1	1	1.3	0.0	0.0	0.0	1	1	1
C-type natriuretic peptide precursor	15391	10	1	71	1	1	1.1	0.0	0.0	0.0	1	1	1
Immunoglobulin lambda light chain	26551	6	1	69	1	1	1.4	0.0	0.0	0.0	1	1	1

Extracellular superoxide dismutase [Cu-Zn] precursor	26858	7	1	68	1	1	0.9	0.0	0.0	0.0	1	1	1
Thyroxine-binding globulin precursor	50564	6	1	67	1	1	1.3	0.0	0.0	0.0	1	1	1
Insulin-like growth factor-binding protein 5	13885	6	1	66	2	2	2.6	0.0	0.0	0.0	1	1	1
CCP modules 3-12, with parts of CCP 2 and 13	84142	6	1	66	2	2	1.5	0.0	0.0	0.0	1	1	1
Ig gamma heavy chain constant region - rabbit (fragment)	22719	8	1	66	0	1	1.1	0.0	0.0	0.2	2	2	2
Phosphatidylcholine-sterol acyltransferase; Lecithin-cholesterol acyltr	22082	5	1	66	1	1	1.9	0.0	0.0	0.0	1	1	1
Plasminogen	15564	6	1	65	1	1	1.3	0.0	0.0	0.0	1	1	1
Neuronal pentraxin-1 precursor	51248	6	1	64	1	2	1.0	0.0	0.0	0.0	1	1	1
SPARC precursor	38326	5	1	64	1	1	1.1	0.0	0.0	0.0	1	1	1
Type I collagen alpha 1 precursor	23336	4	1	63	2	2	1.4	0.0	0.0	0.0	1	1	1
Enkephalin precursor	30836	5	1	62	1	2	1.3	0.0	0.0	0.0	1	1	1
Hypothetical protein LOC478604 isoform 1	24946	5	1	62	2	3	2.2	0.0	0.0	0.0	1	1	1
Cd14	17800	8	1	61	1	1	0.9	0.0	0.0	0.0	1	1	1
Chain c, crystal structure of mouse neuroserpin	32371	5	1	60	1	1	0.7	0.0	0.0	0.0	1	1	1
Calsyntenin-1 isoform 1	117941	5	1	60	2	2	1.2	0.0	0.0	0.0	1	1	1
Fibrinogen A-alpha-chain	49533	6	1	60	1	1	1.2	0.0	0.0	0.0	1	1	1
Dystroglycan	104713	9	1	59	1	1	1.0	0.0	0.2	0.5	2	2	2
Unnamed protein product	10796	5	1	59	1	1	1.8	0.0	0.0	0.0	1	1	1
Beta-actin-like protein 2-like	44904	5	1	59	1	1	1.8	0.0	0.0	0.0	1	1	1
Truncated tenascin XB	31411	5	1	59	2	3	1.2	0.0	0.0	0.0	1	1	1
V-set and transmembrane domain containing 2A	29430	8	1	57	1	1	0.7	0.7	0.2	0.3	2	2	2
Golph2	48655	5	1	57	2	1	1.3	0.0	0.0	0.0	1	1	1
Immunoglobulin V lambda chain	12429	6	1	57	3	1	0.9	0.0	0.0	0.0	1	1	1
Immunoglobulin lambda light chain VLJ region	30883	8	1	56	1	2	1.0	0.1	0.2	0.3	4	4	4
Immunoglobulin light chain variable region	13688	6	1	55	1	2	1.0	0.1	0.2	0.3	4	4	4

EGF containing fibulin-like extracellular matrix protein 1	58743	5	1	55	2	2	1.5	0.0	0.0	0.0	1	1	1
Prosaas	27747	6	1	55	2	2	1.9	0.0	0.0	0.0	1	1	1
Alpha-2-antiplasmin precursor	58364	5	1	55	1	1	1.0	0.0	0.0	0.0	1	1	1
Inter-alpha-trypsin inhibitor;	15382	6	1	55	1	1	1.2	0.0	0.0	0.0	1	1	1
Haptoglobin beta chain {N-terminal}	2452	9	1	54	1	1	1.7	0.0	0.0	0.0	1	1	1
Semaphorin-7A isoform 1 preproprotein	79541	8	1	54	1	1	1.1	0.0	0.0	0.0	1	1	1
Insulin-like growth factor binding protein-6	10490	10	1	53	0	1	1.0	0.0	0.0	0.0	1	1	1
Cadherin-2; Neural cadherin;	105324	5	1	53	1	2	1.3	0.0	0.0	0.0	1	1	1
Complement C2; C3/C5 convertase	89708	7	1	52	1	1	1.0	0.0	0.0	0.0	1	1	1
Retinoic acid receptor responder protein 2	21276	9	1	52	1	1	1.1	0.0	0.0	0.0	1	1	1
Chain a, crystal structure analysis of the bovine npc2 (niemann-pick c2) protein	16756	8	1	51	1	1	1.1	0.0	0.0	0.0	1	1	1
Chain A, Crystal Structure Of A Human Igm Rheumatoid Factor Fab In Complex With Its Autoantigen igg	26076	7	1	51	1	2	1.9	0.0	0.0	0.0	1	1	1
Insulin-like growth factor-binding protein 4 precursor	30999	7	1	51	1	1	0.9	0.0	0.0	0.0	1	1	1
Fibrinogen, gamma A chain	39301	6	1	50	1	2	1.2	0.0	0.0	0.0	1	1	1
Protein disulfide isomerase	64027	6	1	50	1	1	1.0	0.0	0.0	0.0	1	1	1
Glutathione S-transferase P	25625	7	1	50	1	1	1.4	0.0	0.0	0.0	1	1	1
Cell adhesion molecule 4 precursor	44712	6	1	49	1	1	0.9	0.0	0.0	0.0	1	1	1
Complement component 3	8803	5	1	49	1	1	1.2	0.0	0.0	0.0	1	1	1
Adipsin/complement factor D	22043	6	1	49	2	2	1.3	0.0	0.0	0.0	1	1	1
Pro-neuropeptide Y	9115	5	1	49	1	2	1.8	0.0	0.0	0.0	1	1	1
Pyruvate kinase isozymes M1/M2 isoform a	63836	8	1	48	1	1	1.9	0.0	0.0	0.0	1	1	1
Immunoglobulin V lambda chain 5.1.11	11278	6	1	48	2	1	1.5	0.0	0.0	0.0	1	1	1
Immunoglobulin V lambda chain 5.1.5	11332	5	1	48	2	1	1.5	0.0	0.0	0.0	1	1	1

Igg3 heavy chain constant region	42669	8	1	47	1	1	1.2	0.0	0.0	0.0	1	1	1
Nidogen-2	158020	5	1	47	2	2	0.8	0.0	0.0	0.0	1	1	1
Ig mu heavy chain V region precursor - sheep (fragment)	15956	9	1	47	1	1	1.1	0.0	0.0	0.0	1	1	1
Thrombospondin-2 precursor	138958	5	1	47	1	2	1.0	0.0	0.0	0.0	1	1	1
Neuroendocrine protein 7B2 isoform 1	25536	6	1	47	1	3	3.0	0.0	0.0	0.0	1	1	1
SPARC-like protein 1 precursor	77718	5	1	47	1	2	1.8	0.0	0.0	0.0	1	1	1
C4b-binding protein alpha chain precursor	76307	6	1	46	1	1	1.2	0.0	0.0	0.0	1	1	1
Protein C prepropeptide	55951	6	1	46	1	1	0.8	0.0	0.0	0.0	1	1	1
Alpha globin chain	16968	9	1	46	1	2	2.2	0.0	0.0	0.0	1	1	1
Galectin 1	16381	5	1	45	2	2	1.6	0.0	0.0	0.0	1	1	1
Neuroblastoma suppressor of tumorigenicity 1 precursor	20837	5	1	45	1	2	1.6	0.0	0.0	0.0	1	1	1
Plasma glutamate carboxypeptidase precursor	55474	6	1	45	2	2	1.2	0.0	0.0	0.0	1	1	1
Aspartate aminotransferase, cytoplasmic	49640	7	1	44	2	1	1.4	0.0	0.0	0.0	1	1	1
Repulsive guidance molecule A isoform 3	53091	7	1	44	1	1	1.0	0.0	0.0	0.0	1	1	1
14-3-3 protein gamma; Protein kinase C inhibitor protein 1	30967	5	1	44	1	2	1.3	0.0	0.0	0.0	1	1	1
CD166 antigen; Activated leukocyte cell adhesion molecule; altname: Ful	64831	6	1	44	1	1	1.1	0.0	0.0	0.0	1	1	1
Serum paraoxonase/arylesterase 1	43725	6	1	43	1	1	2.6	0.0	0.0	0.0	1	1	1
Cathepsin L2 precursor	41703	7	1	43	1	1	1.0	0.0	0.0	0.0	1	1	1
Unnamed protein product	46412	5	1	43	1	1	0.5	0.0	0.0	0.0	1	1	1
Complement C4B precursor	200574	7	1	42	1	2	1.9	0.0	0.0	0.0	1	1	1
Malate dehydrogenase, cytoplasmic isoform 2	41198	7	1	42	1	1	1.2	0.0	0.0	0.0	1	1	1
Mimecan; osteoglycin	38499	5	1	42	1	1	1.1	0.0	0.0	0.0	1	1	1
Alpha-1-antiproteinase; Alpha-1-antitrypsin; Alpha-1-prot	50821	6	1	41	0	0	0.5	0.0	0.0	0.0	1	1	1
Complement component C6; Flags: Precursor	117535	6	1	41	1	2	1.2	0.0	0.0	0.0	1	1	1

Ig lambda chain C region - horse (fragment)	13899	8	1	41	1	2	1.5	0.0	0.0	0.0	1	1	1
Kininogen-1 isoform 2	53513	6	1	41	1	1	1.3	0.0	0.0	0.0	1	1	1
KIAA0578 protein	182933	6	1	39	1	1	0.8	0.0	0.0	0.0	1	1	1
Fibromodulin	44986	6	1	40	1	1	1.2	0.0	0.0	0.0	1	1	1
Neurocan core protein precursor [Pan troglodytes]	149096	5	1	40	1	1	0.7	0.0	0.0	0.0	1	1	1
Endopin 2B	51047	6	1	40	1	1	1.1	0.0	0.0	0.0	1	1	1
Complement c1r-A subcomponent precursor	86405	5	1	40	1	1	1.7	0.0	0.0	0.0	1	1	1
Lysosomal alpha-mannosidase	117756	7	1	40	1	1	1.2	0.0	0.0	0.0	1	1	1
Immunoglobulin light chain variable region	11310	6	1	40	2	2	1.5	0.0	0.0	0.0	1	1	1
Complement component 3	18508	5	1	40	1	1	1.2	0.0	0.0	0.0	1	1	1
Serum amyloid A protein	8367	6	1	40	1	1	1.2	0.0	0.0	0.0	1	1	1
Unnamed protein product	52913	5	1	40	2	1	1.0	0.0	0.0	0.0	1	1	1
Glutathione S-transferase Mu 1	28494	7	1	40	1	1	2.3	0.0	0.0	0.0	1	1	1
Coagulation factor IX	52234	5	1	40	1	1	1.0	0.0	0.0	0.0	1	1	1
Presequence protease, mitochondrial isoform 2 precursor	127532	6	1	40	1	1	0.7	0.0	0.0	0.0	1	1	1
Immunoglobulin igg-2 heavy chain constant region	46351	6	1	40	2	1	1.3	0.0	0.0	0.0	1	1	1
Secreted nidogen domain protein precursor	161194	6	1	39	2	1	1.5	0.0	0.0	0.0	1	1	1
Protein kinase C-binding protein NELL2	100049	5	1	39	2	2	1.2	0.0	0.0	0.0	1	1	1
Chain a, new crystal forms of a mu class glutathione s-transferase	28786	8	1	39	2	3	3.2	0.0	0.0	0.0	1	1	1
Fibrous sheath interacting protein 1	75849	5	1	39	0	0	0.9	0.0	0.0	0.0	1	1	1
Chain a, crystal structure of tetradeca-(3-fluorotyrosyl)-glutathione s-transferase	28109	9	1	38	1	1	2.3	0.0	0.0	0.0	1	1	1
EGF-containing fibulin-like extracellular matrix protein 2; Fibulin-4;	51861	5	1	38	1	1	1.2	0.0	0.0	0.0	1	1	1
Complement component C7 precursor	103094	6	1	38	1	1	1.2	0.0	0.0	0.0	1	1	1

Secretogranin-2 precursor	76942	5	1	38	1	2	1.1	0.0	0.0	0.0	1	1	1
Complement C8 beta	17458	8	1	38	1	1	0.9	0.0	0.0	0.0	1	1	1
Histone deacetylase 7	28292	10	1	38	5	2	0.9	0.0	0.0	0.0	1	1	1
Complement factor B subunit Bb - pig (fragment)	21793	6	1	38	1	2	1.5	0.0	0.0	0.0	1	1	1
Nuclear factor of activated T-cells, cytoplasmic 2 isoform C	105863	7	1	38	1	2	0.4	0.0	0.0	0.0	1	1	1
Fibroleukin	55998	8	1	38	2	2	1.4	0.0	0.0	0.0	1	1	1
Fibulin-5 precursor	52687	5	1	38	2	2	1.3	0.0	0.0	0.0	1	1	1
Ig lambda chain V region	12660	9	1	38	1	1	1.1	0.0	0.0	0.0	1	1	1
Precursor polypeptide (AA -19 to 206)	28103	6	1	38	1	1	1.4	0.0	0.0	0.0	1	1	1

Molecular weight (MW) is predicted based on amino acid sequence.

Analysis Information

Report Type	Protein-Peptide Summary by Sample Set	Analysis Type	MS/MS
Sample Set Name	iTRAQ Sept11	Database	NewNCBInr
Analysis Name	95% CI pep rank1 NCBInr	Creation Date	10/31/2011 11:18:48
Reported By	11/01/2011 10:22:25 - admin	Last Modified	10/31/2011 20:00:34

MS Acq. : Proc. Methods	(Unspecified) : (Unspecified)
Interpretation Method	(Unspecified)

Rank	Protein Name	Accession No.	Protein MW	Pep. Count	Total Ion Score	Avg. iTRAQ Ratio 114/117*	Avg. iTRAQ Ratio 115/117*	Avg. iTRAQ Ratio 116/117*	iTRAQ SDev. 114/117*	iTRAQ SDev. 115/117*	iTRAQ SDev. 116/117*	iTRAQ Peptides 114/117	iTRAQ Peptides 115/117	iTRAQ Peptides 116/117	Total Ion C. I. %
1	serum albumin precursor [Ovis aries]	gi|57164373	79687.2	43	2879	0.989	1.113	0.950	0.493	0.470	0.244	147	147	147	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1035.5922	1035.6558	0.0636	61	198	204	GACLLPK	42	98.234	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[3]	[2] F4 and F13	954/946	1.053	1.023	0.723	1	Mascot
1057.5802	1057.526	-0.0542	-51	161	167	YLYEVAR	38	95.236	(N-term)_iTRAQ[0]	[5] F5 and F10	306/298	1.030	0.974	0.931	1	Mascot
1077.6765	1077.7052	0.0287	27	257	263	IVTDLTK	41	97.756	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	933/925	0.891	1.154	0.967	1	Mascot
1077.6765	1077.7075	0.031	29	257	263	IVTDLTK	38	95.502	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	239/231	0.953	0.896	0.896	1	Mascot
1092.6147	1092.543	-0.0717	-66	562	568	ATDEQLK	42	98.146	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	112/104	0.764	0.800	0.720	1	Mascot
1125.6401	1125.5978	-0.0423	-38	69	75	ELTEFAK	41	97.505	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	272/264	0.472	0.892	0.887	1	Mascot
1125.6401	1125.6044	-0.0357	-32	69	75	ELTEFAK	38	95.091	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[3] F14,15,16 and F6	165/157	0.957	1.144	0.940	1	Mascot
1125.6401	1125.6508	0.0107	10	69	75	ELTEFAK	39	96.028	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	135/127	0.839	0.903	0.877	1	Mascot
1125.6401	1125.6527	0.0126	11	69	75	ELTEFAK	39	96.436	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	186/178	0.889	0.993	1.017	1	Mascot
1125.6401	1125.6742	0.0341	30	69	75	ELTEFAK	38	95.258	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	933/925	0.771	0.835	0.806	1	Mascot
1174.6201	1174.5458	-0.0743	-63	131	138	DDSPDLPK	39	96.285	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	177/169	0.622	0.702	0.788	1	Mascot
1175.6508	1175.6292	-0.0216	-18	483	489	LCVLHEK	41	97.477	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[1] F8 061011	283/275	0.990	0.972	0.967	1	Mascot
1175.6508	1175.6975	0.0467	40	483	489	LCVLHEK	40	97.109	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[7] F12 and F9 and F7 attempt 2	1293/1285	1.301	1.047	0.748	1	Mascot
1184.6409	1184.5986	-0.0423	-36	249	256	ADFTDVTK	59	99.965	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	221/213	0.738	0.739	0.790	1	Mascot
1184.6409	1184.6216	-0.0193	-16	249	256	ADFTDVTK	56	99.92	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	1095/1087	0.713	0.874	0.783	1	Mascot
1184.6409	1184.6884	0.0475	40	249	256	ADFTDVTK	45	99.082	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	910/902	0.872	0.985	0.689	1	Mascot
1216.5933	1216.5546	-0.0387	-32	414	420	NCELFEK	40	97.296	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[5] F5 and F10	333/325	0.707	1.393	1.199	1	Mascot
1216.5933	1216.605	0.0117	10	414	420	NCELFEK	38	95.645	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[2] F4 and F13	188/180	1.316	1.285	1.000	1	Mascot
1216.5933	1216.6311	0.0378	31	414	420	NCELFEK	38	95.158	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[2] F4 and F13	477/469	1.493	1.661	1.358	1	Mascot
1216.5933	1216.6392	0.0459	38	414	420	NCELFEK	38	95.113	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[3] F14,15,16 and F6	964/956	1.233	1.272	1.089	1	Mascot
1216.5933	1216.6566	0.0633	52	414	420	NCELFEK	43	98.476	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[2] F4 and F13	964/956	1.280	1.295	1.133	1	Mascot
1260.5291	1260.5676	0.0385	31	499	507	CCTESLVNR	43	98.581	(N-term)_iTRAQ[0], MMTS (C)[1,2]	[4] F11 and F3	1071/1063	1.992	2.408	1.293	1	Mascot
1302.8242	1302.7657	-0.0585	-45	549	557	QTALVELLK	44	98.958	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[3] F14,15,16 and F6	226/218	1.249	2.368	1.376	1	Mascot
1302.8242	1302.7715	-0.0527	-40	549	557	QTALVELLK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[5] F5 and F10	409/401	1.135	1.403	0.860	1	Mascot

1302.8242	1302.8359	0.0117	9	549	557	QTALVELLK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1149/1141	1.196	1.443	0.987	1	Mascot
1302.8242	1302.8368	0.0126	10	549	557	QTALVELLK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	235/227	0.663	1.379	1.131	1	Mascot
1302.8242	1302.8618	0.0376	29	549	557	QTALVELLK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	995/987	0.751	1.218	1.051	1	Mascot
1335.6627	1335.6188	-0.0439	-33	310	318	SHCIAEVDK	65	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9], MMTS (C)[3]	[1] F8 061011	216/208	0.960	1.116	0.923	1	Mascot
1338.6526	1338.6294	-0.0232	-17	123	130	NECFLNHK	57	99.948	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8], MMTS (C)[3]	[1] F8 061011	257/249	0.935	0.980	0.912	1	Mascot
1412.7145	1412.7344	0.0199	14	588	597	EGCFVLEGPK	59	99.962	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10], MMTS (C)[3]	[2] F4 and F13	217/209	0.761	0.660	0.721	1	Mascot
1412.7145	1412.757	0.0425	30	588	597	EGCFVLEGPK	59	99.961	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10], MMTS (C)[3]	[2] F4 and F13	985/977	0.784	0.952	0.841	1	Mascot
1427.8131	1427.851	0.0379	27	361	371	HPEYAVSVLLR	41	97.693	(N-term)_iTRAQ[0]	[3] F14,15,16 and F6	902/894	0.682	0.665	0.694	1	Mascot
1488.7906	1488.8635	0.0729	49	413	420	KNCELFEK	45	99.125	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,8], MMTS (C)[3]	[7] F12 and F9 and F7 attempt 2	923/915	0.767	0.779	0.859	1	Mascot
1488.7906	1488.8796	0.089	60	413	420	KNCELFEK	42	98.138	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,8], MMTS (C)[3]	[7] F12 and F9 and F7 attempt 2	971/963	0.728	0.912	0.869	1	Mascot
1575.0216	1574.9834	-0.0382	-24	548	557	KQTALVELLK	61	99.979	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[8] F2	375/367	1.065	1.281	1.002	1	Mascot
1575.0216	1575.0242	0.0026	2	548	557	KQTALVELLK	62	99.981	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[1] F8 061011	365/357	0.570	1.183	1.125	1	Mascot
1575.0216	1575.1365	0.1149	73	548	557	KQTALVELLK	57	99.941	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[7] F12 and F9 and F7 attempt 2	1362/1354	0.912	0.993	0.968	1	Mascot
1593.921	1593.8564	-0.0646	-41	402	412	HLVDEPQNLIK	66	99.993	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	174/166	1.536	1.441	0.941	1	Mascot
1593.921	1593.8634	-0.0576	-36	402	412	HLVDEPQNLIK	82	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[8] F2	306/298	0.873	0.928	0.888	1	Mascot
1593.921	1593.975	0.054	34	402	412	HLVDEPQNLIK	80	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	821/813	1.128	0.994	0.937	1	Mascot
1593.921	1593.9929	0.0719	45	402	412	HLVDEPQNLIK	54	99.879	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	1293/1285	0.851	0.864	0.846	1	Mascot
1593.921	1594.0195	0.0985	62	402	412	HLVDEPQNLIK	62	99.983	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	912/904	1.204	1.723	1.246	1	Mascot
1609.99	1610.0524	0.0624	39	66	75	LVKELTEFAK	40	97.29	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,10]	[7] F12 and F9 and F7 attempt 2	1405/1397	0.894	1.263	0.966	1	Mascot
1641.9296	1641.8838	-0.0458	-28	438	451	APQVSTPTLVEISR	65	99.99	(N-term)_iTRAQ[0]	[8] F2	352/344	0.666	0.756	0.734	1	Mascot
1647.8727	1647.8531	-0.0196	-12	421	433	HGEYGFQNALIVR	60	99.974	(N-term)_iTRAQ[0]	[3] F14,15,16 and F6	203/195	0.917	1.114	0.986	1	Mascot
1647.8727	1647.8931	0.0204	12	421	433	HGEYGFQNALIVR	45	99.06	(N-term)_iTRAQ[0]	[4] F11 and F3	1100/1092	1.575	1.505	1.070	1	Mascot
1647.8727	1647.9025	0.0298	18	421	433	HGEYGFQNALIVR	58	99.957	(N-term)_iTRAQ[0]	[5] F5 and F10	1227/1219	1.821	2.149	1.349	1	Mascot
1647.8727	1647.9867	0.114	69	421	433	HGEYGFQNALIVR	59	99.967	(N-term)_iTRAQ[0]	[3] F14,15,16 and F6	867/859	1.046	0.896	0.933	1	Mascot
1687.8225	1687.7981	-0.0244	-14	300	309	ECCDKPVLEK	48	99.499	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[5,10], MMTS (C)[2,3]	[1] F8 061011	296/288	0.704	0.888	1.066	1	Mascot
1687.8225	1687.8889	0.0664	39	300	309	ECCDKPVLEK	49	99.67	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[5,10], MMTS (C)[2,3]	[7] F12 and F9 and F7 attempt 2	1306/1298	0.897	0.911	0.842	1	Mascot
1687.8975	1687.8418	-0.0557	-33	569	580	TVMENFVAFVDK	100	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[5] F5 and F10	512/504	1.113	1.245	0.975	1	Mascot
1687.8975	1687.8925	-0.005	-3	569	580	TVMENFVAFVDK	67	99.994	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[1] F8 061011	501/493	0.506	1.255	0.753	1	Mascot
1687.8975	1687.9059	0.0084	5	569	580	TVMENFVAFVDK	47	99.392	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1231/1223	0.887	1.062	0.891	1	Mascot
1687.8975	1687.9149	0.0174	10	569	580	TVMENFVAFVDK	90	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[5] F5 and F10	1382/1374	1.453	1.560	0.727	1	Mascot
1687.8975	1687.9182	0.0207	12	569	580	TVMENFVAFVDK	102	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[2] F4 and F13	348/340	0.914	1.109	0.881	1	Mascot
1687.8975	1687.9308	0.0333	20	569	580	TVMENFVAFVDK	107	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1272/1264	1.120	1.121	0.952	1	Mascot
1687.8975	1687.9449	0.0474	28	569	580	TVMENFVAFVDK	49	99.662	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[3] F14,15,16 and F6	1048/1040	1.092	0.966	1.058	1	Mascot
1687.8975	1687.9557	0.0582	34	569	580	TVMENFVAFVDK	46	99.272	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[2] F4 and F13	1031/1023	1.939	1.118	2.089	1	Mascot
1687.8975	1687.9612	0.0637	38	569	580	TVMENFVAFVDK	53	99.852	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[7] F12 and F9 and F7 attempt 2	1084/1076	1.666	1.429	1.798	1	Mascot
1696.8629	1696.818	-0.0449	-26	89	100	SLHTLFGDELCK	95	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[3] F14,15,16 and F6	236/228	0.515	0.534	0.670	1	Mascot
1696.8629	1696.8333	-0.0296	-17	89	100	SLHTLFGDELCK	80	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[1] F8 061011	432/424	0.417	0.545	0.730	1	Mascot
1696.8629	1696.8533	-0.0096	-6	89	100	SLHTLFGDELCK	95	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12],	[4] F11 and F3	360/352	0.533	0.549	0.628	1	Mascot

									MMTS (C)[11]							
1696.8629	1696.8579	-0.005	-3	89	100	SLHTLFGDELCK	45	99.002	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[1] F8 061011	467/459	0.333	0.594	0.650	1	Mascot
1696.8629	1696.8772	0.0143	8	89	100	SLHTLFGDELCK	90	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[5] F5 and F10	1298/1290	1.501	2.002	1.278	1	Mascot
1696.8629	1696.8954	0.0325	19	89	100	SLHTLFGDELCK	90	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[2] F4 and F13	268/260	0.740	1.016	1.053	1	Mascot
1696.8629	1696.897	0.0341	20	89	100	SLHTLFGDELCK	58	99.959	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[2] F4 and F13	395/387	1.702	1.957	2.371	1	Mascot
1696.8629	1696.9061	0.0432	25	89	100	SLHTLFGDELCK	92	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[4] F11 and F3	959/951	0.444	0.630	0.658	1	Mascot
1696.8629	1696.9149	0.052	31	89	100	SLHTLFGDELCK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[7] F12 and F9 and F7 attempt 2	1045/1037	1.127	1.204	1.089	1	Mascot
1696.8629	1696.9293	0.0664	39	89	100	SLHTLFGDELCK	95	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[3] F14,15,16 and F6	963/955	0.565	0.588	0.718	1	Mascot
1696.8629	1696.9674	0.1045	62	89	100	SLHTLFGDELCK	56	99.92	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[7] F12 and F9 and F7 attempt 2	1428/1420	0.293	0.582	0.761	1	Mascot
1703.8925	1703.8389	-0.0536	-31	569	580	TVMENFVAFVDK	65	99.991	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], Oxidation (M)[3]	[5] F5 and F10	512/504	0.947	0.682	0.857	1	Mascot
1703.8925	1703.9235	0.031	18	569	580	TVMENFVAFVDK	60	99.973	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], Oxidation (M)[3]	[4] F11 and F3	1324/1316	0.981	1.153	0.881	1	Mascot
1703.8925	1703.9277	0.0352	21	569	580	TVMENFVAFVDK	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], Oxidation (M)[3]	[4] F11 and F3	1162/1154	1.040	1.306	1.265	1	Mascot
1713.8167	1713.7355	-0.0812	-47	286	297	YICDHQDALSSK	56	99.925	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[1] F8 061011	263/255	1.856	1.835	1.293	1	Mascot
1713.8167	1713.7618	-0.0549	-32	286	297	YICDHQDALSSK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[8] F2	300/292	0.598	0.783	0.774	1	Mascot
1713.8167	1713.7625	-0.0542	-32	286	297	YICDHQDALSSK	82	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[3] F14,15,16 and F6	170/162	0.750	0.756	0.775	1	Mascot
1713.8167	1713.7683	-0.0484	-28	286	297	YICDHQDALSSK	77	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[4] F11 and F3	212/204	0.976	1.094	0.818	1	Mascot
1713.8167	1713.771	-0.0457	-27	286	297	YICDHQDALSSK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[1] F8 061011	272/264	0.596	0.815	0.827	1	Mascot
1713.8167	1713.8224	0.0057	3	286	297	YICDHQDALSSK	66	99.992	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[5] F5 and F10	1139/1131	1.128	1.501	0.763	1	Mascot
1713.8167	1713.8513	0.0346	20	286	297	YICDHQDALSSK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[5] F5 and F10	1165/1157	1.397	1.609	1.181	1	Mascot
1713.8167	1713.8605	0.0438	26	286	297	YICDHQDALSSK	81	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[3] F14,15,16 and F6	811/803	0.839	0.761	0.818	1	Mascot
1713.8167	1713.8965	0.0798	47	286	297	YICDHQDALSSK	46	99.302	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[7] F12 and F9 and F7 attempt 2	1287/1279	0.563	0.829	0.901	1	Mascot
1713.8167	1713.9012	0.0845	49	286	297	YICDHQDALSSK	62	99.984	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[3]	[7] F12 and F9 and F7 attempt 2	917/909	1.249	1.693	1.438	1	Mascot
1715.7069	1715.6229	-0.084	-49	76	88	TCVADESHAGCDK	91	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[2,11]	[5] F5 and F10	234/226	1.468	1.953	1.384	1	Mascot
1715.7069	1715.6355	-0.0714	-42	76	88	TCVADESHAGCDK	99	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[2,11]	[8] F2	240/232	0.910	1.195	0.815	1	Mascot
1715.7069	1715.6476	-0.0593	-35	76	88	TCVADESHAGCDK	104	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[2,11]	[1] F8 061011	220/212	1.117	1.293	1.153	1	Mascot
1715.7069	1715.6571	-0.0498	-29	76	88	TCVADESHAGCDK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[2,11]	[3] F14,15,16 and F6	140/132	1.503	1.461	0.913	1	Mascot
1715.7069	1715.7609	0.054	31	76	88	TCVADESHAGCDK	101	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[2,11]	[3] F14,15,16 and F6	761/753	1.157	1.099	0.900	1	Mascot
1715.7069	1715.7878	0.0809	47	76	88	TCVADESHAGCDK	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[2,11]	[7] F12 and F9 and F7 attempt 2	1238/1230	1.064	1.113	0.939	1	Mascot
1739.8765	1739.8195	-0.057	-33	347	359	DVFLGSFLYEYSR	86	100	(N-term)_iTRAQ[0]	[8] F2	528/520	0.723	0.723	0.784	1	Mascot
1739.8765	1739.8373	-0.0392	-23	347	359	DVFLGSFLYEYSR	69	99.997	(N-term)_iTRAQ[0]	[5] F5 and F10	539/531	1.208	1.740	1.228	1	Mascot
1744.6569	1744.5756	-0.0813	-47	106	117	ETYGDMADCCEK	81	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[5] F5 and F10	372/364	0.601	0.935	0.924	1	Mascot

1744.6569	1744.6769	0.02	11	106	117	ETYGDMADCCEK	85	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[2] F4 and F13	188/180	0.564	1.022	0.953	1	Mascot
1744.6569	1744.6855	0.0286	16	106	117	ETYGDMADCCEK	50	99.723	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[4] F11 and F3	1076/1068	1.209	1.073	0.938	1	Mascot
1744.6569	1744.6956	0.0387	22	106	117	ETYGDMADCCEK	80	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[4] F11 and F3	1110/1102	0.855	0.800	0.763	1	Mascot
1744.6569	1744.717	0.0601	34	106	117	ETYGDMADCCEK	65	99.991	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[2] F4 and F13	975/967	0.542	1.061	0.868	1	Mascot
1744.6569	1744.7797	0.1228	70	106	117	ETYGDMADCCEK	38	95.793	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[7] F12 and F9 and F7 attempt 2	1368/1360	1.180	1.412	0.907	1	Mascot
1754.7317	1754.6647	-0.067	-38	375	386	EYEATLEDCCAK	81	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[5] F5 and F10	434/426	1.193	1.237	0.787	1	Mascot
1754.7317	1754.7434	0.0117	7	375	386	EYEATLEDCCAK	74	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[4] F11 and F3	1181/1173	1.263	1.219	0.852	1	Mascot
1754.7317	1754.7574	0.0257	15	375	386	EYEATLEDCCAK	86	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[2] F4 and F13	265/257	1.329	1.220	0.758	1	Mascot
1754.7317	1754.8008	0.0691	39	375	386	EYEATLEDCCAK	39	96.361	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[3] F14,15,16 and F6	961/953	1.224	1.824	1.030	1	Mascot
1754.7317	1754.8232	0.0915	52	375	386	EYEATLEDCCAK	48	99.572	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[4] F11 and F3	1258/1250	1.016	1.115	0.660	1	Mascot
1760.6517	1760.6782	0.0265	15	106	117	ETYGDMADCCEK	53	99.845	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10], Oxidation (M)[6]	[2] F4 and F13	186/178	0.721	0.962	0.833	1	Mascot
1760.6517	1760.6796	0.0279	16	106	117	ETYGDMADCCEK	80	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10], Oxidation (M)[6]	[4] F11 and F3	1030/1022	0.965	0.949	0.867	1	Mascot
1829.8429	1829.7992	-0.0437	-24	387	399	EDPHACYATVFDK	44	98.962	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[6]	[4] F11 and F3	278/270	1.101	0.923	1.044	1	Mascot
1829.8429	1829.8104	-0.0325	-18	387	399	EDPHACYATVFDK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[6]	[3] F14,15,16 and F6	200/192	1.058	0.737	0.680	1	Mascot
1829.8429	1829.8975	0.0546	30	387	399	EDPHACYATVFDK	98	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[6]	[3] F14,15,16 and F6	879/871	1.304	1.103	0.679	1	Mascot
1829.8429	1829.9292	0.0863	47	387	399	EDPHACYATVFDK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[6]	[7] F12 and F9 and F7 attempt 2	975/967	1.498	1.988	0.928	1	Mascot
1857.9014	1857.882	-0.0194	-10	469	482	MPCTEDYLSLILNR	76	99.999	(N-term)_iTRAQ[0], MMTS (C)[3]	[8] F2	558/550	0.855	0.856	0.879	1	Mascot
1860.6581	1860.5664	-0.0917	-49	267	280	ECCHGDLLECADDR	92	100	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[5] F5 and F10	474/466	1.263	1.107	0.804	1	Mascot
1860.6581	1860.6014	-0.0567	-30	267	280	ECCHGDLLECADDR	52	99.839	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[3] F14,15,16 and F6	221/213	0.796	1.173	0.796	1	Mascot
1860.6581	1860.6028	-0.0553	-30	267	280	ECCHGDLLECADDR	81	100	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[5] F5 and F10	407/399	1.372	1.168	1.163	1	Mascot
1860.6581	1860.6277	-0.0304	-16	267	280	ECCHGDLLECADDR	55	99.916	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[4] F11 and F3	329/321	3.021	1.621	1.794	1	Mascot
1860.6581	1860.6558	-0.0023	-1	267	280	ECCHGDLLECADDR	53	99.854	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[1] F8 061011	400/392	1.452	1.453	1.660	1	Mascot
1860.6581	1860.7362	0.0781	42	267	280	ECCHGDLLECADDR	44	98.798	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[5] F5 and F10	1264/1256	1.608	2.083	1.057	1	Mascot
1860.6581	1860.74	0.0819	44	267	280	ECCHGDLLECADDR	79	100	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[3] F14,15,16 and F6	930/922	1.021	1.161	1.116	1	Mascot
1866.1184	1866.0886	-0.0298	-16	402	413	HLVDEPQNLIKK	91	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11,12]	[5] F5 and F10	1151/1143	1.080	1.402	0.894	1	Mascot
1873.8964	1873.8337	-0.0627	-33	469	482	MPCTEDYLSLILNR	48	99.537	(N-term)_iTRAQ[0], MMTS (C)[3], Oxidation (M)[1]	[8] F2	525/517	0.752	0.937	0.819	1	Mascot
1914.127	1914.0345	-0.0925	-48	437	451	KAPQVSTPTLVEISR	58	99.954	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[5] F5 and F10	316/308	1.282	1.017	1.003	1	Mascot
1914.127	1914.0424	-0.0846	-44	437	451	KAPQVSTPTLVEISR	48	99.503	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[4] F11 and F3	239/231	0.866	0.990	0.889	1	Mascot
1914.127	1914.0715	-0.0555	-29	437	451	KAPQVSTPTLVEISR	71	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[3] F14,15,16 and F6	184/176	0.831	0.937	0.889	1	Mascot
1914.127	1914.2155	0.0885	46	437	451	KAPQVSTPTLVEISR	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[3] F14,15,16 and F6	833/825	1.073	0.930	1.216	1	Mascot
1969.0491	1968.9862	-0.0629	-32	139	151	LKPEPDTLCAEFK	57	99.945	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,13], MMTS (C)[9]	[3] F14,15,16 and F6	230/222	1.025	1.108	0.958	1	Mascot
1969.0491	1968.9873	-0.0618	-31	139	151	LKPEPDTLCAEFK	53	99.843	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,13], MMTS (C)[9]	[4] F11 and F3	347/339	0.799	0.931	0.875	1	Mascot
1969.0491	1969.0894	0.0403	20	139	151	LKPEPDTLCAEFK	46	99.336	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,1	[4] F11 and F3	959/951	0.966	0.935	1.158	1	Mascot

									3], MMTS (C)[9]							
1969.0491	1969.1301	0.081	41	139	151	LKPEPDTLCAEFK	69	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,13], MMTS (C)[9]	[3] F14,15,16 and F6	947/939	1.047	0.910	0.908	1	Mascot
1977.9502	1977.8756	-0.0746	-38	118	130	QEPERNECFLNHK	43	98.411	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[8]	[4] F11 and F3	179/171	0.880	0.897	1.109	1	Mascot
1977.9502	1977.9659	0.0157	8	118	130	QEPERNECFLNHK	46	99.336	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[8]	[5] F5 and F10	1132/1124	1.049	1.105	1.025	1	Mascot
2013.8386	2013.8367	-0.0019	-1	184	197	YNGVFQECCQAEDK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[8,9]	[4] F11 and F3	1229/1221	2.242	2.031	0.895	1	Mascot
2013.8386	2013.8453	0.0067	3	184	197	YNGVFQECCQAEDK	56	99.928	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[8,9]	[4] F11 and F3	1288/1280	2.093	1.654	0.932	1	Mascot
2013.8386	2013.8861	0.0475	24	184	197	YNGVFQECCQAEDK	59	99.968	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[8,9]	[4] F11 and F3	1214/1206	1.826	1.527	1.043	1	Mascot
2013.8386	2013.9429	0.1043	52	184	197	YNGVFQECCQAEDK	74	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[8,9]	[4] F11 and F3	1257/1249	1.930	1.969	0.998	1	Mascot
2073.104	2073.1514	0.0474	23	298	309	LKECCDKPVLEK	59	99.961	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,7,12], MMTS (C)[4,5]	[5] F5 and F10	1226/1218	1.084	1.054	0.971	1	Mascot
2177.1318	2177.0769	-0.0549	-25	169	183	HPYFYAPELLYYANK	99	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[5] F5 and F10	480/472	0.566	0.661	0.736	1	Mascot
2177.1318	2177.1179	-0.0139	-6	169	183	HPYFYAPELLYYANK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[5] F5 and F10	1349/1341	0.465	0.762	0.976	1	Mascot
2177.1318	2177.2087	0.0769	35	169	183	HPYFYAPELLYYANK	40	97.214	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[3] F14,15,16 and F6	1019/1011	0.811	0.811	1.058	1	Mascot
2219.0745	2219.0034	-0.0711	-32	529	544	FFTFHADICTLPDTEK	105	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[9]	[5] F5 and F10	514/506	0.705	1.027	0.870	1	Mascot
2219.0745	2219.0742	-0.0003	0	529	544	FFTFHADICTLPDTEK	88	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[9]	[3] F14,15,16 and F6	262/254	0.844	1.077	0.823	1	Mascot
2219.0745	2219.1094	0.0349	16	529	544	FFTFHADICTLPDTEK	69	99.996	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[9]	[2] F4 and F13	347/339	0.856	1.004	1.010	1	Mascot
2219.0745	2219.1414	0.0669	30	529	544	FFTFHADICTLPDTEK	49	99.648	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[9]	[2] F4 and F13	438/430	1.072	1.012	1.062	1	Mascot
2219.0745	2219.1494	0.0749	34	529	544	FFTFHADICTLPDTEK	46	99.305	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[9]	[2] F4 and F13	1030/1022	0.987	1.128	0.653	1	Mascot
2350.1523	2350.1499	-0.0024	-1	123	138	NECFLNHKDDSPDLPK	47	99.381	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8,16], MMTS (C)[3]	[5] F5 and F10	1194/1186	0.690	0.621	0.812	1	Mascot
2355.03	2354.9087	-0.1213	-52	581	597	CCAADDKEGCFVLEGPK	84	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,17], MMTS (C)[1,2,10]	[5] F5 and F10	474/466	2.389	2.697	1.331	1	Mascot
2355.03	2354.9375	-0.0925	-39	581	597	CCAADDKEGCFVLEGPK	90	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,17], MMTS (C)[1,2,10]	[5] F5 and F10	436/428	2.489	2.259	1.224	1	Mascot
2355.03	2355.052	0.022	9	581	597	CCAADDKEGCFVLEGPK	103	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,17], MMTS (C)[1,2,10]	[5] F5 and F10	1297/1289	3.319	3.761	1.524	1	Mascot
2355.03	2355.1267	0.0967	41	581	597	CCAADDKEGCFVLEGPK	52	99.817	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,17], MMTS (C)[1,2,10]	[3] F14,15,16 and F6	968/960	1.476	2.779	1.087	1	Mascot
2503.0405	2502.9846	-0.0559	-22	267	285	ECCHGDLLECADDRADLAK	82	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[19], MMTS (C)[2,3,10]	[8] F2	420/412	1.456	1.205	0.971	1	Mascot

2	RecName: Full=Serotransferrin; Short=Transferrin; AltName: Full=Beta-1 metal-binding globulin; AltN	gi|2501351	88816.9	20	1321	0.951	0.901	0.884	0.438	0.379	0.333	36	36	36	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1023.6084	1023.5566	-0.0518	-51	554	560	GDVAFVK	42	98.313	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	228/220	0.809	0.707	0.738	1	Mascot
1140.6146	1140.5513	-0.0633	-55	320	327	DSADGFLK	49	99.679	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	248/240	0.845	0.890	1.037	1	Mascot
1140.6146	1140.6289	0.0143	13	320	327	DSADGFLK	40	96.994	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	1119/1111	0.394	0.629	0.385	1	Mascot
1207.766	1207.7739	0.0079	7	448	456	GYLAVAVVK	61	99.976	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1081/1073	0.761	0.721	0.777	1	Mascot
1215.593	1215.6121	0.0191	16	188	195	LCQLCAGK	58	99.95	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8], MMTS (C)[2,5]	[2] F4 and F13	267/259	2.625	2.161	1.404	1	Mascot
1241.6075	1241.6476	0.0401	32	540	548	YYGYTGAFR	38	95.945	(N-term)_iTRAQ[0]	[4] F11 and F3	1063/1055	1.179	1.029	1.001	1	Mascot
1268.6028	1268.5626	-0.0402	-32	61	68	TSHMDCIK	55	99.914	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8], MMTS (C)[6]	[1] F8 061011	220/212	0.912	0.857	0.783	1	Mascot

1455.7563	1455.6851	-0.0712	-49	156	166	ELPDPQESIQR	39	96.643	(N-term)_iTRAQ[0]	[5] F5 and F10	256/248	0.895	0.941	0.940	1	Mascot
1455.7563	1455.7013	-0.055	-38	156	166	ELPDPQESIQR	40	96.83	(N-term)_iTRAQ[0]	[8] F2	265/257	0.997	0.872	0.859	1	Mascot
1455.7563	1455.8163	0.06	41	156	166	ELPDPQESIQR	46	99.277	(N-term)_iTRAQ[0]	[4] F11 and F3	1006/998	0.869	0.816	0.942	1	Mascot
1492.7883	1492.7474	-0.0409	-27	695	704	LLEACTFHKP	51	99.757	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9], MMTS (C)[5]	[3] F14,15,16 and F6	231/223	1.564	1.614	1.149	1	Mascot
1492.7883	1492.7501	-0.0382	-26	695	704	LLEACTFHKP	56	99.928	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9], MMTS (C)[5]	[4] F11 and F3	348/340	1.019	1.067	1.175	1	Mascot
1492.7883	1492.8335	0.0452	30	695	704	LLEACTFHKP	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9], MMTS (C)[5]	[3] F14,15,16 and F6	939/931	1.273	1.133	1.035	1	Mascot
1556.7952	1556.6943	-0.1009	-65	60	68	KTSHMDCIK	49	99.634	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,9], MMTS (C)[7], Oxidation (M)[5]	[6] F12 and F9 and F7	161/153	1.208	1.128	1.012	1	Mascot
1610.7458	1610.7025	-0.0433	-27	671	682	TYDSYLGDDYVR	89	100	(N-term)_iTRAQ[0]	[8] F2	333/325	1.288	1.129	1.053	1	Mascot
1610.7458	1610.7777	0.0319	20	671	682	TYDSYLGDDYVR	67	99.994	(N-term)_iTRAQ[0]	[4] F11 and F3	1076/1068	1.262	1.063	1.189	1	Mascot
1610.7458	1610.7975	0.0517	32	671	682	TYDSYLGDDYVR	43	98.493	(N-term)_iTRAQ[0]	[3] F14,15,16 and F6	853/845	1.543	1.609	1.498	1	Mascot
1623.785	1623.8906	0.1056	65	27	37	WCTISTHEANK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[2]	[7] F12 and F9 and F7 attempt 2	1324/1316	0.933	0.861	0.906	1	Mascot
1639.8778	1639.9443	0.0665	41	424	435	CGLVPVLAENYK	61	99.979	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[1]	[4] F11 and F3	1207/1199	2.141	1.164	0.439	1	Mascot
1839.0084	1839.0402	0.0318	17	480	493	TAGWNIPMGLLYSK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[4] F11 and F3	1256/1248	1.561	1.633	1.284	1	Mascot
1882.9432	1882.8854	-0.0578	-31	670	682	KTYDSYLGDDYVR	55	99.91	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[8] F2	311/303	0.918	0.787	1.095	1	Mascot
1882.9432	1883.0215	0.0783	42	670	682	KTYDSYLGDDYVR	40	97.156	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[7] F12 and F9 and F7 attempt 2	1302/1294	0.932	0.881	0.971	1	Mascot
1893.0116	1892.9187	-0.0929	-49	107	120	DNPQTHYYAVAVVK	54	99.894	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	256/248	0.870	0.549	0.791	1	Mascot
1893.0116	1892.9353	-0.0763	-40	107	120	DNPQTHYYAVAVVK	98	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	306/298	0.696	0.632	1.051	1	Mascot
1893.0116	1892.9382	-0.0734	-39	107	120	DNPQTHYYAVAVVK	121	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	282/274	0.740	0.686	0.761	1	Mascot
1893.0116	1892.9613	-0.0503	-27	107	120	DNPQTHYYAVAVVK	40	96.816	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	303/295	0.695	0.390	0.666	1	Mascot
1893.0116	1892.9622	-0.0494	-26	107	120	DNPQTHYYAVAVVK	91	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[1] F8 061011	269/261	1.034	1.017	0.774	1	Mascot
1893.0116	1893.058	0.0464	25	107	120	DNPQTHYYAVAVVK	118	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[3] F14,15,16 and F6	803/795	0.459	0.696	0.905	1	Mascot
1893.0116	1893.074	0.0624	33	107	120	DNPQTHYYAVAVVK	96	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	1153/1145	0.746	0.829	1.022	1	Mascot
2004.1012	2004.0406	-0.0606	-30	153	166	LYKELPDPQESIQR	58	99.951	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3]	[5] F5 and F10	326/318	1.212	1.390	1.210	1	Mascot
2004.1012	2004.1591	0.0579	29	153	166	LYKELPDPQESIQR	41	97.901	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3]	[3] F14,15,16 and F6	853/845	0.903	1.258	0.855	1	Mascot
2119.0627	2118.9917	-0.071	-34	406	423	GEADAMSLDGGYLYIAGK	96	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[5] F5 and F10	427/419	0.805	0.891	0.843	1	Mascot
2119.0627	2119.0623	-0.0004	0	406	423	GEADAMSLDGGYLYIAGK	78	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[4] F11 and F3	1175/1167	0.625	0.597	0.749	1	Mascot
2190.168	2190.1929	0.0249	11	300	314	DKPDNFQLFQSPHGK	110	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,15]	[5] F5 and F10	1176/1168	0.560	0.619	0.817	1	Mascot
2353.2188	2353.2102	-0.0086	-4	283	299	EDVIWELLNHAQEHFGK	65	99.991	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17]	[1] F8 061011	537/529	0.700	0.746	0.854	1	Mascot
2635.3845	2635.2712	-0.1133	-43	403	423	IMKGEADAMSLDGGYLYIAGK	54	99.894	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,21]	[5] F5 and F10	446/438	0.926	0.583	0.316	1	Mascot

3	RecName: Full=Serum albumin; AltName: Full=BSA; AltName: Allergen=Bos d 6; Flags: Precursor	gi|1351907	79648.2	18	1217	0.953	1.101	0.949	0.568	0.477	0.309	70	70	70	100

Protein Group

serum albumin precursor [Bos taurus]	gi|30794280	79678.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1035.5922	1035.6558	0.0636	61	198	204	GACLLPK	42	98.234	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[3]	[2] F4 and F13	954/946	1.053	1.023	0.723	1	Mascot
1077.6765	1077.7052	0.0287	27	257	263	LVTDLTK	41	97.756	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	933/925	0.891	1.154	0.967	1	Mascot
1077.6765	1077.7075	0.031	29	257	263	LVTDLTK	38	95.502	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	239/231	0.953	0.896	0.896	1	Mascot
1174.6201	1174.5458	-0.0743	-63	131	138	DDSPDLPK	39	96.285	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	177/169	0.622	0.702	0.788	1	Mascot
1175.6508	1175.6292	-0.0216	-18	483	489	LCVLHEK	41	97.477	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7],	[1] F8 061011	283/275	0.990	0.972	0.967	1	Mascot

									MMTS (C)[2]							
1175.6508	1175.6975	0.0467	40	483	489	LCVLHEK	40	97.109	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[7] F12 and F9 and F7 attempt 2	1293/1285	1.301	1.047	0.748	1	Mascot
1260.5291	1260.5676	0.0385	31	499	507	CCTESLVNR	43	98.581	(N-term)_iTRAQ[0], MMTS (C)[1,2]	[4] F11 and F3	1071/1063	1.992	2.408	1.293	1	Mascot
1302.8242	1302.7657	-0.0585	-45	549	557	QTALVELLK	44	98.958	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[3] F14,15,16 and F6	226/218	1.249	2.368	1.376	1	Mascot
1302.8242	1302.7715	-0.0527	-40	549	557	QTALVELLK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[5] F5 and F10	409/401	1.135	1.403	0.860	1	Mascot
1302.8242	1302.8359	0.0117	9	549	557	QTALVELLK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1149/1141	1.196	1.443	0.987	1	Mascot
1302.8242	1302.8368	0.0126	10	549	557	QTALVELLK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	235/227	0.663	1.379	1.131	1	Mascot
1302.8242	1302.8618	0.0376	29	549	557	QTALVELLK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	995/987	0.751	1.218	1.051	1	Mascot
1427.8131	1427.851	0.0379	27	361	371	HPEYAVSVLLR	41	97.693	(N-term)_iTRAQ[0]	[3] F14,15,16 and F6	902/894	0.682	0.665	0.694	1	Mascot
1575.0216	1574.9834	-0.0382	-24	548	557	KQTALVELLK	61	99.979	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[8] F2	375/367	1.065	1.281	1.002	1	Mascot
1575.0216	1575.0242	0.0026	2	548	557	KQTALVELLK	62	99.981	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[1] F8 061011	365/357	0.570	1.183	1.125	1	Mascot
1575.0216	1575.1365	0.1149	73	548	557	KQTALVELLK	57	99.941	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[7] F12 and F9 and F7 attempt 2	1362/1354	0.912	0.993	0.968	1	Mascot
1593.921	1593.8564	-0.0646	-41	402	412	HLVDEPQNLIK	66	99.993	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	174/166	1.536	1.441	0.941	1	Mascot
1593.921	1593.8634	-0.0576	-36	402	412	HLVDEPQNLIK	82	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[8] F2	306/298	0.873	0.928	0.888	1	Mascot
1593.921	1593.975	0.054	34	402	412	HLVDEPQNLIK	80	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	821/813	1.128	0.994	0.937	1	Mascot
1593.921	1593.9929	0.0719	45	402	412	HLVDEPQNLIK	54	99.879	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	1293/1285	0.851	0.864	0.846	1	Mascot
1593.921	1594.0195	0.0985	62	402	412	HLVDEPQNLIK	62	99.983	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	912/904	1.204	1.723	1.246	1	Mascot
1687.8975	1687.8418	-0.0557	-33	569	580	TVMENFVAFVDK	100	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[5] F5 and F10	512/504	1.113	1.245	0.975	1	Mascot
1687.8975	1687.8925	-0.005	-3	569	580	TVMENFVAFVDK	67	99.994	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[1] F8 061011	501/493	0.506	1.255	0.753	1	Mascot
1687.8975	1687.9059	0.0084	5	569	580	TVMENFVAFVDK	47	99.392	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1231/1223	0.887	1.062	0.891	1	Mascot
1687.8975	1687.9149	0.0174	10	569	580	TVMENFVAFVDK	90	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[5] F5 and F10	1382/1374	1.453	1.560	0.727	1	Mascot
1687.8975	1687.9182	0.0207	12	569	580	TVMENFVAFVDK	102	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[2] F4 and F13	348/340	0.914	1.109	0.881	1	Mascot
1687.8975	1687.9308	0.0333	20	569	580	TVMENFVAFVDK	107	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1272/1264	1.120	1.121	0.952	1	Mascot
1687.8975	1687.9449	0.0474	28	569	580	TVMENFVAFVDK	49	99.662	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[3] F14,15,16 and F6	1048/1040	1.092	0.966	1.058	1	Mascot
1687.8975	1687.9557	0.0582	34	569	580	TVMENFVAFVDK	46	99.272	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[2] F4 and F13	1031/1023	1.939	1.118	2.089	1	Mascot
1687.8975	1687.9612	0.0637	38	569	580	TVMENFVAFVDK	53	99.852	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[7] F12 and F9 and F7 attempt 2	1084/1076	1.666	1.429	1.798	1	Mascot
1696.8629	1696.818	-0.0449	-26	89	100	SLHTLFGDELCK	95	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[3] F14,15,16 and F6	236/228	0.515	0.534	0.670	1	Mascot
1696.8629	1696.8333	-0.0296	-17	89	100	SLHTLFGDELCK	80	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[1] F8 061011	432/424	0.417	0.545	0.730	1	Mascot
1696.8629	1696.8533	-0.0096	-6	89	100	SLHTLFGDELCK	95	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[4] F11 and F3	360/352	0.533	0.549	0.628	1	Mascot
1696.8629	1696.8579	-0.005	-3	89	100	SLHTLFGDELCK	45	99.002	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[1] F8 061011	467/459	0.333	0.594	0.650	1	Mascot
1696.8629	1696.8772	0.0143	8	89	100	SLHTLFGDELCK	90	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[5] F5 and F10	1298/1290	1.501	2.002	1.278	1	Mascot
1696.8629	1696.8954	0.0325	19	89	100	SLHTLFGDELCK	90	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[2] F4 and F13	268/260	0.740	1.016	1.053	1	Mascot
1696.8629	1696.897	0.0341	20	89	100	SLHTLFGDELCK	58	99.959	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[2] F4 and F13	395/387	1.702	1.957	2.371	1	Mascot
1696.8629	1696.9061	0.0432	25	89	100	SLHTLFGDELCK	92	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[4] F11 and F3	959/951	0.444	0.630	0.658	1	Mascot
1696.8629	1696.9149	0.052	31	89	100	SLHTLFGDELCK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[7] F12 and F9 and F7 attempt 2	1045/1037	1.127	1.204	1.089	1	Mascot
1696.8629	1696.9293	0.0664	39	89	100	SLHTLFGDELCK	95	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[3] F14,15,16 and F6	963/955	0.565	0.588	0.718	1	Mascot
1696.8629	1696.9674	0.1045	62	89	100	SLHTLFGDELCK	56	99.92	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[11]	[7] F12 and F9 and F7 attempt 2	1428/1420	0.293	0.582	0.761	1	Mascot

1703.8925	1703.8389	-0.0536	-31	569	580	TVMENFVAFVDK	65	99.991	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], Oxidation (M)[3]	[5] F5 and F10	512/504	0.947	0.682	0.857	1	Mascot
1703.8925	1703.9235	0.031	18	569	580	TVMENFVAFVDK	60	99.973	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], Oxidation (M)[3]	[4] F11 and F3	1324/1316	0.981	1.153	0.881	1	Mascot
1703.8925	1703.9277	0.0352	21	569	580	TVMENFVAFVDK	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], Oxidation (M)[3]	[4] F11 and F3	1162/1154	1.040	1.306	1.265	1	Mascot
1729.7225	1729.6005	-0.122	-71	76	88	TCVADESHAGCEK	45	99.133	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[2,11]	[5] F5 and F10	234/226	0.627	1.483	0.380	1	Mascot
1744.6569	1744.5756	-0.0813	-47	106	117	ETYGDMADCCEK	81	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[5] F5 and F10	372/364	0.601	0.935	0.924	1	Mascot
1744.6569	1744.6769	0.02	11	106	117	ETYGDMADCCEK	85	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[2] F4 and F13	188/180	0.564	1.022	0.953	1	Mascot
1744.6569	1744.6855	0.0286	16	106	117	ETYGDMADCCEK	50	99.723	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[4] F11 and F3	1076/1068	1.209	1.073	0.938	1	Mascot
1744.6569	1744.6956	0.0387	22	106	117	ETYGDMADCCEK	80	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[4] F11 and F3	1110/1102	0.855	0.800	0.763	1	Mascot
1744.6569	1744.717	0.0601	34	106	117	ETYGDMADCCEK	65	99.991	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[2] F4 and F13	975/967	0.542	1.061	0.868	1	Mascot
1744.6569	1744.7797	0.1228	70	106	117	ETYGDMADCCEK	38	95.793	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10]	[7] F12 and F9 and F7 attempt 2	1368/1360	1.180	1.412	0.907	1	Mascot
1760.6517	1760.6782	0.0265	15	106	117	ETYGDMADCCEK	53	99.845	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10], Oxidation (M)[6]	[2] F4 and F13	186/178	0.721	0.962	0.833	1	Mascot
1760.6517	1760.6796	0.0279	16	106	117	ETYGDMADCCEK	80	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[9,10], Oxidation (M)[6]	[4] F11 and F3	1030/1022	0.965	0.949	0.867	1	Mascot
1857.9014	1857.882	-0.0194	-10	469	482	MPCTEDYLSLILNR	76	99.999	(N-term)_iTRAQ[0], MMTS (C)[3]	[8] F2	558/550	0.855	0.856	0.879	1	Mascot
1860.6581	1860.5664	-0.0917	-49	267	280	ECCHGDLLECADDR	92	100	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[5] F5 and F10	474/466	1.263	1.107	0.804	1	Mascot
1860.6581	1860.6014	-0.0567	-30	267	280	ECCHGDLLECADDR	52	99.839	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[3] F14,15,16 and F6	221/213	0.796	1.173	0.796	1	Mascot
1860.6581	1860.6028	-0.0553	-30	267	280	ECCHGDLLECADDR	81	100	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[5] F5 and F10	407/399	1.372	1.168	1.163	1	Mascot
1860.6581	1860.6277	-0.0304	-16	267	280	ECCHGDLLECADDR	55	99.916	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[4] F11 and F3	329/321	3.021	1.621	1.794	1	Mascot
1860.6581	1860.6558	-0.0023	-1	267	280	ECCHGDLLECADDR	53	99.854	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[1] F8 061011	400/392	1.452	1.453	1.660	1	Mascot
1860.6581	1860.7362	0.0781	42	267	280	ECCHGDLLECADDR	44	98.798	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[5] F5 and F10	1264/1256	1.608	2.083	1.057	1	Mascot
1860.6581	1860.74	0.0819	44	267	280	ECCHGDLLECADDR	79	100	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[3] F14,15,16 and F6	930/922	1.021	1.161	1.116	1	Mascot
1873.8964	1873.8337	-0.0627	-33	469	482	MPCTEDYLSLILNR	48	99.537	(N-term)_iTRAQ[0], MMTS (C)[3], Oxidation (M)[1]	[8] F2	525/517	0.752	0.937	0.819	1	Mascot
2013.8386	2013.8367	-0.0019	-1	184	197	YNGVFQECCQAEDK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[8,9]	[4] F11 and F3	1229/1221	2.242	2.031	0.895	1	Mascot
2013.8386	2013.8453	0.0067	3	184	197	YNGVFQECCQAEDK	56	99.928	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[8,9]	[4] F11 and F3	1288/1280	2.093	1.654	0.932	1	Mascot
2013.8386	2013.8861	0.0475	24	184	197	YNGVFQECCQAEDK	59	99.968	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[8,9]	[4] F11 and F3	1214/1206	1.826	1.527	1.043	1	Mascot
2013.8386	2013.9429	0.1043	52	184	197	YNGVFQECCQAEDK	74	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[8,9]	[4] F11 and F3	1257/1249	1.930	1.969	0.998	1	Mascot
2177.1318	2177.0769	-0.0549	-25	169	183	HPYFYAPELLYYANK	99	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[5] F5 and F10	480/472	0.566	0.661	0.736	1	Mascot
2177.1318	2177.1179	-0.0139	-6	169	183	HPYFYAPELLYYANK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[5] F5 and F10	1349/1341	0.465	0.762	0.976	1	Mascot
2177.1318	2177.2087	0.0769	35	169	183	HPYFYAPELLYYANK	40	97.214	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[3] F14,15,16 and F6	1019/1011	0.811	0.811	1.058	1	Mascot
2503.0405	2502.9846	-0.0559	-22	267	285	ECCHGDLLECADDRADLAK	82	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[19], MMTS (C)[2,3,10]	[8] F2	420/412	1.456	1.205	0.971	1	Mascot

4	RecName: Full=Angiotensinogen; AltName: Full=Serpin A8; Contains: RecName: Full=Angiotensin-1; AltN	gi|1703309	54003.7	15	1182	0.903	0.834	0.947	0.516	0.419	0.274	19	19	19	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type

1188.6609	1188.7065	0.0456	38	459	468	SSGALHFLGR	52	99.815	(N-term)_iTRAQ[0]	[7] F12 and F9 and F7 attempt 2	1293/1285	0.591	0.537	0.887	1	Mascot
1449.7795	1449.7296	-0.0499	-34	82	91	ATEKLEAEDR	43	98.517	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[4]	[1] F8 061011	154/146	0.682	0.694	0.841	1	Mascot
1449.8927	1449.9207	0.028	19	415	424	VLNSVLFELK	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[4] F11 and F3	1252/1244	2.535	2.093	1.490	1	Mascot
1584.957	1584.9668	0.0098	6	392	404	LPTLLGAEANLGK	97	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[4] F11 and F3	1174/1166	0.968	0.778	0.947	1	Mascot
1622.0251	1621.9331	-0.092	-57	367	378	AIHLTVPQLTLK	107	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[5] F5 and F10	424/416	0.840	0.558	0.725	1	Mascot
1622.0251	1621.9836	-0.0415	-26	367	378	AIHLTVPQLTLK	61	99.976	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	344/336	1.220	1.024	1.722	1	Mascot
1622.0251	1622.0746	0.0495	31	367	378	AIHLTVPQLTLK	111	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[3] F14,15,16 and F6	937/929	0.554	0.611	0.762	1	Mascot
1723.9476	1723.9762	0.0286	17	379	391	ASYDLQDLLAQAK	98	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[4] F11 and F3	1198/1190	0.758	0.711	0.819	1	Mascot
1723.9476	1723.9945	0.0469	27	379	391	ASYDLQDLLAQAK	71	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[2] F4 and F13	276/268	0.577	0.667	0.687	1	Mascot
1731.9667	1731.9246	-0.0421	-24	347	359	VEALIFQHNFLTR	60	99.971	(N-term)_iTRAQ[0]	[5] F5 and F10	479/471	1.725	1.608	1.243	1	Mascot
1761.948	1762.0055	0.0575	33	228	241	SLDLSTDPNLAAEK	94	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[4] F11 and F3	1058/1050	1.260	1.073	0.994	1	Mascot
1878.1	1878.0679	-0.0321	-17	27	39	VYIHPFHLLVHSK	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[4] F11 and F3	316/308	1.129	0.852	0.943	1	Mascot
1901.9729	1901.9436	-0.0293	-15	67	81	SSPVDEEALWEQLVR	99	100	(N-term)_iTRAQ[0]	[8] F2	489/481	0.935	0.783	0.913	1	Mascot
1909.9365	1909.9196	-0.0169	-9	148	164	LQAFLGVPGEGQGCTSR	79	100	(N-term)_iTRAQ[0], MMTS (C)[14]	[8] F2	427/419	1.359	1.156	1.126	1	Mascot
2167.3464	2167.3809	0.0345	16	193	210	LLLSTVVGLFTAPGLHLK	54	99.896	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[2] F4 and F13	465/457	1.124	1.300	1.178	1	Mascot
2213.2039	2213.1631	-0.0408	-18	94	110	ASEVGLLLNFMGFHVYK	127	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17]	[5] F5 and F10	594/586	0.399	0.395	0.692	1	Mascot
2229.1987	2229.1565	-0.0422	-19	94	110	ASEVGLLLNFMGFHVYK	52	99.822	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17], Oxidation (M)[11]	[5] F5 and F10	529/521	0.765	0.722	0.892	1	Mascot
2514.4316	2514.3342	-0.0974	-39	325	345	VPLSANGYLLLIQPHHTLDLR	50	99.702	(N-term)_iTRAQ[0]	[5] F5 and F10	491/483	0.471	0.539	0.663	1	Mascot
2669.5559	2669.6338	0.0779	29	169	192	KVLSSLQTIQGLLVAPGGASSQAR	78	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[2] F4 and F13	331/323	1.167	1.186	1.097	1	Mascot

5	apolipoprotein A-I, apoA-1 [Bos=cattle, Friesian-Holstein male calves aged 2-4 weeks, Peptide, 247	gi|245563	31729.2	15	1043	0.997	0.988	1.018	0.438	0.291	0.215	27	27	27	100

Protein Group

apolipoprotein A-I preproprotein [Bos taurus]	gi|75832056	33716.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1147.6569	1147.5867	-0.0702	-61	139	145	VQELQDK	43	98.568	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	171/163	0.929	0.955	0.924	1	Mascot
1161.6388	1161.6711	0.0323	28	124	132	VAPLGEEFR	38	95.773	(N-term)_iTRAQ[0]	[4] F11 and F3	1059/1051	1.207	1.100	1.100	1	Mascot
1404.7032	1404.6575	-0.0457	-33	113	121	WHEEVEIYR	55	99.917	(N-term)_iTRAQ[0]	[8] F2	314/306	1.102	1.054	1.031	1	Mascot
1404.7032	1404.7605	0.0573	41	113	121	WHEEVEIYR	49	99.642	(N-term)_iTRAQ[0]	[7] F12 and F9 and F7 attempt 2	1306/1298	0.871	0.857	0.940	1	Mascot
1449.7458	1449.7748	0.029	20	166	176	QQLAPYSDDLR	58	99.952	(N-term)_iTRAQ[0]	[4] F11 and F3	1021/1013	1.123	1.058	1.084	1	Mascot
1504.8832	1504.8921	0.0089	6	231	242	VSILAAIDEASK	64	99.989	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[2] F4 and F13	287/279	1.073	1.476	1.183	1	Mascot
1504.8832	1504.9407	0.0575	38	231	242	VSILAAIDEASK	85	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1207/1199	1.467	1.430	1.462	1	Mascot
1506.7798	1506.7072	-0.0726	-48	188	199	EGGGSLAEYHAK	83	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[1] F8 061011	176/168	0.291	0.589	0.721	1	Mascot
1506.7798	1506.8101	0.0303	20	188	199	EGGGSLAEYHAK	43	98.476	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[5] F5 and F10	1051/1043	2.313	1.036	0.883	1	Mascot
1506.7798	1506.8741	0.0943	63	188	199	EGGGSLAEYHAK	77	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[7] F12 and F9 and F7 attempt 2	1208/1200	0.631	0.597	0.825	1	Mascot
1547.9128	1547.9839	0.0711	46	137	145	QKVQELQDK	60	99.974	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,9]	[7] F12 and F9 and F7 attempt 2	804/796	0.971	1.217	1.075	1	Mascot
1554.8413	1554.8055	-0.0358	-23	102	111	VQPYLDEFQK	55	99.901	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[3] F14,15,16 and F6	196/188	1.421	1.066	1.168	1	Mascot
1554.8413	1554.8502	0.0089	6	102	111	VQPYLDEFQK	63	99.985	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	216/208	1.080	1.017	0.922	1	Mascot
1554.8413	1554.8571	0.0158	10	102	111	VQPYLDEFQK	61	99.975	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	188/180	0.891	0.876	1.030	1	Mascot
1554.8413	1554.8671	0.0258	17	102	111	VQPYLDEFQK	71	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	135/127	1.000	1.022	1.013	1	Mascot
1554.8413	1554.9163	0.075	48	102	111	VQPYLDEFQK	61	99.975	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	964/956	0.882	0.969	1.004	1	Mascot
1686.8948	1686.8357	-0.0591	-35	33	45	DYVAQFEASALGK	97	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[5] F5 and F10	432/424	1.190	1.214	1.391	1	Mascot
1686.8948	1686.9039	0.0091	5	33	45	DYVAQFEASALGK	98	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[4] F11 and F3	1179/1171	0.671	0.726	0.836	1	Mascot

1686.8948	1686.9125	0.0177	10	33	45	DYVAQFEASALGK	87	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[2] F4 and F13	262/254	0.727	0.681	0.582	1	Mascot
1777.0806	1777.1949	0.1143	64	231	243	VSILAAIDEASKK	59	99.961	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12,13]	[7] F12 and F9 and F7 attempt 2	1422/1414	1.163	1.194	1.299	1	Mascot
1865.0266	1864.9445	-0.0821	-44	51	64	LLDNWDTLASTLSK	77	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	525/517	1.500	1.185	1.061	1	Mascot
1865.0266	1865.0361	0.0095	5	51	64	LLDNWDTLASTLSK	46	99.292	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[2] F4 and F13	362/354	0.995	1.113	1.094	1	Mascot
1865.0266	1865.041	0.0144	8	51	64	LLDNWDTLASTLSK	124	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[4] F11 and F3	1285/1277	1.116	1.116	1.051	1	Mascot
1915.1276	1915.0759	-0.0517	-27	16	28	VKDFATVYVEAIK	68	99.995	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,13]	[4] F11 and F3	344/336	1.110	0.629	1.317	1	Mascot
2102.0764	2102.1504	0.074	35	29	45	DSGRDYVAQFEASALGK	74	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17]	[3] F14,15,16 and F6	931/923	1.056	1.331	0.977	1	Mascot
2221.1387	2221.1797	0.041	18	67	82	EQLGPVTQEFWDNLEK	60	99.974	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1247/1239	0.628	0.698	0.928	1	Mascot
2476.3081	2476.2375	-0.0706	-29	65	82	VREQLGPVTQEFWDNLEK	67	99.994	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[5] F5 and F10	477/469	1.186	1.309	1.085	1	Mascot

6	ceruloplasmin precursor [Ovis aries]	gi|57619174	129919.1	14	1038	0.850	0.840	1.154	0.342	0.660	0.414	17	17	17	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1468.8158	1468.7639	-0.0519	-35	178	187	IYHSHIDAPK	41	97.72	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[3] F14,15,16 and F6	104/96	0.542	0.123	0.622	1	Mascot
1468.8158	1468.777	-0.0388	-26	178	187	IYHSHIDAPK	64	99.989	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[4] F11 and F3	108/100	0.532	0.644	0.960	1	Mascot
1486.7094	1486.6094	-0.1	-67	942	951	ANEEFMESNK	71	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[5] F5 and F10	213/205	0.651	0.721	0.888	1	Mascot
1503.8767	1503.8049	-0.0718	-48	469	481	AAHPLSIEPIGVR	44	98.82	(N-term)_iTRAQ[0]	[5] F5 and F10	316/308	0.661	0.633	0.802	1	Mascot
1577.7693	1577.8447	0.0754	48	427	437	EYTDASFSNQK	56	99.931	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[2] F4 and F13	901/893	1.243	1.123	1.271	1	Mascot
1662.8248	1662.8744	0.0496	30	70	81	AVYLQYTDENFR	50	99.716	(N-term)_iTRAQ[0]	[4] F11 and F3	1105/1097	0.901	0.815	1.360	1	Mascot
1677.8416	1677.7637	-0.0779	-46	835	849	TESSTVTPTAPGETR	121	100	(N-term)_iTRAQ[0]	[8] F2	175/167	1.187	1.230	1.393	1	Mascot
1697.8619	1697.816	-0.0459	-27	780	792	QFTDSTFQVPVER	60	99.969	(N-term)_iTRAQ[0]	[8] F2	352/344	1.247	1.349	1.447	1	Mascot
1697.8619	1697.887	0.0251	15	780	792	QFTDSTFQVPVER	47	99.407	(N-term)_iTRAQ[0]	[4] F11 and F3	1097/1089	0.966	1.004	1.202	1	Mascot
1770.9836	1770.9229	-0.0607	-34	188	201	DIASGLIGPLIHCK	92	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[13]	[5] F5 and F10	501/493	0.920	1.129	1.501	1	Mascot
1792.0341	1792.0414	0.0073	4	99	110	AETGDKVYVHLK	78	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6,12]	[5] F5 and F10	1127/1119	0.644	0.730	0.989	1	Mascot
1973.0021	1972.9318	-0.0703	-36	939	951	VDKANEEFMESNK	86	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,13]	[1] F8 061011	227/219	0.941	1.207	1.245	1	Mascot
1988.9971	1988.9065	-0.0906	-46	939	951	VDKANEEFMESNK	57	99.945	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,13], Oxidation (M)[9]	[1] F8 061011	183/175	1.092	0.801	1.497	1	Mascot
1998.0756	1998.1329	0.0573	29	520	533	EVGPTYKDPVCLAK	74	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,14], MMTS (C)[11]	[3] F14,15,16 and F6	858/850	0.908	0.988	1.264	1	Mascot
2881.2483	2881.1313	-0.117	-41	238	258	TYCSEPEKVEQDNEDFQESNR	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8], MMTS (C)[3]	[5] F5 and F10	306/298	0.985	1.311	1.526	1	Mascot
2911.4685	2911.4216	-0.0469	-16	992	1014	GIYTSDVFDLFPGTYQTLEMTPK	89	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[23]	[8] F2	558/550	0.414	0.493	0.634	1	Mascot
2921.3845	2921.2	-0.1845	-63	593	613	MFTTAPDQVDKENEDFQESNK	75	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11,21], Oxidation (M)[1]	[5] F5 and F10	268/260	1.423	1.841	1.897	1	Mascot

7	complement C3 [Sus scrofa]	gi|47522844	205367.1	15	969	0.876	0.893	0.962	0.325	0.248	0.197	23	23	23	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1064.6714	1064.7218	0.0504	47	599	605	GVFVLNK	44	98.941	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	952/944	0.754	0.620	0.915	1	Mascot
1088.6925	1088.7196	0.0271	25	591	598	VGLVAVDK	40	97.109	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	931/923	0.739	1.066	0.787	1	Mascot
1176.6875	1176.6422	-0.0453	-38	614	620	IWDVVEK	41	97.741	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	348/340	0.633	1.068	1.041	1	Mascot
1176.6875	1176.6638	-0.0237	-20	614	620	IWDVVEK	42	98.298	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[3] F14,15,16 and F6	202/194	1.023	0.510	0.864	1	Mascot
1176.6875	1176.6947	0.0072	6	614	620	IWDVVEK	44	98.854	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	135/127	1.356	1.093	1.086	1	Mascot
1176.6875	1176.6978	0.0103	9	614	620	IWDVVEK	39	96.696	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	188/180	1.333	1.203	1.166	1	Mascot

1176.6875	1176.7061	0.0186	16	614	620	IWDVVEK	41	97.568	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	216/208	0.959	0.925	0.962	1	Mascot
1176.6875	1176.7257	0.0382	32	614	620	IWDVVEK	44	98.941	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	970/962	1.191	1.109	1.068	1	Mascot
1227.6606	1227.687	0.0264	22	1050	1058	GYTQQLAFR	51	99.775	(N-term)_iTRAQ[0]	[4] F11 and F3	1035/1027	0.872	0.997	1.354	1	Mascot
1331.7808	1331.808	0.0272	20	1309	1318	ILWESASLLR	42	98.317	(N-term)_iTRAQ[0]	[4] F11 and F3	1254/1246	1.909	1.020	1.613	1	Mascot
1336.8688	1336.84	-0.0288	-22	599	606	GVFVLNKK	53	99.85	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,8]	[1] F8 061011	266/258	0.642	0.736	0.845	1	Mascot
1380.8348	1380.8812	0.0464	34	1440	1448	NTLIIYLDK	45	99.145	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1156/1148	0.720	1.363	0.886	1	Mascot
1499.858	1499.8282	-0.0298	-20	1049	1058	KGYTQQLAFR	44	98.764	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[1] F8 061011	253/245	1.075	0.992	1.101	1	Mascot
1577.7571	1577.8538	0.0967	61	1534	1544	ACEPGVDYVYK	82	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[2]	[2] F4 and F13	954/946	0.657	0.867	0.936	1	Mascot
1633.9047	1633.9071	0.0024	1	543	554	EVVADSVWVDVK	83	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1130/1122	0.718	0.801	0.704	1	Mascot
1708.9268	1708.9872	0.0604	35	912	924	AAVYNHFISDGVK	51	99.779	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[3] F14,15,16 and F6	829/821	0.702	0.816	0.837	1	Mascot
1708.9268	1709.0417	0.1149	67	912	924	AAVYNHFISDGVK	61	99.977	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[7] F12 and F9 and F7 attempt 2	1317/1309	0.433	0.553	0.778	1	Mascot
2074.0942	2074.2112	0.117	56	862	877	VELLYNPAFCSLATAK	69	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[10]	[4] F11 and F3	1310/1302	1.014	1.108	1.041	1	Mascot
2090.1897	2090.1255	-0.0642	-31	343	358	TGIPIVTSPYQIHFTK	77	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[5] F5 and F10	425/417	0.774	0.877	0.940	1	Mascot
2090.1897	2090.2029	0.0132	6	343	358	TGIPIVTSPYQIHFTK	81	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[2] F4 and F13	251/243	1.128	0.999	1.108	1	Mascot
2338.3242	2338.2783	-0.0459	-20	795	811	DSITTWEILAVSLSDKK	128	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16, 17]	[5] F5 and F10	535/527	0.668	0.699	0.834	1	Mascot
2338.3242	2338.4331	0.1089	47	795	811	DSITTWEILAVSLSDKK	91	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16, 17]	[3] F14,15,16 and F6	1074/1066	0.939	0.711	0.811	1	Mascot
2967.4597	2967.4065	-0.0532	-18	1259	1282	YYGGGYGSTQATFMVFQALAQYQK	103	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[24]	[8] F2	555/547	0.960	1.010	0.862	1	Mascot

8	alpha-1-antiproteinase precursor [Ovis aries]	gi|57526646	50698.8	13	804	1.067	0.896	1.053	0.475	0.361	0.357	19	19	19	100	

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1148.6772	1148.714	0.0368	32	358	365	AALTIDEK	47	99.452	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	912/904	0.704	0.427	0.930	1	Mascot
1168.646	1168.5886	-0.0574	-49	179	185	INDYVEK	41	97.517	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	228/220	1.350	1.050	1.293	1	Mascot
1215.7181	1215.7311	0.013	11	323	332	TVLGELGINR	55	99.914	(N-term)_iTRAQ[0]	[4] F11 and F3	1114/1106	1.150	1.111	1.055	1	Mascot
1440.8434	1440.9263	0.0829	58	178	185	KINDYVEK	48	99.571	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,8]	[7] F12 and F9 and F7 attempt 2	850/842	0.934	0.796	1.052	1	Mascot
1466.8352	1466.7963	-0.0389	-27	148	157	LVDTFLEDVK	57	99.948	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[5] F5 and F10	480/472	1.648	1.430	1.899	1	Mascot
1466.8352	1466.8562	0.021	14	148	157	LVDTFLEDVK	66	99.993	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[4] F11 and F3	1237/1229	1.187	1.407	1.454	1	Mascot
1466.8352	1466.8593	0.0241	16	148	157	LVDTFLEDVK	46	99.327	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	313/305	2.280	1.763	1.413	1	Mascot
1488.842	1488.9088	0.0668	45	302	312	YASSANLHLPK	41	97.802	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	1282/1274	1.073	0.874	0.898	1	Mascot
1605.8483	1605.7822	-0.0661	-41	229	239	DFHVNEQTTVK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[5] F5 and F10	217/209	1.053	0.996	1.260	1	Mascot
1605.8483	1605.8077	-0.0406	-25	229	239	DFHVNEQTTVK	66	99.993	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[1] F8 061011	208/200	0.635	0.665	0.625	1	Mascot
1605.8483	1605.8666	0.0183	11	229	239	DFHVNEQTTVK	47	99.445	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	752/744	1.710	0.753	0.738	1	Mascot
1605.8483	1605.9216	0.0733	46	229	239	DFHVNEQTTVK	61	99.98	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	1231/1223	0.800	0.650	0.922	1	Mascot
1675.7874	1675.8517	0.0643	38	246	256	LGMFDLHYCDK	60	99.972	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[9]	[3] F14,15,16 and F6	983/975	0.899	0.768	1.000	1	Mascot
1675.7874	1675.8717	0.0843	50	246	256	LGMFDLHYCDK	39	96.517	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[9]	[7] F12 and F9 and F7 attempt 2	1438/1430	0.521	0.696	0.983	1	Mascot
1761.0394	1760.9717	-0.0677	-38	301	312	KYASSANLHLPK	68	99.996	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,12]	[4] F11 and F3	179/171	0.727	0.771	0.827	1	Mascot
1994.111	1994.0408	-0.0702	-35	48	62	IAPNLANFAFSIYHK	101	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[5] F5 and F10	505/497	1.036	0.901	1.353	1	Mascot
2201.2876	2201.3569	0.0693	31	282	296	LQQLEDKLNNELLAK	76	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,15]	[3] F14,15,16 and F6	1000/992	1.758	1.458	1.341	1	Mascot
2276.2061	2276.1802	-0.0259	-11	197	213	DLDQDTVFALVNYISFK	78	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17]	[5] F5 and F10	588/580	1.249	0.843	1.226	1	Mascot
2510.3057	2510.3296	0.0239	10	333	353	VFSNGADLSGITEEQPLMVSK	43	98.483	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[21]	[4] F11 and F3	1183/1175	0.982	0.679	0.587	1	Mascot

9	RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	gi|41016830	38112	10	687	1.084	0.954	1.063	0.346	0.185	0.168	16	16	16	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1177.6449	1177.6891	0.0442	38	269	277	LQAEAFQAR	53	99.845	(N-term)_iTRAQ[0]	[4] F11 and F3	1006/998	1.316	1.075	1.288	1	Mascot
1179.58	1179.6038	0.0238	20	121	129	LGSDMEDLR	57	99.946	(N-term)_iTRAQ[0]	[4] F11 and F3	1037/1029	1.100	1.022	0.981	1	Mascot
1218.7092	1218.6534	-0.0558	-46	292	299	QWAGLVEK	60	99.973	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	310/302	0.678	1.182	1.086	1	Mascot
1218.7092	1218.7697	0.0605	50	292	299	QWAGLVEK	58	99.954	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	950/942	1.438	1.271	1.286	1	Mascot
1565.8043	1565.7266	-0.0777	-50	176	189	LAVYQAGASEGAER	59	99.963	(N-term)_iTRAQ[0]	[5] F5 and F10	248/240	1.470	0.659	1.089	1	Mascot
1565.8043	1565.7374	-0.0669	-43	176	189	LAVYQAGASEGAER	78	100	(N-term)_iTRAQ[0]	[8] F2	256/248	1.461	1.193	1.137	1	Mascot
1565.8043	1565.8868	0.0825	53	176	189	LAVYQAGASEGAER	86	100	(N-term)_iTRAQ[0]	[4] F11 and F3	999/991	1.219	1.103	1.203	1	Mascot
1643.8262	1643.8535	0.0273	17	37	49	GQDSQPWEQVLGR	51	99.775	(N-term)_iTRAQ[0]	[4] F11 and F3	1114/1106	0.735	0.787	0.953	1	Mascot
1680.8176	1680.7826	-0.035	-21	280	291	SWFEPLVEDMQR	71	99.998	(N-term)_iTRAQ[0]	[8] F2	498/490	0.898	0.773	0.963	1	Mascot
1713.9619	1713.9227	-0.0392	-23	209	223	AATLSTQVGQPLLDR	75	99.999	(N-term)_iTRAQ[0]	[8] F2	339/331	1.030	0.894	1.055	1	Mascot
1821.9137	1821.8862	-0.0275	-15	137	151	SEVQAMLGQSTEELR	98	100	(N-term)_iTRAQ[0]	[8] F2	387/379	1.295	1.090	1.204	1	Mascot
1837.9086	1837.8442	-0.0644	-35	137	151	SEVQAMLGQSTEELR	53	99.849	(N-term)_iTRAQ[0], Oxidation (M)[6]	[8] F2	290/282	1.014	0.922	0.964	1	Mascot
2045.0093	2044.9668	-0.0425	-21	93	109	EELEGQLAPMAQETQAR	73	99.999	(N-term)_iTRAQ[0]	[8] F2	323/315	0.660	0.829	1.331	1	Mascot
2435.2109	2435.2227	0.0118	5	90	109	AYREELEGQLAPMAQETQAR	63	99.987	(N-term)_iTRAQ[0]	[2] F4 and F13	188/180	1.015	0.975	0.886	1	Mascot
2435.2109	2435.2546	0.0437	18	90	109	AYREELEGQLAPMAQETQAR	47	99.406	(N-term)_iTRAQ[0]	[2] F4 and F13	135/127	0.973	0.896	0.764	1	Mascot
2451.2058	2451.2578	0.052	21	90	109	AYREELEGQLAPMAQETQAR	49	99.612	(N-term)_iTRAQ[0], Oxidation (M)[13]	[2] F4 and F13	135/127	1.703	0.830	1.001	1	Mascot

10	complement component C3 [Ovis aries]	gi|12649541	43395	10	576	0.956	0.911	1.015	0.483	0.298	0.292	10	10	10	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1227.6606	1227.687	0.0264	22	76	84	GYTQQLAFR	51	99.775	(N-term)_iTRAQ[0]	[4] F11 and F3	1035/1027	0.872	0.997	1.354	1	Mascot
1331.7808	1331.808	0.0272	20	335	344	ILWESASLLR	42	98.317	(N-term)_iTRAQ[0]	[4] F11 and F3	1254/1246	1.909	1.020	1.613	1	Mascot
1362.7753	1362.7961	0.0208	15	244	250	WEEPNKK	38	95.023	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6,7]	[5] F5 and F10	1053/1045	0.728	0.666	0.922	1	Mascot
1365.6671	1365.645	-0.0221	-16	196	205	AGDFLENHYR	51	99.792	(N-term)_iTRAQ[0]	[1] F8 061011	266/258	0.613	0.525	0.887	1	Mascot
1499.858	1499.8282	-0.0298	-20	75	84	KGYTQQLAFR	44	98.764	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[1] F8 061011	253/245	1.075	0.992	1.101	1	Mascot
1663.9503	1663.9076	-0.0427	-26	109	122	VFALSTNLIAIDSR	89	100	(N-term)_iTRAQ[0]	[8] F2	479/471	1.537	1.485	1.206	1	Mascot
2009.0275	2009.0454	0.0179	9	180	195	DICEAQVNSLGPSITK	71	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[3]	[4] F11 and F3	1138/1130	0.448	0.699	0.707	1	Mascot
2079.2576	2079.2175	-0.0401	-19	209	225	RPYTVAIAAYALALLGK	43	98.6	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17]	[5] F5 and F10	595/587	1.304	1.149	1.110	1	Mascot
2472.3457	2472.3337	-0.012	-5	309	327	DVPDHKELNLDVSIHLPSR	44	98.979	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6]	[5] F5 and F10	1255/1247	0.926	0.922	0.725	1	Mascot
2967.4597	2967.4065	-0.0532	-18	285	308	YYGGGYGSTQATFMVFQALAQYQK	103	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[24]	[8] F2	555/547	0.960	1.010	0.862	1	Mascot

11	preprocomplement component C3 [Mus musculus]	gi|309122	205041.7	9	570	0.838	0.842	0.914	0.250	0.227	0.142	16	16	16	100

Protein Group

RecName: Full=Complement C3; Contains: RecName: Full=Complement C3 beta chain; Contains: RecName: F	gi|116597	203965.7
complement C3 [Mus musculus]	gi|126518317	204899.5
complement component C3 prepropeptide, last [Mus musculus]	gi|387114	205042.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1064.6714	1064.7218	0.0504	47	600	606	GVFVLNK	44	98.941	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	952/944	0.754	0.620	0.915	1	Mascot
1088.6925	1088.7196	0.0271	25	592	599	VGLVAVDK	40	97.109	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	931/923	0.739	1.066	0.787	1	Mascot
1176.6875	1176.6422	-0.0453	-38	615	621	IWDVVEK	41	97.741	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	348/340	0.633	1.068	1.041	1	Mascot

1176.6875	1176.6638	-0.0237	-20	615	621	IWDVVEK	42	98.298	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[3] F14,15,16 and F6	202/194	1.023	0.510	0.864	1	Mascot
1176.6875	1176.6947	0.0072	6	615	621	IWDVVEK	44	98.854	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	135/127	1.356	1.093	1.086	1	Mascot
1176.6875	1176.6978	0.0103	9	615	621	IWDVVEK	39	96.696	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	188/180	1.333	1.203	1.166	1	Mascot
1176.6875	1176.7061	0.0186	16	615	621	IWDVVEK	41	97.568	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	216/208	0.959	0.925	0.962	1	Mascot
1176.6875	1176.7257	0.0382	32	615	621	IWDVVEK	44	98.941	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	970/962	1.191	1.109	1.068	1	Mascot
1336.8688	1336.84	-0.0288	-22	600	607	GVFVLNKK	53	99.85	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,8]	[1] F8 061011	266/258	0.642	0.736	0.845	1	Mascot
1577.7571	1577.8538	0.0967	61	1536	1546	ACEPGVDYVYK	82	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[2]	[2] F4 and F13	954/946	0.657	0.867	0.936	1	Mascot
1633.9047	1633.9071	0.0024	1	545	556	EVVADSVWVDVK	83	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1130/1122	0.718	0.801	0.704	1	Mascot
1660.0295	1660.0381	0.0086	5	892	904	SSVAVPYVIVPLK	52	99.813	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[4] F11 and F3	1187/1179	0.971	1.016	0.720	1	Mascot
1999.0331	1999.007	-0.0261	-13	1492	1504	FYHPEKDDGMLSK	44	98.979	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6,13]	[5] F5 and F10	1150/1142	0.666	0.713	1.031	1	Mascot
2015.028	2015.0646	0.0366	18	1492	1504	FYHPEKDDGMLSK	44	98.822	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6,13], Oxidation (M)[10]	[5] F5 and F10	1110/1102	0.651	0.714	0.998	1	Mascot
2338.3242	2338.2783	-0.0459	-20	797	813	DSITTWEILAVSLSDKK	128	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16,17]	[5] F5 and F10	535/527	0.668	0.699	0.834	1	Mascot
2338.3242	2338.4331	0.1089	47	797	813	DSITTWEILAVSLSDKK	91	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16,17]	[3] F14,15,16 and F6	1074/1066	0.939	0.711	0.811	1	Mascot

12	transferrin [Sus scrofa]	gi|833800	86770.7	7	549	0.808	0.777	0.855	0.365	0.271	0.265	16	16	16	100

Protein Group

RecName: Full=Serotransferrin; Short=Transferrin; AltName: Full=Beta-1 metal-binding globulin; AltN	gi|136192	86931.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1023.6084	1023.5566	-0.0518	-51	537	543	GDVAFVK	42	98.313	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	228/220	0.809	0.707	0.738	1	Mascot
1207.766	1207.7739	0.0079	7	430	438	GYLAVAVVK	61	99.976	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1081/1073	0.761	0.721	0.777	1	Mascot
1241.6075	1241.6476	0.0401	32	523	531	YYGYTGAFR	38	95.945	(N-term)_iTRAQ[0]	[4] F11 and F3	1063/1055	1.179	1.029	1.001	1	Mascot
1639.8778	1639.9443	0.0665	41	406	417	CGLVPVLAENYK	61	99.979	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[1]	[4] F11 and F3	1207/1199	2.141	1.164	0.439	1	Mascot
1893.0116	1892.9187	-0.0929	-49	88	101	DNPQTHYYAVAVVK	54	99.894	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	256/248	0.870	0.549	0.791	1	Mascot
1893.0116	1892.9353	-0.0763	-40	88	101	DNPQTHYYAVAVVK	98	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	306/298	0.696	0.632	1.051	1	Mascot
1893.0116	1892.9382	-0.0734	-39	88	101	DNPQTHYYAVAVVK	121	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	282/274	0.740	0.686	0.761	1	Mascot
1893.0116	1892.9613	-0.0503	-27	88	101	DNPQTHYYAVAVVK	40	96.816	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	303/295	0.695	0.390	0.666	1	Mascot
1893.0116	1892.9622	-0.0494	-26	88	101	DNPQTHYYAVAVVK	91	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[1] F8 061011	269/261	1.034	1.017	0.774	1	Mascot
1893.0116	1893.058	0.0464	25	88	101	DNPQTHYYAVAVVK	118	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[3] F14,15,16 and F6	803/795	0.459	0.696	0.905	1	Mascot
1893.0116	1893.074	0.0624	33	88	101	DNPQTHYYAVAVVK	96	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	1153/1145	0.746	0.829	1.022	1	Mascot
2119.0627	2118.9917	-0.071	-34	388	405	GEADAMSLDGGYIYIAGK	96	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[5] F5 and F10	427/419	0.805	0.891	0.843	1	Mascot
2119.0627	2119.0623	-0.0004	0	388	405	GEADAMSLDGGYIYIAGK	78	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[4] F11 and F3	1175/1167	0.625	0.597	0.749	1	Mascot
2603.4126	2603.3179	-0.0947	-36	385	405	IVKGEADAMSLDGGYIYIAGK	130	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,21]	[5] F5 and F10	431/423	0.473	0.765	0.876	1	Mascot
2603.4126	2603.4468	0.0342	13	385	405	IVKGEADAMSLDGGYIYIAGK	51	99.771	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,21]	[5] F5 and F10	1293/1285	0.609	0.977	1.343	1	Mascot
2619.4075	2619.3086	-0.0989	-38	385	405	IVKGEADAMSLDGGYIYIAGK	101	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,21], Oxidation (M)[9]	[5] F5 and F10	394/386	1.330	1.333	1.442	1	Mascot

13	alpha-2-HS-glycoprotein precursor [Ovis aries]	gi|57526674	41650.9	6	534	1.102	0.830	0.862	0.321	0.440	0.282	8	8	8	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type

1442.8213	1442.788	-0.0333	-23	58	67	HTLNQIDSVK	76	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[1] F8 061011	213/205	1.130	0.970	1.063	1	Mascot
1557.8523	1557.8696	0.0173	11	121	131	QDGQFSVLFTK	61	99.979	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[2] F4 and F13	217/209	1.646	1.445	1.267	1	Mascot
1557.8523	1557.9008	0.0485	31	121	131	QDGQFSVLFTK	53	99.862	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[2] F4 and F13	983/975	1.578	1.205	0.838	1	Mascot
2256.0979	2256.0513	-0.0466	-21	104	120	QQTEHAVEGDCDIHVLK	77	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17], MMTS (C)[11]	[1] F8 061011	321/313	1.075	0.893	1.152	1	Mascot
2392.2141	2392.1865	-0.0276	-12	318	338	HTFSGVASVESASGEAFHVGK	60	99.973	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[21]	[1] F8 061011	350/342	0.971	0.891	0.964	1	Mascot
2683.2458	2683.1899	-0.0559	-21	29	50	EPACDDPDTEQAALAAVDYINK	116	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[22], MMTS (C)[4]	[8] F2	463/455	0.881	0.317	0.732	1	Mascot
2683.2458	2683.2727	0.0269	10	29	50	EPACDDPDTEQAALAAVDYINK	38	95.907	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[22], MMTS (C)[4]	[4] F11 and F3	1222/1214	1.102	0.772	0.577	1	Mascot
2754.4436	2754.415	-0.0286	-10	188	211	AQFVPLPGSVSVEFAVAATDCIAK	144	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[24], MMTS (C)[21]	[8] F2	587/579	0.734	0.686	0.576	1	Mascot

14	immunoglobulin lambda light chain constant region segment 1 [Ovis aries]	gi|52366986	13044.6	5	525	1.094	0.964	1.073	0.447	0.378	0.251	15	15	15	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1434.7798	1434.6858	-0.094	-66	44	54	ADGSTINQNVK	91	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[5] F5 and F10	134/126	1.435	1.185	1.203	1	Mascot
1434.7798	1434.8113	0.0315	22	44	54	ADGSTINQNVK	45	99.08	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[5] F5 and F10	997/989	2.295	2.355	2.076	1	Mascot
1965.0215	1964.9554	-0.0661	-34	66	80	YAASSYLTLTGSEWK	143	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[5] F5 and F10	431/423	1.441	1.406	1.111	1	Mascot
1965.0215	1964.9746	-0.0469	-24	66	80	YAASSYLTLTGSEWK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[4] F11 and F3	305/297	0.646	0.651	1.101	1	Mascot
1965.0215	1965.0332	0.0117	6	66	80	YAASSYLTLTGSEWK	98	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[4] F11 and F3	1179/1171	1.222	1.171	1.199	1	Mascot
1965.0215	1965.036	0.0145	7	66	80	YAASSYLTLTGSEWK	99	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[2] F4 and F13	260/252	1.119	0.884	1.125	1	Mascot
1965.0215	1965.1161	0.0946	48	66	80	YAASSYLTLTGSEWK	58	99.951	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[4] F11 and F3	1258/1250	1.435	1.240	1.203	1	Mascot
2062.9653	2062.8677	-0.0976	-47	83	98	SSYTCEVTHEGSTVTK	135	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[5] F5 and F10	260/252	1.407	0.862	1.048	1	Mascot
2062.9653	2062.8889	-0.0764	-37	83	98	SSYTCEVTHEGSTVTK	107	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[4] F11 and F3	173/165	0.641	0.707	0.942	1	Mascot
2062.9653	2062.9084	-0.0569	-28	83	98	SSYTCEVTHEGSTVTK	92	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[1] F8 061011	249/241	1.276	1.003	0.997	1	Mascot
2062.9653	2062.9226	-0.0427	-21	83	98	SSYTCEVTHEGSTVTK	105	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[3] F14,15,16 and F6	155/147	0.814	0.678	0.925	1	Mascot
2062.9653	2063.0234	0.0581	28	83	98	SSYTCEVTHEGSTVTK	131	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[3] F14,15,16 and F6	781/773	0.773	0.696	0.916	1	Mascot
2293.2173	2293.2178	0.0005	0	5	23	SAPSVTLFPPSTEELSTNK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[19]	[4] F11 and F3	1134/1126	1.116	0.901	0.875	1	Mascot
2558.3376	2558.3057	-0.0319	-12	24	43	ATVVCLINDFYPGSVNVVWK	93	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20], MMTS (C)[5]	[5] F5 and F10	584/576	1.013	0.788	0.841	1	Mascot
2558.3376	2558.415	0.0774	30	24	43	ATVVCLINDFYPGSVNVVWK	56	99.928	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20], MMTS (C)[5]	[2] F4 and F13	438/430	0.785	0.853	0.951	1	Mascot

15	keratin 1 [Homo sapiens]	gi|11935049	70199.8	8	504	2.650	3.123	1.530	0.954	1.100	0.475	10	10	10	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1353.7261	1353.6477	-0.0784	-58	356	364	AQYEDIAQK	66	99.992	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[5] F5 and F10	212/204	1.793	2.301	1.310	1	Mascot
1421.8124	1421.7811	-0.0313	-22	473	483	LALDLEIATYR	54	99.888	(N-term)_iTRAQ[0]	[8] F2	459/451	2.369	3.051	1.562	1	Mascot
1590.92	1591.0013	0.0813	51	344	355	SLDLDSIIAEVK	76	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1257/1249	1.889	2.288	1.354	1	Mascot
1671.8951	1671.9244	0.0293	18	186	197	SLNNQFASFIDK	88	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[2] F4 and F13	231/223	3.331	4.145	1.664	1	Mascot
1671.8951	1671.9363	0.0412	25	186	197	SLNNQFASFIDK	56	99.929	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[2] F4 and F13	988/980	2.321	3.168	1.044	1	Mascot
1772.9766	1772.91	-0.0666	-38	365	376	SKAEAESLYQSK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,12]	[1] F8 061011	229/221	3.252	3.392	1.963	1	Mascot

1772.9766	1772.9552	-0.0214	-12	365	376	SKAEAESLYQSK	50	99.7	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,12]	[1] F8 061011	169/161	1.755	1.828	1.161	1	Mascot
1826.0396	1826.1379	0.0983	54	278	289	TNAENEFVTIKK	50	99.728	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11, 12]	[7] F12 and F9 and F7 attempt 2	1279/1271	3.007	3.023	1.254	1	Mascot
1860.9536	1860.9867	0.0331	18	418	432	QISNLQQSISDAEQR	55	99.909	(N-term)_iTRAQ[0]	[4] F11 and F3	1071/1063	3.568	4.925	2.679	1	Mascot
2138.0791	2138.0222	-0.0569	-27	224	239	THNLEPYFESFINNLR	52	99.838	(N-term)_iTRAQ[0]	[5] F5 and F10	546/538	4.493	4.529	1.904	1	Mascot

16	alpha-1-antiproteinase precursor [Bos taurus]	gi|27806941	51106.1	9	502	1.030	0.900	1.071	0.522	0.444	0.354	13	13	13	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1148.6772	1148.714	0.0368	32	358	365	AALTIDEK	47	99.452	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	912/904	0.704	0.427	0.930	1	Mascot
1168.646	1168.5886	-0.0574	-49	179	185	INDYVEK	41	97.517	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	228/220	1.350	1.050	1.293	1	Mascot
1440.8434	1440.9263	0.0829	58	178	185	KINDYVEK	48	99.571	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,8]	[7] F12 and F9 and F7 attempt 2	850/842	0.934	0.796	1.052	1	Mascot
1466.8352	1466.7963	-0.0389	-27	148	157	LVDTFLEDVK	57	99.948	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[5] F5 and F10	480/472	1.648	1.430	1.899	1	Mascot
1466.8352	1466.8562	0.021	14	148	157	LVDTFLEDVK	66	99.993	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[4] F11 and F3	1237/1229	1.187	1.407	1.454	1	Mascot
1466.8352	1466.8593	0.0241	16	148	157	LVDTFLEDVK	46	99.327	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	313/305	2.280	1.763	1.413	1	Mascot
1488.842	1488.9088	0.0668	45	302	312	YASSANLHLPK	41	97.802	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	1282/1274	1.073	0.874	0.898	1	Mascot
1606.8323	1606.866	0.0337	21	229	239	DFHVDEQTTVK	55	99.9	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	758/750	0.819	0.623	0.745	1	Mascot
1606.8323	1606.9128	0.0805	50	229	239	DFHVDEQTTVK	45	99.023	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	1234/1226	0.708	0.616	0.675	1	Mascot
1675.7874	1675.8517	0.0643	38	246	256	LGMFDLHYCDK	60	99.972	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[9]	[3] F14,15,16 and F6	983/975	0.899	0.768	1.000	1	Mascot
1675.7874	1675.8717	0.0843	50	246	256	LGMFDLHYCDK	39	96.517	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[9]	[7] F12 and F9 and F7 attempt 2	1438/1430	0.521	0.696	0.983	1	Mascot
1761.0394	1760.9717	-0.0677	-38	301	312	KYASSANLHLPK	68	99.996	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,12]	[4] F11 and F3	179/171	0.727	0.771	0.827	1	Mascot
2201.2876	2201.3569	0.0693	31	282	296	LQQLEDKLNNELLAK	76	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,15]	[3] F14,15,16 and F6	1000/992	1.758	1.458	1.341	1	Mascot

17	Ig lambda chain C region - sheep (fragment)	gi|109030	13171.8	4	495	0.912	0.897	1.114	0.430	0.315	0.199	15	15	15	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1965.0215	1964.9554	-0.0661	-34	65	79	YAASSYLTLTGSEWK	143	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[5] F5 and F10	431/423	1.441	1.406	1.111	1	Mascot
1965.0215	1964.9746	-0.0469	-24	65	79	YAASSYLTLTGSEWK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[4] F11 and F3	305/297	0.646	0.651	1.101	1	Mascot
1965.0215	1965.0332	0.0117	6	65	79	YAASSYLTLTGSEWK	98	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[4] F11 and F3	1179/1171	1.222	1.171	1.199	1	Mascot
1965.0215	1965.036	0.0145	7	65	79	YAASSYLTLTGSEWK	99	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[2] F4 and F13	260/252	1.119	0.884	1.125	1	Mascot
1965.0215	1965.1161	0.0946	48	65	79	YAASSYLTLTGSEWK	58	99.951	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[4] F11 and F3	1258/1250	1.435	1.240	1.203	1	Mascot
2062.9653	2062.8677	-0.0976	-47	82	97	SSYTCEVTHEGSTVTK	135	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[5] F5 and F10	260/252	1.407	0.862	1.048	1	Mascot
2062.9653	2062.8889	-0.0764	-37	82	97	SSYTCEVTHEGSTVTK	107	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[4] F11 and F3	173/165	0.641	0.707	0.942	1	Mascot
2062.9653	2062.9084	-0.0569	-28	82	97	SSYTCEVTHEGSTVTK	92	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[1] F8 061011	249/241	1.276	1.003	0.997	1	Mascot
2062.9653	2062.9226	-0.0427	-21	82	97	SSYTCEVTHEGSTVTK	105	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[3] F14,15,16 and F6	155/147	0.814	0.678	0.925	1	Mascot
2062.9653	2063.0234	0.0581	28	82	97	SSYTCEVTHEGSTVTK	131	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[3] F14,15,16 and F6	781/773	0.773	0.696	0.916	1	Mascot
2492.3621	2492.2773	-0.0848	-34	4	22	SAPSVTLFPPSKEELDTNK	121	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12, 19]	[5] F5 and F10	359/351	0.744	0.805	1.156	1	Mascot
2492.3621	2492.3149	-0.0472	-19	4	22	SAPSVTLFPPSKEELDTNK	55	99.918	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12, 19]	[5] F5 and F10	601/593	1.239	1.499	1.427	1	Mascot
2492.3621	2492.3928	0.0307	12	4	22	SAPSVTLFPPSKEELDTN	77	99.999	(N-term)_iTRAQ[0],	[5] F5 and F10	1238/1230	0.881	1.122	1.745	1	Mascot

						K			Lysine(K)_iTRAQ[12,19]							
2531.3269	2531.2876	-0.0393	-16	23	42	ATVVCLISDFYPGSVNVVWK	96	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20], MMTS (C)[5]	[5] F5 and F10	593/585	0.362	0.502	1.034	1	Mascot
2531.3269	2531.3806	0.0537	21	23	42	ATVVCLISDFYPGSVNVVWK	46	99.311	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20], MMTS (C)[5]	[2] F4 and F13	446/438	0.646	0.842	1.023	1	Mascot

18	complement C3 preproprotein [Cavia porcellus]	gi|290543340	204039.3	8	483	0.868	0.896	0.915	0.259	0.280	0.130	14	14	14	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1064.6714	1064.7218	0.0504	47	604	610	GVFVLNK	44	98.941	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	952/944	0.754	0.620	0.915	1	Mascot
1088.6925	1088.7196	0.0271	25	596	603	VGLVAVDK	40	97.109	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	931/923	0.739	1.066	0.787	1	Mascot
1176.6875	1176.6422	-0.0453	-38	619	625	IWDVVEK	41	97.741	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	348/340	0.633	1.068	1.041	1	Mascot
1176.6875	1176.6638	-0.0237	-20	619	625	IWDVVEK	42	98.298	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[3] F14,15,16 and F6	202/194	1.023	0.510	0.864	1	Mascot
1176.6875	1176.6947	0.0072	6	619	625	IWDVVEK	44	98.854	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	135/127	1.356	1.093	1.086	1	Mascot
1176.6875	1176.6978	0.0103	9	619	625	IWDVVEK	39	96.696	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	188/180	1.333	1.203	1.166	1	Mascot
1176.6875	1176.7061	0.0186	16	619	625	IWDVVEK	41	97.568	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	216/208	0.959	0.925	0.962	1	Mascot
1176.6875	1176.7257	0.0382	32	619	625	IWDVVEK	44	98.941	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	970/962	1.191	1.109	1.068	1	Mascot
1336.8688	1336.84	-0.0288	-22	604	611	GVFVLNKK	53	99.85	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,8]	[1] F8 061011	266/258	0.642	0.736	0.845	1	Mascot
1380.8348	1380.8812	0.0464	34	1446	1454	NTLIIYLDK	45	99.145	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1156/1148	0.720	1.363	0.886	1	Mascot
1577.7571	1577.8538	0.0967	61	1539	1549	ACEPGVDYVYK	82	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[2]	[2] F4 and F13	954/946	0.657	0.867	0.936	1	Mascot
1660.0295	1660.0381	0.0086	5	897	909	SSVAVPYVLVPLK	52	99.813	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[4] F11 and F3	1187/1179	0.971	1.016	0.720	1	Mascot
2338.3242	2338.2783	-0.0459	-20	802	818	DSITTWEILAVSLSDKK	128	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16,17]	[5] F5 and F10	535/527	0.668	0.699	0.834	1	Mascot
2338.3242	2338.4331	0.1089	47	802	818	DSITTWEILAVSLSDKK	91	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16,17]	[3] F14,15,16 and F6	1074/1066	0.939	0.711	0.811	1	Mascot

19	contactin-1 precursor [Bos taurus]	gi|27805871	122262.6	6	481	1.742	1.450	1.200	0.822	0.821	0.444	7	7	7	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1430.8127	1430.7853	-0.0274	-19	722	732	ELTITWAPLSR	42	98.108	(N-term)_iTRAQ[0]	[8] F2	441/433	1.556	1.216	0.968	1	Mascot
1657.834	1657.7791	-0.0549	-33	654	667	TDPPIIEGNMEAAR	56	99.923	(N-term)_iTRAQ[0]	[8] F2	293/285	1.492	1.166	1.091	1	Mascot
1829.9293	1829.8489	-0.0804	-44	844	856	YWASHDKEAAAHR	57	99.939	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[3] F14,15,16 and F6	123/115	1.163	0.744	0.765	1	Mascot
1999.9553	1999.8577	-0.0976	-49	701	721	TDGAAPNVAPSDVGGGGGSNR	124	100	(N-term)_iTRAQ[0]	[8] F2	196/188	4.003	3.390	1.999	1	Mascot
2039.1913	2039.2516	0.0603	30	236	249	TTKPYPADIVVQFK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,14]	[3] F14,15,16 and F6	918/910	1.228	1.135	0.945	1	Mascot
2385.2368	2385.1453	-0.0915	-38	699	721	IKTDGAAPNVAPSDVGGGGGSNR	42	98.254	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2]	[5] F5 and F10	226/218	2.079	1.841	1.502	1	Mascot
2385.2368	2385.2695	0.0327	14	699	721	IKTDGAAPNVAPSDVGGGGGSNR	124	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2]	[3] F14,15,16 and F6	756/748	1.765	1.802	1.559	1	Mascot

20	transthyretin precursor [Ovis aries]	gi|57526651	17582.2	7	464	0.628	0.729	1.085	0.319	0.479	0.336	11	11	11	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1187.6993	1187.6165	-0.0828	-70	42	51	GSPAANVGVK	51	99.796	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[5] F5 and F10	153/145	0.362	0.774	1.345	1	Mascot
1187.6993	1187.7024	0.0031	3	42	51	GSPAANVGVK	71	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	164/156	0.599	0.761	0.990	1	Mascot
1696.8428	1696.8508	0.008	5	56	68	AADETWEPFASGK	52	99.824	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[2] F4 and F13	136/128	0.823	0.909	1.062	1	Mascot
1696.8428	1696.8597	0.0169	10	56	68	AADETWEPFASGK	50	99.682	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[2] F4 and F13	203/195	0.939	0.739	1.634	1	Mascot
1696.8428	1696.8615	0.0187	11	56	68	AADETWEPFASGK	83	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[2] F4 and F13	188/180	0.806	1.074	1.094	1	Mascot

1696.8428	1696.9285	0.0857	51	56	68	AADETWEPFASGK	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[2] F4 and F13	963/955	0.671	0.720	1.017	1	Mascot
1877.9338	1877.9673	0.0335	18	69	83	TSDSGELHGLTTEDK	101	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[3] F14,15,16 and F6	759/751	0.585	0.626	0.945	1	Mascot
1969.0403	1969.0217	-0.0186	-9	55	68	KAADETWEPFASGK	54	99.876	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,14]	[1] F8 061011	303/295	0.470	1.012	1.555	1	Mascot
2758.4912	2758.5073	0.0161	6	124	146	HYTIAALLSPYSYSTTALVSSPK	46	99.238	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[23]	[2] F4 and F13	364/356	1.156	1.129	1.323	1	Mascot
2858.4795	2858.6121	0.1326	46	69	90	TSDSGELHGLTTEDKFVEGLYK	62	99.98	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15,22]	[5] F5 and F10	1260/1252	0.266	0.162	0.675	1	Mascot
2887.5339	2887.5481	0.0142	5	124	147	HYTIAALLSPYSYSTTALVSSPKE	49	99.643	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[23]	[2] F4 and F13	364/356	0.779	0.867	0.728	1	Mascot

21	complement component C4 [Ovis aries]	gi|1227	15519.9	7	463	0.840	0.957	1.063	0.351	0.317	0.224	7	7	7	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1074.6769	1074.6154	-0.0615	-57	38	44	AVDLIQK	44	98.817	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	258/250	0.525	0.750	0.895	1	Mascot
1305.646	1305.6111	-0.0349	-27	56	65	DGSYGAWLHR	47	99.468	(N-term)_iTRAQ[0]	[1] F8 061011	272/264	0.701	0.715	1.110	1	Mascot
1655.9254	1655.9398	0.0144	9	66	77	DSSTWLTAFVLK	63	99.986	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1279/1271	0.631	0.754	0.755	1	Mascot
1717.9358	1717.9036	-0.0322	-19	93	105	LQETATWLLSQQR	55	99.904	(N-term)_iTRAQ[0]	[8] F2	443/435	1.664	1.525	1.310	1	Mascot
1778.7928	1778.7198	-0.073	-41	106	119	DDGSFHDPFPVMDR	64	99.989	(N-term)_iTRAQ[0]	[5] F5 and F10	369/361	0.826	0.829	0.989	1	Mascot
1830.0219	1830.042	0.0201	11	78	92	ILSLAQDQVGGSPEK	96	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[4] F11 and F3	1094/1086	1.047	1.360	1.205	1	Mascot
2380.3135	2380.197	-0.1165	-49	20	35	YLDKTEQWSLLPPETK	95	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[4,16]	[5] F5 and F10	417/409	0.880	1.062	1.308	1	Mascot

22	RecName: Full=Complement C4; Contains: RecName: Full=Complement C4 alpha chain; Contains: RecName:	gi|31563307	108117.7	9	458	0.939	1.028	1.112	0.436	0.321	0.323	9	9	9	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1074.6769	1074.6154	-0.0615	-57	226	232	AVDLIQK	44	98.817	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	258/250	0.525	0.750	0.895	1	Mascot
1109.6565	1109.5997	-0.0568	-51	351	358	ANTFLGAK	55	99.919	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	247/239	0.998	1.027	0.949	1	Mascot
1305.646	1305.6111	-0.0349	-27	244	253	DGSYGAWLHR	47	99.468	(N-term)_iTRAQ[0]	[1] F8 061011	272/264	0.701	0.715	1.110	1	Mascot
1351.7831	1351.8199	0.0368	27	12	21	LGQYTSPVAK	41	97.714	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	921/913	1.681	1.345	1.936	1	Mascot
1374.8354	1374.892	0.0566	41	823	831	ITQVLHFTK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[7] F12 and F9 and F7 attempt 2	1346/1338	1.146	1.333	1.118	1	Mascot
1655.9254	1655.9398	0.0144	9	254	265	DSSTWLTAFVLK	63	99.986	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1279/1271	0.631	0.754	0.755	1	Mascot
1667.9102	1667.9253	0.0151	9	530	541	LEEELQFSLGSK	47	99.482	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1166/1158	0.823	0.922	1.014	1	Mascot
1712.9429	1712.8804	-0.0625	-36	517	529	SHVLQLTNHQVHR	44	98.967	(N-term)_iTRAQ[0]	[3] F14,15,16 and F6	133/125	0.926	1.225	1.275	1	Mascot
1717.9358	1717.9036	-0.0322	-19	281	293	LQETATWLLSQQR	55	99.904	(N-term)_iTRAQ[0]	[8] F2	443/435	1.664	1.525	1.310	1	Mascot

23	clusterin preproprotein [Bos taurus]	gi|27806907	55864.1	7	455	0.807	0.930	1.102	0.314	0.290	0.180	9	9	9	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1197.6877	1197.6389	-0.0488	-41	209	216	GSLFFNPK	59	99.966	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	332/324	0.444	0.810	0.907	1	Mascot
1197.6877	1197.7462	0.0585	49	209	216	GSLFFNPK	49	99.674	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	964/956	0.828	0.735	0.959	1	Mascot
1390.8403	1390.8541	0.0138	10	63	72	LLLSSLEEAK	48	99.534	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[4] F11 and F3	1168/1160	0.570	0.663	1.052	1	Mascot
1555.7546	1555.7681	0.0135	9	177	188	ASSIMDELFQDR	72	99.998	(N-term)_iTRAQ[0]	[4] F11 and F3	1231/1223	0.815	0.922	1.145	1	Mascot
1555.7546	1555.7887	0.0341	22	177	188	ASSIMDELFQDR	39	96.198	(N-term)_iTRAQ[0]	[4] F11 and F3	1252/1244	0.889	0.820	1.221	1	Mascot
1663.0377	1663.2009	0.1632	98	62	72	KLLLSSLEEAK	54	99.896	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,11]	[7] F12 and F9 and F7 attempt 2	1373/1365	0.735	0.900	1.045	1	Mascot
1814.9899	1815.0369	0.047	26	332	343	LYDQLLQSYQQK	81	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1160/1152	1.545	1.654	1.455	1	Mascot
1954.8759	1954.829	-0.0469	-24	162	176	EQSHVMDVMEDSFTR	96	100	(N-term)_iTRAQ[0]	[5] F5 and F10	376/368	1.012	1.318	1.310	1	Mascot

2120.0322	2119.9683	-0.0639	-30	193	208	RPQDTQYYSPFSSFPR	46	99.234	(N-term)_iTRAQ[0]	[5] F5 and F10	384/376	0.837	0.894	0.940	1	Mascot

24 albumin [Sus scrofa] gi|164318 79319.3 7 442 0.940 1.069 0.924 1.048 1.235 0.607 21 21 21 100

Protein Group

albumin [Sus scrofa] gi|833798 79333.3

serum albumin precursor [Sus scrofa] gi|52353352 79758.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1175.6508	1175.6292	-0.0216	-18	481	487	LCVLHEK	41	97.477	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[1] F8 061011	283/275	0.990	0.972	0.967	1	Mascot
1175.6508	1175.6975	0.0467	40	481	487	LCVLHEK	40	97.109	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[7] F12 and F9 and F7 attempt 2	1293/1285	1.301	1.047	0.748	1	Mascot
1260.5291	1260.5676	0.0385	31	497	505	CCTESLVNR	43	98.581	(N-term)_iTRAQ[0], MMTS (C)[1,2]	[4] F11 and F3	1071/1063	1.992	2.408	1.293	1	Mascot
1302.8242	1302.7657	-0.0585	-45	547	555	QTALVELLK	44	98.958	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[3] F14,15,16 and F6	226/218	1.249	2.368	1.376	1	Mascot
1302.8242	1302.7715	-0.0527	-40	547	555	QTALVELLK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[5] F5 and F10	409/401	1.135	1.403	0.860	1	Mascot
1302.8242	1302.8359	0.0117	9	547	555	QTALVELLK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1149/1141	1.196	1.443	0.987	1	Mascot
1302.8242	1302.8368	0.0126	10	547	555	QTALVELLK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	235/227	0.663	1.379	1.131	1	Mascot
1302.8242	1302.8618	0.0376	29	547	555	QTALVELLK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	995/987	0.751	1.218	1.051	1	Mascot
1344.6519	1344.7135	0.0616	46	411	418	QNCELFEK	50	99.685	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8], MMTS (C)[3]	[5] F5 and F10	1168/1160	0.100	0.100	0.184	1	Mascot
1344.6519	1344.7535	0.1016	76	411	418	QNCELFEK	52	99.836	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8], MMTS (C)[3]	[7] F12 and F9 and F7 attempt 2	921/913	0.158	0.131	0.285	1	Mascot
1575.0216	1574.9834	-0.0382	-24	546	555	KQTALVELLK	61	99.979	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[8] F2	375/367	1.065	1.281	1.002	1	Mascot
1575.0216	1575.0242	0.0026	2	546	555	KQTALVELLK	62	99.981	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[1] F8 061011	365/357	0.570	1.183	1.125	1	Mascot
1575.0216	1575.1365	0.1149	73	546	555	KQTALVELLK	57	99.941	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[7] F12 and F9 and F7 attempt 2	1362/1354	0.912	0.993	0.968	1	Mascot
1860.6581	1860.5664	-0.0917	-49	265	278	ECCHGDLLECADDR	92	100	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[5] F5 and F10	474/466	1.263	1.107	0.804	1	Mascot
1860.6581	1860.6014	-0.0567	-30	265	278	ECCHGDLLECADDR	52	99.839	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[3] F14,15,16 and F6	221/213	0.796	1.173	0.796	1	Mascot
1860.6581	1860.6028	-0.0553	-30	265	278	ECCHGDLLECADDR	81	100	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[5] F5 and F10	407/399	1.372	1.168	1.163	1	Mascot
1860.6581	1860.6277	-0.0304	-16	265	278	ECCHGDLLECADDR	55	99.916	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[4] F11 and F3	329/321	3.021	1.621	1.794	1	Mascot
1860.6581	1860.6558	-0.0023	-1	265	278	ECCHGDLLECADDR	53	99.854	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[1] F8 061011	400/392	1.452	1.453	1.660	1	Mascot
1860.6581	1860.7362	0.0781	42	265	278	ECCHGDLLECADDR	44	98.798	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[5] F5 and F10	1264/1256	1.608	2.083	1.057	1	Mascot
1860.6581	1860.74	0.0819	44	265	278	ECCHGDLLECADDR	79	100	(N-term)_iTRAQ[0], MMTS (C)[2,3,10]	[3] F14,15,16 and F6	930/922	1.021	1.161	1.116	1	Mascot
2503.0405	2502.9846	-0.0559	-22	265	283	ECCHGDLLECADDRADLAK	82	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[19], MMTS (C)[2,3,10]	[8] F2	420/412	1.456	1.205	0.971	1	Mascot

25 fibronectin gi|224863 95322.7 6 421 1.309 1.001 1.011 0.725 0.723 0.350 7 7 7 100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1281.6382	1281.6561	0.0179	14	296	305	FTNVGPDTMR	55	99.917	(N-term)_iTRAQ[0]	[4] F11 and F3	1019/1011	1.953	1.338	1.460	1	Mascot
1707.8938	1707.8341	-0.0597	-35	142	155	QYNVGPAASQYPLR	58	99.958	(N-term)_iTRAQ[0]	[8] F2	301/293	1.451	1.189	0.879	1	Mascot
1707.8938	1707.9291	0.0353	21	142	155	QYNVGPAASQYPLR	49	99.659	(N-term)_iTRAQ[0]	[4] F11 and F3	1040/1032	1.323	1.093	0.813	1	Mascot
1773.9731	1773.9127	-0.0604	-34	40	54	VDVIPVNLPGEHGQR	51	99.767	(N-term)_iTRAQ[0]	[5] F5 and F10	346/338	0.674	0.657	0.731	1	Mascot
1865.9967	1866.0474	0.0507	27	546	560	GDSPASSKPVSINYR	52	99.828	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[3] F14,15,16 and F6	760/752	0.829	0.498	0.774	1	Mascot
1963.111	1963.114	0.003	2	156	171	NLQPGSEYAVSLVAVK	67	99.994	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1137/1129	2.700	2.812	1.632	1	Mascot
2405.3208	2405.2563	-0.0645	-27	616	636	EINLAPDSSSVVVSGLMVATK	138	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[21]	[8] F2	472/464	1.162	0.630	1.119	1	Mascot

26	keratin, type I cytoskeletal 9 [Homo sapiens]	gi|55956899	66101.5	4	411	2.070	2.735	1.391	1.362	2.399	0.635	4	4	4	100

Protein Group

cytokeratin 9 [Homo sapiens]	gi|435476	66166.6
keratin 9 [Homo sapiens]	gi|453155	66024.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1527.8542	1527.944	0.0898	59	185	192	IQDWYDKK	53	99.847	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,8]	[7] F12 and F9 and F7 attempt 2	912/904	4.530	6.290	2.241	1	Mascot
2126.1704	2126.2537	0.0833	39	375	390	HGVQELEIELQSQLSK	96	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[3] F14,15,16 and F6	985/977	1.525	2.142	1.027	1	Mascot
2849.2634	2849.2075	-0.0559	-20	64	95	GGGGSFGYSYGGGSGG GFSASSLGGGFGGGSR	173	100	(N-term)_iTRAQ[0]	[8] F2	398/390	2.238	3.619	1.791	1	Mascot
3511.4863	3511.269	-0.2173	-62	580	619	GGSGGSHGGGSGFGGE SGGSYGGGEEASGSGG GYGGGSGK	89	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[40]	[5] F5 and F10	203/195	1.187	1.147	0.908	1	Mascot

27	immunoglobulin gamma-1 chain [Ovis aries]	gi|388235	55491.8	6	399	1.121	0.908	0.914	0.413	0.297	0.153	14	14	14	100

Protein Group

Ig gamma-1 chain - sheep (fragment)	gi|346578	55377.8
Ig heavy chain C region - sheep (fragment)	gi|109029	36810.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1245.7903	1245.8126	0.0223	18	466	473	SISKPPGK	40	97.201	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[4,8]	[7] F12 and F9 and F7 attempt 2	771/763	1.417	0.696	1.242	1	Mascot
1424.6254	1424.6464	0.021	15	240	249	VEPGCPDPCK	44	98.87	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10], MMTS (C)[5,9]	[2] F4 and F13	217/209	1.191	0.948	0.737	1	Mascot
1424.6254	1424.6941	0.0687	48	240	249	VEPGCPDPCK	53	99.858	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10], MMTS (C)[5,9]	[2] F4 and F13	966/958	1.345	1.015	0.852	1	Mascot
2024.1174	2024.0583	-0.0591	-29	326	341	VVSALPIQHQDWTGGK	120	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[5] F5 and F10	337/329	1.422	1.237	1.113	1	Mascot
2024.1174	2024.0848	-0.0326	-16	326	341	VVSALPIQHQDWTGGK	84	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[5] F5 and F10	601/593	0.943	0.950	0.790	1	Mascot
2024.1174	2024.1013	-0.0161	-8	326	341	VVSALPIQHQDWTGGK	44	98.909	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[1] F8 061011	340/332	1.520	1.610	1.005	1	Mascot
2024.1174	2024.1593	0.0419	21	326	341	VVSALPIQHQDWTGGK	117	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[5] F5 and F10	1223/1215	1.366	1.203	1.170	1	Mascot
2115.1584	2115.1035	-0.0549	-26	369	384	EPQVYVLAPPQEELSK	55	99.91	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[5] F5 and F10	378/370	0.547	0.633	0.801	1	Mascot
2115.1584	2115.1072	-0.0512	-24	369	384	EPQVYVLAPPQEELSK	54	99.885	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[8] F2	379/371	0.803	0.626	0.816	1	Mascot
2115.1584	2115.1665	0.0081	4	369	384	EPQVYVLAPPQEELSK	58	99.95	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1120/1112	0.783	0.742	0.887	1	Mascot
2115.1584	2115.2253	0.0669	32	369	384	EPQVYVLAPPQEELSK	40	96.903	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1286/1278	1.105	0.710	0.773	1	Mascot
2289.0796	2289.0969	0.0173	8	417	435	YGTTTSQLDADGSYFLYS R	76	99.999	(N-term)_iTRAQ[0]	[2] F4 and F13	249/241	1.484	0.868	0.951	1	Mascot
3417.5969	3417.5835	-0.0134	-4	408	435	NGQPESEDKYGTTTSQL DADGSYFLYSR	43	98.616	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1149/1141	0.843	0.735	0.922	1	Mascot
3417.5969	3417.6345	0.0376	11	408	435	NGQPESEDKYGTTTSQL DADGSYFLYSR	53	99.871	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	218/210	1.651	1.277	0.895	1	Mascot

28	antithrombin-III precursor [Ovis aries]	gi|57164383	57635.1	7	397	1.043	1.093	1.051	0.258	0.162	0.143	7	7	7	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1212.6722	1212.6202	-0.052	-43	358	365	IEDSFSVK	38	95.419	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	283/275	0.763	0.897	0.904	1	Mascot
1507.8427	1507.809	-0.0337	-22	447	458	EVALNTIIFMGR	78	100	(N-term)_iTRAQ[0]	[8] F2	483/475	1.075	1.155	0.994	1	Mascot
1510.7322	1510.7089	-0.0233	-15	47	57	DIPVNPMCIYR	49	99.651	(N-term)_iTRAQ[0], MMTS (C)[8]	[8] F2	436/428	0.984	1.000	1.165	1	Mascot
1628.8683	1628.927	0.0587	36	148	158	TSDQIHFFFAK	73	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	926/918	1.314	1.119	1.154	1	Mascot
2065.8928	2065.9199	0.0271	13	275	290	ADGESCSVPMMYQEGK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[6]	[4] F11 and F3	1097/1089	0.820	1.048	0.916	1	Mascot
2147.1794	2147.251	0.0716	33	134	147	QLMEVFKFDTISEK	40	97.156	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,1	[3] F14,15,16 and F6	993/985	1.494	1.450	1.299	1	Mascot

									4]							
2586.3484	2586.3784	0.03	12	104	124	NNNDNIFLSPLSISTAFAMTK	48	99.532	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[21]	[4] F11 and F3	1347/1339	1.031	1.059	0.985	1	Mascot

29	insulin-like growth factor-binding protein 2 precursor [Ovis aries]	gi|57164237	37202.1	7	394	0.900	1.147	1.249	0.349	0.456	0.260	7	7	7	100

Protein Group

insulin-like growth factor-binding protein 2 precursor [Bos taurus]	gi|27807005	37028

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1347.7631	1347.8269	0.0638	47	200	208	HHLGLEEPK	53	99.863	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	897/889	0.659	1.149	1.127	1	Mascot
1477.7369	1477.8073	0.0704	48	115	125	ALVHGEGTCEK	71	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[9]	[7] F12 and F9 and F7 attempt 2	1230/1222	0.645	0.843	1.008	1	Mascot
1535.7451	1535.7174	-0.0277	-18	103	114	CYPNPGSELPLR	51	99.751	(N-term)_iTRAQ[0], MMTS (C)[1]	[8] F2	377/369	1.693	1.930	1.508	1	Mascot
1619.9604	1619.8883	-0.0721	-45	200	209	HHLGLEEPKK	49	99.652	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9,10]	[3] F14,15,16 and F6	120/112	1.121	1.579	1.754	1	Mascot
1748.8412	1748.7885	-0.0527	-30	217	229	TPCQQELDQVLER	70	99.997	(N-term)_iTRAQ[0], MMTS (C)[3]	[8] F2	471/463	1.040	1.206	1.301	1	Mascot
2053.896	2053.8206	-0.0754	-37	294	309	GDPECHLFYNEQQGAR	40	97.315	(N-term)_iTRAQ[0], MMTS (C)[5]	[5] F5 and F10	336/328	0.822	1.121	1.180	1	Mascot
2170.1016	2170.0754	-0.0262	-12	240	255	GPLEHLYSLHIPNCDK	60	99.972	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[14]	[1] F8 061011	448/440	0.696	0.655	1.026	1	Mascot

30	pigment epithelium-derived factor precursor [Bos taurus]	gi|27806487	50038.9	5	388	1.444	1.516	1.330	0.895	1.142	0.283	5	5	5	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1188.8052	1188.8368	0.0316	27	344	350	ITGKPIK	38	95.926	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[4,7]	[7] F12 and F9 and F7 attempt 2	817/809	2.031	1.738	1.551	1	Mascot
1655.889	1655.9127	0.0237	14	332	343	LQSLFDAPDFSK	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1201/1193	1.583	2.048	1.402	1	Mascot
1703.8877	1703.8383	-0.0494	-29	52	65	LAAAVSNFGYDLYR	80	100	(N-term)_iTRAQ[0]	[8] F2	469/461	1.521	1.507	1.149	1	Mascot
2271.1907	2271.1118	-0.0789	-35	105	121	ALYYDLISNPDIHGTYK	98	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17]	[5] F5 and F10	431/423	0.576	0.534	0.993	1	Mascot
2362.3997	2362.3604	-0.0393	-17	261	279	IAQLPLTGSTSIIFFLPQK	99	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[19]	[8] F2	560/552	2.233	2.800	1.675	1	Mascot

31	RecName: Full=Gelsolin; AltName: Full=Actin-depolymerizing factor; Short=ADF; AltName: Full=Brevin;	gi|121118	91483.3	6	371	0.946	1.141	1.045	0.306	0.372	0.239	6	6	6	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1116.5773	1116.5212	-0.0561	-50	659	665	LFACSNK	44	98.986	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[4]	[5] F5 and F10	319/311	1.188	1.847	1.116	1	Mascot
1156.646	1156.5836	-0.0624	-54	351	358	TASDFISK	44	98.767	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	238/230	1.408	1.377	1.390	1	Mascot
2011.0422	2010.9756	-0.0666	-33	138	152	EVQGFESATFLGYFK	88	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[5] F5 and F10	508/500	0.837	0.865	0.824	1	Mascot
2042.0039	2042.002	-0.0019	-1	318	331	SEDCFILDHGKDGK	73	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11,14], MMTS (C)[4]	[5] F5 and F10	1196/1188	0.799	1.148	1.075	1	Mascot
2098.0886	2098.126	0.0374	18	704	718	DSQEEEKTEALTSAK	67	99.994	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,15]	[3] F14,15,16 and F6	758/750	1.065	1.104	1.221	1	Mascot
2590.3035	2590.3271	0.0236	9	617	638	AQPVQVAEGSEPDSFWEALGGK	56	99.932	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[22]	[4] F11 and F3	1221/1213	0.602	0.794	0.777	1	Mascot

32	prostaglandin-H2 D-isomerase [Ovis aries]	gi|57164293	22794.6	4	343	1.025	1.089	1.018	0.382	0.351	0.219	8	8	8	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1608.8176	1608.7279	-0.0897	-56	138	151	GPGPDSLMATLYSR	48	99.581	(N-term)_iTRAQ[0]	[5] F5 and F10	424/416	0.996	1.175	0.837	1	Mascot

1608.8176	1608.781	-0.0366	-23	138	151	GPGPDSLMATLYSR	82	100	(N-term)_iTRAQ[0]	[8] F2	420/412	0.812	0.730	0.887	1	Mascot
1608.8176	1608.8326	0.015	9	138	151	GPGPDSLMATLYSR	88	100	(N-term)_iTRAQ[0]	[4] F11 and F3	1172/1164	0.651	0.740	0.913	1	Mascot
1825.0356	1825.0129	-0.0227	-12	169	182	SLGFTEEGIVFLPK	38	95.615	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[5] F5 and F10	1356/1348	1.538	1.409	1.558	1	Mascot
1825.0356	1825.0688	0.0332	18	169	182	SLGFTEEGIVFLPK	102	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[4] F11 and F3	1247/1239	0.999	0.863	1.011	1	Mascot
1825.0356	1825.0907	0.0551	30	169	182	SLGFTEEGIVFLPK	66	99.992	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[2] F4 and F13	325/317	0.802	1.288	0.873	1	Mascot
2148.1011	2148.1353	0.0342	16	43	58	WFTSGLASNSSWFLEK	40	97.471	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1299/1291	1.796	1.576	1.025	1	Mascot
2313.3076	2313.2129	-0.0947	-41	169	185	SLGFTEEGIVFLPKTDK	113	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14,17]	[5] F5 and F10	442/434	1.046	1.266	1.207	1	Mascot

33	beta-2-microglobulin precursor [Ovis aries]	gi|57164311	14844.8	4	340	0.914	0.991	1.166	0.296	0.384	0.185	4	4	4	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1415.7264	1415.6598	-0.0666	-47	68	77	SEQSDLSFSK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[5] F5 and F10	232/224	0.904	1.050	1.300	1	Mascot
1424.8472	1424.9287	0.0815	57	101	110	VNHVTLTQPK	71	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[7] F12 and F9 and F7 attempt 2	1219/1211	0.846	0.672	1.051	1	Mascot
1801.0078	1800.9515	-0.0563	-31	66	77	IKSEQSDLSFSK	85	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,12]	[1] F8 061011	249/241	1.410	1.629	1.392	1	Mascot
2330.1704	2330.0967	-0.0737	-32	78	94	DWSFYLLSHAEFTPNSK	114	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17]	[5] F5 and F10	498/490	0.646	0.838	0.973	1	Mascot

34	RecName: Full=Plasminogen	gi|3914364	41059.2	4	322	1.081	1.033	1.206	0.280	0.359	0.146	4	4	4	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1358.74	1358.7659	0.0259	19	179	189	EASVQEIPVSR	59	99.967	(N-term)_iTRAQ[0]	[4] F11 and F3	990/982	1.094	1.065	1.428	1	Mascot
1754.8907	1754.85	-0.0407	-23	329	341	VSTYVPWIEETMR	49	99.67	(N-term)_iTRAQ[0]	[8] F2	485/477	1.339	1.485	1.250	1	Mascot
2095.9067	2095.8589	-0.0478	-23	67	83	NPDGDVNGPWCYTTNPR	76	99.999	(N-term)_iTRAQ[0], MMTS (C)[11]	[8] F2	363/355	1.260	1.111	1.064	1	Mascot
3243.3635	3243.3074	-0.0561	-17	274	302	STELCAGDLAGGTDSCQGDSGGPLVCFEK	138	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[29], MMTS (C)[5,16,26]	[8] F2	518/510	0.741	0.648	1.113	1	Mascot

35	ectonucleotide pyrophosphatase/phosphodiesterase family member 2 [Pongo abelii]	gi|197101079	111363.4	7	316	1.151	1.036	1.176	0.521	0.536	0.378	7	7	7	100

Protein Group

Ectonucleotide pyrophosphatase/phosphodiesterase 2 [Homo sapiens]	gi|22137786	108526.8
autotaxin-t [Homo sapiens]	gi|1160616	108540.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1622.8121	1622.7762	-0.0359	-22	314	326	YGPFGPEMTNPLR	40	97.096	(N-term)_iTRAQ[0]	[8] F2	414/406	1.399	1.230	1.244	1	Mascot
1636.8456	1636.7698	-0.0758	-46	850	861	DIEHLTSLDFFR	52	99.84	(N-term)_iTRAQ[0]	[5] F5 and F10	468/460	0.930	0.670	1.345	1	Mascot
1700.6986	1700.6548	-0.0438	-26	59	71	CFELQEAGPPDCR	44	98.781	(N-term)_iTRAQ[0], MMTS (C)[1,12]	[8] F2	421/413	1.613	1.375	1.184	1	Mascot
1748.7751	1748.8528	0.0777	44	465	476	CFFQGDHGFDNK	40	97.062	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[1]	[7] F12 and F9 and F7 attempt 2	1347/1339	1.040	1.108	1.376	1	Mascot
1977.1782	1977.1207	-0.0575	-29	412	422	KPDQHFKPYLK	45	99.086	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,7,11]	[3] F14,15,16 and F6	148/140	0.704	0.780	0.995	1	Mascot
2295.1804	2295.137	-0.0434	-19	715	731	YDAFLVTNMVPMYPAFK	49	99.667	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17]	[8] F2	551/543	2.164	2.163	1.722	1	Mascot
2437.2358	2437.2441	0.0083	3	696	714	QMSYGFLFPPYLSSSPEAK	46	99.267	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[19]	[4] F11 and F3	1282/1274	0.805	0.604	0.665	1	Mascot

36	complement component C4 [Ovis aries]	gi|1235	15731.1	5	287	0.787	0.909	1.057	0.337	0.284	0.263	5	5	5	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1074.6769	1074.6154	-0.0615	-57	38	44	AVDLIQK	44	98.817	(N-term)_iTRAQ[0],	[5] F5 and F10	258/250	0.525	0.750	0.895	1	Mascot

									Lysine(K)_iTRAQ[7]							
1305.646	1305.6111	-0.0349	-27	56	65	DGSYGAWLHR	47	99.468	(N-term)_iTRAQ[0]	[1] F8 061011	272/264	0.701	0.715	1.110	1	Mascot
1655.9254	1655.9398	0.0144	9	66	77	DSSTWLTAFVLK	63	99.986	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1279/1271	0.631	0.754	0.755	1	Mascot
2020.126	2020.2085	0.0825	41	92	105	KLQETAMWLLSQQR	38	95.783	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[3] F14,15,16 and F6	1022/1014	1.478	1.446	1.344	1	Mascot
2380.3135	2380.197	-0.1165	-49	20	35	YLDKTEQWSLLPPETK	95	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[4,16]	[5] F5 and F10	417/409	0.880	1.062	1.308	1	Mascot

37	Chain A, Crystal Structure Of The First Active Autolysate Form Of The Porcine Alpha Trypsin	gi|1942351	14234.1	3	286	0.738	0.640	0.908	0.329	0.307	0.067	5	5	5	100

Protein Group

Chain A, Complex Of The Second Kunitz Domain Of Tissue Factor Pathway Inhibitor With Porcine Trypsi	gi|2914482	25597.4
Chain A, The Refined 1.6 Angstroms Resolution Crystal Structure Of The Complex Formed Between Porci	gi|494360	25595.4
Chain B, Refined 1.8 Angstroms Resolution Crystal Structure Of Porcine Epsilon-Trypsin	gi|999627	9481.9
RecName: Full=Trypsin; Flags: Precursor	gi|136429	26674.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1189.6661	1189.6781	0.012	10	90	99	LSSPATLNSR	38	95.333	(N-term)_iTRAQ[0]	[4] F11 and F3	974/966	1.341	1.152	0.900	1	Mascot
2499.3088	2499.1692	-0.1396	-56	50	69	LGEHNIDVLEGNEQFINAAK	131	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[5] F5 and F10	474/466	0.648	0.528	0.797	1	Mascot
2499.3088	2499.2151	-0.0937	-37	50	69	LGEHNIDVLEGNEQFINAAK	183	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[5] F5 and F10	399/391	0.691	0.566	0.950	1	Mascot
2499.3088	2499.4016	0.0928	37	50	69	LGEHNIDVLEGNEQFINAAK	117	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[5] F5 and F10	1265/1257	0.433	0.371	0.926	1	Mascot
2571.385	2571.4092	0.0242	9	70	89	IITHPNFNGNTLDNDIMLIK	65	99.991	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[2] F4 and F13	306/298	0.842	0.838	0.978	1	Mascot

38	Chain E, Leech-Derived Tryptase InhibitorTRYPSIN COMPLEX	gi|3318722	25594.3	3	286	0.738	0.640	0.908	0.329	0.307	0.067	5	5	5	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1189.6661	1189.6781	0.012	10	90	99	LSSPATLXSR	38	95.333	(N-term)_iTRAQ[0]	[4] F11 and F3	974/966	1.341	1.152	0.900	1	Mascot
2499.3088	2499.1692	-0.1396	-56	50	69	LGEHNIDVLEGNEQFINAAK	131	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[5] F5 and F10	474/466	0.648	0.528	0.797	1	Mascot
2499.3088	2499.2151	-0.0937	-37	50	69	LGEHNIDVLEGNEQFINAAK	183	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[5] F5 and F10	399/391	0.691	0.566	0.950	1	Mascot
2499.3088	2499.4016	0.0928	37	50	69	LGEHNIDVLEGNEQFINAAK	117	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[5] F5 and F10	1265/1257	0.433	0.371	0.926	1	Mascot
2571.385	2571.4092	0.0242	9	70	89	IITHPNFNGNTLDNDIMLIK	65	99.991	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[2] F4 and F13	306/298	0.842	0.838	0.978	1	Mascot

39	serpin A3-1 precursor [Bos taurus]	gi|31340900	49725.6	4	278	0.730	0.625	1.279	0.330	0.329	0.312	5	5	5	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1300.7875	1300.8687	0.0812	62	301	308	IHELYLPK	55	99.915	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[7] F12 and F9 and F7 attempt 2	1320/1312	1.141	0.831	1.636	1	Mascot
1409.825	1409.8518	0.0268	19	395	404	DTQSIIFLGK	79	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[4] F11 and F3	1109/1101	0.888	0.588	1.142	1	Mascot
1548.9094	1548.8564	-0.053	-34	87	98	GSTLTEILEGLK	68	99.995	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[5] F5 and F10	516/508	0.409	0.412	0.987	1	Mascot
1548.9094	1548.9353	0.0259	17	87	98	GSTLTEILEGLK	88	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1272/1264	0.553	0.396	1.102	1	Mascot
1624.9645	1624.9529	-0.0116	-7	182	191	TQGKIEELFK	57	99.938	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[4,10]	[1] F8 061011	342/334	0.904	1.201	1.682	1	Mascot

40	amyloid beta A4 protein isoform b precursor [Homo sapiens]	gi|41406055	91356.8	4	276	1.236	0.919	0.950	0.359	0.256	0.244	5	5	5	100

Protein Group

A4 amyloid protein precursor [Homo sapiens]	gi|871360	84843.2
App protein [Rattus norvegicus]	gi|38303889	89480.9

RecName: Full=Amyloid beta A4 protein; AltName: Full=ABPP; Short=APP; AltName: Full=Alzheimer disea	gi|3912955	91431.8
RecName: Full=Amyloid beta A4 protein; AltName: Full=ABPP; Short=APP; AltName: Full=Alzheimer disea	gi|28558768	93897.2
RecName: Full=Amyloid beta A4 protein; AltName: Full=ABPP; Short=APP; AltName: Full=Alzheimer disea	gi|30172731	93996.4
amyloid beta A4 precursor protein [Macaca fascicularis]	gi|52782183	84206
amyloid beta A4 protein [Canis lupus familiaris]	gi|54633336	94042.5
amyloid beta A4 protein [Pan troglodytes]	gi|61316399	93796.1
amyloid beta A4 protein [Pongo abelii]	gi|197099512	84749.2
amyloid beta A4 protein [Rattus norvegicus]	gi|27436861	93673.2
amyloid beta A4 protein [Sus scrofa]	gi|47523800	93930.3
amyloid beta A4 protein isoform 1 precursor [Mus musculus]	gi|311893401	93691.2
amyloid beta A4 protein isoform 2 precursor [Mus musculus]	gi|47271504	84709.3
amyloid beta A4 protein isoform a precursor [Homo sapiens]	gi|4502167	93768.1
amyloid beta A4 protein isoform c precursor [Homo sapiens]	gi|41406057	84785.2
amyloid beta A4 protein isoform e precursor [Homo sapiens]	gi|209915570	78109.1
amyloid precursor protein [Homo sapiens]	gi|609449	59429.5
amyloid-beta precursor protein-like protein long isoform [Mus musculus]	gi|30385620	93721.2
amyloid-beta protein [Homo sapiens]	gi|178615	67534.8
beta amyloid precursor protein isoform APP695 [Canis lupus familiaris]	gi|40950174	85059.6
beta amyloid precursor protein isoform APP751 [Canis lupus familiaris]	gi|40950176	91659.2
beta-amyloid protein [Mus musculus]	gi|309085	84837.4
hippocampal amyloid precursor protein [Mus musculus]	gi|1805299	84681.2
putative amyloid precursor protein [Cavia sp.]	gi|1418676	85111.5
unnamed protein product [Rattus rattus]	gi|55617	84749.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1387.7943	1387.745	-0.0493	-36	411	419	AVIQHFQEK	63	99.986	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[1] F8 061011	218/210	0.871	0.639	0.974	1	Mascot
1387.7943	1387.8531	0.0588	42	411	419	AVIQHFQEK	48	99.495	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[7] F12 and F9 and F7 attempt 2	1234/1226	1.282	0.803	0.658	1	Mascot
1518.752	1518.7815	0.0295	19	420	431	VESLEQEAANER	50	99.727	(N-term)_iTRAQ[0]	[4] F11 and F3	1015/1007	1.659	1.194	1.085	1	Mascot
2039.0784	2039.1174	0.039	19	117	132	CLVGEFVSDALLVPDK	76	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[1]	[4] F11 and F3	1354/1346	1.587	1.220	1.298	1	Mascot
2211.084	2210.9844	-0.0996	-45	162	178	STNLHDYGMLLPCGIDK	86	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17], MMTS (C)[13]	[5] F5 and F10	470/462	0.983	0.877	0.855	1	Mascot

41	72 kDa type IV collagenase precursor [Bos taurus]	gi|27807447	81088.1	5	275	1.112	0.828	1.011	0.633	0.207	0.249	5	5	5	100	

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1325.71	1325.6624	-0.0476	-36	569	577	VDAAFNWSK	47	99.369	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[5] F5 and F10	332/324	2.493	0.947	0.960	1	Mascot
1562.8451	1562.8724	0.0273	17	148	159	AFQVWSDVTPLR	46	99.269	(N-term)_iTRAQ[0]	[4] F11 and F3	1203/1195	1.013	1.076	1.260	1	Mascot
1695.8013	1695.8027	0.0014	1	177	188	WEHGDGYPFDGK	65	99.991	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[1] F8 061011	292/284	0.640	0.652	0.677	1	Mascot
1723.8636	1723.9016	0.038	22	521	532	IDAVYEDPQEEK	70	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1012/1004	1.172	0.950	1.175	1	Mascot
2568.3193	2568.2312	-0.0881	-34	46	63	TDKELAVQYLNTFYGCPK	49	99.616	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,1	[5] F5 and F10	492/484	0.898	0.617	1.098	1	Mascot

8], MMTS (C)[16]

42	phospholipid transfer protein [Bos taurus]	gi|78042516	59170.3	3	256	0.831	1.094	0.968	0.375	0.495	0.236	4	4	4	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2383.3193	2383.2776	-0.0417	-17	319	338	ASYFGSIVLMSPAVIDSPLK	117	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[8] F2	548/540	0.734	0.738	0.906	1	Mascot
2383.3193	2383.3296	0.0103	4	319	338	ASYFGSIVLMSPAVIDSPLK	43	98.715	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[4] F11 and F3	1331/1323	0.639	1.310	1.014	1	Mascot
2428.3235	2428.4136	0.0901	37	461	480	EVVTNHAGFLTIGADLHFAK	50	99.74	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[3] F14,15,16 and F6	986/978	0.646	0.804	0.721	1	Mascot
2587.4956	2587.4431	-0.0525	-20	409	429	IYSNQSALESLALIPLQTPLK	89	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[21]	[8] F2	550/542	1.574	1.845	1.323	1	Mascot

43	insulin-like growth factor-binding protein 7 [Homo sapiens]	gi|4504619	32244.8	3	253	0.755	0.614	1.007	0.730	0.256	0.350	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1722.0411	1721.9779	-0.0632	-37	263	275	ITVVDALHEIPVK	47	99.493	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[5] F5 and F10	432/424	1.317	0.762	0.991	1	Mascot
1994.2385	1994.2294	-0.0091	-5	263	276	ITVVDALHEIPVKK	66	99.993	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13,14]	[1] F8 061011	394/386	1.122	0.809	1.463	1	Mascot
2574.1062	2573.9592	-0.147	-57	241	262	EDAGEYECHASNSQGQASASAK	140	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[22], MMTS (C)[8]	[5] F5 and F10	202/194	0.292	0.376	0.705	1	Mascot

44	keratin, type II cytoskeletal 2 epidermal [Homo sapiens]	gi|47132620	70810.8	3	243	1.296	1.111	0.995	0.120	0.193	0.149	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1617.9309	1617.9594	0.0285	18	342	353	NLDLDSIIAEVK	63	99.987	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1254/1246	1.303	1.373	0.902	1	Mascot
1823.9874	1823.9167	-0.0707	-39	363	374	SKEEAEALYHSK	44	98.886	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,12]	[4] F11 and F3	147/139	1.160	0.932	0.902	1	Mascot
2543.1206	2543.074	-0.0466	-18	93	122	GGGFGGGSSFGGGSGFSGGGFGGGGFGGGR	135	100	(N-term)_iTRAQ[0]	[8] F2	399/391	1.442	1.073	1.212	1	Mascot

45	RecName: Full=Brevican core protein; Flags: Precursor	gi|2497653	103281.3	3	241	1.521	1.489	1.258	0.275	0.279	0.253	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1027.6299	1027.626	-0.0039	-4	894	899	LVGHWK	39	96.772	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6]	[5] F5 and F10	1132/1124	1.302	1.822	1.520	1	Mascot
1951.9998	1951.9644	-0.0354	-18	284	300	IATTGQLYAAWDGGLDR	94	100	(N-term)_iTRAQ[0]	[8] F2	440/432	1.915	1.512	1.334	1	Mascot
2165.0081	2164.9214	-0.0867	-40	137	153	CEVQHGIDDSSDAVEVK	108	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17], MMTS (C)[1]	[5] F5 and F10	286/278	1.412	1.197	0.982	1	Mascot

46	RecName: Full=Fibrinogen beta chain; Contains: RecName: Full=Fibrinopeptide B; Contains: RecName: F	gi|1346006	59431.9	3	239	1.247	1.404	0.741	0.133	0.021	0.107	3	3	3	100

Protein Group

Chain B, The Crystal Structure Of Modified Bovine Fibrinogen (At ~4 Angstrom Resolution)	gi|6980815	52216.1
fibrinogen beta chain [Bos taurus]	gi|357	54018

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1383.6202	1383.5822	-0.038	-27	404	413	EDGGGWWYNR	43	98.469	(N-term)_iTRAQ[0]	[5] F5 and F10	323/315	1.334	1.391	0.733	1	Mascot
1867.0409	1866.9756	-0.0653	-35	278	291	QGFGNIATNAEGKK	127	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13,14]	[1] F8 061011	233/225	1.345	1.433	0.878	1	Mascot
1899.8986	1899.9613	0.0627	33	423	435	YYWGGAYTWDMAK	69	99.996	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[4] F11 and F3	1211/1203	1.081	1.387	0.632	1	Mascot

47	RecName: Full=Apolipoprotein A-I; Short=Apo-AI; Short=ApoA-I; AltName: Full=Apolipoprotein A1; Flag	gi|3915607	33204	3	232	0.826	0.890	0.907	0.241	0.303	0.293	5	5	5	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1686.8948	1686.8357	-0.0591	-35	51	63	DYVAQFEASALGK	97	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[5] F5 and F10	432/424	1.190	1.214	1.391	1	Mascot
1686.8948	1686.9039	0.0091	5	51	63	DYVAQFEASALGK	98	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[4] F11 and F3	1179/1171	0.671	0.726	0.836	1	Mascot
1686.8948	1686.9125	0.0177	10	51	63	DYVAQFEASALGK	87	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[2] F4 and F13	262/254	0.727	0.681	0.582	1	Mascot
2102.0764	2102.1504	0.074	35	47	63	DSGRDYVAQFEASALGK	74	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17]	[3] F14,15,16 and F6	931/923	1.056	1.331	0.977	1	Mascot
2221.1387	2221.1797	0.041	18	85	100	EQIGPVTQEFWDNLEK	60	99.974	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1247/1239	0.628	0.698	0.928	1	Mascot

48	Chain A, Crystal Structure Of Bovine Holo-Rbp At Ph 4.0	gi|31615476	22018.7	4	230	1.067	1.151	1.126	0.264	0.296	0.113	6	6	6	100

Protein Group

RecName: Full=Retinol-binding protein 4; AltName: Full=Plasma retinol-binding protein; Short=PRBP;	gi|132403	23060.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1311.7644	1311.7521	-0.0123	-9	11	17	VKENFDK	40	97.162	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,7]	[5] F5 and F10	1041/1033	1.030	1.314	1.266	1	Mascot
1433.7498	1433.7698	0.02	14	20	29	FAGTWYAMAK	61	99.977	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	222/214	1.375	1.470	1.046	1	Mascot
1478.7737	1478.8044	0.0307	21	140	150	DPSGFSPEVQK	42	98.134	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[4] F11 and F3	995/987	1.012	0.857	1.065	1	Mascot
1478.7737	1478.8202	0.0465	31	140	150	DPSGFSPEVQK	57	99.94	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[2] F4 and F13	913/905	0.724	0.885	1.092	1	Mascot
1486.8304	1486.8406	0.0102	7	90	99	YWGVASFLQK	57	99.938	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[4] F11 and F3	1228/1220	1.399	1.051	1.019	1	Mascot
1486.8304	1486.8527	0.0223	15	90	99	YWGVASFLQK	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	308/300	1.013	1.506	1.302	1	Mascot

49	complement component 4, gene 2 [Rattus norvegicus]	gi|50657362	205542.6	4	228	0.874	1.080	1.145	0.213	0.359	0.367	4	4	4	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1108.6613	1108.6101	-0.0512	-46	158	164	VFALDQK	43	98.61	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	283/275	0.962	1.522	1.639	1	Mascot
1374.8354	1374.892	0.0566	41	1640	1648	ITQVLHFTK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[7] F12 and F9 and F7 attempt 2	1346/1338	1.146	1.333	1.118	1	Mascot
1641.8676	1641.9149	0.0473	29	773	782	SFFPENWLWK	58	99.954	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	382/374	0.841	0.889	1.241	1	Mascot
1655.9254	1655.9398	0.0144	9	1068	1079	DSSTWLTAFVLK	63	99.986	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1279/1271	0.631	0.754	0.755	1	Mascot

50	hypothetical protein [Homo sapiens]	gi|30722344	263094.8	3	227	0.978	0.766	0.827	0.295	0.215	0.198	3	3	3	100

Protein Group

fibronectin 1 [Homo sapiens]	gi|53791223	263248.7
fibronectin isoform 1 preproprotein [Homo sapiens]	gi|47132557	286441.2
fibronectin isoform 3 preproprotein [Homo sapiens]	gi|16933542	273344.7
fibronectin isoform 4 preproprotein [Homo sapiens]	gi|47132555	270632.3
fibronectin isoform 5 preproprotein [Homo sapiens]	gi|47132553	266655.4
fibronectin isoform 6 preproprotein [Homo sapiens]	gi|47132549	253334.6
fibronectin precursor [Homo sapiens]	gi|31397	270764.3
hypothetical protein [Homo sapiens]	gi|31874109	283329.9
hypothetical protein [Homo sapiens]	gi|31873670	282968.7
hypothetical protein [Homo sapiens]	gi|34364820	283118.8

hypothetical protein [Homo sapiens]	gi|34364617	266596.4
hypothetical protein [Homo sapiens]	gi|51476292	273249.9
hypothetical protein [Homo sapiens]	gi|51476364	260414.5
hypothetical protein [Homo sapiens]	gi|51476362	263051.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1545.7683	1545.7308	-0.0375	-24	147	156	HYQINQQWER	40	96.86	(N-term)_iTRAQ[0]	[1] F8 061011	245/237	1.194	1.086	0.692	1	Mascot
1773.9731	1773.9127	-0.0604	-34	1028	1042	VDVIPVNLPGEHGQR	51	99.767	(N-term)_iTRAQ[0]	[5] F5 and F10	346/338	0.674	0.657	0.731	1	Mascot
2405.3208	2405.2563	-0.0645	-27	1766	1786	EINLAPDSSSVVVSGLMVATK	138	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[21]	[8] F2	472/464	1.162	0.630	1.119	1	Mascot

51	Keratin 10 [Homo sapiens]	gi|21961605	62434.1	3	221	2.039	1.674	1.044	0.703	0.409	0.277	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1397.6947	1397.656	-0.0387	-28	335	343	DAEAWFNEK	46	99.245	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[5] F5 and F10	327/319	1.571	1.362	0.757	1	Mascot
1427.827	1427.9156	0.0886	62	178	184	IKEWYEK	44	98.878	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,7]	[7] F12 and F9 and F7 attempt 2	907/899	3.086	2.265	1.319	1	Mascot
2476.051	2476.0151	-0.0359	-14	60	86	GSSGGGCFGGSSGGYGGLGGFGGGSFR	131	100	(N-term)_iTRAQ[0], MMTS (C)[7]	[8] F2	438/430	1.748	1.520	1.139	1	Mascot

52	RecName: Full=Hemoglobin subunit beta; AltName: Full=Beta-globin; AltName: Full=Hemoglobin beta cha	gi|122686	17982.6	3	219	0.492	1.057	1.901	0.117	0.151	0.130	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1224.6986	1224.6554	-0.0432	-35	8	16	AAVTGFWGK	56	99.929	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[5] F5 and F10	328/320	0.455	1.137	2.081	1	Mascot
2156.1135	2156.1538	0.0403	19	116	131	HHGNEFTPVLQADFQK	50	99.697	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[5] F5 and F10	1221/1213	0.398	0.876	1.852	1	Mascot
2441.1804	2441.0972	-0.0832	-34	40	58	FFEHFGDLSNADAVMNNPK	113	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[19]	[5] F5 and F10	431/423	0.658	1.185	1.781	1	Mascot

53	inter-alpha-trypsin inhibitor heavy chain H2 precursor [Sus scrofa]	gi|47522678	114146.5	4	217	1.032	1.175	0.969	0.510	0.400	0.240	4	4	4	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1481.8236	1481.7925	-0.0311	-21	478	488	FYNQVSTPLLR	56	99.932	(N-term)_iTRAQ[0]	[8] F2	381/373	1.946	1.783	1.165	1	Mascot
1707.9315	1707.9822	0.0507	30	166	176	VQFELHYQEVK	45	99.121	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	857/849	0.851	0.781	0.690	1	Mascot
1726.9572	1726.905	-0.0522	-30	369	383	IQPSGGTNINEALLR	74	99.999	(N-term)_iTRAQ[0]	[8] F2	338/330	1.045	1.135	0.918	1	Mascot
1741.0118	1741.0032	-0.0086	-5	236	248	AHVAFKPTVAQQR	42	98.294	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6]	[5] F5 and F10	1093/1085	0.656	1.208	1.195	1	Mascot

54	neurosecretory protein VGF precursor [Homo sapiens]	gi|17136078	69569.2	2	203	1.392	1.041	0.997	0.246	0.365	0.212	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2060.9646	2060.9053	-0.0593	-29	64	80	NSEPQDEGELFQGVDPR	68	99.995	(N-term)_iTRAQ[0]	[8] F2	334/326	1.638	1.407	1.208	1	Mascot
2306.9868	2306.9287	-0.0581	-25	378	397	VGEEDEEAAEAEAEAEEAER	135	100	(N-term)_iTRAQ[0]	[8] F2	332/324	1.182	0.771	0.822	1	Mascot

55	fibronectin [Sus scrofa]	gi|56608605	69908.3	2	199	1.320	0.881	1.098	0.179	0.351	0.021	2	2	2	100

Protein Group

fibronectin [Sus scrofa]	gi|56407693	59270.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio	iTRAQ Ratio	iTRAQ Ratio	Rank	Result Type

												114/117*	115/117*	116/117*		
1575.8826	1575.8358	-0.0468	-30	405	419	VPGTSASATLTGLTR	62	99.981	(N-term)_iTRAQ[0]	[8] F2	336/328	1.499	1.231	1.078	1	Mascot
2405.3208	2405.2563	-0.0645	-27	47	67	EINLAPDSSSVVVSGLMVATK	138	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[21]	[8] F2	472/464	1.162	0.630	1.119	1	Mascot

56	prothrombin [Bos taurus]	gi|27806947	76293.7	4	196	1.018	0.898	1.037	0.104	0.227	0.568	4	4	4	100

Protein Group

RecName: Full=Prothrombin; AltName: Full=Coagulation factor II; Contains: RecName: Full=Activation	gi|135806	76221.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1778.8882	1778.8273	-0.0609	-34	388	402	SPQELLCGASLISDR	38	95.982	(N-term)_iTRAQ[0], MMTS (C)[7]	[8] F2	474/466	1.197	1.129	1.585	1	Mascot
1976.8558	1976.8105	-0.0453	-23	585	599	WYQMGIVSWGEGCDR	52	99.809	(N-term)_iTRAQ[0], MMTS (C)[13]	[8] F2	509/501	0.936	0.736	0.528	1	Mascot
2145.0698	2144.9844	-0.0854	-40	331	347	TFGAGEADCGLRPLFEK	50	99.699	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17], MMTS (C)[9]	[5] F5 and F10	450/442	0.954	1.118	1.462	1	Mascot
2207.9097	2207.8767	-0.033	-15	101	118	LNECLEGNCAEGVGMNYR	56	99.93	(N-term)_iTRAQ[0], MMTS (C)[4,9]	[8] F2	450/442	1.004	0.698	0.946	1	Mascot

57	pigment epithelium-derived factor [Homo sapiens]	gi|15217079	50486.1	3	196	1.629	1.421	1.363	0.282	0.302	0.183	3	3	3	100

Protein Group

Chain A, 2.85 A Crystal Structure Of Pedf	gi|15988024	48330.1
Serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), membe	gi|15559258	50545.2
pigment epithelial-differentiating factor [Homo sapiens]	gi|189778	50473.1
pigment epithelium-derived factor [Homo sapiens]	gi|1144299	44074.8
pigment epithelium-derived factor precursor [Homo sapiens]	gi|39725934	50456.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1188.8052	1188.8368	0.0316	27	346	352	ITGKPIK	38	95.926	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[4,7]	[7] F12 and F9 and F7 attempt 2	817/809	2.031	1.738	1.551	1	Mascot
1703.8877	1703.8383	-0.0494	-29	54	67	LAAAVSNFGYDLYR	80	100	(N-term)_iTRAQ[0]	[8] F2	469/461	1.521	1.507	1.149	1	Mascot
2118.1262	2118.1643	0.0381	18	175	189	LDLQEINNWVQAQMK	77	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[4] F11 and F3	1324/1316	1.400	1.095	1.422	1	Mascot

58	factor XIIa inhibitor precursor [Bos taurus]	gi|27807349	55333.2	3	193	1.161	1.095	1.276	0.252	0.161	0.278	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1380.733	1380.672	-0.061	-44	365	374	FHPTHLTMPR	40	97.412	(N-term)_iTRAQ[0]	[4] F11 and F3	203/195	0.917	0.993	0.986	1	Mascot
1513.9927	1514.0712	0.0785	52	261	272	LILLNAVALSAK	85	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1257/1249	1.484	0.994	1.324	1	Mascot
1822.967	1822.9375	-0.0295	-16	111	126	SAEAVLGEALTDFSLR	68	99.996	(N-term)_iTRAQ[0]	[8] F2	558/550	1.150	1.330	1.590	1	Mascot

59	apolipoprotein C-III precursor [Bos taurus]	gi|47564119	11982.3	3	186	0.740	1.092	1.220	0.017	0.074	0.104	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1220.6198	1220.5734	-0.0464	-38	72	78	DYWSSFK	43	98.486	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	338/330	0.763	1.060	1.357	1	Mascot
1618.8032	1618.8066	0.0034	2	61	71	DWMTESFSSLK	45	99.073	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[4] F11 and F3	1177/1169	0.728	1.195	1.202	1	Mascot
1860.9535	1860.8761	-0.0774	-42	45	60	DALSSVQESQVAQQAR	98	100	(N-term)_iTRAQ[0]	[8] F2	263/255	0.728	1.027	1.112	1	Mascot

60	primary amine oxidase, lung isozyme [Bos taurus]	gi|30794300	87835.1	3	184	0.753	0.910	1.056	0.090	0.093	0.157	3	3	3	100

Protein Group

Chain A, Crystal Structure Of Bovine Plasma Copper-Containing Amine Oxidase	gi|61680007	85792.4
primary amine oxidase, liver isozyme precursor [Bos taurus]	gi|195539525	87756.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1700.8438	1700.8082	-0.0356	-21	175	186	EYLDIDQMIFNR	67	99.994	(N-term)_iTRAQ[0]	[8] F2	487/479	0.803	0.904	1.284	1	Mascot
2045.0424	2044.9833	-0.0591	-29	568	585	QLETEEQAAFPLGGASPR	60	99.974	(N-term)_iTRAQ[0]	[8] F2	359/351	0.643	0.811	0.972	1	Mascot
2317.2397	2317.1719	-0.0678	-29	567	585	KQLETEEQAAFPLGGASPR	56	99.934	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[5] F5 and F10	326/318	0.828	1.028	0.944	1	Mascot

61	sex hormone-binding globulin [Bos taurus]	gi|38325826	41549.8	2	172	1.481	1.320	1.170	0.339	0.618	0.065	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1586.939	1586.912	-0.027	-17	164	177	IALGGLLFPASDLR	51	99.758	(N-term)_iTRAQ[0]	[8] F2	534/526	1.820	1.937	1.235	1	Mascot
2376.1553	2376.0896	-0.0657	-28	190	209	QDDWLDQQAQTSASVPTSVR	122	100	(N-term)_iTRAQ[0]	[8] F2	343/335	1.206	0.899	1.109	1	Mascot

62	apolipoprotein A-IV precursor [Sus scrofa]	gi|47523830	48023.1	3	171	1.087	0.983	0.893	0.403	0.298	0.116	4	4	4	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1510.8839	1510.9172	0.0333	22	113	123	LLPHATEVSQK	53	99.862	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	775/767	1.101	0.804	0.990	1	Mascot
1510.8839	1510.9908	0.1069	71	113	123	LLPHATEVSQK	72	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	1260/1252	0.794	0.892	0.841	1	Mascot
1816.9989	1817.0597	0.0608	33	234	246	LNHQLEGLAFQMK	40	97.201	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[3] F14,15,16 and F6	928/920	0.884	0.840	0.753	1	Mascot
1953.054	1953.0747	0.0207	11	52	65	SELTQQLNTLFQDK	59	99.967	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[4] F11 and F3	1221/1213	1.803	1.547	1.015	1	Mascot

63	complement C3 alpha chain [Oryctolagus cuniculus]	gi|126723309	90597.5	2	168	1.040	1.334	1.049	0.395	0.071	0.141	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1380.8348	1380.8812	0.0464	34	505	513	NTLIIYLDK	45	99.145	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1156/1148	0.720	1.363	0.886	1	Mascot
2058.1746	2058.0913	-0.0833	-40	526	541	VHQYFNVGLIQPGAVK	123	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[5] F5 and F10	402/394	1.576	1.403	1.200	1	Mascot
2058.1746	2058.2366	0.062	30	526	541	VHQYFNVGLIQPGAVK	77	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[3] F14,15,16 and F6	927/919	0.992	1.242	1.084	1	Mascot

64	beta-1,3-N-acetylglucosaminyltransferase bGnT-6 [Bos taurus]	gi|61553937	45814.3	2	164	1.637	1.383	1.166	0.344	0.282	0.103	2	2	2	100

Protein Group

N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase [Bos taurus]	gi|77736590	49858.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1696.8625	1696.7961	-0.0664	-39	65	80	TALASGGVLDASGDYR	123	100	(N-term)_iTRAQ[0]	[8] F2	318/310	1.981	1.665	1.269	1	Mascot
1802.0084	1801.9594	-0.049	-27	249	263	QWAGTALVVPAFEIR	41	97.709	(N-term)_iTRAQ[0]	[8] F2	503/495	1.353	1.149	1.072	1	Mascot

65	RecName: Full=Serum albumin; Flags: Precursor	gi|2492797	78092.2	4	162	1.144	1.163	0.954	0.361	0.462	0.167	6	6	6	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type

1057.5802	1057.526	-0.0542	-51	154	160	YLYEVAR	38	95.236	(N-term)_iTRAQ[0]	[5] F5 and F10	306/298	1.030	0.974	0.931	1	Mascot
1077.6765	1077.7052	0.0287	27	250	256	LVTDLTK	41	97.756	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	933/925	0.891	1.154	0.967	1	Mascot
1077.6765	1077.7075	0.031	29	250	256	LVTDLTK	38	95.502	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	239/231	0.953	0.896	0.896	1	Mascot
1175.6508	1175.6292	-0.0216	-18	476	482	LCVLHEK	41	97.477	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[1] F8 061011	283/275	0.990	0.972	0.967	1	Mascot
1175.6508	1175.6975	0.0467	40	476	482	LCVLHEK	40	97.109	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7], MMTS (C)[2]	[7] F12 and F9 and F7 attempt 2	1293/1285	1.301	1.047	0.748	1	Mascot
1260.5291	1260.5676	0.0385	31	492	500	CCTESLVNR	43	98.581	(N-term)_iTRAQ[0], MMTS (C)[1,2]	[4] F11 and F3	1071/1063	1.992	2.408	1.293	1	Mascot

66	DKFZP459P137 protein [Pongo abelii]	gi|207079999	58525.5	3	162	1.164	0.905	1.209	0.140	0.205	0.228	3	3	3	100

Protein Group

nucleobindin [Homo sapiens]	gi|1144316	58255.6
nucleobindin [Homo sapiens]	gi|189308	58165.5
nucleobindin-1 precursor [Homo sapiens]	gi|20070228	58169.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1382.7301	1382.6689	-0.0612	-44	88	97	ELDFVSHHVR	40	96.867	(N-term)_iTRAQ[0]	[4] F11 and F3	195/187	1.050	0.778	0.950	1	Mascot
1416.8182	1416.7861	-0.0321	-23	153	163	DLELLIQTATR	49	99.666	(N-term)_iTRAQ[0]	[8] F2	481/473	1.104	0.789	1.319	1	Mascot
1650.9187	1650.8923	-0.0264	-16	311	323	LVTLEEFLASTQR	73	99.999	(N-term)_iTRAQ[0]	[8] F2	542/534	1.363	1.209	1.411	1	Mascot

67	collagen alpha-1(XII) chain long isoform precursor [Homo sapiens]	gi|93141047	356530.3	2	159	1.208	0.932	0.935	0.039	0.083	0.136	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1859.9735	1859.9086	-0.0649	-35	1939	1953	NVQVYNPTPNSLDVR	57	99.941	(N-term)_iTRAQ[0]	[8] F2	316/308	1.248	0.857	0.816	1	Mascot
2254.1072	2254.0161	-0.0911	-40	1785	1804	ITYQPSTGEGNEQTTTIGGR	102	100	(N-term)_iTRAQ[0]	[8] F2	262/254	1.171	1.015	1.071	1	Mascot

68	pigment epithelium-derived factor [Rattus norvegicus]	gi|29293811	49796.5	2	157	1.459	1.285	1.278	0.062	0.222	0.144	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1703.8877	1703.8383	-0.0494	-29	54	67	LAAAVSNFGYDLYR	80	100	(N-term)_iTRAQ[0]	[8] F2	469/461	1.521	1.507	1.149	1	Mascot
2118.1262	2118.1643	0.0381	18	175	189	IDLQEINNWVQAQMK	77	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[4] F11 and F3	1324/1316	1.400	1.095	1.422	1	Mascot

69	transcription factor AEBP1 [Bos taurus]	gi|4105170	85223.4	3	155	1.090	0.841	1.204	0.058	0.434	0.283	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1581.8245	1581.7653	-0.0592	-37	315	327	YLSPDATVSTEVR	66	99.993	(N-term)_iTRAQ[0]	[8] F2	308/300	1.048	1.165	1.110	1	Mascot
1772.9449	1772.9011	-0.0438	-25	360	375	TPSQEQLLAAAMAAAR	51	99.753	(N-term)_iTRAQ[0]	[8] F2	463/455	1.053	1.093	0.978	1	Mascot
2563.1895	2563.2383	0.0488	19	181	201	IYAMEISDNPGDHELGEPEFR	39	96.189	(N-term)_iTRAQ[0]	[4] F11 and F3	1162/1154	1.172	0.468	1.608	1	Mascot

70	fibrinogen A-alpha chain [Bos taurus]	gi|3789962	46124.2	3	155	1.026	1.147	0.868	0.140	0.050	0.136	3	3	3	100

Protein Group

Chain A, The Crystal Structure Of Modified Bovine Fibrinogen (At ~4 Angstrom Resolution)	gi|6980814	46278.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio	iTRAQ Ratio	iTRAQ Ratio	Rank	Result Type

												114/117*	115/117*	116/117*		
1169.63	1169.5842	-0.0458	-39	22	28	VDLEDYK	39	96.11	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	278/270	1.220	1.155	0.707	1	Mascot
1738.0347	1737.9945	-0.0402	-23	33	46	QLEQVIAINLLPSR	57	99.946	(N-term)_iTRAQ[0]	[8] F2	483/475	0.984	1.204	0.942	1	Mascot
1892.05	1892.0819	0.0319	17	17	28	ALEHKVDLEDYK	59	99.963	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[5,12]	[5] F5 and F10	1171/1163	0.900	1.085	0.981	1	Mascot

71	haptoglobin heavy chain, HpH chain [dogs, Peptide, 245 aa]	gi|258499	30383.8	3	153	0.576	0.514	1.563	0.136	0.158	0.245	3	3	3	100

Protein Group

RecName: Full=Haptoglobin; Contains: RecName: Full=Haptoglobin alpha chain; Contains: RecName: Full	gi|123511	41125.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1045.6866	1045.7325	0.0459	44	84	90	VDIGLIK	39	96.696	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	962/954	0.631	0.463	1.385	1	Mascot
1208.6674	1208.6146	-0.0528	-44	10	17	GSFPWQAK	54	99.896	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	311/303	0.429	0.395	1.436	1	Mascot
1566.8447	1566.8649	0.0202	13	137	147	YVMLPVADQDK	59	99.967	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[4] F11 and F3	1090/1082	0.704	0.742	1.919	1	Mascot

72	chromogranin B [Bos taurus]	gi|12	79124.7	2	151	0.997	1.128	1.323	0.094	0.068	0.024	2	2	2	100

Protein Group

RecName: Full=Secretogranin-1; AltName: Full=Chromogranin-B; Short=CgB; AltName: Full=Secretogranin	gi|12644006	79151.7
chromogranin B	gi|228903	79374.9
chromogranin B [Bos taurus]	gi|202	77524.9
secretogranin-1 [Bos taurus]	gi|30794308	79228.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2031.9868	2032.0377	0.0509	25	437	451	NYLDYGEEKGEEAAR	44	98.817	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[4] F11 and F3	1061/1053	1.091	1.196	1.300	1	Mascot
2445.0886	2444.9426	-0.146	-60	102	124	EDSGEGDAQVPTVADTESGGHSR	107	100	(N-term)_iTRAQ[0]	[5] F5 and F10	206/198	0.912	1.063	1.347	1	Mascot

73	RecName: Full=Metalloproteinase inhibitor 2; AltName: Full=Tissue inhibitor of metalloproteinases 2	gi|3915132	25216.4	2	149	0.770	0.860	0.930	0.150	0.066	0.081	2	2	2	100

Protein Group

Chain C, Prommp-2TIMP-2 Complex	gi|22218677	25030.3
RecName: Full=Metalloproteinase inhibitor 2; AltName: Full=Collagenase inhibitor; AltName: Full=Tis	gi|135853	27530.7
RecName: Full=Metalloproteinase inhibitor 2; AltName: Full=Tissue inhibitor of metalloproteinases 2	gi|267133	27601.9
RecName: Full=Metalloproteinase inhibitor 2; AltName: Full=Tissue inhibitor of metalloproteinases 2	gi|8478957	24980.3
TIMP-2 [Mus musculus]	gi|202054	27496.7
metalloproteinase inhibitor 2 [Cavia porcellus]	gi|290491246	27591.8
metalloproteinase inhibitor 2 precursor [Canis lupus familiaris]	gi|50978760	27570.9
metalloproteinase inhibitor 2 precursor [Homo sapiens]	gi|4507511	27672.9

metalloproteinase inhibitor 2 precursor [Rattus norvegicus]	gi|11464979	27629.9
tissue inhibitor of metalloproteinases-2 [Homo sapiens]	gi|1517893	27484.8
tissue inhibitor of metalloproteinases-2 [Rattus norvegicus]	gi|540205	27642.9
unnamed protein product [Mus musculus]	gi|26328599	27615.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1915.0059	1915.0286	0.0227	12	182	196	GAAPPKQEFLDIEDP	74	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6]	[4] F11 and F3	1114/1106	0.644	0.798	0.856	1	Mascot
1965.0287	1965.0791	0.0504	26	30	44	EVDSGNDIYGNPIKR	76	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[3] F14,15,16 and F6	775/767	0.920	0.926	1.011	1	Mascot

74	RecName: Full=Chitinase-3-like protein 1; AltName: Full=BP40; AltName: Full=Mammary gland protein 4	gi|55976543	46168.8	3	148	1.195	0.930	1.256	0.200	0.230	0.281	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1537.8458	1537.7867	-0.0591	-38	272	286	TDVGAPISGPGIPGR	66	99.994	(N-term)_iTRAQ[0]	[8] F2	287/279	1.488	0.683	1.670	1	Mascot
1676.8881	1676.8188	-0.0693	-41	92	105	TLLSVGGWNFGPER	43	98.597	(N-term)_iTRAQ[0]	[8] F2	476/468	1.083	1.039	1.113	1	Mascot
1961.9994	1961.9126	-0.0868	-44	129	144	THGFDGLDLAWLYPGR	38	95.85	(N-term)_iTRAQ[0]	[5] F5 and F10	527/519	1.060	1.134	1.066	1	Mascot

75	Tetranectin [Homo sapiens]	gi|37409	25323.9	2	145	1.234	1.367	0.835	0.153	0.088	0.500	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1594.8524	1594.9194	0.067	42	63	73	EQQALQTVCLK	81	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11], MMTS (C)[9]	[4] F11 and F3	1102/1094	1.387	1.455	1.335	1	Mascot
1833.9229	1834.0176	0.0947	52	156	169	NWETEITAQPDGGK	65	99.991	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[4] F11 and F3	1049/1041	1.099	1.285	0.523	1	Mascot

76	vitamin D-binding protein [Sus scrofa]	gi|51863317	28956.2	3	140	0.824	0.771	0.977	0.346	0.212	0.353	4	4	4	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1266.7191	1266.7223	0.0032	3	22	29	ELPEYTVK	41	97.877	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	198/190	1.488	1.110	1.631	1	Mascot
1266.7191	1266.7574	0.0383	30	22	29	ELPEYTVK	49	99.634	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	928/920	0.771	0.829	0.945	1	Mascot
2332.0339	2332.1123	0.0784	34	148	164	GQELCADYSENTFTEYK	53	99.849	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17], MMTS (C)[5]	[4] F11 and F3	1156/1148	0.620	0.633	0.785	1	Mascot
2604.2314	2604.2991	0.0677	26	148	165	GQELCADYSENTFTEYKK	38	95.366	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[17, 18], MMTS (C)[5]	[3] F14,15,16 and F6	901/893	0.647	0.606	0.752	1	Mascot

77	transferrin [Ovis aries]	gi|2318026	7637.4	2	137	1.398	1.092	0.981	0.260	0.067	0.021	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1241.6075	1241.6476	0.0401	32	50	58	YYGYTGAFR	38	95.945	(N-term)_iTRAQ[0]	[4] F11 and F3	1063/1055	1.179	1.029	1.001	1	Mascot
1824.7786	1824.7451	-0.0335	-18	9	23	FDEYFSAGCAPGSQR	98	100	(N-term)_iTRAQ[0], MMTS (C)[9]	[8] F2	399/391	1.659	1.159	0.961	1	Mascot

78	limbic system-associated membrane protein precursor [Rattus norvegicus]	gi|25742796	40308.9	2	136	1.118	1.027	0.851	0.108	0.145	0.096	2	2	2	100

Protein Group

LAMP [Homo sapiens]	gi|1276899	40292.9

limbic system-associated membrane protein 6c-isoform [Rattus norvegicus]	gi|37499114	43276.6
limbic system-associated membrane protein precursor [Mus musculus]	gi|30425330	41554.7
limbic system-associated membrane protein preproprotein [Homo sapiens]	gi|45594240	40377.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1930.8568	1930.8184	-0.0384	-20	239	253	CEASAVPAPDFEWYR	39	96.501	(N-term)_iTRAQ[0], MMTS (C)[1]	[8] F2	453/445	1.019	0.900	0.764	1	Mascot
2619.1934	2619.136	-0.0574	-22	101	120	VDVYDEGSYTCSVQTQHEPK	97	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20], MMTS (C)[11]	[5] F5 and F10	322/314	1.226	1.173	0.947	1	Mascot

79	RecName: Full=Fibrinogen alpha chain; Contains: RecName: Full=Fibrinopeptide A	gi|75039944	1990.9	1	136	0.625	0.859	1.390	0.000	0.000	0.000	1	1	1	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1991.943	1991.8911	-0.0519	-26	1	19	ADDSDPVGGEFLAEGGGVR	136	100	(N-term)_iTRAQ[0]	[8] F2	346/338	0.625	0.859	1.390	1	Mascot

80	insulin-like growth factor II preproprotein [Ovis aries]	gi|57164331	20980.4	2	134	0.832	1.434	1.203	0.073	0.006	0.016	2	2	2	100

Protein Group

insulin-like growth factor II [Ovis aries]	gi|552424	14279.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1346.6991	1346.6503	-0.0488	-36	113	120	FFQSDTWK	42	98.193	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	353/345	0.904	1.440	1.187	1	Mascot
2048.9736	2049.0042	0.0306	15	74	89	SCDLALLETYCAAPAK	93	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[2,11]	[4] F11 and F3	1329/1321	0.765	1.428	1.220	1	Mascot

81	complement component C7 precursor [Sus scrofa]	gi|47523630	103502.2	2	130	0.662	0.702	0.827	0.148	0.032	0.053	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1656.7496	1656.7067	-0.0429	-26	812	824	EQTMTECEAGVLR	55	99.918	(N-term)_iTRAQ[0], MMTS (C)[7]	[8] F2	361/353	0.810	0.734	0.777	1	Mascot
2517.2871	2517.197	-0.0901	-36	295	314	LIDQYGTHYLQSGSLGGEYK	75	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[5] F5 and F10	390/382	0.540	0.672	0.880	1	Mascot

82	unnamed protein product [Bos taurus]	gi|218	55266.1	2	130	1.008	1.103	0.901	0.114	0.178	0.021	2	2	2	100

Protein Group

RecName: Full=Chromogranin-A; Short=CgA; AltName: Full=Pituitary secretory protein I; Short=SP-I; C	gi|116548	55166
RecName: Full=Chromogranin-A; Short=CgA; Contains: RecName: Full=Pancreastatin; Contains: RecName:	gi|116551	53901.9
chromogranin A	gi|225693	55194
chromogranin A [Bos taurus]	gi|163728	55252.1
chromogranin A [Bos taurus]	gi|244424	55114
chromogranin-A [Bos taurus]	gi|30794306	55182

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1556.8405	1556.7944	-0.0461	-30	392	404	EDSVEAGLPLQVR	61	99.975	(N-term)_iTRAQ[0]	[8] F2	342/334	1.123	1.281	0.922	1	Mascot
2474.2871	2474.2	-0.0871	-35	420	438	RPEDQELESLSAIEAELEK	69	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[19]	[5] F5 and F10	488/480	0.906	0.949	0.880	1	Mascot

83	dickkopf-related protein 3 precursor [Homo sapiens]	gi|40548389	40483.6	2	129	0.827	0.909	0.736	0.402	0.141	0.152	3	3	3	100

Protein Group

dickkopf-3 [Homo sapiens]	gi|6049608	40384.6
dickkopf-related protein 3 [Pongo abelii]	gi|197099502	40676
hypothetical protein [Pongo abelii]	gi|55730213	39809.3
unnamed protein product [Homo sapiens]	gi|21749214	25207.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1752.8571	1752.8989	0.0418	24	67	80	SAVEEMEAEEAAAK	76	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[4] F11 and F3	1060/1052	1.331	1.080	0.922	1	Mascot
1768.8521	1768.8704	0.0183	10	67	80	SAVEEMEAEEAAAK	64	99.988	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], Oxidation (M)[6]	[4] F11 and F3	975/967	0.842	0.759	0.743	1	Mascot
2686.2947	2686.2502	-0.0445	-17	225	247	GLLFPVCTPLPVEGELCHDPASR	54	99.881	(N-term)_iTRAQ[0], MMTS (C)[7,17]	[8] F2	572/564	0.505	0.916	0.583	1	Mascot

84	beta-2-glycoprotein 1 precursor [Canis lupus familiaris]	gi|54792721	43614.4	2	129	0.794	1.014	1.065	0.319	0.456	0.069	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1392.7522	1392.7346	-0.0176	-13	328	336	EHSSLAFWK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[1] F8 061011	334/326	0.492	0.622	1.012	1	Mascot
1592.8954	1592.8424	-0.053	-33	286	295	FKDGMLHGQK	65	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,10]	[4] F11 and F3	120/112	1.019	1.097	1.163	1	Mascot
1608.8904	1608.8298	-0.0606	-38	286	295	FKDGMLHGQK	44	98.901	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,10], Oxidation (M)[5]	[4] F11 and F3	120/112	0.998	1.527	1.026	1	Mascot

85	WAP, kazal, immunoglobulin, kunitz and NTR domain-containing protein 2 precursor [Mus musculus]	gi|267844918	68543.1	2	128	0.728	0.965	0.937	0.179	0.043	0.000	2	2	2	100

Protein Group

Bikunin hlg [Homo sapiens]	gi|37181390	68978.2
PREDICTED: WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 [Rattus no	gi|27675188	68579.3
WAP, kazal, immunoglobulin, kunitz and NTR domain-containing protein 2 [Homo sapiens]	gi|28212222	69006.3
growth and differentiation factor-associated serum protein 1 [Mus musculus]	gi|32187114	68531.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1891.1123	1891.1708	0.0585	31	476	488	ALVTVDEVLKDEK	68	99.995	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10,13]	[3] F14,15,16 and F6	923/915	0.907	0.924	0.937	1	Mascot
1986.7649	1986.7932	0.0283	14	60	72	ECETDQECETYEK	60	99.973	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[2,8]	[4] F11 and F3	1030/1022	0.584	1.007	0.936	1	Mascot

86	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) [Bos taurus]	gi|59857769	108789.4	2	125	0.952	1.159	1.572	0.032	0.074	0.138	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1636.9758	1636.933	-0.0428	-26	216	225	FKPTLSQQQK	52	99.821	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,10]	[1] F8 061011	207/199	0.921	1.233	1.711	1	Mascot
2122.2244	2122.2793	0.0549	26	125	140	KTEQFQVSVSVAPAAK	73	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,16]	[3] F14,15,16 and F6	818/810	0.984	1.090	1.445	1	Mascot

87	calcium uniporter channel component [cattle, heart, Peptide Mitochondrial Partial, 18 aa, segment 3	gi|833995	2470.3	1	123	1.284	0.876	2.364	0.000	0.000	0.000	1	1	1	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2471.3152	2471.2144	-0.1008	-41	1	18	NVGVSFYADKPEVTQEQK	123	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10,18]	[5] F5 and F10	306/298	1.284	0.876	2.364	1	Mascot

88	plasminogen precursor [Bos taurus]	gi|27806815	101001.3	2	121	0.889	0.868	1.116	0.079	0.140	0.060	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1601.7557	1601.7241	-0.0316	-20	149	160	FPLAGLEENYCR	53	99.863	(N-term)_iTRAQ[0], MMTS (C)[11]	[8] F2	488/480	0.817	0.748	1.059	1	Mascot
2334.1489	2334.075	-0.0739	-32	144	160	FSPEKFPLAGLEENYCR	68	99.996	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[5], MMTS (C)[16]	[5] F5 and F10	513/505	0.968	1.008	1.176	1	Mascot

89	calreticulin [cattle, brain, Peptide, 400 aa]	gi|545920	52543.1	2	119	0.948	1.107	0.640	0.042	0.132	0.111	2	2	2	100

Protein Group

calreticulin precursor [Bos taurus]	gi|27806723	54199.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1753.8229	1753.781	-0.0419	-24	82	94	HEQNIDCGGGYVK	76	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13], MMTS (C)[7]	[1] F8 061011	245/237	0.908	0.989	0.545	1	Mascot
2203.1367	2203.157	0.0203	9	191	205	IKDPDAAKPEDWDDR	42	98.306	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,8]	[5] F5 and F10	1126/1118	0.990	1.240	0.751	1	Mascot

90	amyloid precursor-like protein 1 [Homo sapiens]	gi|1709301	74870.6	2	117	0.769	0.461	0.775	0.354	0.480	0.138	2	2	2	100

Protein Group

amyloid-like protein 1 isoform 2 precursor [Homo sapiens]	gi|4885065	74844.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1467.7148	1467.6428	-0.072	-49	331	340	EWAMADNQSK	63	99.984	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[5] F5 and F10	232/224	1.123	0.941	0.914	1	Mascot
1681.8907	1681.8435	-0.0472	-28	430	441	HYQHVAAVDPEK	55	99.908	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[3] F14,15,16 and F6	107/99	0.527	0.226	0.658	1	Mascot

91	unnamed protein product [Homo sapiens]	gi|21757045	55766.8	2	116	0.465	0.440	1.060	0.067	0.053	0.071	2	2	2	100

Protein Group

RecName: Full=Vimentin	gi|138535	57057.4
RecName: Full=Vimentin	gi|1353212	55177.6
VIM [Homo sapiens]	gi|47115317	56907.4
unnamed protein product [Mus musculus]	gi|55291	56957.4

vimentin [Bos taurus]	gi|289450	57004.4
vimentin [Cricetulus griseus]	gi|860908	47903.7
vimentin [Homo sapiens]	gi|62414289	56979.4
vimentin [Homo sapiens]	gi|5030431	44799.3
vimentin [Homo sapiens]	gi|340219	57041.4
vimentin [Mus musculus]	gi|2078001	54893.4
vimentin [Mus musculus]	gi|31982755	57015.4
vimentin [Mus musculus]	gi|55408	57049.4
vimentin [Pan troglodytes]	gi|57114172	56975.4
vimentin [Rattus norvegicus]	gi|14389299	57060.4
vimentin protein [Mus musculus]	gi|202368	57001.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1457.9188	1457.941	0.0222	15	118	127	ILLAELEQLK	43	98.613	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[4] F11 and F3	1297/1289	0.407	0.393	1.131	1	Mascot
1980.902	1980.8199	-0.0821	-41	439	454	DGQVINETSQHHDDLE	73	99.998	(N-term)_iTRAQ[0]	[5] F5 and F10	217/209	0.532	0.493	0.994	1	Mascot

92	immunoglobulin kappa light chain constant region [Ovis aries]	gi|52367058	13395.7	2	114	1.262	1.033	0.931	0.308	0.076	0.046	3	3	3	100

Protein Group

kappa light chain [Ovis aries]	gi|147904806	27495.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1116.7239	1116.7499	0.026	23	92	99	SLPTALVK	39	96.25	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	944/936	1.171	0.939	0.989	1	Mascot
2366.2603	2366.1663	-0.094	-40	1	18	SDAQPSVFLFKPSEEQLR	75	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[5] F5 and F10	401/393	1.011	1.053	0.928	1	Mascot
2366.2603	2366.3062	0.0459	19	1	18	SDAQPSVFLFKPSEEQLR	42	98.068	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[2] F4 and F13	227/219	1.698	1.114	0.879	1	Mascot

93	insulin-like growth factor-binding protein 7 [Rattus norvegicus]	gi|61556795	32026.8	2	113	1.216	0.786	1.204	0.101	0.024	0.259	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1722.0411	1721.9779	-0.0632	-37	262	274	ITVVDAIHEIPVK	47	99.493	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[5] F5 and F10	432/424	1.317	0.762	0.991	1	Mascot
1994.2385	1994.2294	-0.0091	-5	262	275	ITVVDAIHEIPVKK	66	99.993	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13, 14]	[1] F8 061011	394/386	1.122	0.809	1.463	1	Mascot

94	beta-2-glycoprotein 1 [Rattus norvegicus]	gi|57528174	43956.6	2	109	0.648	0.814	1.135	0.206	0.251	0.139	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio	iTRAQ Ratio	iTRAQ Ratio	Rank	Result Type

												114/117*	115/117*	116/117*		
1392.7522	1392.7346	-0.0176	-13	328	336	EHSSLAFWK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[1] F8 061011	334/326	0.492	0.622	1.012	1	Mascot
2056.0662	2056.115	0.0488	24	64	78	FTCPLTGMWPINTLK	44	98.943	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15], MMTS (C)[3]	[4] F11 and F3	1359/1351	0.854	1.065	1.274	1	Mascot

95	RecName: Full=Superoxide dismutase [Cu-Zn]	gi|75061021	17556	2	106	1.105	0.962	0.926	0.052	0.073	0.095	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1226.7103	1226.7273	0.017	14	79	87	HVGDLGNVK	50	99.733	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[7] F12 and F9 and F7 attempt 2	828/820	1.055	0.894	0.839	1	Mascot
1784.9575	1785.0632	0.1057	59	115	127	TMVVHEKPDDLGR	56	99.928	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[7] F12 and F9 and F7 attempt 2	854/846	1.157	1.035	1.021	1	Mascot

96	immunoglobulin lambda-6c light chain variable region [Ovis aries]	gi|2746699	12870.2	1	106	1.705	0.934	1.258	0.000	0.000	0.000	1	1	1	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1884.9535	1884.8937	-0.0598	-32	80	97	FSGSNSGNTATLTISGAR	106	100	(N-term)_iTRAQ[0]	[8] F2	286/278	1.705	0.934	1.258	1	Mascot

97	alpha-macroglobulin [Cavia porcellus]	gi|290543549	178258.9	2	104	0.777	0.923	1.175	0.331	0.272	0.135	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1053.619	1053.5586	-0.0604	-57	807	813	GEAFTLK	40	96.823	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	260/252	0.545	0.714	1.054	1	Mascot
1751.9564	1751.9291	-0.0273	-16	1150	1164	ALLAYAFALAGNQER	65	99.99	(N-term)_iTRAQ[0]	[8] F2	544/536	1.108	1.195	1.310	1	Mascot

98	IgG1 heavy chain constant region [Bos taurus]	gi|7547266	39259.3	2	100	1.131	0.961	1.001	0.678	0.509	0.274	7	7	7	100

Protein Group

Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine	gi|108750	54983.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1445.8348	1445.7682	-0.0666	-46	203	214	VHNEGLPAPIVR	43	98.568	(N-term)_iTRAQ[0]	[4] F11 and F3	197/189	2.222	1.945	1.440	1	Mascot
1445.8348	1445.7845	-0.0503	-35	203	214	VHNEGLPAPIVR	43	98.545	(N-term)_iTRAQ[0]	[3] F14,15,16 and F6	167/159	1.642	1.315	1.330	1	Mascot
1445.8348	1445.8787	0.0439	30	203	214	VHNEGLPAPIVR	42	98.077	(N-term)_iTRAQ[0]	[3] F14,15,16 and F6	794/786	1.707	1.419	1.169	1	Mascot
2115.1584	2115.1035	-0.0549	-26	225	240	EPQVYVLAPPQEELSK	55	99.91	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[5] F5 and F10	378/370	0.547	0.633	0.801	1	Mascot
2115.1584	2115.1072	-0.0512	-24	225	240	EPQVYVLAPPQEELSK	54	99.885	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[8] F2	379/371	0.803	0.626	0.816	1	Mascot
2115.1584	2115.1665	0.0081	4	225	240	EPQVYVLAPPQEELSK	58	99.95	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1120/1112	0.783	0.742	0.887	1	Mascot
2115.1584	2115.2253	0.0669	32	225	240	EPQVYVLAPPQEELSK	40	96.903	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1286/1278	1.105	0.710	0.773	1	Mascot

99	RecName: Full=Myocilin; AltName: Full=Trabecular meshwork-induced glucocorticoid response protein;	gi|12585283	58154.6	2	99	1.273	1.119	1.029	0.226	0.285	0.446	2	2	2	100

Protein Group

myocilin [Bos taurus]	gi|4760473	36578.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1631.7859	1631.7487	-0.0372	-23	459	470	YSSMIDYNPLER	43	98.67	(N-term)_iTRAQ[0]	[8] F2	401/393	1.499	1.404	1.475	1	Mascot
2230.1475	2230.0581	-0.0894	-40	392	408	LNPETLELEQTWETNIR	56	99.927	(N-term)_iTRAQ[0]	[8] F2	476/468	1.081	0.892	0.718	1	Mascot

100	immunoglobulin mu chain [Ovis aries]	gi|165945	57810.9	2	99	0.557	0.612	1.212	0.026	0.069	0.019	2	2	2	100

Protein Group

Ig mu chain - sheep	gi|478694	69348.6
This CDS feature is included to show the translation of the corresponding C_region. Presently trans	gi|561876	56422.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1410.7137	1410.8064	0.0927	66	282	291	ALETHTYFER	43	98.727	(N-term)_iTRAQ[0]	[7] F12 and F9 and F7 attempt 2	1272/1264	0.583	0.680	1.193	1	Mascot
1894.0472	1894.0812	0.034	18	370	383	GFAPADVFVQWLQK	55	99.913	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[4] F11 and F3	1351/1343	0.532	0.550	1.231	1	Mascot

101	Chain C, The Crystal Structure Of Modified Bovine Fibrinogen (At ~4 Angstrom Resolution)	gi|6980816	51472.4	2	98	1.232	1.416	0.923	0.043	0.079	0.040	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1610.9515	1611.0001	0.0486	30	163	173	ESGLYFIRPLK	46	99.29	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	922/914	1.191	1.495	0.963	1	Mascot
1885.1031	1885.1543	0.0512	27	233	247	IHLISTQSTIPYVLR	52	99.803	(N-term)_iTRAQ[0]	[2] F4 and F13	275/267	1.276	1.341	0.884	1	Mascot

102	proactivator polypeptide [Bos taurus]	gi|27806447	64671.9	2	97	0.598	0.763	0.828	0.103	0.258	0.061	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1302.7878	1302.8336	0.0458	35	431	439	EQILAALEK	59	99.966	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	978/970	0.701	1.021	0.889	1	Mascot
1377.7849	1377.7327	-0.0522	-38	144	152	HLAELNHQK	38	95.584	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[6] F12 and F9 and F7	172/164	0.510	0.571	0.771	1	Mascot

103	apolipoprotein D, apoD [human, plasma, Peptide, 246 aa]	gi|619383	31277.2	1	95	1.287	1.463	1.186	0.000	0.000	0.000	1	1	1	100

Protein Group

apolipoprotein D precursor [Homo sapiens]	gi|4502163	23220.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1934.9331	1934.9568	0.0237	12	8	21	CPNPPVQENFDVNK	95	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14], MMTS (C)[1]	[4] F11 and F3	1081/1073	1.287	1.463	1.186	1	Mascot

104	insulin-like growth factor-binding protein 6 [Bos taurus]	gi|5705897	14741.4	1	93	0.793	1.130	0.961	0.000	0.000	0.000	1	1	1	100

Protein Group

RecName: Full=Insulin-like growth factor-binding protein 6; Short=IBP-6; Short=IGF-binding protein	gi|1352416	26986.4
insulin-like growth factor binding protein 6 [Bos taurus]	gi|28630915	9734.6
insulin-like growth factor binding protein 6 [Ovis aries]	gi|12061034	9071.5
insulin-like growth factor-binding protein 6 precursor [Mus musculus]	gi|168693654	26930.4
insulin-like growth factor-binding protein 6 precursor [Rattus norvegicus]	gi|6981090	25686

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type

1957.0627	1957.0239	-0.0388	-20	79	93	HLDSVLQQLQTEVFR	93	100	(N-term)_iTRAQ[0]	[5] F5 and F10	537/529	0.793	1.130	0.961	1	Mascot

105	hepatocarcinogenesis-specific protein/hemopexin homolog {clone HC34} [woodchucks, hepatitis B virus	gi|1087020	33129.3	2	93	1.350	1.210	1.307	0.353	0.272	0.249	3	3	3	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1261.7555	1261.7815	0.026	21	196	202	LWWLDLK	43	98.538	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	374/366	1.009	0.913	1.217	1	Mascot
1261.7555	1261.796	0.0405	32	196	202	LWWLDLK	39	96.154	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	1045/1037	1.368	1.335	1.103	1	Mascot
1269.641	1269.6816	0.0406	32	219	227	VDGALCTEK	50	99.697	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9], MMTS (C)[6]	[2] F4 and F13	935/927	1.781	1.454	1.662	1	Mascot

106	inter-alpha-trypsin inhibitor heavy chain H4 [Sus scrofa]	gi|48374067	108849.5	2	90	0.824	1.126	1.680	0.097	0.107	0.031	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1373.6796	1373.7531	0.0735	54	534	542	YIFHSFMER	38	95.822	(N-term)_iTRAQ[0]	[7] F12 and F9 and F7 attempt 2	1391/1383	0.737	1.029	1.650	1	Mascot
1636.9758	1636.933	-0.0428	-26	213	222	FKPTLSQQQK	52	99.821	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,10]	[1] F8 061011	207/199	0.921	1.233	1.711	1	Mascot

107	phospholipid transfer protein [Pongo abelii]	gi|197100925	57666.5	2	89	0.795	1.001	0.833	0.183	0.245	0.130	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1370.7136	1370.6759	-0.0377	-28	153	162	MHAAFGGTFK	39	96.065	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10], Oxidation (M)[1]	[1] F8 061011	231/223	0.979	1.246	0.963	1	Mascot
2428.3235	2428.4136	0.0901	37	447	466	EVVTNHAGFLTIGADLHFAK	50	99.74	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[3] F14,15,16 and F6	986/978	0.646	0.804	0.721	1	Mascot

108	inhibitor of carbonic anhydrase precursor [Sus scrofa]	gi|47523160	85723.8	2	89	0.837	0.821	0.927	0.029	0.132	0.237	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1023.6084	1023.5566	-0.0518	-51	554	560	GDVAFVK	42	98.313	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	228/220	0.809	0.707	0.738	1	Mascot
1750.9612	1750.9208	-0.0404	-23	675	688	YLGPEYLQAIANVR	48	99.497	(N-term)_iTRAQ[0]	[8] F2	483/475	0.866	0.953	1.164	1	Mascot

109	unnamed protein product [Mus musculus]	gi|12835087	12781.6	2	89	1.206	0.967	1.204	0.012	0.163	0.247	2	2	2	100

Protein Group

D6Wsu176e protein precursor [Mus musculus]	gi|42734496	27992.8
Fam3c protein [Mus musculus]	gi|33417025	28022.8
Fam3c protein [Mus musculus]	gi|47125071	36097
PREDICTED: protein FAM3C-like isoform 2 [Pan troglodytes]	gi|55629272	27901.6
family with sequence similarity 3, member C [Rattus norvegicus]	gi|38454280	27953.7
family with sequence similarity 3, member C precursor [Homo sapiens]	gi|7661714	27920.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type

1359.6416	1359.5864	-0.0552	-41	54	62	DNWVFCGGK	49	99.652	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9], MMTS (C)[6]	[5] F5 and F10	402/394	1.218	1.130	1.451	1	Mascot
1646.9602	1646.8857	-0.0745	-45	66	75	TKSPFEQHIK	39	96.794	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,10]	[4] F11 and F3	130/122	1.194	0.828	0.999	1	Mascot

110	collagen type I alpha 1 [Sus scrofa]	gi|37811669	10249	1	87	1.328	2.093	1.125	0.000	0.000	0.000	1	1	1	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2838.2852	2838.2363	-0.0489	-17	7	28	VFCNMETGETCVYPTQPSVPQK	87	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[22], MMTS (C)[3,11]	[8] F2	448/440	1.328	2.093	1.125	1	Mascot

111	contactin-2 precursor [Homo sapiens]	gi|4827022	119638.3	2	87	1.253	0.729	0.774	0.057	0.043	0.010	2	2	2	100

Protein Group

TAG-1 protein (axonin 1)	gi|444868	119652.4
contactin-2 [Pongo abelii]	gi|197098330	119769.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1390.7616	1390.785	0.0234	17	129	137	FGFLQEFSK	48	99.563	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	296/288	1.199	0.771	0.765	1	Mascot
1428.8546	1428.8223	-0.0323	-23	465	476	VTVTPDGTLIIR	38	95.973	(N-term)_iTRAQ[0]	[8] F2	375/367	1.310	0.688	0.784	1	Mascot

112	RecName: Full=Fibulin-1; Short=FIBL-1	gi|30580425	70865.5	2	85	1.231	1.058	0.988	0.598	0.215	0.316	2	2	2	100

Protein Group

Fibulin 1 [Homo sapiens]	gi|18490682	80422.8
fibulin-1 C [Homo sapiens]	gi|31419	80474.9
fibulin-1 isoform C precursor [Homo sapiens]	gi|34734062	80460.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1320.7522	1320.7183	-0.0339	-26	580	589	HGTVSSFVAK	41	97.857	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[1] F8 061011	213/205	0.829	0.879	0.749	1	Mascot
1580.6451	1580.6099	-0.0352	-22	466	476	CLAFECPENYR	44	98.755	(N-term)_iTRAQ[0], MMTS (C)[1,6]	[8] F2	463/455	1.829	1.274	1.304	1	Mascot

113	cadherin-15 preproprotein [Homo sapiens]	gi|4826669	91488.9	1	84	1.394	0.891	0.719	0.000	0.000	0.000	1	1	1	100

Protein Group

M-cadherin [Mus musculus]	gi|3228372	87808.8
cadherin-15 [Rattus norvegicus]	gi|46485501	88045.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1918.875	1918.7867	-0.0883	-46	174	190	AEATDADDPETDNAALR	84	100	(N-term)_iTRAQ[0]	[8] F2	213/205	1.394	0.891	0.719	1	Mascot

114	vitamin K-dependent protein S precursor [Bos taurus]	gi|27806095	83177.9	2	83	0.800	0.744	0.619	0.348	0.108	0.068	2	2	2	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type

1065.6554	1065.6118	-0.0436	-41	359	364	IEIQFK	40	96.924	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6]	[5] F5 and F10	329/321	0.558	0.650	0.558	1	Mascot
1683.8336	1683.7052	-0.1284	-76	591	601	KDSFHSEDFQR	44	98.75	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1]	[6] F12 and F9 and F7	211/203	1.148	0.852	0.686	1	Mascot

115	PREDICTED: apolipoprotein D-like [Cavia porcellus]	gi|348582766	23364.9	1	83	0.712	0.988	0.899	0.000	0.000	0.000	1	1	1	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1662.916	1662.9722	0.0562	34	165	176	DILTSNNIDIEK	83	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1055/1047	0.712	0.988	0.899	1	Mascot

116	unnamed protein product [Homo sapiens]	gi|22761800	75687.3	2	81	1.441	1.103	1.131	0.387	0.171	0.173	2	2	2	100

Protein Group

RecName: Full=Fibulin-1; Short=FIBL-1; Flags: Precursor	gi|215274249	83067.2
fibulin-1 isoform D precursor [Homo sapiens]	gi|34734066	83095.2
fibulin-1 isoform D precursor [Homo sapiens]	gi|13661193	83128.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1580.6451	1580.6099	-0.0352	-22	486	496	CLAFECPENYR	44	98.755	(N-term)_iTRAQ[0], MMTS (C)[1,6]	[8] F2	463/455	1.829	1.274	1.304	1	Mascot
1693.9397	1693.8815	-0.0582	-34	543	554	EFTRPEEIIFLR	38	95.192	(N-term)_iTRAQ[0]	[5] F5 and F10	439/431	1.136	0.955	0.981	1	Mascot

117	glutaminyl cyclase [Ovis aries]	gi|3170172	28410.5	1	80	2.087	1.600	2.044	0.000	0.000	0.000	1	1	1	100

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1960.1477	1960.1471	-0.0006	0	199	213	LEAIEHGLHELGLLK	80	100	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[1] F8 061011	531/523	2.087	1.600	2.044	1	Mascot

118	Chain A, Divalent Cation Tolerant Protein Cuta From Homo Sapiens O60888	gi|56554578	16966.7	1	79	1.370	1.035	1.003	0.000	0.000	0.000	1	1	1	100

Protein Group

brain acetylcholinesterase putative membrane anchor [Homo sapiens]	gi|7341255	15755.2
protein CutA isoform 2 [Homo sapiens]	gi|7706244	17922.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1677.9296	1677.8711	-0.0585	-35	93	106	TQSSLVPALTDFVR	79	100	(N-term)_iTRAQ[0]	[8] F2	474/466	1.370	1.035	1.003	1	Mascot

119	vitronectin precursor [Homo sapiens]	gi|88853069	57941.1	1	79	0.968	0.802	1.161	0.000	0.000	0.000	1	1	1	100

Protein Group

Vitronectin [Homo sapiens]	gi|13477169	57971.1
unnamed protein product [Homo sapiens]	gi|36573	57978
unnamed protein product [Homo sapiens]	gi|36575	58037.1
vitronectin [Pongo abelii]	gi|197100902	57802.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start	End	Sequence	Ion	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700	iTRAQ	iTRAQ	iTRAQ	Rank	Result Type

				Seq.	Seq.		Score				Sample Name]	Ratio 114/117*	Ratio 115/117*	Ratio 116/117*		
1790.9197	1790.8745	-0.0452	-25	198	212	DVWGIEGPIDAAFTR	79	100	(N-term)_iTRAQ[0]	[8] F2	496/488	0.968	0.802	1.161	1	Mascot

120	V-type proton ATPase subunit S1 precursor [Bos taurus]	gi|28461231	53615.2	1	77	0.836	0.812	0.783	0.000	0.000	0.000	1	1	1	99.999

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2233.2358	2233.2573	0.0215	10	191	208	EVLMGNDEVIGQVLSTLK	77	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[4] F11 and F3	1333/1325	0.836	0.812	0.783	1	Mascot

121	calreticulin [rabbits, sketetal muscle, Peptide, 401 aa]	gi|237420	52957.4	1	76	0.908	0.989	0.545	0.000	0.000	0.000	1	1	1	99.999

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1753.8229	1753.781	-0.0419	-24	82	94	HEQNIDXGGGYVK	76	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[1] F8 061011	245/237	0.908	0.989	0.545	1	Mascot

122	brain-type ribonuclease [Antilocapra americana]	gi|12381819	20326.4	1	75	0.822	1.371	1.217	0.000	0.000	0.000	1	1	1	99.999

Protein Group

RecName: Full=Brain ribonuclease; Short=BRB	gi|3024568	18156

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1895.9348	1895.8885	-0.0463	-24	107	119	ETGGSKYPNCAYK	75	99.999	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6,13], MMTS (C)[10]	[1] F8 061011	236/228	0.822	1.371	1.217	1	Mascot

123	similar to pro alpha 1(I) collagen [Bos taurus]	gi|28189559	14422.3	1	73	1.042	0.910	1.106	0.000	0.000	0.000	1	1	1	99.998

Protein Group

Collagen, type I, alpha 1 [Homo sapiens]	gi|22328092	148111.3
collagen alpha-1(I) chain precursor [Canis lupus familiaris]	gi|50978774	147718.9
pro alpha 1(I) collagen [Bos taurus]	gi|14043011	34495.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1599.9189	1599.8799	-0.039	-24	101	113	ALLLQGSNEIEIR	73	99.998	(N-term)_iTRAQ[0]	[8] F2	399/391	1.042	0.910	1.106	1	Mascot

124	alpha 1 (I) chain propeptide [Homo sapiens]	gi|180392	105491.5	1	73	1.042	0.910	1.106	0.000	0.000	0.000	1	1	1	99.998

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1599.9189	1599.8799	-0.039	-24	963	975	ALLLXGSNEIEIR	73	99.998	(N-term)_iTRAQ[0]	[8] F2	399/391	1.042	0.910	1.106	1	Mascot

125	type I collagen alpha 1 chain [Mus sp.]	gi|455975	37820.6	1	73	1.042	0.910	1.106	0.000	0.000	0.000	1	1	1	99.998

Protein Group

Col1a1 protein [Mus musculus]	gi|13096810	62883.2
Col1a1 protein [Mus musculus]	gi|37589303	125532.7
alpha-1 type I procollagen [Mus musculus]	gi|424104	38170.7

collagen alpha-1(I) chain precursor [Mus musculus]	gi|34328108	146845.5
collagen pro-alpha-1 type I chain [Mus musculus]	gi|470674	146756.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1599.9189	1599.8799	-0.039	-24	246	258	ALLLQGSNEIELR	73	99.998	(N-term)_iTRAQ[0]	[8] F2	399/391	1.042	0.910	1.106	1	Mascot

126	C-type natriuretic peptide precursor [Sus scrofa]	gi|56606059	15390.5	1	71	0.628	0.779	0.950	0.000	0.000	0.000	1	1	1	99.998

Protein Group

C-type natriuretic peptide precursor [Ovis aries]	gi|57164165	15464.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2011.0342	2011.1312	0.097	48	34	51	TPPGEEVAEPQAAGGGQK	71	99.998	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[4] F11 and F3	947/939	0.628	0.779	0.950	1	Mascot

127	immunoglobulin lambda light chain [Bos taurus]	gi|15088675	26551.1	1	69	1.204	0.701	1.143	0.000	0.000	0.000	1	1	1	99.997

Protein Group

anti-testosterone antibody [Bos taurus]	gi|432627	26305

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2018.939	2018.8159	-0.1231	-61	212	227	GSYSCEVTHEGSTVTK	69	99.997	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16], MMTS (C)[5]	[8] F2	308/300	1.204	0.701	1.143	1	Mascot

128	extracellular superoxide dismutase [Cu-Zn] precursor [Oryctolagus cuniculus]	gi|130508879	26858.4	1	68	0.542	0.846	0.718	0.000	0.000	0.000	1	1	1	99.995

Protein Group

extracellular superoxide dismutase [Cu-Zn] precursor [Homo sapiens]	gi|118582275	27067.2
extracellular-superoxide dismutase (EC 1.15.1.1) [Homo sapiens]	gi|338284	27097.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1481.7832	1481.8273	0.0441	30	181	193	AVVVHAGEDDLGR	68	99.995	(N-term)_iTRAQ[0]	[3] F14,15,16 and F6	760/752	0.542	0.846	0.718	1	Mascot

129	thyroxine-binding globulin precursor [Ovis aries]	gi|155369640	50563.6	1	67	0.655	0.622	1.069	0.000	0.000	0.000	1	1	1	99.995

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1347.8035	1347.8147	0.0112	8	298	306	GWVNLFVPK	67	99.995	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[2] F4 and F13	309/301	0.655	0.622	1.069	1	Mascot

130	insulin-like growth factor-binding protein 5 [Bos taurus]	gi|263306	13885.5	1	66	1.605	1.316	2.188	0.000	0.000	0.000	1	1	1	99.993

Protein Group

IGFBP5 [Homo sapiens]	gi|48145735	34534
insulin-like growth factor binding protein 5 [Mus musculus]	gi|437125	34220.8
insulin-like growth factor binding protein-5 [Equus caballus]	gi|56849566	12886

insulin-like growth factor-binding protein 5	gi|1586428	34346.8
insulin-like growth factor-binding protein 5 precursor [Homo sapiens]	gi|10834982	34548
insulin-like growth factor-binding protein 5 precursor [Mus musculus]	gi|70909322	34349.8
insulin-like growth factor-binding protein 5 precursor [Rattus norvegicus]	gi|6981088	34321.7
insulin-like growth factor-binding protein 5 precursor [Sus scrofa]	gi|47523008	34360.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2383.0857	2382.9753	-0.1104	-46	84	101	EHEEPTTSEMAEETYSPK	66	99.993	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[5] F5 and F10	243/235	1.605	1.316	2.188	1	Mascot

131	CCP modules 3-12, with parts of CCP 2 and 13 [Bos taurus]	gi|1419424	84142	1	66	1.441	1.501	1.245	0.000	0.000	0.000	1	1	1	99.992

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1616.8492	1616.8114	-0.0378	-23	384	394	CKPGYVTADGK	66	99.992	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,11], MMTS (C)[1]	[1] F8 061011	215/207	1.441	1.501	1.245	1	Mascot

132	Ig gamma heavy chain constant region - rabbit (fragment)	gi|2136983	22718.7	1	66	0.415	0.589	0.961	0.007	0.017	0.191	2	2	2	99.992

Protein Group

Ig gamma H-chain C-region [Oryctolagus cuniculus]	gi|457366	38755.7
Ig gamma H-chain [Oryctolagus cuniculus]	gi|165128	48079.4
RecName: Full=Ig gamma chain C region	gi|121088	38867.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2651.2395	2651.2898	0.0503	19	153	172	GDVFTCSVMHEALHNHYTQK	66	99.992	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20], MMTS (C)[6]	[5] F5 and F10	1289/1281	0.422	0.573	1.152	1	Mascot
2667.2344	2667.3342	0.0998	37	153	172	GDVFTCSVMHEALHNHYTQK	64	99.989	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20], MMTS (C)[6], Oxidation (M)[9]	[5] F5 and F10	1209/1201	0.408	0.607	0.801	1	Mascot

133	RecName: Full=Phosphatidylcholine-sterol acyltransferase; AltName: Full=Lecithin-cholesterol acyltr	gi|21542351	22081.9	1	66	1.102	0.904	1.619	0.000	0.000	0.000	1	1	1	99.992

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1814.9421	1814.9829	0.0408	22	85	96	LEPSQQEEYYLK	66	99.992	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1064/1056	1.102	0.904	1.619	1	Mascot

134	RecName: Full=Plasminogen	gi|51702791	15564.2	1	65	0.835	0.990	1.121	0.000	0.000	0.000	1	1	1	99.992

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2006.8876	2006.8495	-0.0381	-19	76	91	TPESYPNAGLTMNYCR	65	99.992	(N-term)_iTRAQ[0], MMTS (C)[15]	[8] F2	396/388	0.835	0.990	1.121	1	Mascot

135	neuronal pentraxin-1 precursor [Mus musculus]	gi|6679120	51248.3	1	64	0.666	1.248	0.816	0.000	0.000	0.000	1	1	1	99.99

Protein Group

neuronal pentraxin 1 [Homo sapiens]	gi|1438954	51166.3
neuronal pentraxin-1 precursor [Homo sapiens]	gi|55770878	51109.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2174.2278	2174.3406	0.1128	52	124	141	TPAAETLSQLGQTLQSLK	64	99.99	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[18]	[4] F11 and F3	1310/1302	0.666	1.248	0.816	1	Mascot

136	SPARC precursor [Homo sapiens]	gi|4507171	38325.6	1	64	0.925	0.839	0.961	0.000	0.000	0.000	1	1	1	99.989

Protein Group

Chain A, Bm-40, FsEC DOMAIN PAIR	gi|2624793	30724.1
Chain A, Helix C Deletion Mutant Of Bm-40 Fs-Ec Domain Pair	gi|4139513	30132.8
RecName: Full=SPARC; AltName: Full=Basement-membrane protein 40; Short=BM-40; AltName: Full=Osteone	gi|13959711	34312.7
SPARC [Bos taurus]	gi|27806147	38455.6
SPARC precursor [Mus musculus]	gi|6678077	37999.5
SPARC precursor [Pongo abelii]	gi|197102212	38357.6
SPARC precursor [Rattus norvegicus]	gi|6981574	37845.4
osteonectin [Homo sapiens]	gi|338325	38120.6
osteonectin [Rattus norvegicus]	gi|600381	37792.2
secreted acidic cysteine rich glycoprotein [Mus musculus]	gi|56800090	21219.9
secreted acidic cysteine rich glycoprotein [Mus musculus]	gi|56800089	37871.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1492.7883	1492.8629	0.0746	50	141	150	LHLDYIGPCK	64	99.989	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10], MMTS (C)[9]	[7] F12 and F9 and F7 attempt 2	1392/1384	0.925	0.839	0.961	1	Mascot

137	type I collagen alpha 1 precursor [Ovis aries]	gi|8809712	23335.9	1	63	1.822	1.248	1.212	0.000	0.000	0.000	1	1	1	99.986

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1640.855	1640.795	-0.06	-37	164	179	STGISVPGPMGPSGPR	63	99.986	(N-term)_iTRAQ[0]	[8] F2	306/298	1.822	1.248	1.212	1	Mascot

138	enkephalin precursor	gi|223387	30835.5	1	62	0.863	1.070	1.102	0.000	0.000	0.000	1	1	1	99.982

Protein Group

proenkephalin-A [Bos taurus]	gi|27806489	33404.9
unnamed protein product [Bos taurus]	gi|331	28259.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2087.0066	2087.0425	0.0359	17	209	224	FAEPLPSEEEGESYSK	62	99.982	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1047/1039	0.863	1.070	1.102	1	Mascot

139	PREDICTED: hypothetical protein LOC478604 isoform 1 [Canis lupus familiaris]	gi|57109608	24945.8	1	62	1.564	1.863	1.833	0.000	0.000	0.000	1	1	1	99.981

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1823.02	1823.0228	0.0028	2	168	180	NPYLPPETVTYLK	62	99.981	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[4] F11 and F3	1137/1129	1.564	1.863	1.833	1	Mascot

140	CD14 [Ovis aries]	gi|31096292	17799.6	1	61	0.703	0.496	0.792	0.000	0.000	0.000	1	1	1	99.975

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1446.795	1446.7805	-0.0145	-10	3	13	GGGHSLDQFLK	61	99.975	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[1] F8 061011	299/291	0.703	0.496	0.792	1	Mascot

141	Chain C, Crystal Structure Of Mouse Neuroserpin (Cleaved Form)	gi|18158628	32370.6	1	60	0.428	0.657	0.580	0.000	0.000	0.000	1	1	1	99.974

Protein Group

Serine (or cysteine) peptidase inhibitor, clade I, member 1 [Mus musculus]	gi|13904990	49462.2
neuroserpin precursor [Mus musculus]	gi|6678091	49534.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1675.9265	1675.9668	0.0403	24	173	184	AQLIEEWANSVK	60	99.974	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[2] F4 and F13	290/282	0.428	0.657	0.580	1	Mascot

142	calsyntenin-1 isoform 1 [Homo sapiens]	gi|57242757	117940.5	1	60	1.310	1.134	1.015	0.000	0.000	0.000	1	1	1	99.971

Protein Group

Calsyntenin 1 [Homo sapiens]	gi|21706696	116719.8
Clstn1 protein [Mus musculus]	gi|31753169	115754.6
KIAA0911 protein [Homo sapiens]	gi|40788983	125894.7
calsyntenin-1 [Rattus norvegicus]	gi|347300280	114365.2
calsyntenin-1 isoform 2 [Homo sapiens]	gi|57242755	116646.9
calsyntenin-1 precursor [Mus musculus]	gi|12746426	117048.3
mKIAA0911 protein [Mus musculus]	gi|50510703	122835.2
non-classical cadherin XB31alpha1 [Homo sapiens]	gi|33315782	116541.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1926.0695	1926.1344	0.0649	34	89	103	IHGQNVPFDAVVVDK	60	99.971	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15]	[3] F14,15,16 and F6	864/856	1.310	1.134	1.015	1	Mascot

143	fibrinogen A-alpha-chain [Canis lupus familiaris]	gi|1304047	49533.3	1	60	0.613	0.849	0.979	0.000	0.000	0.000	1	1	1	99.969

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1661.981	1661.9297	-0.0513	-31	295	305	GEKELLIGNEK	60	99.969	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,11]	[1] F8 061011	249/241	0.613	0.849	0.979	1	Mascot

144	dystroglycan [Homo sapiens]	gi|398026	104712.6	1	59	0.683	0.768	0.840	0.020	0.118	0.413	2	2	2	99.967

Protein Group

Chain A, Crystal Structure Of A-Dystroglycan	gi|55670138	28003.6
Dystroglycan [Mus musculus]	gi|2924287	75845.5
alpha dystroglycan	gi|1587060	75862.5
dystroglycan precursor [Bos taurus]	gi|27806449	104355
dystroglycan precursor [Canis lupus familiaris]	gi|77404203	104324.3
dystroglycan precursor [Mus musculus]	gi|33859532	104325.4
dystroglycan preproprotein [Homo sapiens]	gi|294997282	104672.5
unnamed protein product [Mus musculus]	gi|26331204	104163.3
unnamed protein product [Mus musculus]	gi|26343839	104355.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2416.2693	2416.1841	-0.0852	-35	283	302	EGAMSAQLGYPVVGWHIANK	59	99.967	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[5] F5 and F10	427/419	0.663	0.666	0.563	1	Mascot
2416.2693	2416.2795	0.0102	4	283	302	EGAMSAQLGYPVVGWHIANK	53	99.852	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20]	[2] F4 and F13	253/245	0.703	0.886	1.253	1	Mascot

145	unnamed protein product [Oryctolagus cuniculus]	gi|929752	10796.3	1	59	0.778	0.822	1.548	0.000	0.000	0.000	1	1	1	99.966

Protein Group

48 kda histamine receptor subunit peptide 4 {internal fragment} [human, peripheral blood mononuclea	gi|998467	3257.5
A-X actin [Mus musculus]	gi|309090	44824.7
ACTB protein [Homo sapiens]	gi|15277503	43352
ACTG1 protein [Homo sapiens]	gi|40225338	20398.2
ACTG1 protein [Homo sapiens]	gi|40226101	31784.2
ACTG2 [Homo sapiens]	gi|49168516	45101.7
Actin, beta [Homo sapiens]	gi|16359158	44893.7
Chain A, Complex Between Rabbit Muscle Alpha-Actin: Human Gelsolin Domain 1	gi|7766848	45155.8
Chain A, Crystal Structure Of Human Vitamin D-Binding Protein In Complex With Skeletal Actin	gi|21730554	44901.8

Chain A, Polylysine Induces An Antiparallel Actin Dimer That Nucleates Filament Assembly: Crystal S	gi|20664362	44240.5
Chain A, Structural Basis Of Actin Sequestration By Thymosin-B4: Implications For Arp23 ACTIVATION	gi|55669843	44312.6
Chain A, Structure Of Rabbit Actin In Complex With Kabiramide C	gi|39654752	44875.7
PREDICTED: actin, alpha skeletal muscle-like isoform 3 [Macaca mulatta]	gi|297281875	40813.7
RecName: Full=Actin, cytoplasmic 1; AltName: Full=Beta-actin; Contains: RecName: Full=Actin, cytopl	gi|47116231	44849.7
RecName: Full=Actin, cytoplasmic 1; AltName: Full=Beta-actin; Contains: RecName: Full=Actin, cytopl	gi|60389477	44978.7
RecName: Full=Putative beta-actin-like protein 3; AltName: Full=Kappa-actin; AltName: Full=POTE ank	gi|74739412	45579.1
Unknown (protein for IMAGE:3538275) [Homo sapiens]	gi|16924319	43635.2
Unknown (protein for IMAGE:3897065) [Homo sapiens]	gi|16306948	19383.6
actin prepeptide [Homo sapiens]	gi|178067	39508.8
actin, alpha 1, skeletal muscle [Homo sapiens]	gi|56204817	34897.6
actin, alpha cardiac muscle 1 proprotein [Homo sapiens]	gi|4885049	45149.8
actin, alpha skeletal muscle [Bos taurus]	gi|27819614	45266.9
actin, alpha skeletal muscle [Homo sapiens]	gi|4501881	45181.8
actin, aortic smooth muscle [Homo sapiens]	gi|4501883	45185.8
actin, beta [Homo sapiens]	gi|14250401	44136.4
actin, beta [Macaca fascicularis]	gi|57281683	14491.4
actin, cytoplasmic 1 [Cricetulus griseus]	gi|347360906	44868.7
actin, cytoplasmic 1 [Homo sapiens]	gi|4501885	44867.7
actin, cytoplasmic 1 [Oryctolagus cuniculus]	gi|156119364	44886.7
actin, cytoplasmic 1 [Pongo abelii]	gi|197099682	44866.7
actin, cytoplasmic 2 [Homo sapiens]	gi|4501887	44923.8
actin, gamma-enteric smooth muscle isoform 1 precursor [Homo sapiens]	gi|4501889	45053.7
alpha 2 actin [Bos taurus]	gi|61553131	48919.9
alpha-actin (AA 27-375) [Mus musculus]	gi|49870	42147.7
alpha-actin (aa 40-375) [Mus musculus]	gi|49864	40709.8

alpha-actin [Homo sapiens]	gi|178027	45284.8
alpha-cardiac actin [Mus musculus]	gi|387090	44869.8
alpha-smooth muscle actin - rabbit (fragment)	gi|2136927	27633.2
beta actin [Cricetinae gen. sp.]	gi|2318133	44859.8
beta actin [Cricetinae gen. sp.]	gi|2318135	34828.6
beta actin [Lama glama]	gi|29603621	36251.3
beta actin [Meriones unguiculatus]	gi|41387701	22995.6
beta actin [Sus scrofa]	gi|476332	27871.1
beta-actin FE-3 [Rattus norvegicus]	gi|13516471	16264.2
beta-actin [Didelphis virginiana]	gi|61375223	36150.5
beta-actin [Felis catus]	gi|11191964	34425.7
beta-actin [Macaca fuscata]	gi|6636344	31385.2
beta-actin [Macaca mulatta]	gi|40744574	33666.2
beta-actin [Marmota monax]	gi|9864780	34175.4
beta-actin [Mus musculus]	gi|48237757	9302.5
beta-actin [Mustela putorius furo]	gi|2724046	38781.9
beta-actin [Oryctolagus cuniculus]	gi|12240086	16512.3
beta-actin [Ovis aries]	gi|8809716	26728.3
beta-actin [Ovis aries]	gi|2665740	29781.1
beta-actin [Sus scrofa]	gi|20068082	19962.9
beta-actin-like [Canis lupus familiaris]	gi|55741585	44749.9
beta-actin-like protein 2 [Mus musculus]	gi|30425250	44990.9
cardiac actin [Canis lupus familiaris]	gi|11493749	8151
cardiac alpha actin [Equus caballus]	gi|14456493	8899.3
cytoskeletal beta actin [Sus scrofa]	gi|45269029	47967.2
gamma actin-like protein [Mus musculus]	gi|6425087	46678.3

gamma-actin [Homo sapiens]	gi|178045	28109.3
gamma-actin [Mus musculus]	gi|809561	44150.4
mutant beta-actin (beta'-actin) [Homo sapiens]	gi|28336	44943.6
put. beta-actin (aa 27-375) [Mus musculus]	gi|49868	42128.5
similar to beta actin [Bos taurus]	gi|28189611	22161
skeletal muscle alpha-actin [Mus musculus]	gi|387082	40672.6
smooth muscle alpha actin [Mesocricetus auratus]	gi|21070328	17433.8
smooth muscle gamma-actin [Mus musculus]	gi|950002	45623.9
unnamed protein product [Mus musculus]	gi|12852068	45077.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#]	Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1934.9944	1934.9412	-0.0532	-27	48	63	SYELPDGQVITIGNER	59	99.966	(N-term)_iTRAQ[0]	[8] F2		421/413	0.778	0.822	1.548	1	Mascot

146	PREDICTED: beta-actin-like protein 2-like [Canis lupus familiaris]	gi|57043600	44903.7	1	59	0.778	0.822	1.548	0.000	0.000	0.000	1	1	1	99.966

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#]	Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1934.9944	1934.9412	-0.0532	-27	240	255	SYELPDGQVITLGNER	59	99.966	(N-term)_iTRAQ[0]	[8] F2		421/413	0.778	0.822	1.548	1	Mascot

147	truncated tenascin XB [Homo sapiens]	gi|6448761	31411.2	1	59	1.296	1.895	1.022	0.000	0.000	0.000	1	1	1	99.964

Protein Group

RecName: Full=Putative tenascin-XA; Short=TN-XA	gi|74706767	34917.8
tenascin-X [Bos taurus]	gi|27807269	469186.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#]	Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2149.0645	2148.9951	-0.0694	-32	253	271	VSYQLADGGEPQSVQVDGR	59	99.964	(N-term)_iTRAQ[0]	[8] F2		304/296	1.296	1.895	1.022	1	Mascot

148	V-set and transmembrane domain containing 2A [Homo sapiens]	gi|20306326	29430.1	1	57	1.124	0.810	0.589	0.564	0.110	0.255	2	2	2	99.945

Protein Group

V-set and transmembrane domain containing 2A [Mus musculus]	gi|20072584	28028.4
V-set and transmembrane domain containing 2A [Mus musculus]	gi|56205459	33336.9
V-set and transmembrane domain containing 2A [Mus musculus]	gi|56205460	27929.4
V-set and transmembrane domain-containing protein 2A precursor [Mus musculus]	gi|281182810	28159.5
hypothetical protein MGC33530 [Homo sapiens]	gi|51094556	29286.9

unnamed protein product [Mus musculus]	gi|26347777	32545.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1791.9122	1791.9662	0.054	30	128	140	VTDANYGELQEHK	57	99.945	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[3] F14,15,16 and F6	767/759	1.688	0.920	0.411	1	Mascot
1791.9122	1791.9716	0.0594	33	128	140	VTDANYGELQEHK	42	98.218	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[7] F12 and F9 and F7 attempt 2	1246/1238	0.749	0.713	0.844	1	Mascot

149	GOLPH2 [Homo sapiens]	gi|48146519	48655.1	1	57	1.413	0.991	1.087	0.000	0.000	0.000	1	1	1	99.942

Protein Group

Golgi membrane protein 1 [Homo sapiens]	gi|29550838	48758.1
golgi membrane protein 1 [Homo sapiens]	gi|55662179	49697.6
golgi membrane protein GP73 [Homo sapiens]	gi|7271867	48627

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1653.9183	1654.004	0.0857	52	66	75	KNEFQGELEK	57	99.942	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[1,10]	[7] F12 and F9 and F7 attempt 2	863/855	1.413	0.991	1.087	1	Mascot

150	immunoglobulin V lambda chain [Ovis aries]	gi|2766639	12428.9	1	57	2.230	0.501	0.750	0.000	0.000	0.000	1	1	1	99.937

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1808.9568	1808.8837	-0.0731	-40	51	65	YGVGWFQQLPGSGLR	57	99.937	(N-term)_iTRAQ[0]	[8] F2	476/468	2.230	0.501	0.750	1	Mascot

151	immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669651	30883.4	1	56	1.249	1.145	0.875	0.101	0.111	0.250	4	4	4	99.933

Protein Group

Bence Jones protein HAG=monoclonal IgM lambda VIII light chain {V region} [human, multiple myeloma, Peptide Partial, 117 aa]	gi|632814	13347.6
Chain A, Bence Jones Protein Cle, A Lambda Iii Immunoglobulin Light- Chain Dimer	gi|2194054	24521.1
Chain A, Crystal Structure Of Monoclonal Antibody 2d12.5 Fab Complexed With Y-Dota	gi|40889110	24644.1
Chain A, Crystal Structure Of The Fab Fragment From The Human Myeloma Immunoglobulin Igg Hil At 1.8 Angstroms Resolution	gi|443559	24694.3
Chain A, Three-Dimensional Structure Of An Immunoglobulin Light Chain Dimer Acting As A Lethal Amyloid Precursor	gi|21465749	24966.5
Chain L, Anti-Morphine Antibody 9b1 Unliganded Form	gi|48425241	24260.2
Chain L, Cocaine Hydrolytic Antibody 15a10	gi|46014931	24571.2
Chain L, Crystal Structure Of A Human Igm Rheumatoid Factor Fab In Complex With Its Autoantigen Igg Fc	gi|3659942	24637.3
Chain L, Crystal Structure Of An Anti-Carbohydrate Antibody Directed Against Vibrio Cholerae O1 In Complex With Antigen	gi|9954938	24105
Chain L, Crystal Structure Of An Anti-Carbohydrate Antibody Directed Against Vibrio Cholerae O1 In Complex With Antigen	gi|9954942	24119
Chain L, Crystal Structure Of Human Factor Ix Gla	gi|42543068	25086.7

Domain In Complex Of An Inhibitory Antibody, 10c12		
Chain L, Fab Fragment	gi|1633069	24263.1
Chain L, Free Conformation Ab1 Of The Ige Spe-7	gi|42543147	13308.8
Chain L, High Resolution Structures Of Antibody Fab Fragment Complexed With Cell-Surface Oligosaccharide Of Pathogenic Salmonella	gi|494368	24807.2
Chain L, How The Anti-(Metal Chelate) Antibody Cha255 Is Specific For The Metal Ion Of Its Antigen: X-Ray Structures For Two Fab'(Slash)hapten Complexes With Different Metals In The Chelate	gi|443045	24838.2
Chain L, N1g9 (Igg1-Lambda) Fab Fragment	gi|1633154	24766.2
Chain L, Recognition Of A Cell-Surface Oligo-Saccharide Of Pathogenic Salmonella By An Antibody Fab Fragment	gi|494374	24790.1
Chain L, Refined Three-Dimensional Structure Of The Fab Fragment Of A Murine Igg1, Lambda Antibody	gi|515129	24188
Chain L, The Three-Dimensional Structure Of An Anti-Sweetener Fab, Nc10.14, Shows The Extent Of Structural Diversity In Antigen Recognition By Immunoglobulins	gi|11514460	24802.3
Chain L, Three-Dimensional Structure Of A Human Fab With High Affinity For Tetanus Toxoid	gi|2914164	24624.3
Chain W, Murine 6a6 Fab In Complex With Humanized Anti-Tissue Factor D3h44 Fab	gi|34810347	24361.1
IGL@ protein [Homo sapiens]	gi|48735306	28028.1
IGL@ protein [Homo sapiens]	gi|49522736	27880.8
IGL@ protein [Homo sapiens]	gi|21595392	27094.4
IGL@ protein [Homo sapiens]	gi|20380868	26782.3
IGL@ protein [Homo sapiens]	gi|49256434	26787.4
IGL@ protein [Homo sapiens]	gi|49258104	26655.2
IGL@ protein [Homo sapiens]	gi|47939570	26911.4
IGL@ protein [Homo sapiens]	gi|21410208	27442.7
Ig A L	gi|229536	25060.5
Ig L-chain V-region [Homo sapiens]	gi|27552515	25023.6
Ig V lambda	gi|226513	15750.9
Ig VJC-region [Homo sapiens]	gi|306977	26885.4
Ig lambda C Sut	gi|224503	13263.8
Ig lambda VI THO	gi|224892	25411.5
Ig lambda chain (BJP-DIA) - human	gi|539617	24726.3

Ig lambda chain - human	gi|106637	26662.2
Ig lambda chain - human	gi|106642	26700.2
Ig lambda chain - human	gi|106643	26734.5
Ig lambda chain - human	gi|106640	26917.4
Ig lambda chain - human	gi|106639	26723.4
Ig lambda chain - human	gi|106655	27005.6
Ig lambda chain - human	gi|106653	26623.3
Ig lambda chain - human	gi|106651	26506.2
Ig lambda chain - human	gi|106649	28312.2
Ig lambda chain - human	gi|106648	26653.1
Ig lambda chain - human	gi|106636	26618.1
Ig lambda chain - human	gi|106645	26947.4
Ig lambda chain - human (fragment)	gi|106657	26903.5
Ig lambda chain - human (fragment)	gi|106660	26675.3
Ig lambda chain - human (fragment)	gi|106656	17109.4
Ig lambda chain - human (fragment)	gi|106661	22181.1
Ig lambda chain V region (Zim) - human (fragment)	gi|87899	12695.4
Ig lambda chain V region - human	gi|478602	24485.3
Ig lambda chain V region - human	gi|346196	13069.5
Ig lambda chain V region - human	gi|7439053	24713.4
Ig lambda chain V region - human (fragment)	gi|478653	16264.1
Ig lambda chain V region MabB23 - mouse	gi|2135590	24658.2
Ig lambda chain V-region (V-J) [Homo sapiens]	gi|186112	15814.9
Ig lambda chain V-region [Homo sapiens]	gi|1864143	15653.1
Ig lambda chain precursor - human	gi|87890	26978.5
Ig lambda chain precursor V region (JP-DL-3) - human (fragment)	gi|87891	15229.6

Ig lambda light chain variable region (VJC) [Homo sapiens]	gi|439517	14408
Ig lambda,anti-Rh(c)	gi|227167	25272.6
Ig lambda-1 chain V region (hybridoma Se155-4) - mouse	gi|627941	12752.4
Ig rearranged L-chain V-region [Homo sapiens]	gi|28559048	17981.9
IgG1/L immunoglobulin light chain VL2 variable region [Homo sapiens]	gi|33340655	13207.4
IgM heavy chain variable region [Homo sapiens]	gi|4100378	13233.5
IgM heavy chain variable region [Homo sapiens]	gi|4100376	13435.7
IgM light chain [Homo sapiens]	gi|4261790	14170.1
Shigella dysenteriae type 1-specific antibody light chain variable region [Mus sp.]	gi|1087011	12209.2
This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal [Homo sapiens]	gi|619634	15022.5
Unknown (protein for MGC:27152) [Homo sapiens]	gi|16198375	26910.5
Unknown (protein for MGC:31936) [Homo sapiens]	gi|18044241	26886.3
Unknown (protein for MGC:31944) [Homo sapiens]	gi|18380972	26874.3
amyloid fibril protein Es492,Ig lambda	gi|224730	19163.6
amyloid lambda 6 light chain variable region SAR [Homo sapiens]	gi|14279407	13099.4
amyloidogenic immunoglobulin lambda VI chain variable region [Homo sapiens]	gi|4732060	12825.2
anti-HIV-1 gp120 immunoglobulin 23e lambda light chain [Homo sapiens]	gi|40647140	21791.8
anti-Rh(D) antibody [Homo sapiens]	gi|7765075	22710.4
anti-carcinoma surface antigen monoclonal antibody AC6C3 [Homo sapiens]	gi|998391	15218.5
anti-flavocytochrome b2 IgG [Mus musculus]	gi|12584580	26584.3
anti-peptide/MHC complex HLA-A1/MAGE-A1 monoclonal antibody light chain [Homo sapiens]	gi|16974104	24982.5
anti-rabies SO57 immunoglobulin lambda light chain [Homo sapiens]	gi|27728683	27766.8
anti-rabies SOJB immunoglobulin lambda light chain [Homo sapiens]	gi|27728687	26882.4
antiporphyrin immunoglobulin G lambda chain variable region [Mus musculus]	gi|27763668	25955.1
antiporphyrin immunoglobulin G lambda chain variable region [Mus musculus]	gi|27762580	26098.1
immunoglobin anti-granzymeB light chain variable	gi|13235108	14099

region [Homo sapiens]		
immunoglobulin kappa light chain V region [Homo sapiens]	gi|2599538	13492.9
immunoglobulin kappa light chain V region [Homo sapiens]	gi|2599540	12635.3
immunoglobulin kappa light chain variable region DPL5 [Homo sapiens]	gi|5731247	15163.6
immunoglobulin lambda chain [Macaca mulatta]	gi|40287807	15247.7
immunoglobulin lambda chain [Macaca mulatta]	gi|40287765	15392.8
immunoglobulin lambda chain [Macaca mulatta]	gi|40287823	14669.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287763	15350.7
immunoglobulin lambda chain [Macaca mulatta]	gi|40287819	15406.7
immunoglobulin lambda chain [Macaca mulatta]	gi|40287821	14758.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287769	15283.7
immunoglobulin lambda chain [Macaca mulatta]	gi|40287813	15048.6
immunoglobulin lambda chain [Macaca mulatta]	gi|40287815	15018.6
immunoglobulin lambda chain [Macaca mulatta]	gi|40287817	14909.5
immunoglobulin lambda chain [Macaca mulatta]	gi|40287771	15345.6
immunoglobulin lambda chain [Macaca mulatta]	gi|40287809	15203.7
immunoglobulin lambda chain [Macaca mulatta]	gi|40287827	15006.6
immunoglobulin lambda chain [Macaca mulatta]	gi|40287851	14125.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287837	14169.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287839	14185.3
immunoglobulin lambda chain [Macaca mulatta]	gi|40287767	15461.6
immunoglobulin lambda chain [Macaca mulatta]	gi|40287847	14155.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287849	14155.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287773	15436.7
immunoglobulin lambda chain [Macaca mulatta]	gi|40287825	14857.4
immunoglobulin lambda chain [Macaca mulatta]	gi|40287833	14161
immunoglobulin lambda chain [Macaca mulatta]	gi|40287843	14169.2

immunoglobulin lambda chain [Macaca mulatta]	gi|40287841	14155.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287811	15240.6
immunoglobulin lambda chain [Macaca mulatta]	gi|40287845	14203.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287831	14283.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287803	15296.7
immunoglobulin lambda chain [Macaca mulatta]	gi|40287829	14309.2
immunoglobulin lambda chain [Macaca mulatta]	gi|40287835	14199.3
immunoglobulin lambda chain [Mus musculus]	gi|393152	12729.5
immunoglobulin lambda chain [Mus musculus]	gi|37196479	25204.5
immunoglobulin lambda chain [Mus musculus]	gi|37196529	25111.5
immunoglobulin lambda chain [Mus musculus]	gi|393148	12644.4
immunoglobulin lambda chain [Mus musculus]	gi|37196444	25085.4
immunoglobulin lambda chain [Mus musculus]	gi|37196442	24898.5
immunoglobulin lambda chain [Mus musculus]	gi|37196465	25043.6
immunoglobulin lambda chain [Mus musculus]	gi|37221169	24995.6
immunoglobulin lambda chain [Mus musculus]	gi|37221129	25103.5
immunoglobulin lambda chain [Mus musculus]	gi|37221125	25062.5
immunoglobulin lambda chain [Mus musculus]	gi|37221133	25059.5
immunoglobulin lambda chain [Mus musculus]	gi|37221064	24848.6
immunoglobulin lambda chain [Mus musculus]	gi|37221147	25075.5
immunoglobulin lambda chain [Mus musculus]	gi|37221090	24972.5
immunoglobulin lambda chain [Mus musculus]	gi|37221143	25107.5
immunoglobulin lambda chain [Mus musculus]	gi|37221163	24858.5
immunoglobulin lambda chain [Mus musculus]	gi|37221094	25217.7
immunoglobulin lambda chain [Mus musculus]	gi|37196450	25183.6
immunoglobulin lambda chain [Mus musculus]	gi|37196446	24931.4

immunoglobulin lambda chain [Mus musculus]	gi|37196494	25188.7
immunoglobulin lambda chain [Mus musculus]	gi|37196485	25089.5
immunoglobulin lambda chain [Mus musculus]	gi|37196498	25077.5
immunoglobulin lambda chain [Mus musculus]	gi|37196440	25026.4
immunoglobulin lambda chain [Mus musculus]	gi|37196527	25040.4
immunoglobulin lambda chain [Mus musculus]	gi|37196508	25095.6
immunoglobulin lambda chain [Mus musculus]	gi|37196512	25133.6
immunoglobulin lambda chain [Mus musculus]	gi|37221117	25075.4
immunoglobulin lambda chain [Mus musculus]	gi|37196481	25056.6
immunoglobulin lambda chain [Mus musculus]	gi|37196514	25130.5
immunoglobulin lambda chain [Mus musculus]	gi|37196504	25009.4
immunoglobulin lambda chain [Mus musculus]	gi|37196467	25154.6
immunoglobulin lambda chain [Mus musculus]	gi|37196483	24927.4
immunoglobulin lambda chain [Mus musculus]	gi|37196525	25134.5
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immunoglobulin lambda chain [Mus musculus]	gi|37196500	25119.5
immunoglobulin lambda chain [Mus musculus]	gi|37221153	25061.5
immunoglobulin lambda chain [Mus musculus]	gi|37221139	25116.5
immunoglobulin lambda chain [Mus musculus]	gi|37221105	25117.6
immunoglobulin lambda chain [Mus musculus]	gi|37221085	24867.5
immunoglobulin lambda chain [Mus musculus]	gi|37221141	25119.5
immunoglobulin lambda chain [Mus musculus]	gi|37221059	25089.5
immunoglobulin lambda chain [Mus musculus]	gi|37221071	25187.6
immunoglobulin lambda chain [Mus musculus]	gi|37221159	25203.6
immunoglobulin lambda chain [Mus musculus]	gi|37221131	25016.5
immunoglobulin lambda chain [Mus musculus]	gi|37221087	25117.6

immunoglobulin lambda chain [Mus musculus]	gi|37221135	25131.6
immunoglobulin lambda chain [Mus musculus]	gi|37221145	25000.5
immunoglobulin lambda chain [Mus musculus]	gi|37221137	25075.5
immunoglobulin lambda chain [Mus musculus]	gi|37221113	25027.6
immunoglobulin lambda chain [Mus musculus]	gi|37221155	25117.5
immunoglobulin lambda chain [Mus musculus]	gi|37221167	25164.5
immunoglobulin lambda chain [Mus musculus]	gi|37221127	25101.6
immunoglobulin lambda chain [Mus musculus]	gi|37221115	25088.6
immunoglobulin lambda chain [Mus musculus]	gi|37196531	25138.5
immunoglobulin lambda chain [Mus musculus]	gi|37196496	25106.5
immunoglobulin lambda chain variable and joining regions [Mus musculus]	gi|623386	12824.5
immunoglobulin lambda chain variable and joining regions [Mus musculus]	gi|619963	12757.4
immunoglobulin lambda chain variable region [Homo sapiens]	gi|5578834	12793.3
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587378	13906.9
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587360	13715.8
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587388	14077
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587416	14177
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587384	14013.9
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587398	13734.9
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587358	13772.9
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587402	13598.8
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587412	14255.9
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587408	14243.9
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587414	14181.9
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587395	13885
immunoglobulin lambda chain variable region [Homo	gi|587382	13693.7

sapiens]		
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587364	13915.9
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immunoglobulin lambda chain variable region [Homo sapiens]	gi|587404	13820
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587406	13840.8
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587418	14481.1
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587420	14617.1
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587368	13590.7
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587410	14198.9
immunoglobulin lambda chain variable region [Homo sapiens]	gi|587400	14112.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669669	30256.8
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669665	30175.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669501	30537.3
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669677	30251.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669243	14016
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669537	30567.2
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669521	30351.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669511	30644.2
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669533	30618.2
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669643	30722.3
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669619	29766.8
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669595	30373
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669573	30091.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669645	30601.2
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669505	30517.3
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669529	30366.1
immunoglobulin lambda light chain VLJ region [Homo	gi|21669495	30717.4

sapiens]		
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immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669659	30438.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669509	30377.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669625	30205
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669535	30444
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669515	30255.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669639	29578.7
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669493	30544.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669547	29959.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669615	31355.7
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669587	30073.7
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669623	29785.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669599	30191.8
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669575	30189
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669525	30323
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669545	29977.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669581	30673.3
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669593	30264.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669597	30318
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669671	30021.7
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669551	30043.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669675	30201.8
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669543	30148
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669655	31077.5
immunoglobulin lambda light chain VLJ region [Homo	gi|21669517	30384.1

sapiens]		
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immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669503	30487.2
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669629	29913.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669591	30235.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669635	30205
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669607	30874.3
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669609	31423.8
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669613	30852.3
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669539	30268.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669531	30406.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669563	30382.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669567	30375.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669247	12858.3
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669653	31564.9
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669627	29857.8
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669603	31291.6
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669601	31364.7
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669541	30559.2
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669565	30760.3
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669667	29903
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669661	30436.1
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669561	30736.3
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669657	30520.2
immunoglobulin lambda light chain VLJ region [Homo sapiens]	gi|21669663	30520.1
immunoglobulin lambda light chain VLJ region [Homo	gi|21669577	30361.1

sapiens]		
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immunoglobulin lambda light chain [Homo sapiens]	gi|21311293	15402.9
immunoglobulin lambda light chain [Homo sapiens]	gi|468247	24988.4
immunoglobulin lambda light chain [Homo sapiens]	gi|6467839	25015.6
immunoglobulin lambda light chain [Homo sapiens]	gi|1684928	22607.3
immunoglobulin lambda light chain variable and constant region [Homo sapiens]	gi|27818835	12711.3
immunoglobulin lambda light chain variable region 4a [Homo sapiens]	gi|3335588	13423.7
immunoglobulin lambda light chain variable region 4a [Homo sapiens]	gi|3335580	13977
immunoglobulin lambda light chain variable region 4a [Homo sapiens]	gi|3335594	13307.6
immunoglobulin lambda light chain variable region 4a [Homo sapiens]	gi|3335586	13472.6
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|47271324	12792.4
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|47271328	12809.3
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|3388057	13025.4
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324232	12255.3
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324110	12176
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324062	11591.7
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|3388053	13116.5
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324186	12346.3
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324128	12202.1
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324088	11406.7
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324044	12366.1
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324178	12060
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|3388059	13262.6
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324056	12062.1
immunoglobulin lambda light chain variable region	gi|4324244	12626.4

[Homo sapiens]		
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|3388063	13155.7
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|3388075	13079.6
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|27369054	15208.4
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324152	12537.3
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324040	12512.4
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324200	11772.7
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324098	12517.2
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324026	12285.1
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324102	11790.8
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324230	11932
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|27369050	12756.3
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324268	12233.1
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|27369034	12963.4
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324124	12315.2
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324142	11873.8
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|27369083	15745.7
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|3388061	13160.6
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324164	12846.4
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324262	11933.8
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324280	12134
immunoglobulin lambda light chain variable region	gi|4324204	11849.9

[Homo sapiens]		
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324144	12083
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324246	12210
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324038	11924.9
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324028	13021.6
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324190	12568.1
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324116	12722.3
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|3388073	12875.4
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324080	10741.5
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324046	12364.2
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324284	12283.2
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324174	12252.3
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324092	11817.7
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immunoglobulin lambda light chain variable region	gi|4324064	12023

[Homo sapiens]		
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324042	11677.8
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immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324122	12453.2
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immunoglobulin lambda-1 light chain precursor [Mus musculus]	gi|387376	26693.3
immunoglobulin lambda-chain [Homo sapiens]	gi|185364	27123.5
immunoglobulin lambda-chain [Homo sapiens]	gi|434698	15026.4
immunoglobulin lambda-chain [Homo sapiens]	gi|186135	16522.3
immunoglobulin lambda-chain [Homo sapiens]	gi|186083	15465.5
immunoglobulin lambda-chain [Homo sapiens]	gi|186091	14936.3
immunoglobulin lambda-chain [Homo sapiens]	gi|186093	15096.4
immunoglobulin lambda-chain [Homo sapiens]	gi|186095	14728.3
immunoglobulin lambda-chain [Mus musculus]	gi|197685	14931.8
immunoglobulin lambda-chain [Mus musculus]	gi|197683	14849.6
immunoglobulin light chain Fab fragment [Homo sapiens]	gi|3954950	14179
immunoglobulin light chain [Homo sapiens]	gi|553496	15735.8
immunoglobulin light chain [Homo sapiens]	gi|1684927	23162.6
immunoglobulin light chain [Mus musculus]	gi|34481886	23062.4
immunoglobulin light chain lambda 1 [Homo sapiens]	gi|11992192	14157.1
immunoglobulin light chain lambda 2 [Homo sapiens]	gi|11992186	13981.7

immunoglobulin light chain lambda 3 [Homo sapiens]	gi|11992196	13870.9
immunoglobulin light chain lambda 6 [Homo sapiens]	gi|11992204	14329
immunoglobulin light chain lambda 6 [Homo sapiens]	gi|11992202	14123.9
immunoglobulin light chain lambda 6 [Homo sapiens]	gi|11992200	14482.2
immunoglobulin light chain variable region [Homo sapiens]	gi|11558190	14416.3
immunoglobulin light chain variable region [Homo sapiens]	gi|12734074	13701.6
immunoglobulin light chain variable region [Homo sapiens]	gi|12734067	13965
immunoglobulin light chain variable region [Homo sapiens]	gi|12734092	14357.1
immunoglobulin light chain variable region [Homo sapiens]	gi|11121491	14551.4
immunoglobulin light chain variable region [Homo sapiens]	gi|11121493	14528.5
immunoglobulin light chain variable region [Homo sapiens]	gi|22095259	14951.8
immunoglobulin light chain variable region [Homo sapiens]	gi|18025610	16551.1
immunoglobulin light chain variable region [Homo sapiens]	gi|22095217	13432.6
immunoglobulin light chain variable region [Homo sapiens]	gi|22095251	12732.3
immunoglobulin light chain variable region [Homo sapiens]	gi|3327990	14795.4
immunoglobulin light chain variable region [Homo sapiens]	gi|7688925	12809.5
immunoglobulin light chain variable region [Homo sapiens]	gi|3327988	14945.5
immunoglobulin light chain variable region [Homo sapiens]	gi|3327992	14693.2
immunoglobulin light chain variable region [Homo sapiens]	gi|22095229	12736.4
immunoglobulin light chain variable region [Homo sapiens]	gi|3328010	14432.5
immunoglobulin light chain variable region [Homo sapiens]	gi|22095189	12931.4
immunoglobulin light chain variable region [Homo sapiens]	gi|12698680	13614.8
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immunoglobulin light chain variable region [Homo sapiens]	gi|465170	17501.8
immunoglobulin light chain variable region [Homo sapiens]	gi|12698674	14424.1
immunoglobulin light chain variable region [Homo	gi|1087002	12240.2

sapiens]		
immunoglobulin light chain variable region [Homo sapiens]	gi|12734088	13990.9
immunoglobulin light chain variable region [Homo sapiens]	gi|12734083	14088.9
immunoglobulin light chain variable region [Homo sapiens]	gi|12734077	14040.1
immunoglobulin light chain variable region [Homo sapiens]	gi|12698676	14601.2
immunoglobulin light chain variable region [Homo sapiens]	gi|22095209	12737.3
immunoglobulin light chain variable region [Homo sapiens]	gi|3327994	14805.5
immunoglobulin light chain variable region [Homo sapiens]	gi|465176	17312.9
immunoglobulin light chain variable region [Mus musculus]	gi|37784142	14451.3
immunoglobulin variable region [Homo sapiens]	gi|306918	15384.7
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524117	14477
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524109	13891.7
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524095	14282.2
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524093	13955
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524125	13933.7
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524091	13849.8
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524131	14165.9
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524121	14225.9
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524123	14359
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524115	14219.9
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524103	14226.1
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524097	13878.9
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524107	13715.9
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524087	13770.9
lambda 1 immunoglobin light chain variable region [Homo sapiens]	gi|5524127	14108.8
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023127	14226.9
lambda 1 immunoglobulin light chain variable region	gi|3023107	14024

[Homo sapiens]		
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023105	13742.8
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023133	14147.8
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023119	14027.1
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023123	14218
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023113	13680
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023115	13947.8
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023125	14149.9
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|4761260	13789.8
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023103	13900
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023129	14287.9
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|4761254	13634.7
lambda 1 immunoglobulin light chain variable region [Homo sapiens]	gi|3023121	14378
lambda 2 immunoglobulin light chain variable region [Homo sapiens]	gi|4927958	14181.1
lambda 2 immunoglobulin light chain variable region [Homo sapiens]	gi|4761264	13799.8
lambda 3 immunoglobulin light chain variable region [Homo sapiens]	gi|4761270	13778.7
lambda 3 immunoglobulin light chain variable region [Homo sapiens]	gi|4761268	13708.7
lambda 6 immunoglobulin light chain variable region [Homo sapiens]	gi|4927956	12587.1
lambda 6 immunoglobulin light chain variable region [Homo sapiens]	gi|4761278	14492
lambda 6 immunoglobulin light chain variable region [Homo sapiens]	gi|4761276	14367
lambda 6 immunoglobulin light chain variable region [Homo sapiens]	gi|4761280	13936.7
monoclonal antibody HB4C5 light chain [Homo sapiens]	gi|1524073	13428.9
protein CAP,Bence-Jones	gi|223968	12540.1
protein MES,Bence-Jones	gi|223971	12715.2
protein NIG51 lambda,Bence-Jones	gi|223229	24586.2
protein OKA,Bence-Jones	gi|223972	12681.2
protein SUT,Bence-Jones	gi|223863	13261.4

rheumatoid factor G9 light chain [Homo sapiens]	gi|298557	13845.9
unnamed protein product [Homo sapiens]	gi|34526178	26825.4
unnamed protein product [Mus musculus]	gi|12841278	15580.6
unnamed protein product [Mus musculus]	gi|12842122	26529.2
variable immunoglobulin anti-HLA lambda light chain [Homo sapiens]	gi|2654044	13058.5
variable immunoglobulin anti-HLA lambda light chain [Homo sapiens]	gi|2654036	12391.2
variable immunoglobulin anti-steroid light chain [Homo sapiens]	gi|1695139	14414.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1143.7347	1143.745	0.0103	9	129	136	LTVLGQPK	52	99.802	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	239/231	1.285	1.227	1.137	1	Mascot
1143.7347	1143.7556	0.0209	18	129	136	LTVLGQPK	49	99.639	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	135/127	1.096	1.276	0.863	1	Mascot
1143.7347	1143.7593	0.0246	22	129	136	LTVLGQPK	44	98.738	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	477/469	1.284	1.079	0.587	1	Mascot
1143.7347	1143.7604	0.0257	22	129	136	LTVLGQPK	56	99.933	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	936/928	1.346	1.016	1.020	1	Mascot

152	immunoglobulin light chain variable region [Homo sapiens]	gi|3328006	13687.7	1	55	1.249	1.145	0.875	0.101	0.111	0.250	4	4	4	99.912

Protein Group

immunoglobulin lambda light chain variable region [Homo sapiens]	gi|27369079	12877.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1143.7347	1143.745	0.0103	9	107	114	LTVXGQPK	52	99.802	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	239/231	1.285	1.227	1.137	1	Mascot
1143.7347	1143.7556	0.0209	18	107	114	LTVXGQPK	49	99.639	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	135/127	1.096	1.276	0.863	1	Mascot
1143.7347	1143.7593	0.0246	22	107	114	LTVXGQPK	44	98.738	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	477/469	1.284	1.079	0.587	1	Mascot
1143.7347	1143.7604	0.0257	22	107	114	LTVXGQPK	56	99.933	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	936/928	1.346	1.016	1.020	1	Mascot

153	PREDICTED: EGF containing fibulin-like extracellular matrix protein 1 [Canis lupus familiaris]	gi|57092953	58743.1	1	55	1.307	1.403	1.245	0.000	0.000	0.000	1	1	1	99.916

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1825.8314	1825.7839	-0.0475	-26	372	385	NPCQDPYVLTSENR	55	99.916	(N-term)_iTRAQ[0], MMTS (C)[3]	[8] F2	366/358	1.307	1.403	1.245	1	Mascot

154	proSAAS [Mus musculus]	gi|6653209	27747	1	55	1.366	1.389	1.570	0.000	0.000	0.000	1	1	1	99.914

Protein Group

proSAAS [Mus musculus]	gi|257153448	27732
proSAAS [Rattus norvegicus]	gi|9507061	27876.1
proSAAS precursor [Homo sapiens]	gi|7019519	27834.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1315.709	1315.7361	0.0271	21	66	77	GEAAGAVQELAR	55	99.914	(N-term)_iTRAQ[0]	[4] F11 and F3	1012/1004	1.366	1.389	1.570	1	Mascot

155	alpha-2-antiplasmin precursor [Bos taurus]	gi|27807209	58364.5	1	55	0.576	0.722	0.822	0.000	0.000	0.000	1	1	1	99.905

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1563.8754	1563.8358	-0.0396	-25	467	476	GDKPFDPDLK	56	99.928	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,10]	[1] F8 061011	242/234	0.576	0.722	0.822	1	Mascot

156	RecName: Full=Inter-alpha-trypsin inhibitor; Short=ITI; AltName: Full=GIK-14; AltName: Full=Inhibit	gi|51317404	15381.8	1	55	0.977	0.980	1.043	0.000	0.000	0.000	1	1	1	99.904

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1607.9043	1607.9338	0.0295	18	72	83	AGIELWAFDAVK	55	99.904	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[4] F11 and F3	1252/1244	0.977	0.980	1.043	1	Mascot

157	haptoglobin beta chain {N-terminal} [Ursus arctos=brown bears, serum, Peptide Partial, 20 aa]	gi|998960	2452.3	1	54	0.429	0.395	1.436	0.000	0.000	0.000	1	1	1	99.896

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1208.6674	1208.6146	-0.0528	-44	10	17	GSFPXQAK	54	99.896	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	311/303	0.429	0.395	1.436	1	Mascot

158	semaphorin-7A isoform 1 preproprotein [Homo sapiens]	gi|4504237	79540.7	1	54	0.717	0.437	0.889	0.000	0.000	0.000	1	1	1	99.878

Protein Group

semaphorin L [Homo sapiens]	gi|3551779	71769.3
semaphorin L [Mus musculus]	gi|3523117	46843.7
semaphorin-7A precursor [Mus musculus]	gi|6755466	79376.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1791.9124	1792.0386	0.1262	70	227	239	ATIVHQDQAYDDK	54	99.878	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[7] F12 and F9 and F7 attempt 2	1213/1205	0.717	0.437	0.889	1	Mascot

159	insulin-like growth factor binding protein-6 [Equus caballus]	gi|56849568	10490.1	1	53	0.389	0.719	0.818	0.000	0.000	0.000	1	1	1	99.871

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1688.7738	1688.7689	-0.0049	-3	63	75	GSHTLYVPNCDHR	53	99.871	(N-term)_iTRAQ[0], MMTS (C)[10]	[5] F5 and F10	1145/1137	0.389	0.719	0.818	1	Mascot

160	RecName: Full=Cadherin-2; AltName: Full=Neural cadherin; Short=N-cadherin; AltName: CD_antigen=CD32	gi|13431334	105324	1	53	1.056	1.282	1.115	0.000	0.000	0.000	1	1	1	99.853

Protein Group

Cadherin 2, type 1, N-cadherin (neuronal) [Homo sapiens]	gi|22209070	105700.1
N-cadherin [Homo sapiens]	gi|253483	105664.1
RecName: Full=Cadherin-2; AltName: Full=Neural	gi|115421	102583.6

cadherin; Short=N-cadherin; AltName: CD_antigen=CD32		
cadherin-2 precursor [Mus musculus]	gi|161760627	105434.1
cadherin-2 precursor [Rattus norvegicus]	gi|13786162	105593.2
cadherin-2 preproprotein [Homo sapiens]	gi|14589889	105735.2
hypothetical protein [Pongo abelii]	gi|55728602	102906.8
neural cadherin precursor [Mus musculus]	gi|309125	105254.9
unnamed protein product [Homo sapiens]	gi|34999	105790.3
unnamed protein product [Mus musculus]	gi|26328611	105494.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2045.129	2045.1973	0.0683	33	102	114	FLIYAQDKETQEK	53	99.853	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8,13]	[3] F14,15,16 and F6	852/844	1.056	1.282	1.115	1	Mascot

161	RecName: Full=Complement C2; AltName: Full=C3/C5 convertase; Contains: RecName: Full=Complement C2b	gi|48427894	89707.8	1	52	0.436	0.857	0.844	0.000	0.000	0.000	1	1	1	99.814

Protein Group

C2 [Homo sapiens]	gi|15277207	68378.1
DKFZP469A1324 protein [Pongo abelii]	gi|207079949	88115.9
RecName: Full=Complement C2; AltName: Full=C3/C5 convertase; Contains: RecName: Full=Complement C2b	gi|62286486	89801.9
RecName: Full=Complement C2; AltName: Full=C3/C5 convertase; Contains: RecName: Full=Complement C2b	gi|38257345	89563.6
complement C2 [Pongo abelii]	gi|197098872	89541.7
complement C2 [Sus scrofa]	gi|38455778	87999.3
complement C2 isoform 1 preproprotein [Homo sapiens]	gi|14550407	89649.8
hypothetical protein [Homo sapiens]	gi|31873561	44416.4
unnamed protein product [Homo sapiens]	gi|34628	89615.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1639.0067	1638.9542	-0.0525	-32	478	487	TPWHVTIKPK	52	99.814	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8,10]	[4] F11 and F3	212/204	0.436	0.857	0.844	1	Mascot

162	retinoic acid receptor responder protein 2 [Cricetulus griseus]	gi|346716116	21276.2	1	52	0.578	0.970	0.908	0.000	0.000	0.000	1	1	1	99.807

Protein Group

retinoic acid receptor responder protein 2 precursor [Homo sapiens]	gi|4506427	20610.9

retinoic acid receptor responder protein 2 precursor [Pongo abelii]	gi|197100983	20636.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1558.8839	1558.929	0.0451	29	31	41	GLQVALEEFHK	52	99.807	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[3] F14,15,16 and F6	920/912	0.578	0.970	0.908	1	Mascot

163	Chain A, Crystal Structure Analysis Of The Bovine Npc2 (Niemann-Pick C2) Protein	gi|28373999	16755.6	1	51	0.741	0.712	0.938	0.000	0.000	0.000	1	1	1	99.797

Protein Group

epididymal secretory protein E1 precursor [Bos taurus]	gi|27806881	18778.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1576.8706	1576.9209	0.0503	32	85	93	DKTYNYVNK	51	99.797	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,9]	[7] F12 and F9 and F7 attempt 2	817/809	0.741	0.712	0.938	1	Mascot

164	Chain A, Crystal Structure Of A Human Igm Rheumatoid Factor Fab In Complex With Its Autoantigen Igg	gi|3659940	26076.4	1	51	1.071	1.417	1.603	0.000	0.000	0.000	1	1	1	99.784

Protein Group

Chain A, Crystal Structure Of The C2 Fragment Of Streptococcal Protein G In Complex With The Fc Dom	gi|1065199	26396.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1689.0475	1689.0439	-0.0036	-2	1	11	PSVFLFPPKPK	51	99.784	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9,11]	[1] F8 061011	357/349	1.071	1.417	1.603	1	Mascot

165	insulin-like growth factor-binding protein 4 precursor [Bos taurus]	gi|27807009	30998.8	1	50	0.587	0.820	0.755	0.000	0.000	0.000	1	1	1	99.747

Protein Group

RecName: Full=Insulin-like growth factor-binding protein 4; Short=IBP-4; Short=IGF-binding protein	gi|2497252	28933.7
insulin-like growth factor binding protein 4 [Homo sapiens]	gi|54696644	30826.5
insulin-like growth factor binding protein-4 [Homo sapiens]	gi|695254	30762.5
insulin-like growth factor-binding protein 4 [Bos taurus]	gi|17864013	17787.8
insulin-like growth factor-binding protein 4 precursor [Homo sapiens]	gi|62243290	30754.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1809.8	1809.739	-0.061	-34	245	258	GELDCHQLADSFRE	50	99.747	(N-term)_iTRAQ[0], MMTS (C)[5]	[5] F5 and F10	394/386	0.587	0.820	0.755	1	Mascot

166	fibrinogen, gamma A chain [Mustela putorius]	gi|881556	39301.2	1	50	0.912	1.637	0.970	0.000	0.000	0.000	1	1	1	99.746

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1785.9381	1785.9547	0.0166	9	14	25	FLQEIYNSNNQK	50	99.746	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12]	[2] F4 and F13	193/185	0.912	1.637	0.970	1	Mascot

167	protein disulfide isomerase [Homo sapiens]	gi|860986	64026.6	1	50	0.710	0.755	0.879	0.000	0.000	0.000	1	1	1	99.731

Protein Group

ER-60 protease [Homo sapiens]	gi|1208427	64143.7
ER-60 protein [Homo sapiens]	gi|2245365	64130.6
RecName: Full=Protein disulfide-isomerase A3; AltName: Full=58 kDa glucose-regulated protein; AltNa	gi|729433	64709.1
phospholipase C-alpha [Homo sapiens]	gi|303618	64048.7
protein disulfide-isomerase A3 precursor [Homo sapiens]	gi|21361657	64129.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2012.1399	2012.1421	0.0022	1	483	496	EATNPPVIQEEKPK	50	99.731	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12, 14]	[3] F14,15,16 and F6	746/738	0.710	0.755	0.879	1	Mascot

168	glutathione S-transferase P [Rattus norvegicus]	gi|25453420	25625.4	1	50	1.245	0.757	1.213	0.000	0.000	0.000	1	1	1	99.691

Protein Group

Chain A, Structure Of Porcine Class Pi Glutathione S-Transferase	gi|1943418	25697.4
RecName: Full=Glutathione S-transferase P; AltName: Full=GST P1-1; AltName: Full=GST class-pi	gi|544445	25683.4
RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|1170100	25968.8
RecName: Full=Glutathione S-transferase P; AltName: Full=GST class-pi	gi|1346208	25943.7
glutathione S-transferase P [Macaca mulatta]	gi|111185949	25480.3
glutathione S-transferase P [Pongo abelii]	gi|197097848	25432.3
glutathione S-transferase Pi [Capra hircus]	gi|6013379	25541.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1889.9398	1889.9111	-0.0287	-15	86	101	EAALVDMVNDGVEDLR	50	99.691	(N-term)_iTRAQ[0]	[8] F2	483/475	1.245	0.757	1.213	1	Mascot

169	cell adhesion molecule 4 precursor [Homo sapiens]	gi|21686977	44711.9	1	49	1.113	0.504	0.773	0.000	0.000	0.000	1	1	1	99.656

Protein Group

F22162_1 [Homo sapiens]	gi|3451335	43714.2
cell adhesion molecule 4 precursor [Mus musculus]	gi|23346547	44649.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1912.9889	1912.9436	-0.0453	-24	213	227	QTQYVLDVQYSPTAR	49	99.656	(N-term)_iTRAQ[0]	[8] F2	339/331	1.113	0.504	0.773	1	Mascot

170	complement component 3 [Bos taurus]	gi|47271264	8802.6	1	49	0.794	0.891	0.985	0.000	0.000	0.000	1	1	1	99.651

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type

2812.231	2812.2727	0.0417	15	43	62	DTWVELWPEAEECQDEENQK	49	99.651	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[20], MMTS (C)[13]	[4] F11 and F3	1256/1248	0.794	0.891	0.985	1	Mascot

171	adipsin/complement factor D [Sus scrofa]	gi|773265	22043.2	1	49	1.498	1.270	1.087	0.000	0.000	0.000	1	1	1	99.643

Protein Group

PREDICTED: complement factor D [Sus scrofa]	gi|311248224	29600.9
complement factor D [Sus scrofa]	gi|34329339	9673.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1460.9073	1460.8372	-0.0701	-48	99	109	LQHLLLPVLDR	49	99.643	(N-term)_iTRAQ[0]	[5] F5 and F10	472/464	1.498	1.270	1.087	1	Mascot

172	RecName: Full=Pro-neuropeptide Y; Contains: RecName: Full=Neuropeptide Y; AltName: Full=Neuropeptid	gi|30923117	9114.6	1	49	0.783	1.401	1.536	0.000	0.000	0.000	1	1	1	99.642

Protein Group

neuropeptide Y [Homo sapiens]	gi|386984	11367.9
neuropeptide Y precursor [Ovis aries]	gi|3822548	10388.5
pro-neuropeptide Y precursor [Bos taurus]	gi|62460382	11380
pro-neuropeptide Y precursor [Macaca mulatta]	gi|74136189	11455.9
pro-neuropeptide Y precursor [Ovis aries]	gi|57164209	11366
pro-neuropeptide Y precursor [Rattus norvegicus]	gi|6981286	11693.9
pro-neuropeptide Y preproprotein [Homo sapiens]	gi|4505449	11467

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1605.8643	1605.8296	-0.0347	-22	49	61	SSPETLISDLLMR	49	99.642	(N-term)_iTRAQ[0]	[8] F2	555/547	0.783	1.401	1.536	1	Mascot

173	pyruvate kinase isozymes M1/M2 isoform a [Homo sapiens]	gi|33286418	63835.8	1	48	1.060	0.592	1.616	0.000	0.000	0.000	1	1	1	99.592

Protein Group

Chain A, Pyruvate Kinase From Rabbit Muscle With Mg, K, And L- Phospholactate	gi|3659945	63769.6
Chain A, Recombinant Rabbit Muscle Pyruvate Kinase	gi|15987970	63753.6
Chain A, S402p Mutant Of Rabbit Muscle Pyruvate Kinase	gi|15987978	63763.6
M2 pyruvate kinase [Rattus norvegicus]	gi|206205	63679.7
M2-type pyruvate kinase [Homo sapiens]	gi|189998	63812.8
PKM2 protein [Homo sapiens]	gi|34782802	40842.7
Pkm2 protein [Rattus norvegicus]	gi|38181543	58261.7

Pyruvate kinase, muscle [Homo sapiens]	gi|31416989	63877.8
RecName: Full=Pyruvate kinase isozymes M1/M2; AltName: Full=Pyruvate kinase muscle isozyme	gi|2851533	63900.6
cytosolic thyroid hormone-binding protein (EC 2.7.1.40) [Homo sapiens]	gi|338827	63899.8
pyruvate kinase [Homo sapiens]	gi|35505	63776.7
pyruvate kinase [Oryctolagus cuniculus]	gi|2623945	63672.7
pyruvate kinase isozyme M1 [Pongo abelii]	gi|197101195	63870.7
pyruvate kinase isozymes M1/M2 [Mus musculus]	gi|31981562	63743.8
pyruvate kinase isozymes M1/M2 [Rattus norvegicus]	gi|16757994	63526.5
pyruvate kinase isozymes M1/M2 isoform b [Homo sapiens]	gi|33286420	63914.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2298.241	2298.1831	-0.0579	-25	320	336	AGKPVICATQMLESMIK	48	99.592	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,17], MMTS (C)[7]	[5] F5 and F10	565/557	1.060	0.592	1.616	1	Mascot

174	immunoglobulin V lambda chain 5.1.11 [Ovis aries]	gi|26245557	11278.4	1	48	1.310	0.793	1.245	0.000	0.000	0.000	1	1	1	99.588

Protein Group

immunoglobulin V lambda chain 5.1.12 [Ovis aries]	gi|26245559	11303.4
immunoglobulin V lambda chain 5.1.14 [Ovis aries]	gi|26245563	11248.3
immunoglobulin lambda-1a light chain variable region [Ovis aries]	gi|2746683	12195.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1862.9845	1862.8909	-0.0936	-50	56	71	TVIYGSTNRPSGVPDR	48	99.588	(N-term)_iTRAQ[0]	[5] F5 and F10	237/229	1.310	0.793	1.245	1	Mascot

175	immunoglobulin V lambda chain 5.1.5 [Ovis aries]	gi|26245545	11332.4	1	48	1.310	0.793	1.245	0.000	0.000	0.000	1	1	1	99.588

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1862.9845	1862.8909	-0.0936	-50	56	71	TVIYGTSNRPSGVPDR	48	99.588	(N-term)_iTRAQ[0]	[5] F5 and F10	237/229	1.310	0.793	1.245	1	Mascot

176	IgG3 heavy chain constant region [Bos taurus]	gi|1575493	42668.8	1	47	1.089	0.438	0.995	0.000	0.000	0.000	1	1	1	99.493

Protein Group

IgG3 heavy chain constant region [Bos taurus]	gi|1575495	42480.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1412.8022	1412.7606	-0.0416	-29	248	258	EPQVYVLAPPR	47	99.493	(N-term)_iTRAQ[0]	[8] F2	339/331	1.089	0.438	0.995	1	Mascot

177	nidogen-2 [Homo sapiens]	gi|2791962	158019.9	1	47	1.253	1.218	0.705	0.000	0.000	0.000	1	1	1	99.488

Protein Group

entactin-2 [Mus musculus]	gi|3513368	160198
hypothetical protein [Homo sapiens]	gi|60219225	135257
nidogen-2 [Mus musculus]	gi|23592218	159959.2
nidogen-2 precursor [Mus musculus]	gi|84370361	159816
osteonidogen [Homo sapiens]	gi|1449167	158060.9
unnamed protein product [Mus musculus]	gi|26343027	146200.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1561.8458	1561.866	0.0202	13	213	224	ESYNVQLQLPAR	47	99.488	(N-term)_iTRAQ[0]	[4] F11 and F3	1083/1075	1.253	1.218	0.705	1	Mascot

178	Ig mu heavy chain V region precursor - sheep (fragment)	gi|1083124	15956.1	1	47	0.637	0.926	0.901	0.000	0.000	0.000	1	1	1	99.449

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1345.7937	1345.8352	0.0415	31	23	32	LQESGPSLVK	47	99.449	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[2] F4 and F13	922/914	0.637	0.926	0.901	1	Mascot

179	thrombospondin-2 precursor [Bos taurus]	gi|28875793	138958.5	1	47	0.978	1.137	0.879	0.000	0.000	0.000	1	1	1	99.436

Protein Group

Thbs2 protein [Mus musculus]	gi|21594089	67873.9
Thrombospondin 2 [Mus musculus]	gi|31565630	140001.7
hypothetical protein [Homo sapiens]	gi|34365397	50905.6
thrombospondin 2 [Homo sapiens]	gi|307506	139483.5
thrombospondin 2 [Mus musculus]	gi|567241	140016.5
thrombospondin-2 precursor [Homo sapiens]	gi|40317628	139519.4
thrombospondin-2 precursor [Mus musculus]	gi|239787900	139986.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2072.9832	2072.917	-0.0662	-32	1130	1147	QVMADSGPIYDQTYAGGR	47	99.436	(N-term)_iTRAQ[0]	[8] F2	308/300	0.978	1.137	0.879	1	Mascot

180	neuroendocrine protein 7B2 isoform 1 [Homo sapiens]	gi|221139785	25535.9	1	47	1.171	1.829	2.496	0.000	0.000	0.000	1	1	1	99.381

Protein Group

7B2 protein	gi|1585794	23354.8
RecName: Full=Neuroendocrine protein 7B2; AltName: Full=Secretogranin V; AltName: Full=Secretograni	gi|112850	25030.7
Secretogranin V (7B2 protein) [Homo sapiens]	gi|13529158	25475.9

neuroendocrine protein 7B2 isoform 2 [Homo sapiens]	gi|4506917	25464.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1305.7035	1305.7239	0.0204	16	182	191	SVNPYLQGQR	47	99.381	(N-term)_iTRAQ[0]	[4] F11 and F3	982/974	1.171	1.829	2.496	1	Mascot

181	SPARC-like protein 1 precursor [Rattus norvegicus]	gi|6978789	77718.5	1	47	1.218	1.311	1.488	0.000	0.000	0.000	1	1	1	99.375

Protein Group

DKFZP459N0428 protein [Pongo abelii]	gi|207080142	82764
Hevin-like protein [Homo sapiens]	gi|809027	82663.9
SC1 precursor [Mus musculus]	gi|1854948	79504.3
SPARC-like 1 (hevin) [Homo sapiens]	gi|21707436	82645.8
SPARC-like 1 (hevin) [Rattus norvegicus]	gi|38197696	77696.4
SPARC-like protein 1 [Pongo abelii]	gi|197101799	82599.9
Sparcl1 protein [Mus musculus]	gi|13277723	79444.2
extracellular matrix associated protein [Mus musculus]	gi|1498641	79446.2
hevin [Homo sapiens]	gi|758066	82631.8
hypothetical protein [Pongo abelii]	gi|55732071	82656.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1546.7645	1546.6946	-0.0699	-45	588	599	ASLVPMEHCITR	47	99.375	(N-term)_iTRAQ[0], MMTS (C)[9]	[5] F5 and F10	371/363	1.218	1.311	1.488	1	Mascot

182	C4b-binding protein alpha chain precursor [Bos taurus]	gi|27806291	76307	1	46	1.140	0.584	0.981	0.000	0.000	0.000	1	1	1	99.299

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2120.863	2120.8184	-0.0446	-21	541	556	CEWEYPEGCEQVVTGR	46	99.299	(N-term)_iTRAQ[0], MMTS (C)[1,9]	[8] F2	477/469	1.140	0.584	0.981	1	Mascot

183	protein C prepropeptide [Bos taurus]	gi|163487	55951.3	1	46	0.934	0.678	0.687	0.000	0.000	0.000	1	1	1	99.289

Protein Group

RecName: Full=Vitamin K-dependent protein C; AltName: Full=Anticoagulant protein C; AltName: Full=A	gi|131065	55937.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1595.8832	1595.9568	0.0736	46	435	444	YLDWIYGHIK	46	99.289	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[3] F14,15,16 and F6	1038/1030	0.934	0.678	0.687	1	Mascot

184	alpha globin chain [Ovis aries]	gi|1787	16968.1	1	46	0.948	1.562	1.878	0.000	0.000	0.000	1	1	1	99.217

Protein Group

RecName: Full=Hemoglobin subunit alpha-1/2; AltName: Full=Alpha-1/2-globin; AltName: Full=Hemoglobi	gi|62901553	16930.1
alpha globin chain [Ovis aries]	gi|1789	17002.1
alpha globin chain [Ovis aries]	gi|1791	16944.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1578.7996	1578.8236	0.024	15	18	32	VGGNAGAYGAEALER	46	99.217	(N-term)_iTRAQ[0]	[4] F11 and F3	1023/1015	0.948	1.562	1.878	1	Mascot

185	galectin 1 [Ovis aries]	gi|57164313	16381.1	1	45	1.461	1.097	1.359	0.000	0.000	0.000	1	1	1	99.159

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1997.0953	1997.1047	0.0094	5	114	129	LNLEAINYLAAGGDFK	45	99.159	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[16]	[4] F11 and F3	1282/1274	1.461	1.097	1.359	1	Mascot

186	neuroblastoma suppressor of tumorigenicity 1 precursor [Rattus norvegicus]	gi|13928832	20836.7	1	45	1.039	1.068	1.354	0.000	0.000	0.000	1	1	1	99.109

Protein Group

DAN [Mus musculus]	gi|780124	20764.7
Neuroblastoma, suppression of tumorigenicity 1 [Rattus norvegicus]	gi|38197666	20744.7
RecName: Full=Neuroblastoma suppressor of tumorigenicity 1; AltName: Full=DAN domain family member	gi|729293	20876.8
neuroblastoma suppressor of tumorigenicity 1 isoform 2 precursor [Homo sapiens]	gi|323276673	21007.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1091.671	1091.7037	0.0327	30	24	30	LALFPDK	45	99.109	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[2] F4 and F13	973/965	1.039	1.068	1.354	1	Mascot

187	plasma glutamate carboxypeptidase precursor [Pongo abelii]	gi|197099774	55473.9	1	45	1.364	1.124	1.051	0.000	0.000	0.000	1	1	1	99.023

Protein Group

blood plasma glutamate carboxypeptidase precursor [Homo sapiens]	gi|4877698	64872.1
plasma glutamate carboxypeptidase precursor [Homo sapiens]	gi|7706387	55641
unnamed protein product [Homo sapiens]	gi|22761023	55393.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1297.7964	1297.7694	-0.027	-21	67	77	LALLVDTVGPR	45	99.023	(N-term)_iTRAQ[0]	[8] F2	441/433	1.364	1.124	1.051	1	Mascot

188	aspartate aminotransferase, cytoplasmic [Bos taurus]	gi|29135295	49639.8	1	44	1.325	0.998	1.163	0.000	0.000	0.000	1	1	1	98.979

Protein Group

RecName: Full=Aspartate aminotransferase, cytoplasmic; AltName: Full=Glutamate oxaloacetate transam	gi|122065118	49753.7
aspartate aminotransferase 1 [Bos taurus]	gi|59858077	49464.5

cytosolic aspartate aminotransferase [Rattus norvegicus]	gi|220684	49752.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1655.8877	1655.8508	-0.0369	-22	43	55	TDDSQPWVLPVVR	44	98.979	(N-term)_iTRAQ[0]	[8] F2	417/409	1.325	0.998	1.163	1	Mascot

189	repulsive guidance molecule A isoform 3 [Homo sapiens]	gi|261878452	53091.5	1	44	0.853	0.576	0.838	0.000	0.000	0.000	1	1	1	98.847

Protein Group

hypothetical protein [Homo sapiens]	gi|9368530	54438.1
repulsive guidance molecule A isoform 2 [Homo sapiens]	gi|261878459	51257.5
repulsive guidance molecule A precursor [Mus musculus]	gi|164663868	53359.8
repulsive guidance molecule A, RgmA protein [Mus musculus]	gi|32400242	51525.8
unnamed protein product [Homo sapiens]	gi|22760663	53063.5
unnamed protein product [Mus musculus]	gi|26349781	40992.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1483.8478	1483.9391	0.0913	62	265	275	VSGQHVEIQAK	44	98.847	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[7] F12 and F9 and F7 attempt 2	1208/1200	0.853	0.576	0.838	1	Mascot

190	RecName: Full=14-3-3 protein gamma; AltName: Full=Protein kinase C inhibitor protein 1; Short=KCIP-	gi|71153781	30966.7	1	44	1.153	1.035	1.072	0.000	0.000	0.000	1	1	1	98.82

Protein Group

14-3-3 gamma protein [Homo sapiens]	gi|5726310	30944.5
14-3-3 protein gamma [Mus musculus]	gi|3065929	31076.8
14-3-3 protein gamma [Rattus norvegicus]	gi|9507245	31016.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1787.8895	1787.8372	-0.0523	-29	29	42	NVTELNEPLSNEER	44	98.82	(N-term)_iTRAQ[0]	[8] F2	277/269	1.153	1.035	1.072	1	Mascot

191	RecName: Full=CD166 antigen; AltName: Full=Activated leukocyte cell adhesion molecule; AltName: Ful	gi|47605370	64831.1	1	44	0.883	0.945	0.920	0.000	0.000	0.000	1	1	1	98.767

Protein Group

CD166 antigen [Pongo abelii]	gi|197099250	70942
CD166 antigen precursor [Bos taurus]	gi|41386784	72914.2
MEMD protein [Homo sapiens]	gi|3183975	72254.7
RecName: Full=CD166 antigen; AltName: Full=Activated leukocyte cell adhesion molecule; AltName: Ful	gi|47605369	64248.6
activated leukocyte cell adhesion molecule [Sus scrofa]	gi|13446215	15032.1

alcam [Homo sapiens]	gi|886258	72415.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1544.9384	1544.8738	-0.0646	-42	71	80	QPSKPEIVSK	44	98.767	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[4,10]	[1] F8 061011	186/178	0.883	0.945	0.920	1	Mascot

192	serum paraoxonase/arylesterase 1 [Oryctolagus cuniculus]	gi|126722853	43725	1	43	0.985	0.907	2.178	0.000	0.000	0.000	1	1	1	98.632

Protein Group

Chain A, Serum Paraoxonase By Directed Evolution	gi|48425851	42559.2
Paraoxonase 1 [Mus musculus]	gi|15215219	42776.4
paraoxonase	gi|736808	43663
paraoxonase	gi|736809	42826.3
paraoxonase 1 [Oryctolagus cuniculus]	gi|12743893	40293
paraoxonase 1A [Oryctolagus cuniculus]	gi|12743897	43557.8
paraoxonase 1B [Oryctolagus cuniculus]	gi|12743895	43741
paraoxonase B-type/arylesterase B-type precursor [Homo sapiens]	gi|408299	42785.3
paraoxonase [Rattus norvegicus]	gi|1945471	41209.3
paraoxonase/arylesterase [Homo sapiens]	gi|298532	42916.3
serum paraoxonase [Homo sapiens]	gi|190192	42888.3
serum paraoxonase [Homo sapiens]	gi|190194	40831.1
serum paraoxonase [Homo sapiens]	gi|190196	39512.5
serum paraoxonase [Mus musculus]	gi|1272236	42670.4
serum paraoxonase/arylesterase 1 [Mus musculus]	gi|261823995	42704.4
serum paraoxonase/arylesterase 1 [Rattus norvegicus]	gi|54292130	42255
serum paraoxonase/arylesterase 1 precursor [Homo sapiens]	gi|19923106	42870.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1607.9407	1607.8881	-0.0526	-33	234	244	YVYIAELLAHK	43	98.632	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[11]	[5] F5 and F10	506/498	0.985	0.907	2.178	1	Mascot

193	cathepsin L2 precursor [Bos taurus]	gi|27806673	41703.5	1	43	0.859	0.752	0.817	0.000	0.000	0.000	1	1	1	98.616

Protein Group

RecName: Full=Cathepsin L2; Flags: Precursor	gi|75060921	41719.5

preprocathepsin L [Bos taurus]	gi|3641698	37673.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1948.0076	1948.0419	0.0343	18	21	33	LDPNLDAHWHQWK	43	98.616	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[13]	[5] F5 and F10	1239/1231	0.859	0.752	0.817	1	Mascot

194	unnamed protein product [Homo sapiens]	gi|7022277	46412.3	1	43	0.722	0.726	0.439	0.000	0.000	0.000	1	1	1	98.469

Protein Group

ASPIC [Homo sapiens]	gi|9368808	73657.1
ASPIC [Homo sapiens]	gi|9368807	74031.2
CRTAC1 protein [Homo sapiens]	gi|21706428	50809.6
CRTAC1-B protein [Homo sapiens]	gi|19171211	72854.8
cartilage acidic protein 1 [Homo sapiens]	gi|55957679	58643.4
cartilage acidic protein 1 isoform A precursor [Homo sapiens]	gi|47777317	74757.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2324.0776	2324.041	-0.0366	-16	62	83	GDGTFVDAAASAGVDDPHQHGR	43	98.469	(N-term)_iTRAQ[0]	[1] F8 061011	259/251	0.722	0.726	0.439	1	Mascot

195	complement C4B precursor [Homo sapiens]	gi|1314244	200573.8	1	42	0.962	1.522	1.639	0.000	0.000	0.000	1	1	1	98.178

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1108.6613	1108.6101	-0.0512	-46	160	166	VFXLDQK	43	98.61	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	283/275	0.962	1.522	1.639	1	Mascot

196	malate dehydrogenase, cytoplasmic isoform 2 [Homo sapiens]	gi|5174539	41198.2	1	42	0.745	0.721	0.993	0.000	0.000	0.000	1	1	1	98.086

Protein Group

Malate dehydrogenase 1, NAD (soluble) [Rattus norvegicus]	gi|37590235	41066.2
cytosolic malate dehydrogenase [Mus musculus]	gi|387129	41059.2
malate dehydrogenase, cytoplasmic [Mus musculus]	gi|254540027	41093.2
malate dehydrogenase, cytoplasmic [Rattus norvegicus]	gi|15100179	41065.2
unnamed protein product [Mus musculus]	gi|12837652	41050.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2184.1924	2184.2771	0.0847	39	206	220	EVGVYEALKDDSWLK	42	98.086	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9,15]	[3] F14,15,16 and F6	991/983	0.745	0.721	0.993	1	Mascot

197	RecName: Full=Mimecan; AltName: Full=Osteoglycin; Contains: RecName: Full=Corneal keratan sulfate p	gi|129077	38498.7	1	42	0.927	0.873	0.941	0.000	0.000	0.000	1	1	1	98.068

Protein Group

mimecan precursor [Bos taurus]	gi|27806829	38413.6
mimecan precursor [Mus musculus]	gi|6679166	38301.4
mimecan precursor [Oryctolagus cuniculus]	gi|126723013	38063.5
mimecan precursor [Pongo abelii]	gi|197102868	38245.6
mimecan preproprotein [Homo sapiens]	gi|7661704	38211.7
osteoglycin OG [Homo sapiens]	gi|33150528	38067.5
osteoglycin [Homo sapiens]	gi|55957237	34944.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2458.2712	2458.2031	-0.0681	-28	148	166	RLDFTGNLIEDIEDGTFSK	42	98.068	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[19]	[5] F5 and F10	548/540	0.927	0.873	0.941	1	Mascot

198	RecName: Full=Alpha-1-antiproteinase; AltName: Full=Alpha-1-antitrypsin; AltName: Full=Alpha-1-prot	gi|461443	50820.6	1	41	0.275	0.280	0.395	0.000	0.000	0.000	1	1	1	97.807

Protein Group

Chain A, 2.0 Angstrom Structure Of Intact Alpha-1-Antitrypsin: A Canonical Template For Active Serp	gi|6137432	49388.3
Chain A, A 2.1 Angstrom Structure Of An Uncleaved Alpha-1- Antitrypsin Shows Variability Of The Rea	gi|13787109	49339.2
Chain A, Cleaved Alpha-1-Antitrypsin Polymer	gi|7245932	40780.9
Chain A, Crystal Structure Of A Serpin:protease Complex	gi|11514321	41849.4
Chain A, Crystal Structure Of A1pi-Pittsburgh In The Native Conformation	gi|34810820	49093.3
Chain A, Crystal Structure Of Cleaved Antitrypsin Polymer	gi|7546268	41790.4
Chain A, Interactions Causing The Kinetic Trap In Serpin Protein Folding	gi|28948408	49067.1
Chain A, The S Variant Of Human Alpha1-Antitrypsin, Structure And Implications For Function And Met	gi|231240	43267
DKFZP470L1511 protein [Pongo abelii]	gi|207079907	49945.4
PRO0684 [Homo sapiens]	gi|6855601	51872.5
RecName: Full=Alpha-1-antitrypsin; AltName: Full=Alpha-1 protease inhibitor; AltName: Full=Alpha-1-	gi|68052067	51868.6
Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Homo sapiens]	gi|15080499	51874.6
Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Homo sapiens]	gi|15990507	51860.5
alpha-1 antitrypsin [Homo sapiens]	gi|28637	26174.3
alpha-1-antiproteinase 2 precursor [Equus caballus]	gi|167621418	50987.8

alpha-1-antitrypsin [Homo sapiens]	gi|177827	51797.5
alpha-1-antitrypsin [Homo sapiens]	gi|177831	51858.6
alpha-1-antitrypsin [Pongo abelii]	gi|197098210	51944.6
alpha-1-antitrypsin precursor [Homo sapiens]	gi|50363217	51888.6
alpha-1-antitrypsin precursor [Homo sapiens]	gi|177836	52003.7
antitrypsin alpha1 mutant	gi|224224	51883.5
inhibitor,alpha1 protease	gi|223433	49495.5
unnamed protein product [Homo sapiens]	gi|28193184	38592.1
unnamed protein product [Homo sapiens]	gi|28207863	45595

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1296.7046	1296.7727	0.0681	53	173	180	QINDYVEK	41	97.807	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[7] F12 and F9 and F7 attempt 2	823/815	0.275	0.280	0.395	1	Mascot

199	RecName: Full=Complement component C6; Flags: Precursor	gi|47115536	117534.9	1	41	0.762	1.200	0.983	0.000	0.000	0.000	1	1	1	97.772

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1215.662	1215.5988	-0.0632	-52	510	517	AFQEYAAK	41	97.772	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[5] F5 and F10	232/224	0.762	1.200	0.983	1	Mascot

200	Ig lambda chain C region - horse (fragment)	gi|346446	13899	1	41	1.206	1.171	1.302	0.000	0.000	0.000	1	1	1	97.573

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1993.035	1993.0155	-0.0195	-10	78	92	YAASSYLTLSPAMWK	41	97.573	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[15], Oxidation (M)[13]	[4] F11 and F3	1175/1167	1.206	1.171	1.302	1	Mascot

201	PREDICTED: kininogen-1 isoform 2 [Canis lupus familiaris]	gi|57109938	53513.5	1	41	0.744	0.966	1.110	0.000	0.000	0.000	1	1	1	97.494

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1277.8164	1277.8474	0.031	24	36	43	AVDTALKK	41	97.494	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,8]	[7] F12 and F9 and F7 attempt 2	815/807	0.744	0.966	1.110	1	Mascot

202	KIAA0578 protein [Homo sapiens]	gi|20521087	182933	1	39	0.741	0.694	0.646	0.000	0.000	0.000	1	1	1	96.646

Protein Group

mKIAA0578 protein [Mus musculus]	gi|28394197	183988.4
neurexin 1 [Rattus norvegicus]	gi|37620151	178694.5
neurexin-1-beta isoform alpha1 precursor [Homo sapiens]	gi|14149613	175147.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1617.9224	1617.8665	-0.0559	-35	324	333	GKEEYIATFK	40	97.441	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,10]	[1] F8 061011	279/271	0.741	0.694	0.646	1	Mascot

203	fibromodulin [Homo sapiens]	gi|453157	44985.6	1	40	0.776	0.835	0.986	0.000	0.000	0.000	1	1	1	97.382

Protein Group

Fmod protein [Mus musculus]	gi|30851675	48402.3
RecName: Full=Fibromodulin; Short=FM; AltName: Full=Collagen-binding 59 kDa protein; AltName: Full=	gi|21542068	17122.9
RecName: Full=Fibromodulin; Short=FM; AltName: Full=Keratan sulfate proteoglycan lumican; Short=KSP	gi|21542112	17252
fibromodulin [Bos taurus]	gi|27806623	45101.6
fibromodulin [Homo sapiens]	gi|297091	44936.4
fibromodulin precursor [Homo sapiens]	gi|71040111	45012.6
fibromodulin precursor [Mus musculus]	gi|10946680	44790.4
fibromodulin precursor [Rattus norvegicus]	gi|18104933	44954.5
unnamed protein product [Mus musculus]	gi|26348627	44933.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1505.7944	1505.743	-0.0514	-34	180	190	ELHLDHNQISR	40	97.382	(N-term)_iTRAQ[0]	[4] F11 and F3	120/112	0.776	0.835	0.986	1	Mascot

204	neurocan core protein precursor [Pan troglodytes]	gi|77681353	149095.9	1	40	1.108	0.706	0.610	0.000	0.000	0.000	1	1	1	97.352

Protein Group

PGCN_HUMAN, PARTIAL CDS [Homo sapiens]	gi|3288885	39691.8
chondroitin sulfate proteoglycan 3 [Saimiri boliviensis]	gi|56122258	134967
neurocan [Homo sapiens]	gi|2739089	149057.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2201.0173	2200.9438	-0.0735	-33	1155	1170	DFQWTDNTGLQFENWR	40	97.352	(N-term)_iTRAQ[0]	[8] F2	474/466	1.108	0.706	0.610	1	Mascot

205	endopin 2B [Bos taurus]	gi|38683423	51047	1	40	0.768	0.671	0.934	0.000	0.000	0.000	1	1	1	97.302

Protein Group

alpha1-antichymotrypsin isoform pHHK12 [Bos taurus]	gi|535509	50998.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1122.6075	1122.5343	-0.0732	-65	280	286	MQDLEAK	40	97.302	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	202/194	0.768	0.671	0.934	1	Mascot

206	complement C1r-A subcomponent precursor [Mus musculus]	gi|164518925	86404.9	1	40	0.911	0.913	1.444	0.000	0.000	0.000	1	1	1	97.265

Protein Group

Complement component 1, r subcomponent [Mus musculus]	gi|13435522	86427.9
complement C1r-B subcomponent precursor [Mus musculus]	gi|164518919	85979.7
complement component C1RB [Mus musculus]	gi|27462718	25478.7
serine protease [Mus musculus]	gi|9909196	86474

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1156.6599	1156.7358	0.0759	66	542	549	VIIHPDYR	40	97.265	(N-term)_iTRAQ[0]	[7] F12 and F9 and F7 attempt 2	1257/1249	0.911	0.913	1.444	1	Mascot

207	lysosomal alpha-mannosidase [Homo sapiens]	gi|2209015	117755.7	1	40	0.796	0.478	0.968	0.000	0.000	0.000	1	1	1	97.258

Protein Group

Chain C, The Structure Of The Bovine Lysosomal A-Mannosidase Suggests A Novel Mechanism For Low Ph	gi|29726876	18855.7
RecName: Full=Lysosomal alpha-mannosidase; Short=Laman; AltName: Full=Lysosomal acid alpha-mannosid	gi|62510916	118292.4
alpha-mannosidase [Homo sapiens]	gi|1419374	115325.7
lysosomal acid alpha-mannosidase [Homo sapiens]	gi|1658374	115477.8
lysosomal alpha-mannosidase [Bos taurus]	gi|31341666	118928.4
lysosomal alpha-mannosidase [Homo sapiens]	gi|3522867	117810.8
lysosomal alpha-mannosidase [Pongo abelii]	gi|197101359	117958.8
lysosomal alpha-mannosidase isoform 1 precursor [Homo sapiens]	gi|51873064	117826.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1449.8337	1449.8043	-0.0294	-20	509	519	FQVIVYNPLGR	40	97.258	(N-term)_iTRAQ[0]	[8] F2	443/435	0.796	0.478	0.968	1	Mascot

208	immunoglobulin light chain variable region [Ovis aries]	gi|5802448	11309.5	1	40	1.299	1.474	1.231	0.000	0.000	0.000	1	1	1	97.22

Protein Group

immunoglobin light chain VJ region [Bos taurus]	gi|4680177	11510.5
immunoglobulin light chain variable region [Bos taurus]	gi|2323372	11971.7
immunoglobulin light chain variable region [Bos taurus]	gi|2323398	11648.7
immunoglobulin light chain variable region [Bos taurus]	gi|2323380	11665.6
immunoglobulin light chain variable region [Bos taurus]	gi|2323374	11681.6
immunoglobulin light chain variable region [Bos taurus]	gi|2323406	11324.5
immunoglobulin light chain variable region [Bos taurus]	gi|2323390	11645.6

immunoglobulin light chain variable region [Bos taurus]	gi|2555149	12097.9
immunoglobulin light chain variable region [Bos taurus]	gi|2323386	11651.6
immunoglobulin light chain variable region [Bos taurus]	gi|2323394	11608.6
immunoglobulin light chain variable region [Bos taurus]	gi|2323382	11606.6
immunoglobulin light chain variable region [Bos taurus]	gi|2323404	11643.6
immunoglobulin light chain variable region [Bos taurus]	gi|2323384	11595.5
immunoglobulin light chain variable region [Bos taurus]	gi|2323396	11455.5
immunoglobulin light chain variable region [Bos taurus]	gi|2323402	11553.6
immunoglobulin light chain variable region [Bos taurus]	gi|2323400	11438.5
immunoglobulin light chain variable region [Bos taurus]	gi|2323376	11635.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1859.0106	1858.9402	-0.0704	-38	1	17	QAVLTQPSSVSGSLGQR	40	97.22	(N-term)_iTRAQ[0]	[8] F2	279/271	1.299	1.474	1.231	1	Mascot

209	complement component 3 [Bos taurus]	gi|4093220	18508	1	40	0.757	0.958	1.030	0.000	0.000	0.000	1	1	1	97.214

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1626.8574	1626.9343	0.0769	47	77	88	AQFILQGDACVK	40	97.214	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12], MMTS (C)[10]	[4] F11 and F3	1153/1145	0.757	0.958	1.030	1	Mascot

210	serum amyloid A protein [Oryctolagus cuniculus]	gi|1450	8367.2	1	40	1.027	0.837	0.973	0.000	0.000	0.000	1	1	1	97.169

Protein Group

serum amyloid A [Felis catus]	gi|52352265	9179.4
serum amyloid A [Felis catus]	gi|52352277	9338.5
serum amyloid A [Felis catus]	gi|52352267	9151.4
serum amyloid A [Homo sapiens]	gi|259352	15996.1
serum amyloid A protein, SAA [rabbits, acute phase serum, Peptide Partial, 103 aa]	gi|299487	12453.1
serum amyloid A, SAA [rabbits, acute-phase serum, Peptide, 104 aa]	gi|239908	12538.1
serum amyloid A-1 protein precursor [Oryctolagus cuniculus]	gi|126722709	14701.3
serum amyloid A-2 protein precursor [Oryctolagus cuniculus]	gi|126723243	14497.2
unknown [Oryctolagus cuniculus]	gi|517271	14555.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1130.6567	1130.5991	-0.0576	-51	13	21	GPGGVWAAK	40	97.169	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[9]	[5] F5 and F10	251/243	1.027	0.837	0.973	1	Mascot

211	unnamed protein product [Homo sapiens]	gi|22761577	52913.5	1	40	1.267	1.009	0.878	0.000	0.000	0.000	1	1	1	97.062

Protein Group

PI16 protein [Homo sapiens]	gi|37574025	47970.7
peptidase inhibitor 16 precursor [Bos taurus]	gi|66792752	53017.9
peptidase inhibitor 16 precursor [Homo sapiens]	gi|70780384	53017.5
unnamed protein product [Homo sapiens]	gi|34530413	31741.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1467.7729	1467.7799	0.007	5	59	68	WDEELAAFAK	40	97.062	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10]	[4] F11 and F3	1181/1173	1.267	1.009	0.878	1	Mascot

212	glutathione S-transferase Mu 1 [Bos taurus]	gi|28461273	28494.1	1	40	1.054	0.427	1.913	0.000	0.000	0.000	1	1	1	96.938

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1228.7188	1228.7435	0.0247	20	137	144	LFSEFLGK	40	96.938	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	295/287	1.054	0.427	1.913	1	Mascot

213	RecName: Full=Coagulation factor IX; AltName: Full=Christmas factor; Contains: RecName: Full=Coagul	gi|119769	52234.2	1	40	0.923	0.690	0.836	0.000	0.000	0.000	1	1	1	96.924

Protein Group

RecName: Full=Coagulation factor IX; AltName: Full=Christmas factor	gi|119777	33203.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
2539.3738	2539.3005	-0.0733	-29	230	248	ITVVAGEHNTEKPEPTEQK	40	96.924	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[12, 19]	[1] F8 061011	215/207	0.923	0.690	0.836	1	Mascot

214	presequence protease, mitochondrial isoform 2 precursor [Homo sapiens]	gi|41352061	127532.5	1	40	0.558	0.650	0.558	0.000	0.000	0.000	1	1	1	96.924

Protein Group

KIAA1104 protein [Homo sapiens]	gi|40789078	79221.5
Pitrilysin metallopeptidase 1 [Homo sapiens]	gi|13477137	127616.6
metalloprotease 1 [Homo sapiens]	gi|3779244	127588.5
pitrilysin metallopeptidase 1 [Homo sapiens]	gi|57162484	127529.5
pitrilysin metallopeptidase 1 [Homo sapiens]	gi|57162481	29420.4
presequence protease, mitochondrial precursor [Pongo abelii]	gi|207080086	127436.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1065.6224	1065.6118	-0.0106	-10	432	437	IEIQMK	40	96.924	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6], Oxidation (M)[5]	[5] F5 and F10	329/321	0.558	0.650	0.558	1	Mascot

215	immunoglobulin IgG-2 heavy chain constant region [Tursiops truncatus]	gi|58701034	46350.8	1	40	1.574	0.980	1.085	0.000	0.000	0.000	1	1	1	96.86

Protein Group

immunoglobulin IgG-1 heavy chain constant region [Tursiops truncatus]	gi|49355314	43863.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1922.111	1921.8835	-0.2275	-118	234	247	VVSALPIQHQDWLK	40	96.86	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[14]	[8] F2	381/373	1.574	0.980	1.085	1	Mascot

216	secreted nidogen domain protein precursor [Mus musculus]	gi|37605781	161194.4	1	39	1.450	0.945	1.251	0.000	0.000	0.000	1	1	1	96.711

Protein Group

FLJ00133 protein [Homo sapiens]	gi|18676472	147862
secreted protein SST3 [Mus musculus]	gi|29568116	121217

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1991.9828	1991.9224	-0.0604	-30	233	250	TADMAEVETTTNVGVPGR	39	96.711	(N-term)_iTRAQ[0]	[8] F2	307/299	1.450	0.945	1.251	1	Mascot

217	RecName: Full=Protein kinase C-binding protein NELL2; AltName: Full=MEL91 protein; AltName: Full=NE	gi|2494290	100048.6	1	39	1.813	1.402	1.003	0.000	0.000	0.000	1	1	1	96.588

Protein Group

DKFZP459E232 protein [Pongo abelii]	gi|207079905	100063.5
RecName: Full=Protein kinase C-binding protein NELL2; AltName: Full=NEL-like protein 2; Flags: Prec	gi|2494291	99883.4
hypothetical protein [Pongo abelii]	gi|55727761	99972.6
mel [Mus musculus]	gi|1389827	100387.7
neuron-specific epidermal growth factor-like repeat domain-containing protein [Rattus norvegicus]	gi|19568159	99751.4
protein kinase C-binding protein NELL2 [Mus musculus]	gi|133922561	100361.7
protein kinase C-binding protein NELL2 [Pongo abelii]	gi|197097656	100052.5
protein kinase C-binding protein NELL2 isoform b precursor [Homo sapiens]	gi|5453766	100276.7
protein kinase C-binding protein NELL2 isoform c [Homo sapiens]	gi|223029474	100195.7
unnamed protein product [Mus musculus]	gi|26330366	96480.7
unnamed protein product [Mus musculus]	gi|26333475	104708.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#]	Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1557.6616	1557.6276	-0.034	-22	755	766	CVTDPCQADTIR	39	96.588	(N-term)_iTRAQ[0], MMTS (C)[1,6]	[8] F2		373/365	1.813	1.402	1.003	1	Mascot

218	Chain A, New Crystal Forms Of A Mu Class Glutathione S-Transferase From Rat Liver	gi|442967	28786.1	1	39	1.547	2.020	2.672	0.000	0.000	0.000	1	1	1	96.541

Protein Group

Chain A, Crystal Structures Of Class Mu Chimeric Gst Isoenzymes M1-2 And M2-1	gi|33356830	28707.1
Chain A, First-Sphere And Second-Sphere Electrostatic Effects In The Active Site Of A Class Mu Glut	gi|1943397	28770.1
Chain A, First-Sphere And Second-Sphere Electrostatic Effects In The Active Site Of A Class Mu Glut	gi|1943435	28784.1
Chain A, First-Sphere And Second-Sphere Electrostatic Effects In The Active Site Of A Class Mu Glut	gi|1943433	28772.1
Chain A, First-Sphere And Second-Sphere Electrostatic Effects In The Active Site Of A Class Mu Glut	gi|1943431	28756.1
Chain A, Glutathione Transferase Mutant Y115f	gi|29726512	28770.1
Chain A, Tetra-(5-Fluorotryptophanyl)-Glutathione Transferase	gi|4388948	28485.8
RecName: Full=Glutathione S-transferase Mu 6; AltName: Full=GST class-mu 6; AltName: Full=Glutathio	gi|51338739	27888.4
glutathione S-transferase (EC 2.5.1.18) [Rattus norvegicus]	gi|204501	28689
glutathione S-transferase Mu 1 [Rattus norvegicus]	gi|8393502	28917.1
glutathione S-transferase Mu 6 [Mus musculus]	gi|113680506	28192.6
glutathione S-transferase Yb-1 subunit (EC 2.5.1.18) [Rattus norvegicus]	gi|204503	28820.9
glutathione-S-transferase class M5 [Mus musculus]	gi|2275021	11865.1
glutathione-S-transferase class M5 [Mus musculus]	gi|2275019	27966.3
unnamed protein product [Mus musculus]	gi|12853535	29718.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#]	Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1417.6178	1417.5051	-0.1127	-79	32	42	YAMGDAPDYDR	39	96.541	(N-term)_iTRAQ[0]	[8] F2		238/230	1.547	2.020	2.672	1	Mascot

219	Fibrous sheath interacting protein 1 [Homo sapiens]	gi|28175039	75848.8	1	39	0.230	0.342	0.780	0.000	0.000	0.000	1	1	1	96.525

Protein Group

HSD10 [Homo sapiens]	gi|37956233	75915.8
RecName: Full=Fibrous sheath-interacting protein 1	gi|75048806	75358.6
fibrous sheath-interacting protein 1 [Homo sapiens]	gi|116089284	75860.7
hypothetical protein [Macaca fascicularis]	gi|15207939	60696.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1158.782	1158.7306	-0.0514	-44	278	284	RLVELLK	39	96.525	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[4] F11 and F3	1138/1130	0.230	0.342	0.780	1	Mascot

220	Chain A, Crystal Structure Of Tetradeca-(3-Fluorotyrosyl)- Glutathione S-Transferase	gi|5107744	28109.2	1	38	1.054	0.427	1.913	0.000	0.000	0.000	1	1	1	95.986

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1228.7188	1228.7435	0.0247	20	136	143	LXSEFLGK	40	96.938	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	295/287	1.054	0.427	1.913	1	Mascot

221	RecName: Full=EGF-containing fibulin-like extracellular matrix protein 2; AltName: Full=Fibulin-4;	gi|9973149	51861.1	1	38	1.206	0.897	0.975	0.000	0.000	0.000	1	1	1	95.841

Protein Group

EGF-containing fibulin-like extracellular matrix protein 2 [Mus musculus]	gi|7634795	51881.1
EGF-containing fibulin-like extracellular matrix protein 2 [Rattus norvegicus]	gi|54400722	46862.1
EGF-containing fibulin-like extracellular matrix protein 2 isoform 1 [Mus musculus]	gi|256355190	51854.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1598.7407	1598.6863	-0.0544	-34	315	326	CVEPYVQVSDNR	38	95.841	(N-term)_iTRAQ[0], MMTS (C)[1]	[8] F2	316/308	1.206	0.897	0.975	1	Mascot

222	complement component C7 precursor [Homo sapiens]	gi|45580688	103093.5	1	38	0.985	0.978	1.044	0.000	0.000	0.000	1	1	1	95.831

Protein Group

complement C7 [Homo sapiens]	gi|899271	100354.2
complement component C7 precursor [Pongo abelii]	gi|197100316	103387.9
complement protein C7 precursor [Homo sapiens]	gi|179716	103089.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1220.7338	1220.7637	0.0299	24	737	744	ILPLTVCK	38	95.831	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8], MMTS (C)[7]	[2] F4 and F13	285/277	0.985	0.978	1.044	1	Mascot

223	secretogranin-2 precursor [Bos taurus]	gi|27806421	76941.6	1	38	1.071	1.324	0.914	0.000	0.000	0.000	1	1	1	95.754

Protein Group

PREDICTED: secretogranin-2 isoform 1 [Canis lupus familiaris]	gi|57111253	77353.9
Secretogranin II (chromogranin C) [Homo sapiens]	gi|18490917	76878.4
secretogranin II [Gorilla gorilla]	gi|23379613	43127.9
secretogranin II [Homo sapiens]	gi|338051	77021.4
secretogranin II [Macaca sp.]	gi|23379617	43170
secretogranin II [Pan troglodytes]	gi|23379611	42998.9

secretogranin II [Pongo pygmaeus]	gi|23379615	43247
secretogranin II [Saguinus oedipus]	gi|23379619	43364.1
secretogranin-2 precursor [Pongo abelii]	gi|197101383	77456.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1782.9457	1782.8641	-0.0816	-46	297	308	ESKDQLSDDVSK	38	95.754	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[3,12]	[1] F8 061011	177/169	1.071	1.324	0.914	1	Mascot

224	complement C8 beta [Rattus norvegicus]	gi|841248	17458.3	1	38	0.611	0.728	0.782	0.000	0.000	0.000	1	1	1	95.754

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1152.651	1152.5862	-0.0648	-56	42	48	ALEEFQK	38	95.754	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7]	[5] F5 and F10	257/249	0.611	0.728	0.782	1	Mascot

225	RecName: Full=Histone deacetylase 7; Short=HD7; AltName: Full=Histone deacetylase 7A; Short=HD7a	gi|30913010	28292.3	1	38	3.847	1.394	0.757	0.000	0.000	0.000	1	1	1	95.675

Protein Group

RecName: Full=Histone deacetylase 7; Short=HD7; AltName: Full=Histone deacetylase 7A; Short=HD7a	gi|30913097	108072.1
histone deacetylase 7 [Homo sapiens]	gi|7542540	97325.3
histone deacetylase 7 [Mus musculus]	gi|6911184	106700.9
histone deacetylase 7 isoform 3 [Mus musculus]	gi|324073138	107291.5
histone deacetylase 7 isoform 4 [Mus musculus]	gi|40254548	106668.9
histone deacetylase 7 isoform a [Homo sapiens]	gi|169234807	112020.7
histone deacetylase 7 isoform d [Homo sapiens]	gi|148539870	108188.4
histone deacetylase 7A variant 3 [Homo sapiens]	gi|32482808	104239.9
hypothetical protein [Homo sapiens]	gi|5911907	99192.4
mFLJ00062 protein [Mus musculus]	gi|47847402	95956.4
unnamed protein product [Mus musculus]	gi|26326835	108247.2
unnamed protein product [Mus musculus]	gi|26331526	107367.6
unnamed protein product [Mus musculus]	gi|26354072	104486.9
unnamed protein product [Mus musculus]	gi|26353936	101963.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1473.974	1473.9379	-0.0361	-24	96	104	QKLAEVILK	38	95.675	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[2,9]	[2] F4 and F13	257/249	3.847	1.394	0.757	1	Mascot

226	complement factor B subunit Bb - pig (fragment)	gi|543095	21792.7	1	38	1.228	1.177	1.292	0.000	0.000	0.000	1	1	1	95.533

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1380.8586	1380.7924	-0.0662	-48	1	9	VASYGVKPK	38	95.533	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,9]	[1] F8 061011	175/167	1.228	1.177	1.292	1	Mascot

227	nuclear factor of activated T-cells, cytoplasmic 2 isoform C [Homo sapiens]	gi|27886541	105862.5	1	38	0.961	1.561	0.377	0.000	0.000	0.000	1	1	1	95.502

Protein Group

Chain L, Structure Of Nfat1 Bound As A Dimer To The Hiv-1 Ltr Kb Element	gi|37927427	35436.7
Chain M, Crystal Structure Of Human Nfat1 Bound Monomerically To Dna	gi|46015057	35262.7
Chain N, Structure Of The Dna Binding Domains Of Nfat, Fos And Jun Bound To Dna	gi|3212242	37211.5
NFAT1-A [Mus musculus]	gi|1353237	121352.1
Nfatc2 protein [Mus musculus]	gi|39793877	70671.8
T cell transcription factor NFAT1 isoform B [Mus musculus]	gi|1353399	105114
T cell transcription factor NFAT1 isoform C [Mus musculus]	gi|1353401	105635.2
nuclear factor of activated T-cells, cytoplasmic 2 isoform B [Homo sapiens]	gi|27886539	105357.3
nuclear factor of activated T-cells, cytoplasmic 2 isoform c [Mus musculus]	gi|81295412	52075.1
transcription factor NFAT [Sus scrofa]	gi|3335546	14988.2
transcription factor NFAT1 isoform B [Homo sapiens]	gi|1353774	105375.2
transcription factor NFAT1 isoform C [Homo sapiens]	gi|1353776	105880.5
transcription factor NFAT1-D [Mus musculus]	gi|13936689	75714.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1338.7352	1338.749	0.0138	10	511	520	ATIDCAGILK	38	95.502	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[10], MMTS (C)[5]	[2] F4 and F13	217/209	0.961	1.561	0.377	1	Mascot

228	fibroleukin [Sus scrofa]	gi|52346216	55998.3	1	38	1.403	1.350	1.137	0.000	0.000	0.000	1	1	1	95.419

Protein Group

FGL2 protein [Homo sapiens]	gi|17389565	18653.7
fibroleukin precursor [Homo sapiens]	gi|5730075	55890.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1362.8691	1362.8411	-0.028	-21	89	96	EIVNSLKK	38	95.419	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[7,8]	[1] F8 061011	215/207	1.403	1.350	1.137	1	Mascot

229	fibulin-5 precursor [Rattus norvegicus]	gi|42476116	52686.6	1	38	1.296	1.182	1.122	0.000	0.000	0.000	1	1	1	95.376

Protein Group

FBLN5 [Homo sapiens]	gi|37182914	52718.6
UP50 [Homo sapiens]	gi|3676822	52939.7
embryonic vascular EGF repeat-containing protein EVEC [Rattus norvegicus]	gi|4583509	52670.6
fibulin-5 precursor [Bos taurus]	gi|62460592	52736.5
fibulin-5 precursor [Homo sapiens]	gi|19743803	52752.6
fibulin-5 precursor [Mus musculus]	gi|6753824	52719.5
fibulin-5 precursor [Pongo abelii]	gi|197102314	52851.7
unnamed protein product [Homo sapiens]	gi|28207929	62962.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1708.8812	1708.8511	-0.0301	-18	360	373	SVPADIFQMQATTR	38	95.376	(N-term)_iTRAQ[0]	[8] F2	393/385	1.296	1.182	1.122	1	Mascot

230	Ig lambda chain V region (JP-FL-4) - human (fragment)	gi|87898	12660.5	1	38	0.928	0.884	0.961	0.000	0.000	0.000	1	1	1	95.181

Protein Group

Ig lambda chain precursor V region (JP-FL-3) - human (fragment)	gi|87892	15663
immunoglobulin lambda light chain variable region [Homo sapiens]	gi|4324216	12229.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
1155.7711	1155.8285	0.0574	50	101	108	LIVLGQPK	38	95.181	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[8]	[2] F4 and F13	959/951	0.928	0.884	0.961	1	Mascot

231	precursor polypeptide (AA -19 to 206) [Mus musculus]	gi|50564	28102.5	1	38	0.654	0.729	1.192	0.000	0.000	0.000	1	1	1	95.091

Protein Group

C-reactive protein [Homo sapiens]	gi|30224	27390.2
C-reactive protein [Oryctolagus cuniculus]	gi|986939	28036.4
C-reactive protein precursor [Homo sapiens]	gi|55770842	27322.2
C-reactive protein precursor [Oryctolagus cuniculus]	gi|126722616	27904.3
C-reactive protein precursor [Sus scrofa]	gi|55742770	26821.7
C-reactive protein, pentraxin-related [Homo sapiens]	gi|55665343	13012.9
CRP protein [Homo sapiens]	gi|18088467	11797.3
Chain A, Human C-Reactive Protein	gi|1942435	25142
RecName: Full=C-reactive protein; Flags: Precursor	gi|117487	28076.5

RecName: Full=C-reactive protein; Flags: Precursor gi|117490 27920.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Plate [#] Name	Gel Idx/Pos [4700 Sample Name]	iTRAQ Ratio 114/117*	iTRAQ Ratio 115/117*	iTRAQ Ratio 116/117*	Rank	Result Type
996.6127	996.5723	-0.0404	-41	27	32	AFVFPK	38	95.091	(N-term)_iTRAQ[0], Lysine(K)_iTRAQ[6]	[5] F5 and F10	325/317	0.654	0.729	1.192	1	Mascot