Serum proteome signatures associated with ileal and colonic ulcers in Crohn's disease

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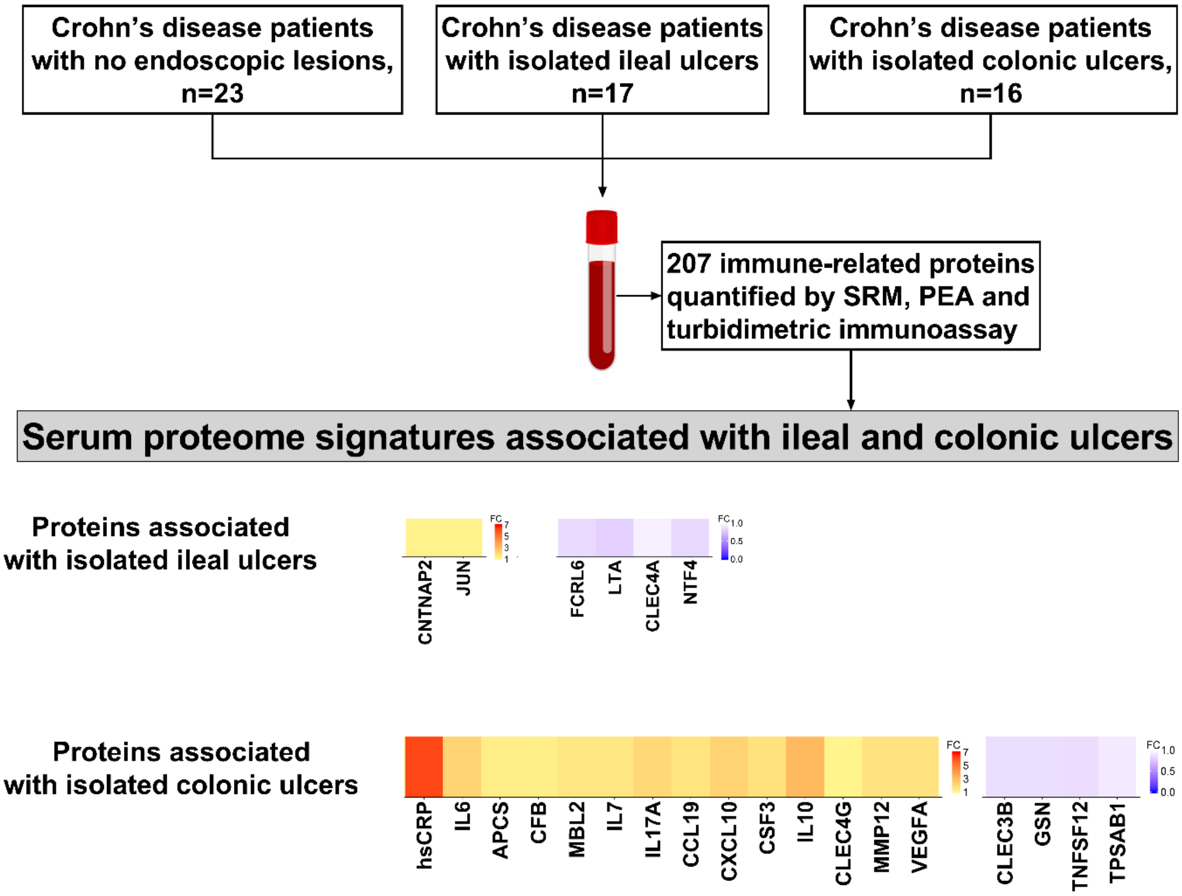

Crohn's disease patients with no endoscopic lesions, n=23

Crohn's disease patients with isolated ileal ulcers n=17

Crohn's disease patients with isolated colonic ulcers, n=16

207 immune-related proteins quantified by SRM, PEA and turbidimetric immunoassay

Serum proteome signatures associated with ileal and colonic ulcers

Proteins associated with isolated ileal ulcers

Proteins associated with isolated colonic ulcers

Abstract

At a clinical level, ileal and colonic Crohn's disease (CD) are considered as separate entities. These subphenotypes need to be better supported by biological data to develop personalised medicine in CD. To this end, we combined different technologies (proximity extension assay, selected reaction monitoring, and high-sensitivity turbidimetric immunoassay (hsCRP)) to measure 207 immune-related serum proteins in CD patients presenting no endoscopic lesions (endoscopic remission) (n=23), isolated ileal ulcers (n=17), or isolated colonic ulcers (n=16). We showed that isolated ileal ulcers and isolated colonic ulcers were specifically associated with 6 and 18 serum proteins, respectively: (high level: JUN, CNTNAP2; low level: FCRL6, LTA, CLEC4A, NTF4); (high level: hsCRP, IL6, APCS, CFB, MBL2, IL7, IL17A, CCL19, CXCL10, CSF3, IL10, CLEC4G, MMP12, VEGFA; low level: CLEC3B, GSN, TNFSF12, TPSAB1). Isolated ileal ulcers and isolated colonic ulcers was detected by hsCRP with an area under the receiver operating characteristics curve of 0.64 (p-value=0.07) and 0.77 (p-value=0.001), respectively. We highlighted distinct serum proteome profiles associated with ileal and colonic ulcers in CD, this finding might support the development of therapeutics and biomarkers tailored to disease location.

1. Introduction

Crohn's disease (CD) is an inflammatory bowel disease (IBD). IBD is a global burden with rising incidence in newly industrialised countries and rising prevalence in Western countries[1]. This pattern of IBD will pose major challenges for the health systems and policymakers in the near future.

The diagnosis of CD is based on a combination of investigations: clinical (eg, abdominal pain, diarrhoea, weight loss, and fatigue), biochemical (eg, CRP and faecal calprotectin) endoscopic, and histological[2]. There is no cure for CD, and the treatment relies on the combination of anti-inflammatory drugs (corticosteroids and 5-ASA), biologics (anti-TNFα, anti-α4β7 integrin, anti-IL12/IL23, and anti-IL23), and immunosuppressant (methotrexate, azathioprine, and mercaptopurine). The failure of pharmacological treatments can lead to surgical resection, and this concerns ~50% of patients 10 years after diagnosis[3].

CD is characterised by patchy inflammation that affects mostly the terminal ileum and colon with a relapsing-remitting pattern. Ileal and colonic CD are nowadays considered as distinct entities and this modern view of CD classification is well supported by epidemiological, clinical, and biological data[4]. Compared with other disease sites, isolated colonic CD has been associated with an older age at diagnosis (~10 years), a predominance of women (~65%), and a weaker association with smoking[5]. At a clinical level, ileal CD poses particular challenges. Compared with colonic CD, ileal CD has a more aggressive progression with a higher risk of penetrating disease and surgery[6–8]. Besides, more and more data indicate that, compared with colonic lesions, ileal lesions are more refractory to the biologics currently used in CD[9]. On top of this, the endoscopic access to the small intestine remains difficult, and the biomarkers used in routine practice (C-reactive protein (CRP) and faecal calprotectin) showed lower performance to monitor ileal than colonic CD[10–16].

The specificities of ileal and colonic CD have been highlighted by various biological data including genetics[6], gut transcriptomics[17], gut proteomics[18], gut metabolomics[19], T-cell composition in mesenteric fat[20], and microbiota[4]. The serum proteome associated with CD location has been poorly studied despite its interest for the development of personalised medicine. To date, this research has been conducted by measuring a maximum of 35 serum proteins[21].

The present study aimed to support the development of personalised medicine by identifying specific blood protein profiles associated with ileal and colonic CD.

2. Materials and Methods

2.1 Study population

This study received approval from the ethics committee of the Liege University Hospital (Belgium) [2022-059]. All patients gave their written informed consent. Figure 1 summarises the patient selection. Adult CD patients (n=56) were retrospectively selected from the database of the Liege University Hospital (2012-2020). All selected patients underwent an endoscopic examination performed as part of their disease management. Based on this information, the inclusion criteria included endoscopic remission (no endoscopic lesions), isolated ileal ulcers (deep or superficial), or isolated colonic ulcers (deep or superficial). The exclusion criteria included anastomotic ulcers, Bauhin's valve ulcers, Montreal L4 (upper disease), or suspicion of non-CD-related inflammation. Selected patients were grouped into three categories: 1) endoscopic remission (n=23); 2) isolated ileal ulcers (n=17); and 3) isolated colonic ulcers (n=16). Of note, aphthoid lesions were not considered as ulcers. To compare the endoscopic activity between the ileum and colon, and to assess the overall lesion burden, we used the CD endoscopic index (CDEIS) without dividing its total score (sum of each gut segment) by the number of inspected segments. This score was called “total CDEIS”. The patients’ clinical characteristics are showed in Table 1.

2.2 Study design

Serum samples were obtained at the time of the endoscopic examination to measure immune-related proteins with three technologies. First, a method of selected reaction monitoring (SRM) which generates a relative quantification. The proteins measured by SRM (n=74) are mainly produced by the liver and are related to the inflammatory response (eg, acute-phase response, complement pathway, and blood coagulation)[22]. Second, the proximity extension assay (PEA) used to measure proteins belonging to panels called “immune response panel” (relative quantification; n=92) and “cytokine panel” (absolute quantification; n=45) (Olink, Sweden). The proteins measured by PEA are involved in the adaptive immune response, inflammation, lymphocyte activation, cytokine-mediated signalling pathways, and defence response to virus. Third, a high-sensitivity turbidimetric immunoassay (hsCRP) used to measure the absolute concentration of CRP. Of note, CRP, CCL11, CXCL12, IL6, and IL10 were measured twice. Thus, 207 proteins were studied (74+92+45+1-5) (Figure 1 and Supplementary Table 1). CRP was measured in routine practice (hsCRP) and by SRM, while CCL11, CXCL12, IL6, and IL10 are included in the two PEA panels. These replicates of measurement were correlated (Spearman) to evaluate their reproducibility (CXCL12, r=0.52; CCL11, r=0.93; IL6, r=0.92; IL10, r=0.76; and CRP, r=0.91). For the final analysis, we excluded the following measurements: 1) IL6, IL10, and CCL11 measured with the PEA immune response panel since the absolute concentrations of these proteins were obtained with the PEA cytokine panel; 2) CXCL12 due to the low correlation between its replicates of measurement (see above); and 3) CRP measured by SRM since the hsCRP provides absolute values and it is the reference measurement.

2.3 Proximity extension assay

The PEA technology has been fully described elsewhere[23]. The analytical performances of the PEA measurements are provided on Olink's website (https://www.olink.com/): intra-assay precision, inter-assay precision, dynamic range, limit of detection, lower limit of quantification, upper limit of quantification, and hook effect.

2.4 Selected reaction monitoring method

The SRM method was in-house developed[22]. In the present study, our SRM method was upgraded by using synthetic peptides with stable isotope-labelling to normalise the signal of every endogenous targeted peptide. The reliability of this new development was assessed using the following quality controls: intra-day precision, inter-day precision, stability of the instrumental set-up over time, guarantees on target identity, and quantotypic properties of the selected peptides (Supplementary Methods and Supplementary Table 2). The present SRM method targets 75 proteins (including the internal standard ENO1, see below), 208 peptides, 416 precursors, and 1318 fragments (Supplementary Table 2).

Sample preparation

Serum proteins spiked with internal standard (ENO1, P00924, Sigma-Aldrich, USA) were digested as previously described[22]. Before injection into the LC-MS system, the dried and frozen (–20 °C) peptide mixture was spiked with: 1) a synthetic peptide (VNQIGTLSESIK, ENO1) with stable isotope-labelling (^{13}C, ^{15}N on the C-terminal K) (HeavyPeptide AQUA Ultimate, Thermo Fisher Scientific, USA): 5.2 µL of the peptide solution concentrated at 50 fmol.µL^{-1} in 5% acetonitrile; 2) crude synthetic peptides with stable isotope-labelling (^{13}C, ^{15}N on the C-terminal R/K or internal L) (SpikeTides L, JPT Peptide Technologies, DE) which are analogues of the endogenous targeted peptides: 10 µL of the peptide solution concentrated at 52 fmol.µL^{-1} (each peptide) in 11.3% acetonitrile and 80% ammonium bicarbonate 0.1 M; and 3) 31.5 µL of 0.1% formic acid. Finally, 9 µL of this mix was injected into the LC-MS system, corresponding to 0.675 µg of protein digest, 50 fmol of the VNQIGTLSESIK synthetic peptide, and 100 fmol of each SpikeTides L synthetic peptide.

Liquid chromatography and mass spectrometry

As previously described[22], samples were injected into UPLC M-Class (Waters, USA) chromatography coupled online with a triple quadrupole mass spectrometer Xevo TQ-S (Waters). The SRM method (Supplementary Table 2) was applied with the following settings: scheduled mode, at least 12 points per peak (considering a peak width of 25 s), and a retention time window of 4 minutes. By using these parameters, the dwell times ranged from 11 to 257 ms, the cycle times ranged from 1.03 to 2.11 s, and the number of points per peak ranged from 14 to 29 (considering a minimum peak width of 30 s).

Raw data processing

The raw data were processed using Skyline (version 21.2.0.369). The automatic integration of SRM traces was systematically checked and corrected if necessary. Each peptide was quantified by summing its two most intense fragments (total area). Each protein was quantified using the following formula:

$$\frac{((\text{total area peptide 1} + \ldots + \text{total area peptide n}) / (\text{total area peptide heavy 1} + \ldots + \text{total area peptide heavy n}))}{(\text{total area VNQIGTLSESIK} / \text{total area VNQIGTLSESIK heavy})}$$

2.5 Statistical analysis

The Wilcoxon-Mann-Whitney test was used for the differential analyses (isolated ileal ulcers vs endoscopic remission; isolated colonic ulcers vs endoscopic remission). The classification performance (isolated ileal ulcers vs endoscopic remission; isolated colonic ulcers vs endoscopic remission) of the hsCRP was evaluated by the area under the receiver operating characteristics curve (AUROC). The AUROC values were statistically compared to a random classifier (AUROC=0.5) using the bootstrap test (2000 replicates), as previously described[24]. The significance threshold was set at a p-value <0.05 (two-sided for the differential analysis, and one-sided for the AUROC analysis). The statistical analyses and plots were performed using Python 3.9, R 3.3.1 and GraphPad Prism 9.4.1.

3. Results

3.1 Characteristics of the patients

There were no major differences in age, sex, disease duration, or medication use between patients with isolated ileal ulcers and those with isolated colonic ulcers (Table 1). There were more active and former smokers among patients with isolated ileal ulcers than among those with isolated colonic ulcers (6 vs 2, 5 vs 2, respectively) (Table 1). The median (IQR) of the total CDEIS (endoscopic activity of the disease) was higher in patients with isolated colonic ulcers than in those with isolated ileal ulcers: 23.1 (13.0-38.4) vs 8.0 (6.5-14.0) (Table 1). This last result was expected because, in the colon, the total CDEIS is a sum of four gut segments.

3.2 Detection of isolated ileal ulcers and isolated colonic ulcers with hsCRP

All patients in endoscopic remission showed normal levels of hsCRP (<5 mg.L^{-1}) (Figure 2A). Compared with patients in endoscopic remission, patients with isolated colonic ulcers showed a higher median level of hsCRP (1.3 vs 5.9 mg.L^{-1}, p-value=0.0045) and this was not the case for CD patients presenting isolated ileal ulcers (1.3 vs 2.2 mg.L^{-1}, p-value=0.1288) (Figure 2A). Normal hsCRP levels were observed in 76% (13/17) of patients with isolated ileal ulcers and 44% (7/16) of patients with isolated colonic ulcers. Based on the AUROC, hsCRP had a higher performance in detecting isolated colonic ulcers than isolated ileal ulcers (0.77, p-value=0.001; 0.64, p-value=0.067; respectively) (Figures 2B and 2C).

3.3 Serum protein levels according to ulcer location

When compared to endoscopic remission, the serum abundance of 6 and 18 proteins were specifically associated with the presence of isolated ileal ulcers and isolated colonic ulcers, respectively (Figures 3 and 4, Supplementary Tables 3 and 4). No protein was associated with both isolated ileal ulcers and isolated colonic ulcers (Figures 3 and 4).

4. Discussion

By quantifying 207 serum proteins in CD patients, we revealed that isolated ileal ulcers and isolated colonic ulcers are associated with distinct proteome signatures. This finding could foster the development of therapeutics and biomarkers tailored to CD location.

Remarkably, the presence of inflammation was objectified with ten blood markers in the patients with isolated colonic ulcers but not in those with isolated ileal ulcers. This result is consistent with the literature showing that, inflammatory biomarkers used in clinical routine (CRP and feacal calprotectin), are less impacted by active CD in the ileum than active CD in the colon[14,25]. As already proposed[25], this difference could be partially explained by anatomical considerations. Indeed, the length of the terminal ileum is much shorter than the colon (~30 cm vs ~150 cm), which has a direct influence on the surface area affected and inflammatory load. This idea was substantiated by our result showing lower total CDEIS (an approximation of the inflammatory load) with isolated ileal ulcers compared with isolated colonic ulcers. Furthermore, the passage of bacteria or their products (pathogen-associated molecular patterns) across the intestinal barrier could be more important with colonic than with ileal ulcers, which would influence results at blood level. Two pieces of evidence support this hypothesis: 1) bacterial load is much higher in the colon than the ileum ($10^{10\text{-}11}$ vs 10^{8} bacteria per millilitre of human intestinal content)[26]; and 2) the abnormal development of the intestinal mesenteric fat (i.e., creeping fat), which is specifically observed in ileal CD, could be a defence mechanism preventing systemic bacterial spread[20].

Our data showed that the serum proteome was more disturbed with isolated colonic ulcers than with isolated ileal ulcers. This observation is consistent with the above discussion and agrees with another study investigating 35 serum proteins in CD patients and healthy controls[21]. Indeed, in this work, the authors reported that, among the nine serum proteins associated with disease location, all were associated with colonic CD. Furthermore, in that study, the levels of IL6, IL7, IL10, CSF3 (also known as G-CSF), and VEGF were specifically elevated in colonic CD, which is consistent with our current observations. These converging results were obtained using a different experimental design to ours: 1) comparison between CD patients and healthy controls; 2) disease behaviour not restricted to ulcers (B1 in the Montreal classification) but also included stricturing and penetrating disease (B2 and B3 in the Montreal classification, respectively). Thus, the interest of our results seems to go beyond the study of ulcers.

CSF3 plays a central role in the production of mature neutrophils by stimulating their proliferation, differentiation, and survival[27]. In our study, the CSF3 serum level was specifically increased in CD patients with isolated colonic ulcers. On the other hand, our previous proteomic study showed higher levels of neutrophil degranulation markers in colonic than in ileal ulcer edges[18]. Considering the available evidence, we hypothesise that CSF3 is involved in the relation between neutrophil degranulation markers and CD location.

In our study, hsCRP was increased with isolated colonic ulcers but not with isolated ileal ulcers. We therefore suggest that a normal hsCRP level needs to be interpreted with particular caution in patients with ileal or ileocolonic CD. This message is important for clinical practice, as normalisation of CRP became formally recognised as a therapeutic target[28] and CD affects the ileum in ~75% of cases[6]. Our results on hsCRP agree with previous observations. Among 22 patients with clinically active CD and low CRP level (<10 mg.L^{-1}), the ileal disease was systematically observed (95% with a pure ileal disease and 5% with an ileocolonic disease)[14]. In a Korean population of 435 CD patients taken at diagnosis, the CRP level was lower with ileal CD than with ileocolonic and colonic CD (2.0 vs 3.9 vs 4.8 mg.L^{-1}, respectively)[16]. Another study found no correlation between the CRP level and the radiologic disease activity in the small bowel of CD patients[15]. Finally, the correlation between disease activity (clinical and endoscopic) and CRP level appears weaker in ileal than in colonic CD[16,29].

Compared with colonic CD, ileal CD is more difficult to treat with the current biologics[9]. In this context, the pathophysiological specificities of ileal CD are of particular interest to identify novel therapeutic targets. Our current study shows that isolated ileal ulcers were specifically associated with a low serum level of immune regulators (FCRL6, LTA, CLEC4A). FCRL6 is an MHC class II receptor selectively expressed in natural killer cells and cytotoxic T cells[30]. CLEC4A is a pattern recognition receptor mainly expressed in dendritic cells (DC) that recognises the human immunodeficiency viruses-1[31]. When they FCRL6 and CLEC4A are engaged, they inhibit the immune response through their immunoreceptor tyrosine-based inhibitory motif[31,32]. To the best of our knowledge, the implication of FCRL6 in CD is unknown. As for CLEC4A, we previously reported an association between a low serum level of CLEC4A and the risk of short-term relapse (<6 months) in CD patients stopping infliximab[33]. LTA is a cytokine of the tumour necrosis factor family, mainly produced by lymphocytes, which promotes the maturation of T cells, DC, and macrophages[34]. LTA also regulates the formation and maintenance of Peyer's patches, i.e., the secondary lymphatic organs found specifically in the small intestine[34]. Based on these evidence, we speculate that LTA could be involved in ileal CD.

SRM is a targeted mass spectrometry technique that allows a robust quantification of multiple proteins (50-100)[35]. However, the reliability of SRM data is affected by a lack of transparency and methodological guarantees[36]. In the present study, the reliability of the SRM data is supported by a series of quality controls including intra-day precision, inter-day precision, stability of the instrumental set-up over time, guarantees on target identity, and quantotypic properties of the selected peptides. For transparency, we have provided public access to all the SRM raw data (including quality control samples). The use of synthetic peptides with stable isotope-labelling is another strength of our methodology. As SRM, the PEA technology presents excellent specificity[23] and precision (mean intra-day precision <10%). All these elements support the high quality of our dataset.

Our work has some limitations. Our sample size was relatively small, and without an independent cohort, the generalisability of our results cannot be formally demonstrated. Note, however, that our results are consistent with previous studies. We also recognise that some upper lesions may have been missed since the endoscopic examination was restricted to the colon and terminal ileum. The absence of faecal samples to measure calprotectin is another limitation of our study. However, calprotectin has been well studied in CD and some data showed that it is not correlated with the ileal disease activity (endoscopy or imaging)[13]. Another study reported that, in patients with ileal CD, faecal calprotectin was not highly elevated (< 200 $\mu g.g^{-1}$) even in cases of large (0.5-2 cm) or very large ulcers (> 2 cm)[25].

In summary, we showed that the presence of isolated ileal ulcers and isolated colonic ulcers are associated with distinct serum proteome signatures in CD patients. This knowledge might be useful for the development of personalised medicine in CD. We also reported that CRP is ineffective in detecting ileal ulcers, providing practical information for clinicians.

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Declaration of Competing Interest

The authors declare no conflicts of interest.

Data availability

PEA raw data are available upon request. All the SRM raw data (including quality control samples) and Skyline files have been deposited in a public repository (https://panoramaweb.org/syTB3r.url, username: panorama+reviewer211@proteinms.net; password: ewqMbogk, ProteomeXchange identifier: PXD045278). All the processed data are available in the Supplementary tables.

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Table 1. Patients' characteristics

	No endoscopic lesions	Isolated ileal ulcers	Isolated colonic ulcers
Patients, n [m/f]	23 [11/12]	17 [7/10]	16 [8/8]
Age, median years [IQR]	45 [33-55]	50 [39-55]	42 [29-52]
Disease duration, median years [IQR]	10 [4-22]	10 [3-17]; n=16	11 [8-21]
Total CDEIS, median [IQR]	0.0 [0.0-0.0]	8.0 [6.5-14.0]	23.1 [13.0-38.4]
Smoking			
Active	5	6	2
Former	1	5	2
No	17	6	12
Medication*			
None	4	6	8
Corticoids	5	3	0
Antibiotics	0	0	0
5-ASA	8	3	2
Immunomodulators	3	5	3
Anti-TNFα	4	4	3
Anti-α4β7 integrin	3	0	1
Anti-IL12/23	1	1	1

*Some patients may have several medications.

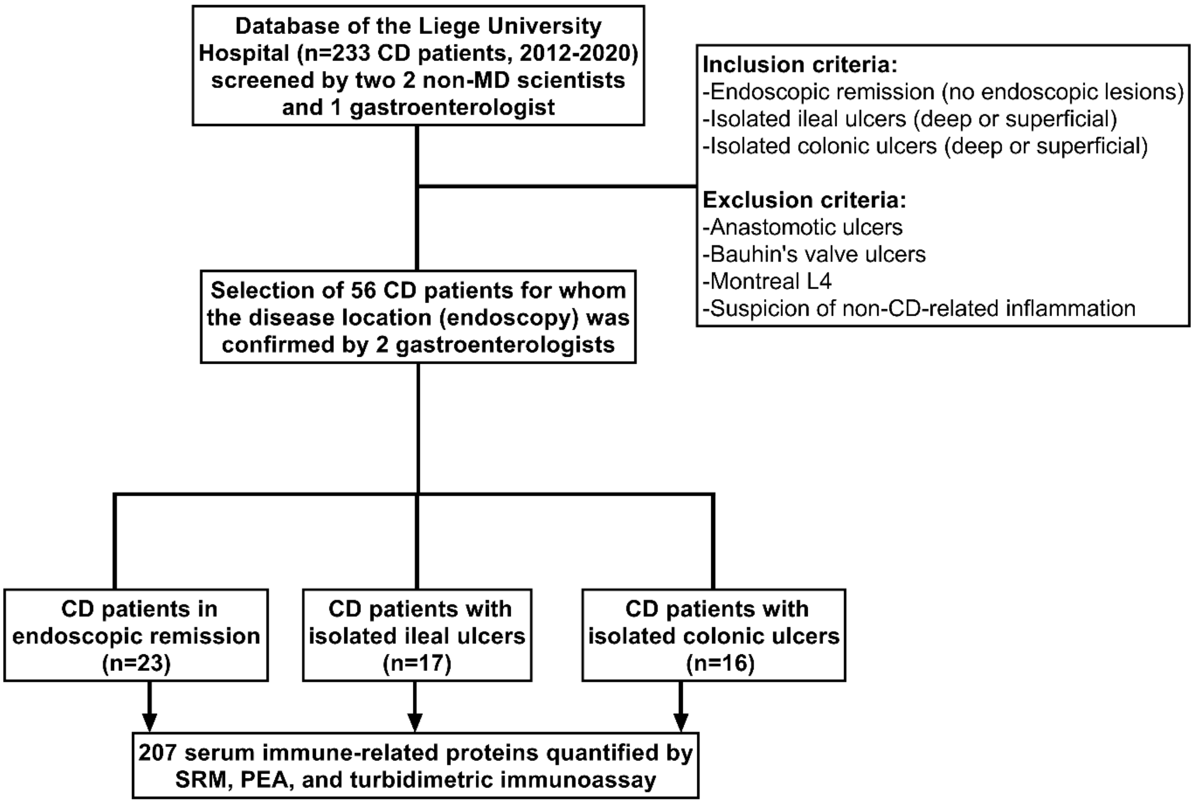

Figure 1. Cohort selection and experimental design

CD, Crohn’s disease; PEA, proximity extension assay; SRM, selected reaction monitoring.

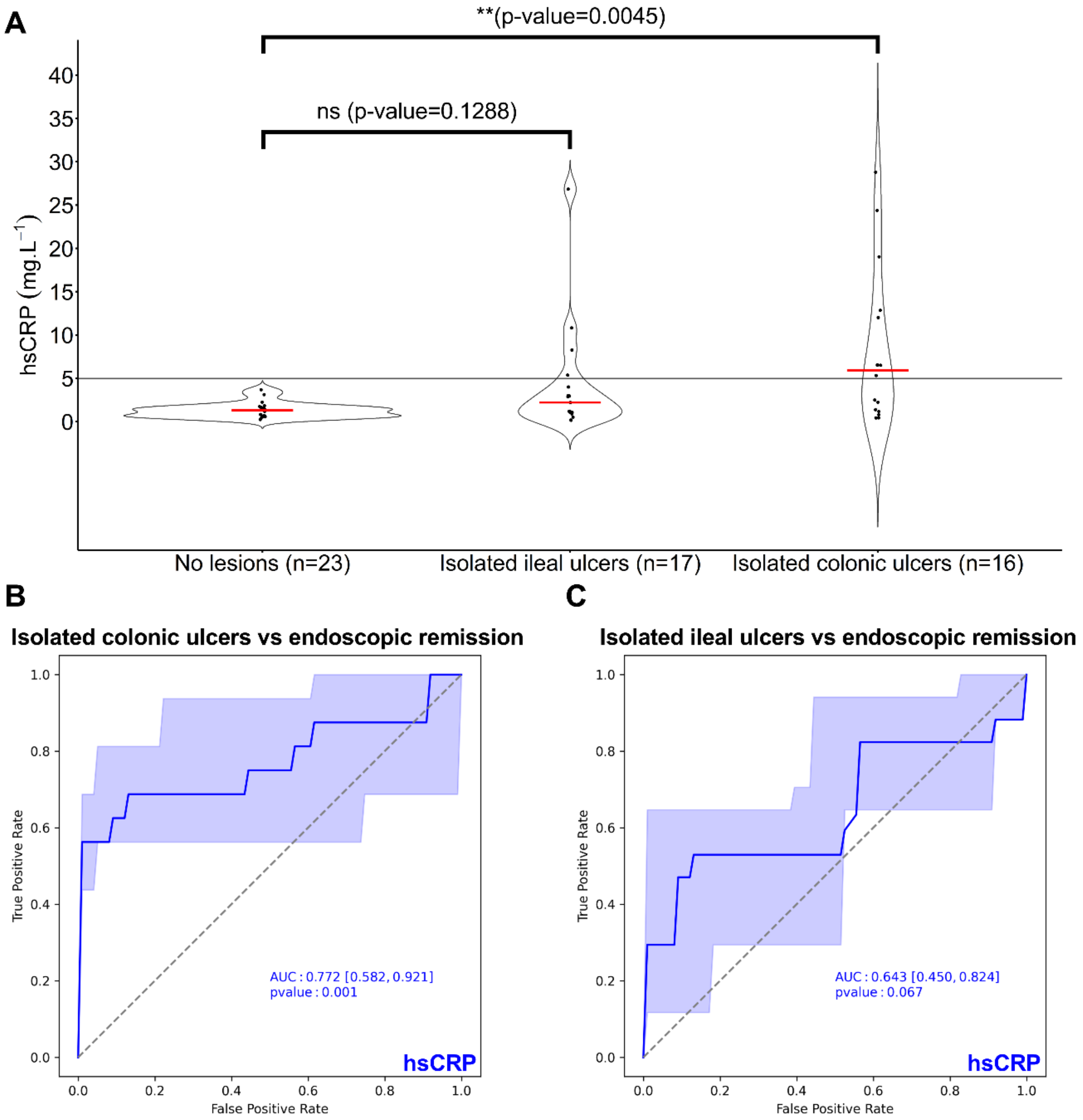

Figure 2. Detection of isolated ileal ulcers and isolated colonic ulcers with hsCRP. hsCRP concentration in CD patients with no endoscopic lesions, isolated ileal ulcers or isolated colonic ulcers (A). The differences between groups were evaluated using Wilcoxon-Mann-Whitney test. ROC curves evaluating the capacity of hsCRP to detect ulcers: isolated colonic ulcers vs endoscopic remission (B); isolated ileal ulcers vs endoscopic remission (C). The differences between AUROC were tested with the bootstrap test (2000 replicates). hsCRP, high-sensitivity C-reactive protein.

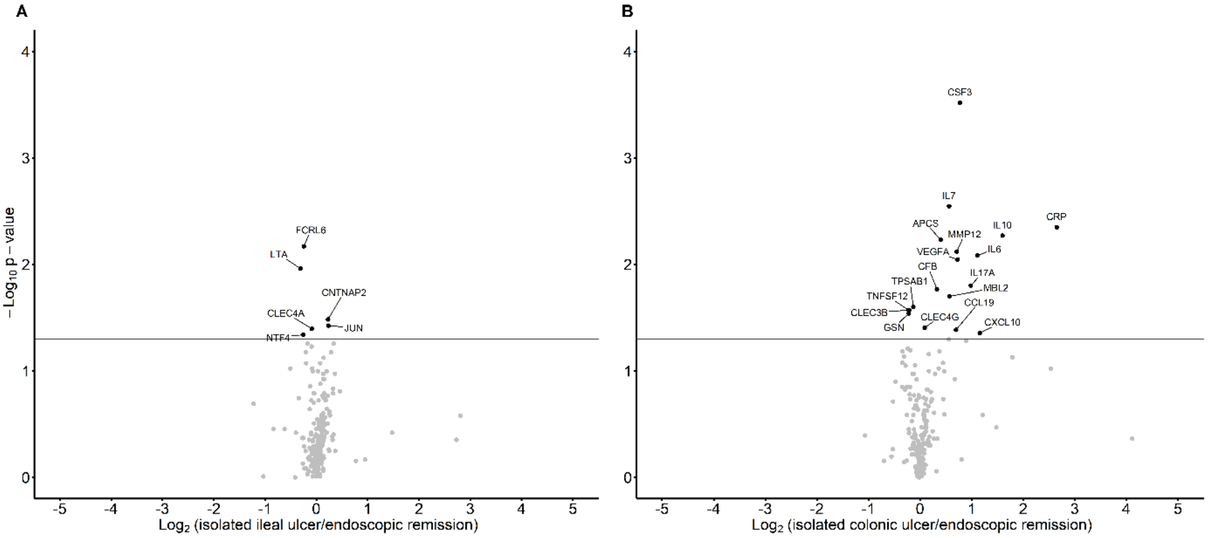

Figure 3. Serum protein levels according to ulcer location. Volcano plots illustrating the differential analysis (Wilcoxon-Mann-Whitney test): isolated ileal ulcers vs endoscopic remission (A); isolated colonic ulcers vs endoscopic remission (B). The statistical threshold (p-value=0.05) is represented by the horizontal lines. APCS, Serum amyloid P-component; CCL19, C-C motif chemokine 19; CFB, Complement factor B; CLEC3B, Tetranectin; CLEC4A, C-type lectin domain family 4 member A; CLEC4G, C-type lectin domain family 4 member G; CNTNAP2, Contactin-associated protein-like 2; CRP, C-reactive protein; CSF3, Granulocyte colony-stimulating factor; CXCL10, C-X-C motif chemokine 10; FCRL6, Fc receptor-like protein 6; GSN, Gelsolin; IL6, Interleukin-6; IL7, Interleukin-7; IL10, interleukin-10; IL17A, Interleukin-17A; JUN, Transcription factor Jun; LTA, Lymphotoxin-alpha; MBL2, Mannose-binding protein C; MMP12, Macrophage metalloelastase; NTF4, Neurotrophin-4; TNFSF12, Tumor necrosis factor ligand superfamily member 12; TPSAB1, Tryptase alpha/beta-1; VEGFA, Vascular endothelial growth factor A.

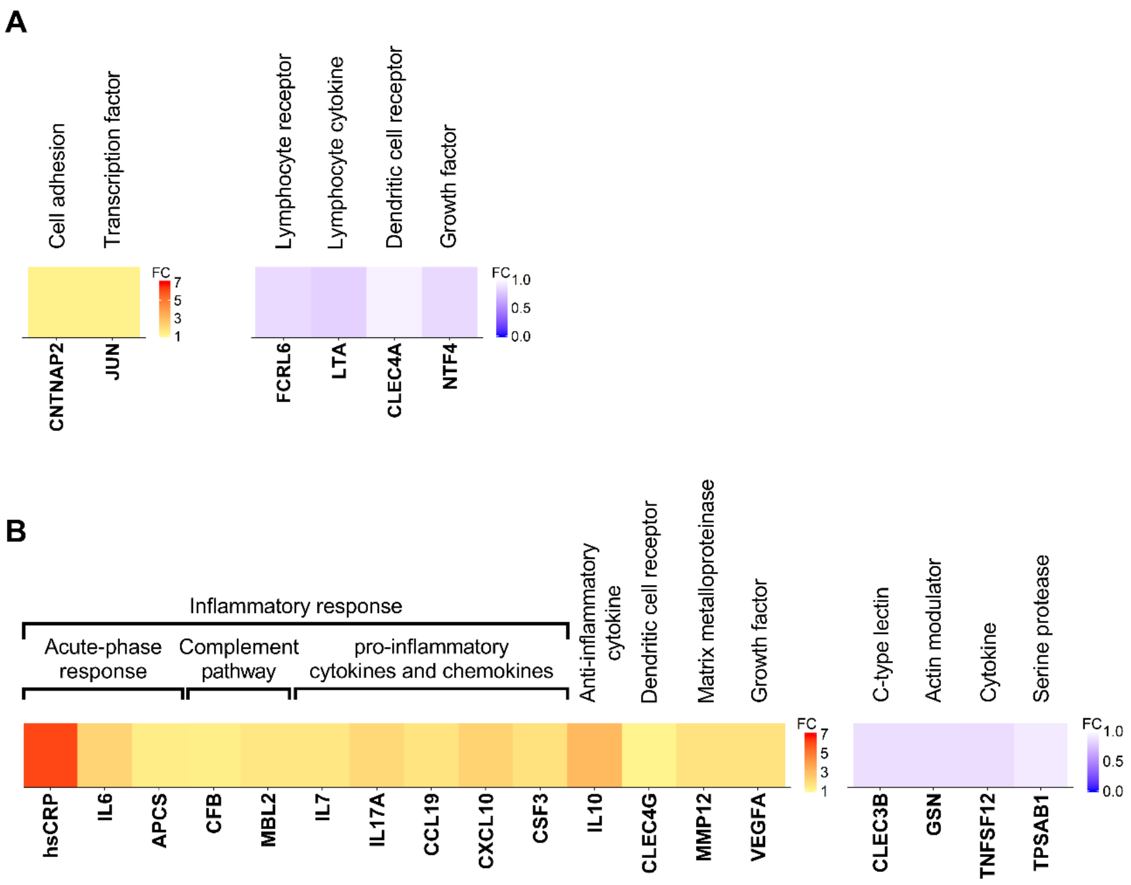

Figure 4. Distinct blood protein profiles associated with isolated ileal ulcers and isolated colonic ulcers. Heat map presenting the function of serum proteins with a differential abundance: isolated ileal ulcers vs endoscopic remission (A); isolated colonic ulcers vs endoscopic remission (B). FC, fold change. APCS, Serum amyloid P-component; CCL19, C-C motif chemokine 19; CFB, Complement factor B; CLEC3B, Tetranectin; CLEC4A, C-type lectin domain family 4 member A; CLEC4G, C-type lectin domain family 4 member G; CNTNAP2, Contactin-associated protein-like 2; CRP, C-reactive protein; CSF3, Granulocyte colony-stimulating factor; CXCL10, C-X-C motif chemokine 10; FCRL6, Fc receptor-like protein 6; GSN, Gelsolin; IL6, Interleukin-6; IL7, Interleukin-7; IL10, interleukin-10; IL17A, Interleukin-17A; JUN, Transcription factor Jun; LTA, Lymphotoxin-alpha; MBL2, Mannose-binding protein C; MMP12, Macrophage metalloelastase; NTF4, Neurotrophin-4; TNFSF12,

Tumor necrosis factor ligand superfamily member 12; TPSAB1, Tryptase alpha/beta-1; VEGFA, Vascular endothelial growth factor A.

Supplementary methods: quality controls

Intra-day precision

The intra-day precision was determined by calculating the coefficient of variation (CV) of 3 digestion replicates (technical replicates) performed in 2 serum pools representative of the study: CD patients in endoscopic remission (n=5) and CD patients with active endoscopic disease (n=5). The 74 proteins measured (excluding the internal standard ENO1) showed a mean intra-day CV (±SD) of 6.2% (2.7) and 4.6% (2.8) in the serum pools of CD patients in endoscopic remission and CD patients with active endoscopic disease, respectively. The intra-day CV reached a maximum of 16.5% (serum amyloid A-1 protein (SAA1) in the serum pool of CD patients in endoscopic remission).

Inter-day precision

The samples were prepared in 3 days and by groups of 15-24. They were injected in the LC-MS system over a period of ~11 days. The inter-day variation of this procedure was controlled using an external standard (a serum pool), digested each day of the sample processing and injected every 25 samples (3 in all). The analysis of these external standards allowed to calculate a mean inter-day CV (±SD) of 5.5% (3.3) for the 74 targeted proteins (excluding the internal standard ENO1). The inter-day CV reached a maximum of 16.4% (serotransferrin (TF)).

Stability of the instrumental set-up over time

During the injection period (~11 days), the stability of the instrumental set-up was evaluated through the injections, every 24 samples (4 in all), of purification replicates performed in a digested sample (serum pool). For this quality control, the 74 targeted proteins (excluding the internal standard ENO1) were measured with a mean CV (±SD) of 6.3% (3.7) and a maximum CV of 28.4% (serum amyloid A-1 protein (SAA1)).

Guaranties on target identity

As previously described[1], MS/MS data from preliminary experiments were used for the peptide identification. In this upgraded SRM method, the identity of endogenous peptides was further guaranteed by the co-elution of their heavy counterparts whose sequences were verified through MS/MS analysis. As recommended, identity of the targeted peptides was also supported by the co-elution of their targeted fragments[3].

Quantotypic properties of the selected peptides

In bottom-up proteomics, the quantification of a given protein relies on the quantification of its peptides which are thus supposed to have quantotypic properties. In this context, measuring a protein or its peptides is assumed to be stoichiometrically equivalent. However, there is currently no mean to verify this assumption[4]. Intuitively, if peptides of the same protein have quantotypic properties, their signal should be highly correlated. In other words, evaluating these correlations can be used to appreciate the quantotypic properties of peptides[4]. Thus, in our study, we generated correlation matrices for each protein based on the signal intensity of their peptides across all samples. This analysis led to 214 correlations which exhibited a mean (± SD) coefficient of correlation of 0.91 (0.08) and a minimum of 0.54 (VNEPSILEMSR vs VTEPISAESGEQVER, apolipoprotein L1 (APOL1)). The correlations matrices abovementioned were not performed for 7 proteins since they were measured with 1 peptide (apolipoprotein A-II (APOA2), monocyte differentiation antigen (CD14), C-reactive protein (CRP), enolase 1 (ENO1), fibrinogen beta chain (FGB), immunoglobulin heavy variable 3-23 (IGHV3-23), mannan-binding lectin serine protease 2 (MASP2)).

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Supplementary Table 1. Serum proteins measured

Technology	Protein names	Gene names	Uniprot accession number
PEA (immune response)	Neurabin-2	PPP1R9B	Q96SB3
PEA (immune response)	Beta-galactosidase	GLB1	P16278
PEA (immune response)	PC4 and SFRS1-interacting protein	PSIP1	O75475
PEA (immune response)	Zinc finger and BTB domain-containing protein 16	ZBTB16	Q05516
PEA (immune response)	Interleukin-1 receptor-associated kinase 4	IRAK4	Q9NWZ3
PEA (immune response)	Tryptase alpha/beta-1	TPSAB1	Q15661
PEA (immune response)	Hematopoietic lineage cell-specific protein	HCLS1	P14317
PEA (immune response)	Contactin-associated protein-like 2	CNTNAP2	Q9UHC6
PEA (immune response)	C-type lectin domain family 4 member G	CLEC4G	Q6UXB4
PEA (immune response)	Interferon regulatory factor 9	IRF9	Q00978
PEA (immune response)	Tumor necrosis factor receptor superfamily member EDAR	EDAR	Q9UNE0
PEA (immune response)	Interleukin-6	IL6	P05231
PEA (immune response)	Diacylglycerol kinase zeta	DGKZ	Q13574
PEA (immune response)	C-type lectin domain family 4 member C	CLEC4C	Q8WTT0
PEA (immune response)	Interleukin-1 receptor-associated kinase 1	IRAK1	P51617
PEA (immune response)	C-type lectin domain family 4 member A	CLEC4A	Q9UMR7
PEA (immune response)	Peroxiredoxin-1	PRDX1	Q06830
PEA (immune response)	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	P30048
PEA (immune response)	Fibroblast growth factor 2	FGF2	P09038
PEA (immune response)	Peroxiredoxin-5, mitochondrial	PRDX5	P30044
PEA (immune response)	Inactive dipeptidyl peptidase 10	DPP10	Q8N608
PEA (immune response)	Tripartite motif-containing protein 5	TRIM5	Q9C035
PEA (immune response)	Dynactin subunit 1	DCTN1	Q14203
PEA (immune response)	Integrin alpha-6	ITGA6	P23229
PEA (immune response)	Corneodesmosin	CDSN	Q15517
PEA (immune response)	Polypeptide N-acetylgalactosaminyltransferase 3	GALNT3	Q14435
PEA (immune response)	FXYD domain-containing ion transport regulator 5	FXYD5	Q96DB9
PEA (immune response)	TNF receptor-associated factor 2	TRAF2	Q12933
PEA (immune response)	E3 ubiquitin-protein ligase TRIM21	TRIM21	P19474
PEA (immune response)	Leukocyte immunoglobulin-like receptor subfamily B member 4	LILRB4	Q8NHJ6
PEA (immune response)	Neurotrophin-4	NTF4	P34130
PEA (immune response)	Keratin, type I cytoskeletal 19	KRT19	P08727
PEA (immune response)	Integral membrane protein 2A	ITM2A	O43736
PEA (immune response)	Histamine N-methyltransferase	HNMT	P50135
PEA (immune response)	Eotaxin	CCL11	P51671
PEA (immune response)	Allergin-1	MILR1	Q7Z6M3
PEA (immune response)	Egl nine homolog 1	EGLN1	Q9GZT9
PEA (immune response)	Nuclear factor of activated T-cells, cytoplasmic 3	NFATC3	Q12968
PEA (immune response)	Lymphocyte antigen 75	LY75	O60449
PEA (immune response)	Eukaryotic translation initiation factor 5A-1	EIF5A	P63241
PEA (immune response)	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	Q04637
PEA (immune response)	T-cell-specific surface glycoprotein CD28	CD28	P10747
PEA (immune response)	Parathyroid hormone/parathyroid hormone-related peptide receptor	PTH1R	Q03431
PEA (immune response)	Baculoviral IAP repeat-containing protein 2	BIRC2	Q13490
PEA (immune response)	11-beta-hydroxysteroid dehydrogenase 1	HSD11B1	P28845
PEA (immune response)	Merlin	NF2	P35240

PEA (immune response)	Plexin-A4	PLXNA4	Q9HCM2
PEA (immune response)	SH2B adapter protein 3	SH2B3	Q9UQQ2
PEA (immune response)	Fc receptor-like protein 3	FCRL3	Q96P31
PEA (immune response)	Cytoskeleton-associated protein 4	CKAP4	Q07065
PEA (immune response)	Transcription factor Jun	JUN	P05412
PEA (immune response)	Protein HEXIM1	HEXIM1	O94992
PEA (immune response)	C-type lectin domain family 4 member D	CLEC4D	Q8WXI8
PEA (immune response)	Protein kinase C theta type	PRKCQ	Q04759
PEA (immune response)	Methylated-DNA--protein-cysteine methyltransferase	MGMT	P16455
PEA (immune response)	Triggering receptor expressed on myeloid cells 1	TREM1	Q9NP99
PEA (immune response)	Coxsackievirus and adenovirus receptor	CXADR	P78310
PEA (immune response)	Interleukin-10	IL10	P22301
PEA (immune response)	SRSF protein kinase 2	SRPK2	P78362
PEA (immune response)	Natural killer cells antigen CD94	KLRD1	Q13241
PEA (immune response)	Transcription regulator protein BACH1	BACH1	O14867
PEA (immune response)	Phosphoinositide 3-kinase adapter protein 1	PIK3AP1	Q6ZUJ8
PEA (immune response)	Protein sprouty homolog 2	SPRY2	O43597
PEA (immune response)	Stanniocalcin-1	STC1	P52823
PEA (immune response)	Aryl hydrocarbon receptor nuclear translocator	ARNT	P27540
PEA (immune response)	Protein FAM3B	FAM3B	P58499
PEA (immune response)	SH2 domain-containing protein 1A	SH2D1A	O60880
PEA (immune response)	Islet cell autoantigen 1	ICA1	Q05084
PEA (immune response)	DNA fragmentation factor subunit alpha	DFFA	O00273
PEA (immune response)	Discoidin, CUB and LCCL domain-containing protein 2	DCBLD2	Q96PD2
PEA (immune response)	Fc receptor-like protein 6	FCRL6	Q6DN72
PEA (immune response)	Natural cytotoxicity triggering receptor 1	NCR1	O76036
PEA (immune response)	Stromal cell-derived factor 1	CXCL12	P48061
PEA (immune response)	Amphiregulin	AREG	P15514
PEA (immune response)	Interferon lambda receptor 1	IFNLR1	Q8IU57
PEA (immune response)	Dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide	DAPP1	Q9UN19
PEA (immune response)	Protein-arginine deiminase type-2	PADI2	Q9Y2J8
PEA (immune response)	Signaling threshold-regulating transmembrane adapter 1	SIT1	Q9Y3P8
PEA (immune response)	Mannan-binding lectin serine protease 1	MASP1	P48740
PEA (immune response)	Lysosome-associated membrane glycoprotein 3	LAMP3	Q9UQV4
PEA (immune response)	C-type lectin domain family 7 member A	CLEC7A	Q9BXN2
PEA (immune response)	C-type lectin domain family 6 member A	CLEC6A	Q6EIG7
PEA (immune response)	Antiviral innate immune response receptor RIG-I	RIGI	O95786
PEA (immune response)	Interleukin-12 receptor subunit beta-1	IL12RB1	P42701
PEA (immune response)	TRAF family member-associated NF-kappa-B activator	TANK	Q92844
PEA (immune response)	Integrin alpha-11	ITGA11	Q9UKX5
PEA (immune response)	Importin subunit alpha-5	KPNA1	P52294
PEA (immune response)	Lymphocyte activation gene 3 protein	LAG3	P18627
PEA (immune response)	Interleukin-5	IL5	P05113
PEA (immune response)	CD83 antigen	CD83	Q01151
PEA (immune response)	Integrin beta-6	ITGB6	P18564
PEA (immune response)	Butyrophilin subfamily 3 member A2	BTN3A2	P78410
PEA (cytokines)	C-C motif chemokine 8	CCL8	P80075
PEA (cytokines)	Interleukin-33	IL33	O95760
PEA (cytokines)	Stromal cell-derived factor 1	CXCL12	P48061
PEA (cytokines)	Oxidized low-density lipoprotein receptor 1	OLR1	P78380

PEA (cytokines)	Interleukin-2	IL2	P60568
PEA (cytokines)	C-X-C motif chemokine 9	CXCL9	Q07325
PEA (cytokines)	Protransforming growth factor alpha	TGFA	P01135
PEA (cytokines)	Interleukin-1 beta	IL1B	P01584
PEA (cytokines)	Interleukin-6	IL6	P05231
PEA (cytokines)	Interleukin-4	IL4	P05112
PEA (cytokines)	Tumor necrosis factor ligand superfamily member 12	TNFSF12	O43508
PEA (cytokines)	Thymic stromal lymphopoietin	TSLP	Q969D9
PEA (cytokines)	Eotaxin	CCL11	P51671
PEA (cytokines)	Hepatocyte growth factor	HGF	P14210
PEA (cytokines)	Fms-related tyrosine kinase 3 ligand	FLT3LG	P49771
PEA (cytokines)	Interleukin-17F	IL17F	Q96PD4
PEA (cytokines)	Interleukin-7	IL7	P13232
PEA (cytokines)	Interleukin-13	IL13	P35225
PEA (cytokines)	Interleukin-18	IL18	Q14116
PEA (cytokines)	C-C motif chemokine 13	CCL13	Q99616
PEA (cytokines)	Tumor necrosis factor ligand superfamily member 10	TNFSF10	P50591
PEA (cytokines)	C-X-C motif chemokine 10	CXCL10	P02778
PEA (cytokines)	Interferon gamma	IFNG	P01579
PEA (cytokines)	Interleukin-10	IL10	P22301
PEA (cytokines)	C-C motif chemokine 19	CCL19	Q99731
PEA (cytokines)	Tumor necrosis factor	TNF	P01375
PEA (cytokines)	Interleukin-15	IL15	P40933
PEA (cytokines)	C-C motif chemokine 3	CCL3	P10147
PEA (cytokines)	Interleukin-8	CXCL8	P10145
PEA (cytokines)	Macrophage metalloelastase	MMP12	P39900
PEA (cytokines)	Granulocyte-macrophage colony-stimulating factor	CSF2	P04141
PEA (cytokines)	Granulocyte colony-stimulating factor	CSF3	P09919
PEA (cytokines)	Vascular endothelial growth factor A	VEGFA	P15692
PEA (cytokines)	Interleukin-17C	IL17C	Q9P0M4
PEA (cytokines)	Pro-epidermal growth factor	EGF	P01133
PEA (cytokines)	C-C motif chemokine 2	CCL2	P13500
PEA (cytokines)	Interleukin-17A	IL17A	Q16552
PEA (cytokines)	Oncostatin-M	OSM	P13725
PEA (cytokines)	Macrophage colony-stimulating factor 1	CSF1	P09603
PEA (cytokines)	C-C motif chemokine 4	CCL4	P13236
PEA (cytokines)	C-X-C motif chemokine 11	CXCL11	O14625
PEA (cytokines)	Lymphotoxin-alpha	LTA	P01374
PEA (cytokines)	C-C motif chemokine 7	CCL7	P80098
PEA (cytokines)	Interstitial collagenase	MMP1	P03956
PEA (cytokines)	Interleukin-27	IL27	Q8NEV9_Q14213
SRM	Thrombospondin-1	THBS1	P07996
SRM	Fibronectin	FN1	P02751
SRM	Fibrinogen beta chain	FGB	P02675
SRM	Monocyte differentiation antigen CD14	CD14	P08571
SRM	Neutrophil defensin 1	DEFA1	P59665
SRM	Apolipoprotein B-100	APOB	P04114
SRM	Apolipoprotein A-IV	APOA4	P06727
SRM	C-reactive protein	CRP	P02741
SRM	Haptoglobin	HP	P00738

SRM	Alpha-1-acid glycoprotein 1	ORM1	P02763
SRM	Protein AMBP	AMBP	P02760
SRM	Serum amyloid A-1 protein	SAA1	P0DJI8
SRM	Beta-Ala-His dipeptidase	CNDP1	Q96KN2
SRM	Leucine-rich alpha-2-glycoprotein	LRG1	P02750
SRM	Kallistatin	SERPINA4	P29622
SRM	Alpha-2-HS-glycoprotein	AHSG	P02765
SRM	Immunoglobulin kappa variable 4-1	IGKV4-1	P06312
SRM	Immunoglobulin lambda constant 6	IGLC6	P0CF74
SRM	Sex hormone-binding globulin	SHBG	P04278
SRM	Immunoglobulin J chain	JCHAIN	P01591
SRM	Inter-alpha-trypsin inhibitor heavy chain H3	ITIH3	Q06033
SRM	Apolipoprotein A-I	APOA1	P02647
SRM	Complement component C9	C9	P02748
SRM	Complement C5	C5	P01031
SRM	Alpha-1-antichymotrypsin	SERPINA3	P01011
SRM	Mannose-binding protein C	MBL2	P11226
SRM	Complement component C7	C7	P10643
SRM	Complement C3	C3	P01024
SRM	Apolipoprotein A-II	APOA2	P02652
SRM	Apolipoprotein C-II	APOC2	P02655
SRM	Apolipoprotein C-III	APOC3	P02656
SRM	Apolipoprotein C-IV	APOC4	P55056
SRM	Apolipoprotein L1	APOL1	O14791
SRM	Attractin	ATRN	O75882
SRM	Beta-2-glycoprotein 1	APOH	P02749
SRM	C4b-binding protein beta chain	C4BPB	P20851
SRM	Carboxypeptidase N subunit 2	CPN2	P22792
SRM	Ceruloplasmin	CP	P00450
SRM	Clusterin	CLU	P10909
SRM	Coagulation factor IX	F9	P00740
SRM	Coagulation factor X	F10	P00742
SRM	Complement C2	C2	P06681
SRM	Complement C4-B	C4B	P0C0L5
SRM	Complement component C6	C6	P13671
SRM	Complement component C8 alpha chain	C8A	P07357
SRM	Complement component C8 beta chain	C8B	P07358
SRM	Complement component C8 gamma chain	C8G	P07360
SRM	Complement factor B	CFB	P00751
SRM	Complement factor H	CFH	P08603
SRM	Complement factor H-related protein 2	CFHR2	P36980
SRM	Complement factor I	CFI	P05156
SRM	Ficolin-3	FCN3	O75636
SRM	Gelsolin	GSN	P06396
SRM	Haptoglobin-related protein	HPR	P00739
SRM	Heparin cofactor 2	SERPIND1	P05546
SRM	Histidine-rich glycoprotein	HRG	P04196
SRM	Immunoglobulin heavy constant alpha 1	IGHA1	P01876
SRM	Immunoglobulin heavy variable 3-23	IGHV3-23	P01764
SRM	Insulin-like growth factor-binding protein complex acid labile subunit	IGFALS	P35858

SRM	Inter-alpha-trypsin inhibitor heavy chain H1	ITIH1	P19827
SRM	Inter-alpha-trypsin inhibitor heavy chain H2	ITIH2	P19823
SRM	L-selectin	SELL	P14151
SRM	Lumican	LUM	P51884
SRM	Mannan-binding lectin serine protease 2	MASP2	O00187
SRM	Pigment epithelium-derived factor	SERPINF1	P36955
SRM	Plasma protease C1 inhibitor	SERPING1	P05155
SRM	Plasminogen	PLG	P00747
SRM	Pregnancy zone protein	PZP	P20742
SRM	Serotransferrin	TF	P02787
SRM	Serum amyloid A-4 protein	SAA4	P35542
SRM	Serum amyloid P-component	APCS	P02743
SRM	Tetranectin	CLEC3B	P05452
SRM	Thyroxine-binding globulin	SERPINA7	P05543
SRM	Vitronectin	VTN	P04004
Turbidimetric immunoassay	C-reactive protein	CRP	P02741

Supplementary Table 2. SRM method

Protein Description	Gene name	Protein Accession	Peptide	Modified Sequence Monoisotopic Masses	Precursor	Precursor m/z	Precursor Charge	Collision Energy	Product m/z	Fragment Ion	Product Charge	Predicted Retention Time	Average Measured Retention Time	CV in CD patients in endoscopic remission (%)	CV in CD patients with active endoscopic disease (%)
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR	808.9106++	808.91061	2	28.9	913.52139	y8	1	64.06	75.87	6.136390941	7.950956795
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR	808.9106++	808.91061	2	28.9	785.462812	y7	1	64.06	75.87		
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR	808.9106++	808.91061	2	28.9	629.372935	y5	1	64.06	75.87		
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR[+10.008269]	813.9147++ (heavy)	813.914744	2	28.9	923.529659	y8	1	64.06	75.87		
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR[+10.008269]	813.9147++ (heavy)	813.914744	2	28.9	795.471081	y7	1	64.06	75.87		
Thrombospondin-1	THBS1	P07996	GGVNDNFQGVLQNVR	GGVNDNFQGVLQNVR[+10.008269]	813.9147++ (heavy)	813.914744	2	28.9	639.381204	y5	1	64.06	75.87		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR	697.8694++	697.869359	2	24.8	1148.594615	y10	1	89.28	101.01		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR	697.8694++	697.869359	2	24.8	1001.526201	y9	1	89.28	101.01		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR	697.8694++	697.869359	2	24.8	247.144104	b2	1	89.28	101.01		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR[+10.008269]	702.8735++ (heavy)	702.873494	2	24.8	1158.602884	y10	1	89.28	101.01		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR[+10.008269]	702.8735++ (heavy)	702.873494	2	24.8	1011.53447	y9	1	89.28	101.01		
Thrombospondin-1	THBS1	P07996	FVFGTTPEDILR	FVFGTTPEDILR[+10.008269]	702.8735++ (heavy)	702.873494	2	24.8	247.144104	b2	1	89.28	101.01		
Fibronectin	FN1	P02751	VDVIPVNLPGEHGQR	VDVIPVNLPGEHGQR	543.9618+++	543.961761	3	18.3	1007.501717	y9	1	55.07	68.72	3.945807838	4.045471592
Fibronectin	FN1	P02751	VDVIPVNLPGEHGQR	VDVIPVNLPGEHGQR	543.9618+++	543.961761	3	18.3	780.374726	y7	1	55.07	68.72		
Fibronectin	FN1	P02751	VDVIPVNLPGEHGQR	VDVIPVNLPGEHGQR	543.9618+++	543.961761	3	18.3	314.171047	b3	1	55.07	68.72		
Fibronectin	FN1	P02751	VDVIPVNLPGEHGQR	VDVIPVNLPGEHGQR[+10.008269]	547.2979+++ (heavy)	547.29785	3	18.3	1017.509986	y9	1	55.07	68.72		
Fibronectin	FN1	P02751	VDVIPVNLPGEHGQR	VDVIPVNLPGEHGQR[+10.008269]	547.2979+++ (heavy)	547.29785	3	18.3	790.382995	y7	1	55.07	68.72		
Fibronectin	FN1	P02751	VDVIPVNLPGEHGQR	VDVIPVNLPGEHGQR[+10.008269]	547.2979+++ (heavy)	547.29785	3	18.3	314.171047	b3	1	55.07	68.72		
Fibronectin	FN1	P02751	STTPDITGYR	STTPDITGYR	555.7749++	555.774927	2	19.5	821.415194	y7	1	28.45	36.16		
Fibronectin	FN1	P02751	STTPDITGYR	STTPDITGYR	555.7749++	555.774927	2	19.5	609.335487	y5	1	28.45	36.16		
Fibronectin	FN1	P02751	STTPDITGYR	STTPDITGYR	555.7749++	555.774927	2	19.5	496.251423	y4	1	28.45	36.16		
Fibronectin	FN1	P02751	STTPDITGYR	STTPDITGYR[+10.008269]	560.7791++ (heavy)	560.779062	2	19.5	831.423463	y7	1	28.45	36.16		
Fibronectin	FN1	P02751	STTPDITGYR	STTPDITGYR[+10.008269]	560.7791++ (heavy)	560.779062	2	19.5	619.343756	y5	1	28.45	36.16		
Fibronectin	FN1	P02751	STTPDITGYR	STTPDITGYR[+10.008269]	560.7791++ (heavy)	560.779062	2	19.5	506.259692	y4	1	28.45	36.16		
Fibronectin	FN1	P02751	SYTITGLQPGTDYK	SYTITGLQPGTDYK	772.3856++	772.38557	2	27.5	1079.536765	y10	1	58.74	62.03		
Fibronectin	FN1	P02751	SYTITGLQPGTDYK	SYTITGLQPGTDYK	772.3856++	772.38557	2	27.5	680.324982	y6	1	58.74	62.03		
Fibronectin	FN1	P02751	SYTITGLQPGTDYK	SYTITGLQPGTDYK	772.3856++	772.38557	2	27.5	352.150312	b3	1	58.74	62.03		
Fibronectin	FN1	P02751	SYTITGLQPGTDYK	SYTITGLQPGTDYK[+8.014199]	776.3927++ (heavy)	776.39267	2	27.5	1087.550964	y10	1	58.74	62.03		
Fibronectin	FN1	P02751	SYTITGLQPGTDYK	SYTITGLQPGTDYK[+8.014199]	776.3927++ (heavy)	776.39267	2	27.5	688.339181	y6	1	58.74	62.03		
Fibronectin	FN1	P02751	SYTITGLQPGTDYK	SYTITGLQPGTDYK[+8.014199]	776.3927++ (heavy)	776.39267	2	27.5	352.150312	b3	1	58.74	62.03		
Fibronectin	FN1	P02751	IYLYTLNDNAR	IYLYTLNDNAR	678.3513++	678.351334	2	24	966.463935	y8	1	65.25	67.51		
Fibronectin	FN1	P02751	IYLYTLNDNAR	IYLYTLNDNAR	678.3513++	678.351334	2	24	803.400606	y7	1	65.25	67.51		
Fibronectin	FN1	P02751	IYLYTLNDNAR	IYLYTLNDNAR	678.3513++	678.351334	2	24	277.154669	b2	1	65.25	67.51		
Fibronectin	FN1	P02751	IYLYTLNDNAR	IYLYTLNDNAR[+10.008269]	683.3555++ (heavy)	683.355468	2	24	976.472204	y8	1	65.25	67.51		
Fibronectin	FN1	P02751	IYLYTLNDNAR	IYLYTLNDNAR[+10.008269]	683.3555++ (heavy)	683.355468	2	24	813.408875	y7	1	65.25	67.51		
Fibronectin	FN1	P02751	IYLYTLNDNAR	IYLYTLNDNAR[+10.008269]	683.3555++ (heavy)	683.355468	2	24	277.154669	b2	1	65.25	67.51		
Fibrinogen beta chain	FGB	P02675	QGFGNVATNTDGK	QGFGNVATNTDGK	654.8126++	654.812573	2	23.2	706.336609	y7	1	22.34	26.55	13.92908907	4.453303756
Fibrinogen beta chain	FGB	P02675	QGFGNVATNTDGK	QGFGNVATNTDGK	654.8126++	654.812573	2	23.2	635.299495	y6	1	22.34	26.55		
Fibrinogen beta chain	FGB	P02675	QGFGNVATNTDGK	QGFGNVATNTDGK	654.8126++	654.812573	2	23.2	204.134267	y2	1	22.34	26.55		
Fibrinogen beta chain	FGB	P02675	QGFGNVATNTDGK	QGFGNVATNTDGK[+8.014199]	658.8197++ (heavy)	658.819672	2	23.2	714.350808	y7	1	22.34	26.55		
Fibrinogen beta chain	FGB	P02675	QGFGNVATNTDGK	QGFGNVATNTDGK[+8.014199]	658.8197++ (heavy)	658.819672	2	23.2	643.313694	y6	1	22.34	26.55		
Fibrinogen beta chain	FGB	P02675	QGFGNVATNTDGK	QGFGNVATNTDGK[+8.014199]	658.8197++ (heavy)	658.819672	2	23.2	212.148466	y2	1	22.34	26.55		
Monocyte differentiation a	CD14	P08571	ELTLEDLK	ELTLEDLK	480.7660++	480.76604	2	16.7	617.350468	y5	1	52.41	63.52	6.606018179	5.050704034

Monocyte differentiation a	CD14	P08571	ELTLEDLK	ELTLEDLK	480.7660++	480.76604	2	16.7	504.266404	y4	1	52.41	63.52		
Monocyte differentiation a	CD14	P08571	ELTLEDLK	ELTLEDLK	480.7660++	480.76604	2	16.7	260.196868	y2	1	52.41	63.52		
Monocyte differentiation a	CD14	P08571	ELTLEDLK	ELTLEDLK[+8.014199]	484.7731++ (heavy)	484.773139	2	16.7	625.364667	y5	1	52.41	63.52		
Monocyte differentiation a	CD14	P08571	ELTLEDLK	ELTLEDLK[+8.014199]	484.7731++ (heavy)	484.773139	2	16.7	512.280603	y4	1	52.41	63.52		
Monocyte differentiation a	CD14	P08571	ELTLEDLK	ELTLEDLK[+8.014199]	484.7731++ (heavy)	484.773139	2	16.7	268.211067	y2	1	52.41	63.52		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER	493.7580++	493.758026	2	17.2	873.424713	y8	1	22.31	28.98	2.397340344	4.566906069
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER	493.7580++	493.758026	2	17.2	776.371949	y7	1	22.31	28.98		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER	493.7580++	493.758026	2	17.2	705.334835	y6	1	22.31	28.98		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER	493.7580++	493.758026	2	17.2	432.220122	y4	1	22.31	28.98		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER[+10.008269]	498.7622++ (heavy)	498.762161	2	17.2	883.432982	y8	1	22.31	28.98		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER[+10.008269]	498.7622++ (heavy)	498.762161	2	17.2	786.380218	y7	1	22.31	28.98		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER[+10.008269]	498.7622++ (heavy)	498.762161	2	17.2	715.343104	y6	1	22.31	28.98		
Neutrophil defensin 1	DEFA1	P59665	IPACIAGER	IPAC[+57.021464]IAGER[+10.008269]	498.7622++ (heavy)	498.762161	2	17.2	442.228391	y4	1	22.31	28.98		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR	559.2584++	559.25839	2	19.6	796.377034	y6	1	29.57	29.27		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR	559.2584++	559.25839	2	19.6	636.346386	y5	1	29.57	29.27		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR	559.2584++	559.25839	2	19.6	523.262322	y4	1	29.57	29.27		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR[+10.008269]	564.2625++ (heavy)	564.262525	2	19.6	806.385303	y6	1	29.57	29.27		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR[+10.008269]	564.2625++ (heavy)	564.262525	2	19.6	646.354655	y5	1	29.57	29.27		
Neutrophil defensin 1	DEFA1	P59665	YGTCIYQGR	YGTC[+57.021464]IYQGR[+10.008269]	564.2625++ (heavy)	564.262525	2	19.6	533.270591	y4	1	29.57	29.27		
Apolipoprotein B-100	APOB	P04114	TGISPLALIK	TGISPLALIK	506.8237++	506.823692	2	17.7	741.486902	y7	1	70.59	88.97	3.87903914	4.254471702
Apolipoprotein B-100	APOB	P04114	TGISPLALIK	TGISPLALIK	506.8237++	506.823692	2	17.7	654.454873	y6	1	70.59	88.97		
Apolipoprotein B-100	APOB	P04114	TGISPLALIK	TGISPLALIK	506.8237++	506.823692	2	17.7	159.076418	b2	1	70.59	88.97		
Apolipoprotein B-100	APOB	P04114	TGISPLALIK	TGISPLALIK[+8.014199]	510.8308++ (heavy)	510.830792	2	17.7	749.501101	y7	1	70.59	88.97		
Apolipoprotein B-100	APOB	P04114	TGISPLALIK	TGISPLALIK[+8.014199]	510.8308++ (heavy)	510.830792	2	17.7	662.469072	y6	1	70.59	88.97		
Apolipoprotein B-100	APOB	P04114	TGISPLALIK	TGISPLALIK[+8.014199]	510.8308++ (heavy)	510.830792	2	17.7	159.076418	b2	1	70.59	88.97		
Apolipoprotein B-100	APOB	P04114	SVSLPSLDPASAK	SVSLPSLDPASAK	636.3457++	636.345717	2	22.5	885.467623	y9	1	50.51	66.68		
Apolipoprotein B-100	APOB	P04114	SVSLPSLDPASAK	SVSLPSLDPASAK	636.3457++	636.345717	2	22.5	473.271824	y5	1	50.51	66.68		
Apolipoprotein B-100	APOB	P04114	SVSLPSLDPASAK	SVSLPSLDPASAK	636.3457++	636.345717	2	22.5	274.139747	b3	1	50.51	66.68		
Apolipoprotein B-100	APOB	P04114	SVSLPSLDPASAK	SVSLPSLDPASAK[+8.014199]	640.3528++ (heavy)	640.352816	2	22.5	893.481822	y9	1	50.51	66.68		
Apolipoprotein B-100	APOB	P04114	SVSLPSLDPASAK	SVSLPSLDPASAK[+8.014199]	640.3528++ (heavy)	640.352816	2	22.5	481.286023	y5	1	50.51	66.68		
Apolipoprotein B-100	APOB	P04114	SVSLPSLDPASAK	SVSLPSLDPASAK[+8.014199]	640.3528++ (heavy)	640.352816	2	22.5	274.139747	b3	1	50.51	66.68		
Apolipoprotein B-100	APOB	P04114	TEVIPPLIENR	TEVIPPLIENR	640.8641++	640.864077	2	22.6	951.562192	y8	1	63.05	73.16		
Apolipoprotein B-100	APOB	P04114	TEVIPPLIENR	TEVIPPLIENR	640.8641++	640.864077	2	22.6	838.478128	y7	1	63.05	73.16		
Apolipoprotein B-100	APOB	P04114	TEVIPPLIENR	TEVIPPLIENR	640.8641++	640.864077	2	22.6	330.165962	b3	1	63.05	73.16		
Apolipoprotein B-100	APOB	P04114	TEVIPPLIENR	TEVIPPLIENR[+10.008269]	645.8682++ (heavy)	645.868211	2	22.6	961.570461	y8	1	63.05	73.16		
Apolipoprotein B-100	APOB	P04114	TEVIPPLIENR	TEVIPPLIENR[+10.008269]	645.8682++ (heavy)	645.868211	2	22.6	848.486397	y7	1	63.05	73.16		
Apolipoprotein B-100	APOB	P04114	TEVIPPLIENR	TEVIPPLIENR[+10.008269]	645.8682++ (heavy)	645.868211	2	22.6	330.165962	b3	1	63.05	73.16		
Apolipoprotein A-IV	APOA4	P06727	LGEVNTYAGDLQK	LGEVNTYAGDLQK	704.3594++	704.359356	2	25	1009.4949	y9	1	52.52	48.54	6.584459013	2.912761261
Apolipoprotein A-IV	APOA4	P06727	LGEVNTYAGDLQK	LGEVNTYAGDLQK	704.3594++	704.359356	2	25	631.340966	y6	1	52.52	48.54		
Apolipoprotein A-IV	APOA4	P06727	LGEVNTYAGDLQK	LGEVNTYAGDLQK	704.3594++	704.359356	2	25	300.155397	b3	1	52.52	48.54		
Apolipoprotein A-IV	APOA4	P06727	LGEVNTYAGDLQK	LGEVNTYAGDLQK[+8.014199]	708.3665++ (heavy)	708.366455	2	25	1017.509099	y9	1	52.52	48.54		
Apolipoprotein A-IV	APOA4	P06727	LGEVNTYAGDLQK	LGEVNTYAGDLQK[+8.014199]	708.3665++ (heavy)	708.366455	2	25	639.355165	y6	1	52.52	48.54		
Apolipoprotein A-IV	APOA4	P06727	LGEVNTYAGDLQK	LGEVNTYAGDLQK[+8.014199]	708.3665++ (heavy)	708.366455	2	25	300.155397	b3	1	52.52	48.54		
Apolipoprotein A-IV	APOA4	P06727	LVPFATELHER	LVPFATELHER	437.9067+++	437.906705	3	14.4	855.431906	y7	1	64.72	60.42		
Apolipoprotein A-IV	APOA4	P06727	LVPFATELHER	LVPFATELHER	437.9067+++	437.906705	3	14.4	784.394792	y6	1	64.72	60.42		
Apolipoprotein A-IV	APOA4	P06727	LVPFATELHER	LVPFATELHER	437.9067+++	437.906705	3	14.4	441.220457	y3	1	64.72	60.42		
Apolipoprotein A-IV	APOA4	P06727	LVPFATELHER	LVPFATELHER[+10.008269]	441.2428+++ (heavy)	441.242794	3	14.4	865.440175	y7	1	64.72	60.42		
Apolipoprotein A-IV	APOA4	P06727	LVPFATELHER	LVPFATELHER[+10.008269]	441.2428+++ (heavy)	441.242794	3	14.4	794.403061	y6	1	64.72	60.42		

Apolipoprotein A-IV	APOA4	P06727	LVPFATELHER	LVPFATELHER[+10.008269]	441.2428+++ (heavy)	441.242794	3	14.4	451.228726	y3	1	64.72	60.42		
Apolipoprotein A-IV	APOA4	P06727	LTPYADEFK	LTPYADEFK	542.2715++	542.271489	2	19	869.40396	y7	1	53.59	49.99		
Apolipoprotein A-IV	APOA4	P06727	LTPYADEFK	LTPYADEFK	542.2715++	542.271489	2	19	772.351196	y6	1	53.59	49.99		
Apolipoprotein A-IV	APOA4	P06727	LTPYADEFK	LTPYADEFK	542.2715++	542.271489	2	19	609.287868	y5	1	53.59	49.99		
Apolipoprotein A-IV	APOA4	P06727	LTPYADEFK	LTPYADEFK[+8.014199]	546.2786++ (heavy)	546.278589	2	19	877.418159	y7	1	53.59	49.99		
Apolipoprotein A-IV	APOA4	P06727	LTPYADEFK	LTPYADEFK[+8.014199]	546.2786++ (heavy)	546.278589	2	19	780.365395	y6	1	53.59	49.99		
Apolipoprotein A-IV	APOA4	P06727	LTPYADEFK	LTPYADEFK[+8.014199]	546.2786++ (heavy)	546.278589	2	19	617.302067	y5	1	53.59	49.99		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK	564.7746++	564.774593	2	19.8	696.392667	y6	1	35.55	35.52	14.74717527	2.280569802
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK	564.7746++	564.774593	2	19.8	609.360639	y5	1	35.55	35.52		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK	564.7746++	564.774593	2	19.8	446.29731	y4	1	35.55	35.52		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK	564.7746++	564.774593	2	19.8	347.228896	y3	1	35.55	35.52		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK[+8.014199]	568.7817++ (heavy)	568.781693	2	19.8	704.406866	y6	1	35.55	35.52		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK[+8.014199]	568.7817++ (heavy)	568.781693	2	19.8	617.374838	y5	1	35.55	35.52		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK[+8.014199]	568.7817++ (heavy)	568.781693	2	19.8	454.311509	y4	1	35.55	35.52		
C-reactive protein	CRP	P02741	ESDTSYVSLK	ESDTSYVSLK[+8.014199]	568.7817++ (heavy)	568.781693	2	19.8	355.243095	y3	1	35.55	35.52		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK	429.7502++	429.750193	2	14.8	730.434532	y6	1	31.64	32.39	5.449981732	3.868309559
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK	429.7502++	429.750193	2	14.8	617.350468	y5	1	31.64	32.39		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK	429.7502++	429.750193	2	14.8	518.282054	y4	1	31.64	32.39		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK	429.7502++	429.750193	2	14.8	389.239461	y3	1	31.64	32.39		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK[+8.014199]	433.7573++ (heavy)	433.757292	2	14.8	738.448731	y6	1	31.64	32.39		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK[+8.014199]	433.7573++ (heavy)	433.757292	2	14.8	625.364667	y5	1	31.64	32.39		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK[+8.014199]	433.7573++ (heavy)	433.757292	2	14.8	526.296253	y4	1	31.64	32.39		
Haptoglobin	HP	P00738	QLVEIEK	QLVEIEK[+8.014199]	433.7573++ (heavy)	433.757292	2	14.8	397.25366	y3	1	31.64	32.39		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR	490.7511++	490.751058	2	17.1	661.341635	y6	1	49.19	47.22		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR	490.7511++	490.751058	2	17.1	562.273221	y5	1	49.19	47.22		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR	490.7511++	490.751058	2	17.1	320.160482	b3	1	49.19	47.22		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR[+10.008269]	495.7552++ (heavy)	495.755193	2	17.1	671.349904	y6	1	49.19	47.22		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR[+10.008269]	495.7552++ (heavy)	495.755193	2	17.1	572.28149	y5	1	49.19	47.22		
Haptoglobin	HP	P00738	VGYVSGWGR	VGYVSGWGR[+10.008269]	495.7552++ (heavy)	495.755193	2	17.1	320.160482	b3	1	49.19	47.22		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK	602.3220++	602.322045	2	21.2	1003.520721	y8	1	55.16	60.96		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK	602.3220++	602.322045	2	21.2	803.404629	y6	1	55.16	60.96		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK	602.3220++	602.322045	2	21.2	675.346051	y5	1	55.16	60.96		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK[+8.014199]	606.3291++ (heavy)	606.329144	2	21.2	1011.53492	y8	1	55.16	60.96		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK[+8.014199]	606.3291++ (heavy)	606.329144	2	21.2	811.418828	y6	1	55.16	60.96		
Haptoglobin	HP	P00738	VTSIQDWVQK	VTSIQDWVQK[+8.014199]	606.3291++ (heavy)	606.329144	2	21.2	683.36025	y5	1	55.16	60.96		
Alpha-1-acid glycoprotein	ORM1	P02763	WFYIASAFR	WFYIASAFR	580.7980++	580.798009	2	20.4	827.441014	y7	1	93.38	103.84	16.28247242	14.12928991
Alpha-1-acid glycoprotein	ORM1	P02763	WFYIASAFR	WFYIASAFR	580.7980++	580.798009	2	20.4	664.377686	y6	1	93.38	103.84		
Alpha-1-acid glycoprotein	ORM1	P02763	WFYIASAFR	WFYIASAFR	580.7980++	580.798009	2	20.4	551.293622	y5	1	93.38	103.84		
Alpha-1-acid glycoprotein	ORM1	P02763	WFYIASAFR	WFYIASAFR[+10.008269]	585.8021++ (heavy)	585.802143	2	20.4	837.449283	y7	1	93.38	103.84		
Alpha-1-acid glycoprotein	ORM1	P02763	WFYIASAFR	WFYIASAFR[+10.008269]	585.8021++ (heavy)	585.802143	2	20.4	674.385955	y6	1	93.38	103.84		
Alpha-1-acid glycoprotein	ORM1	P02763	WFYIASAFR	WFYIASAFR[+10.008269]	585.8021++ (heavy)	585.802143	2	20.4	561.301891	y5	1	93.38	103.84		
Alpha-1-acid glycoprotein	ORM1	P02763	TEDTIFLR	TEDTIFLR	497.7638++	497.763831	2	17.4	764.430115	y6	1	60.76	55.57		
Alpha-1-acid glycoprotein	ORM1	P02763	TEDTIFLR	TEDTIFLR	497.7638++	497.763831	2	17.4	649.403172	y5	1	60.76	55.57		
Alpha-1-acid glycoprotein	ORM1	P02763	TEDTIFLR	TEDTIFLR	497.7638++	497.763831	2	17.4	435.27143	y3	1	60.76	55.57		
Alpha-1-acid glycoprotein	ORM1	P02763	TEDTIFLR	TEDTIFLR[+10.008269]	502.7680++ (heavy)	502.767966	2	17.4	774.438384	y6	1	60.76	55.57		
Alpha-1-acid glycoprotein	ORM1	P02763	TEDTIFLR	TEDTIFLR[+10.008269]	502.7680++ (heavy)	502.767966	2	17.4	659.411441	y5	1	60.76	55.57		
Alpha-1-acid glycoprotein	ORM1	P02763	TEDTIFLR	TEDTIFLR[+10.008269]	502.7680++ (heavy)	502.767966	2	17.4	445.279699	y3	1	60.76	55.57		
Alpha-1-acid glycoprotein	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR	871.9063++	871.906344	2	31.2	1186.556121	y9	1	125.52	110.2		

Alpha-1-acid glycoprotein	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR	871.9063++	871.906344	2	31.2	1039.487707	y8	1	125.52	110.2		
Alpha-1-acid glycoprotein	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR	871.9063++	871.906344	2	31.2	747.381785	y6	1	125.52	110.2		
Alpha-1-acid glycoprotein	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR[+10.008269]	876.9105++ (heavy)	876.910479	2	31.2	1196.56439	y9	1	125.52	110.2		
Alpha-1-acid glycoprotein	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR[+10.008269]	876.9105++ (heavy)	876.910479	2	31.2	1049.495976	y8	1	125.52	110.2		
Alpha-1-acid glycoprotein	ORM1	P02763	EQLGEFYEALDCLR	EQLGEFYEALDC[+57.021464]LR[+10.008269]	876.9105++ (heavy)	876.910479	2	31.2	757.390054	y6	1	125.52	110.2		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK	665.2850++	665.284999	2	23.5	1013.442196	y9	1	7.09	19.02	6.36075639	5.033447804
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK	665.2850++	665.284999	2	23.5	884.399603	y8	1	7.09	19.02		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK	665.2850++	665.284999	2	23.5	755.35701	y7	1	7.09	19.02		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK[+8.014199]	669.2921++ (heavy)	669.292099	2	23.5	1021.456395	y9	1	7.09	19.02		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK[+8.014199]	669.2921++ (heavy)	669.292099	2	23.5	892.413802	y8	1	7.09	19.02		
Protein AMBP	AMBP	P02760	GVCEETSGAYEK	GVC[+57.021464]EETSGAYEK[+8.014199]	669.2921++ (heavy)	669.292099	2	23.5	763.371209	y7	1	7.09	19.02		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR	511.2693++	511.269281	2	17.9	678.35695	y5	1	65.44	69.39		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR	511.2693++	511.269281	2	17.9	565.272886	y4	1	65.44	69.39		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR	511.2693++	511.269281	2	17.9	322.187366	y2	1	65.44	69.39		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR[+10.008269]	516.2734++ (heavy)	516.273415	2	17.9	688.365219	y5	1	65.44	69.39		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR[+10.008269]	516.2734++ (heavy)	516.273415	2	17.9	575.281155	y4	1	65.44	69.39		
Protein AMBP	AMBP	P02760	ETLLQDFR	ETLLQDFR[+10.008269]	516.2734++ (heavy)	516.273415	2	17.9	332.195635	y2	1	65.44	69.39		
Serum amyloid A-1 proteir	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR	775.8673++	775.867348	2	27.6	935.458121	y9	1	127.08	138.68	16.45024253	13.85218923
Serum amyloid A-1 proteir	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR	775.8673++	775.867348	2	27.6	636.31	y6	1	127.08	138.68		
Serum amyloid A-1 proteir	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR	775.8673++	775.867348	2	27.6	303.177529	y3	1	127.08	138.68		
Serum amyloid A-1 proteir	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR	775.8673++	775.867348	2	27.6	235.107718	b2	1	127.08	138.68		
Serum amyloid A-1 proteir	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR[+10.008269]	780.8715++ (heavy)	780.871482	2	27.6	945.46639	y9	1	127.08	138.68		
Serum amyloid A-1 proteir	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR[+10.008269]	780.8715++ (heavy)	780.871482	2	27.6	646.318269	y6	1	127.08	138.68		
Serum amyloid A-1 proteir	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR[+10.008269]	780.8715++ (heavy)	780.871482	2	27.6	313.185798	y3	1	127.08	138.68		
Serum amyloid A-1 proteir	SAA1	P0DJI8	SFFSFLGEAFDGAR	SFFSFLGEAFDGAR[+10.008269]	780.8715++ (heavy)	780.871482	2	27.6	235.107718	b2	1	127.08	138.68		
Serum amyloid A-1 proteir	SAA1	P0DJI8	FFGHGAEDSLADQAANEV	FFGHGAEDSLADQAANEWGR	726.6594+++	726.659358	3	24.8	803.379477	y7	1	87.59	78.73		
Serum amyloid A-1 proteir	SAA1	P0DJI8	FFGHGAEDSLADQAANEV	FFGHGAEDSLADQAANEWGR	726.6594+++	726.659358	3	24.8	732.342363	y6	1	87.59	78.73		
Serum amyloid A-1 proteir	SAA1	P0DJI8	FFGHGAEDSLADQAANEV	FFGHGAEDSLADQAANEWGR	726.6594+++	726.659358	3	24.8	661.305249	y5	1	87.59	78.73		
Serum amyloid A-1 proteir	SAA1	P0DJI8	FFGHGAEDSLADQAANEV	FFGHGAEDSLADQAANEWGR[+10.008269]	729.9954+++ (heavy)	729.995447	3	24.8	813.387746	y7	1	87.59	78.73		
Serum amyloid A-1 proteir	SAA1	P0DJI8	FFGHGAEDSLADQAANEV	FFGHGAEDSLADQAANEWGR[+10.008269]	729.9954+++ (heavy)	729.995447	3	24.8	742.350632	y6	1	87.59	78.73		
Serum amyloid A-1 proteir	SAA1	P0DJI8	FFGHGAEDSLADQAANEV	FFGHGAEDSLADQAANEWGR[+10.008269]	729.9954+++ (heavy)	729.995447	3	24.8	671.313518	y5	1	87.59	78.73		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK	620.3508++	620.350802	2	21.9	798.47198	y7	1	54.42	66.96	8.741228134	6.657717732
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK	620.3508++	620.350802	2	21.9	683.445037	y6	1	54.42	66.96		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK	620.3508++	620.350802	2	21.9	570.360973	y5	1	54.42	66.96		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK[+8.014199]	624.3579++ (heavy)	624.357902	2	21.9	806.486179	y7	1	54.42	66.96		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK[+8.014199]	624.3579++ (heavy)	624.357902	2	21.9	691.459236	y6	1	54.42	66.96		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	ALEQDLPVNIK	ALEQDLPVNIK[+8.014199]	624.3579++ (heavy)	624.357902	2	21.9	578.375172	y5	1	54.42	66.96		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR	420.2191+++	420.21906	3	13.8	596.267467	y4	1	55.58	64.25		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR	420.2191+++	420.21906	3	13.8	467.224873	y3	1	55.58	64.25		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR	420.2191+++	420.21906	3	13.8	338.18228	y2	1	55.58	64.25		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR	420.2191+++	420.21906	3	13.8	550.298373	b5	1	55.58	64.25		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR[+10.008269]	423.5551+++ (heavy)	423.555149	3	13.8	606.275736	y4	1	55.58	64.25		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR[+10.008269]	423.5551+++ (heavy)	423.555149	3	13.8	477.233142	y3	1	55.58	64.25		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR[+10.008269]	423.5551+++ (heavy)	423.555149	3	13.8	348.190549	y2	1	55.58	64.25		
Beta-Ala-His dipeptidase	CNDP1	Q96KN2	AIHLDLEEYR	AIHLDLEEYR[+10.008269]	423.5551+++ (heavy)	423.555149	3	13.8	550.298373	b5	1	55.58	64.25		
Leucine-rich alpha-2-glycc	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR	576.8096++	576.809636	2	20.3	774.410442	y7	1	37.43	37.51	4.807526885	5.603546401
Leucine-rich alpha-2-glycc	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR	576.8096++	576.809636	2	20.3	661.326378	y6	1	37.43	37.51		
Leucine-rich alpha-2-glycc	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR	576.8096++	576.809636	2	20.3	546.299435	y5	1	37.43	37.51		

Leucine-rich alpha-2-glycc	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR	576.8096++	576.809636	2	20.3	379.208829	b4	1	37.43	37.51		
Leucine-rich alpha-2-glycc	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR[+10.008269]	581.8138++ (heavy)	581.81377	2	20.3	784.418711	y7	1	37.43	37.51		
Leucine-rich alpha-2-glycc	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR[+10.008269]	581.8138++ (heavy)	581.81377	2	20.3	671.334647	y6	1	37.43	37.51		
Leucine-rich alpha-2-glycc	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR[+10.008269]	581.8138++ (heavy)	581.81377	2	20.3	556.307704	y5	1	37.43	37.51		
Leucine-rich alpha-2-glycc	LRG1	P02750	ALGHLDLSGNR	ALGHLDLSGNR[+10.008269]	581.8138++ (heavy)	581.81377	2	20.3	379.208829	b4	1	37.43	37.51		
Leucine-rich alpha-2-glycc	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR	590.3402++	590.340238	2	20.8	725.394064	y6	1	78.07	83.27		
Leucine-rich alpha-2-glycc	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR	590.3402++	590.340238	2	20.8	229.118283	b2	1	78.07	83.27		
Leucine-rich alpha-2-glycc	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR	590.3402++	590.340238	2	20.8	342.202347	b3	1	78.07	83.27		
Leucine-rich alpha-2-glycc	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR[+10.008269]	595.3444++ (heavy)	595.344372	2	20.8	735.402333	y6	1	78.07	83.27		
Leucine-rich alpha-2-glycc	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR[+10.008269]	595.3444++ (heavy)	595.344372	2	20.8	229.118283	b2	1	78.07	83.27		
Leucine-rich alpha-2-glycc	LRG1	P02750	DLLLPQPDLR	DLLLPQPDLR[+10.008269]	595.3444++ (heavy)	595.344372	2	20.8	342.202347	b3	1	78.07	83.27		
Leucine-rich alpha-2-glycc	LRG1	P02750	GQTLLAVAK	GQTLLAVAK	450.7793++	450.779285	2	15.6	715.471252	y7	1	35.33	40.23		
Leucine-rich alpha-2-glycc	LRG1	P02750	GQTLLAVAK	GQTLLAVAK	450.7793++	450.779285	2	15.6	501.339509	y5	1	35.33	40.23		
Leucine-rich alpha-2-glycc	LRG1	P02750	GQTLLAVAK	GQTLLAVAK	450.7793++	450.779285	2	15.6	388.255445	y4	1	35.33	40.23		
Leucine-rich alpha-2-glycc	LRG1	P02750	GQTLLAVAK	GQTLLAVAK[+8.014199]	454.7864++ (heavy)	454.786384	2	15.6	723.485451	y7	1	35.33	40.23		
Leucine-rich alpha-2-glycc	LRG1	P02750	GQTLLAVAK	GQTLLAVAK[+8.014199]	454.7864++ (heavy)	454.786384	2	15.6	509.353708	y5	1	35.33	40.23		
Leucine-rich alpha-2-glycc	LRG1	P02750	GQTLLAVAK	GQTLLAVAK[+8.014199]	454.7864++ (heavy)	454.786384	2	15.6	396.269644	y4	1	35.33	40.23		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR	596.8091++	596.809105	2	21	911.436992	y8	1	62.95	64.07	6.148287482	5.627790721
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR	596.8091++	596.809105	2	21	840.399878	y7	1	62.95	64.07		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR	596.8091++	596.809105	2	21	655.319837	y5	1	62.95	64.07		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR[+10.008269]	601.8132++ (heavy)	601.813239	2	21	921.445261	y8	1	62.95	64.07		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR[+10.008269]	601.8132++ (heavy)	601.813239	2	21	850.408147	y7	1	62.95	64.07		
Kallistatin	SERPINA4	P29622	IAPANADFAFR	IAPANADFAFR[+10.008269]	601.8132++ (heavy)	601.813239	2	21	665.328106	y5	1	62.95	64.07		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK	514.2766++	514.276575	2	18	914.461809	y8	1	80.56	97.55		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK	514.2766++	514.276575	2	18	710.371932	y6	1	80.56	97.55		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK	514.2766++	514.276575	2	18	381.213246	y3	1	80.56	97.55		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK[+8.014199]	518.2837++ (heavy)	518.283674	2	18	922.476008	y8	1	80.56	97.55		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK[+8.014199]	518.2837++ (heavy)	518.283674	2	18	718.386131	y6	1	80.56	97.55		
Kallistatin	SERPINA4	P29622	LGFTDLFSK	LGFTDLFSK[+8.014199]	518.2837++ (heavy)	518.283674	2	18	389.227445	y3	1	80.56	97.55		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK	495.7664++	495.766374	2	17.3	804.446159	y8	1	50.82	59.22		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK	495.7664++	495.766374	2	17.3	733.409046	y7	1	50.82	59.22		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK	495.7664++	495.766374	2	17.3	505.298038	y5	1	50.82	59.22		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK[+8.014199]	499.7735++ (heavy)	499.773474	2	17.3	812.460358	y8	1	50.82	59.22		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK[+8.014199]	499.7735++ (heavy)	499.773474	2	17.3	741.423245	y7	1	50.82	59.22		
Kallistatin	SERPINA4	P29622	WADLSGITK	WADLSGITK[+8.014199]	499.7735++ (heavy)	499.773474	2	17.3	513.312237	y5	1	50.82	59.22		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK	554.2594+++	554.259367	3	18.6	763.434866	y6	1	69.93	60.24	5.419811269	2.037866997
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK	554.2594+++	554.259367	3	18.6	648.407923	y5	1	69.93	60.24		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK	554.2594+++	554.259367	3	18.6	338.145895	b3	1	69.93	60.24		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK[+8.014199]	556.9308+++ (heavy)	556.930766	3	18.6	771.449065	y6	1	69.93	60.24		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK[+8.014199]	556.9308+++ (heavy)	556.930766	3	18.6	656.422122	y5	1	69.93	60.24		
Alpha-2-HS-glycoprotein	AHSG	P02765	EHAVEGDCDFQLLK	EHAVEGDC[+57.021464]DFQLLK[+8.014199]	556.9308+++ (heavy)	556.930766	3	18.6	338.145895	b3	1	69.93	60.24		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK	407.2289++	407.228896	2	14	666.382102	y6	1	35.99	40.12		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK	407.2289++	407.228896	2	14	480.28166	y4	1	35.99	40.12		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK	407.2289++	407.228896	2	14	235.107718	b2	1	35.99	40.12		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK[+8.014199]	411.2360++ (heavy)	411.235996	2	14	674.396301	y6	1	35.99	40.12		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK[+8.014199]	411.2360++ (heavy)	411.235996	2	14	488.295859	y4	1	35.99	40.12		
Alpha-2-HS-glycoprotein	AHSG	P02765	FSVVYAK	FSVVYAK[+8.014199]	411.2360++ (heavy)	411.235996	2	14	235.107718	b2	1	35.99	40.12		
Immunoglobulin kappa vai	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER	959.4829++	959.482947	2	34.4	1143.600428	y11	1	82.5	90.52	8.181096425	5.600798306

Immunoglobulin kappa va	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER	959.4829++	959.482947	2	34.4	229.118283	b2	1	82.5	90.52		
Immunoglobulin kappa va	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER	959.4829++	959.482947	2	34.4	328.186697	b3	1	82.5	90.52		
Immunoglobulin kappa va	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER[+10.008269]	964.4871++ (heavy)	964.487082	2	34.4	1153.608697	y11	1	82.5	90.52		
Immunoglobulin kappa va	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER[+10.008269]	964.4871++ (heavy)	964.487082	2	34.4	229.118283	b2	1	82.5	90.52		
Immunoglobulin kappa va	IGKV4-1	P06312	DIVMTQSPDSLAVSLGER	DIVMTQSPDSLAVSLGER[+10.008269]	964.4871++ (heavy)	964.487082	2	34.4	328.186697	b3	1	82.5	90.52		
Immunoglobulin kappa va	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK	606.6493+++	606.649294	3	20.5	623.351137	y6	1	59.71	60.14		
Immunoglobulin kappa va	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK	606.6493+++	606.649294	3	20.5	341.218332	y3	1	59.71	60.14		
Immunoglobulin kappa va	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK	606.6493+++	606.649294	3	20.5	391.197596	b3	1	59.71	60.14		
Immunoglobulin kappa va	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK[+8.014199]	609.3207+++ (heavy)	609.320694	3	20.5	631.365336	y6	1	59.71	60.14		
Immunoglobulin kappa va	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK[+8.014199]	609.3207+++ (heavy)	609.320694	3	20.5	349.23253	y3	1	59.71	60.14		
Immunoglobulin kappa va	IGKV4-1	P06312	NYLAWYQQKPGQPPK	NYLAWYQQKPGQPPK[+8.014199]	609.3207+++ (heavy)	609.320694	3	20.5	391.197596	b3	1	59.71	60.14		
Immunoglobulin kappa va	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR	561.8189++	561.818941	2	19.7	896.462478	y7	1	77.9	85.12		
Immunoglobulin kappa va	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR	561.8189++	561.818941	2	19.7	783.378414	y6	1	77.9	85.12		
Immunoglobulin kappa va	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR	561.8189++	561.818941	2	19.7	620.315085	y5	1	77.9	85.12		
Immunoglobulin kappa va	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR[+10.008269]	566.8231++ (heavy)	566.823076	2	19.7	906.470747	y7	1	77.9	85.12		
Immunoglobulin kappa va	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR[+10.008269]	566.8231++ (heavy)	566.823076	2	19.7	793.386683	y6	1	77.9	85.12		
Immunoglobulin kappa va	IGKV4-1	P06312	LLIYWASTR	LLIYWASTR[+10.008269]	566.8231++ (heavy)	566.823076	2	19.7	630.323354	y5	1	77.9	85.12		
Immunoglobulin lambda c	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK	872.4331++	872.433052	2	31.2	788.39373	y6	1	90.35	92.69	5.178928526	3.699877495
Immunoglobulin lambda c	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK	872.4331++	872.433052	2	31.2	687.346051	y5	1	90.35	92.69		
Immunoglobulin lambda c	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK	872.4331++	872.433052	2	31.2	235.107718	b2	1	90.35	92.69		
Immunoglobulin lambda c	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK[+8.014199]	876.4402++ (heavy)	876.440151	2	31.2	796.407929	y6	1	90.35	92.69		
Immunoglobulin lambda c	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK[+8.014199]	876.4402++ (heavy)	876.440151	2	31.2	695.36025	y5	1	90.35	92.69		
Immunoglobulin lambda c	IGLC6	P0CF74	YAASSYLSLTPEQWK	YAASSYLSLTPEQWK[+8.014199]	876.4402++ (heavy)	876.440151	2	31.2	235.107718	b2	1	90.35	92.69		
Immunoglobulin lambda c	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK	571.2579+++	571.257914	3	19.2	987.474165	y9	1	14.25	20.01		
Immunoglobulin lambda c	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK	571.2579+++	571.257914	3	19.2	749.367575	y7	1	14.25	20.01		
Immunoglobulin lambda c	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK	571.2579+++	571.257914	3	19.2	620.324982	y6	1	14.25	20.01		
Immunoglobulin lambda c	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK[+8.014199	573.9293+++ (heavy)	573.929314	3	19.2	995.488364	y9	1	14.25	20.01		
Immunoglobulin lambda c	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK[+8.014199	573.9293+++ (heavy)	573.929314	3	19.2	757.381774	y7	1	14.25	20.01		
Immunoglobulin lambda c	IGLC6	P0CF74	SYSCQVTHEGSTVEK	SYSC[+57.021464]QVTHEGSTVEK[+8.014199	573.9293+++ (heavy)	573.929314	3	19.2	628.339181	y6	1	14.25	20.01		
Sex hormone-binding glob	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR	721.4299++	721.429918	2	25.6	917.520327	y8	1	105.33	117.1	7.360161156	9.703839498
Sex hormone-binding glob	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR	721.4299++	721.429918	2	25.6	804.436263	y7	1	105.33	117.1		
Sex hormone-binding glob	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR	721.4299++	721.429918	2	25.6	657.367849	y6	1	105.33	117.1		
Sex hormone-binding glob	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR[+10.008269]	726.4341++ (heavy)	726.434053	2	25.6	927.528596	y8	1	105.33	117.1		
Sex hormone-binding glob	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR[+10.008269]	726.4341++ (heavy)	726.434053	2	25.6	814.444532	y7	1	105.33	117.1		
Sex hormone-binding glob	SHBG	P04278	IALGGLLFPASNLR	IALGGLLFPASNLR[+10.008269]	726.4341++ (heavy)	726.434053	2	25.6	667.376118	y6	1	105.33	117.1		
Sex hormone-binding glob	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR	662.3763++	662.376297	2	23.4	901.456013	y8	1	82.79	97.11		
Sex hormone-binding glob	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR	662.3763++	662.376297	2	23.4	211.144104	b2	1	82.79	97.11		
Sex hormone-binding glob	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR	662.3763++	662.376297	2	23.4	324.228168	b3	1	82.79	97.11		
Sex hormone-binding glob	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR	662.3763++	662.376297	2	23.4	423.296582	b4	1	82.79	97.11		
Sex hormone-binding glob	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR[+10.008269]	667.3804++ (heavy)	667.380432	2	23.4	911.464282	y8	1	82.79	97.11		
Sex hormone-binding glob	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR[+10.008269]	667.3804++ (heavy)	667.380432	2	23.4	211.144104	b2	1	82.79	97.11		
Sex hormone-binding glob	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR[+10.008269]	667.3804++ (heavy)	667.380432	2	23.4	324.228168	b3	1	82.79	97.11		
Sex hormone-binding glob	SHBG	P04278	LPLVPALDGCLR	LPLVPALDGC[+57.021464]LR[+10.008269]	667.3804++ (heavy)	667.380432	2	23.4	423.296582	b4	1	82.79	97.11		
Sex hormone-binding glob	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR	665.8517++	665.851698	2	23.6	889.473771	y9	1	40.5	41.62		
Sex hormone-binding glob	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR	665.8517++	665.851698	2	23.6	731.404629	y7	1	40.5	41.62		
Sex hormone-binding glob	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR	665.8517++	665.851698	2	23.6	573.335487	y5	1	40.5	41.62		
Sex hormone-binding glob	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR	665.8517++	665.851698	2	23.6	329.14556	b3	1	40.5	41.62		
Sex hormone-binding glob	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR[+10.008269]	670.8558++ (heavy)	670.855832	2	23.6	899.48204	y9	1	40.5	41.62		

Sex hormone-binding glob	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR[+10.008269]	670.8558++ (heavy)	670.855832	2	23.6	741.412898	y7	1	40.5	41.62		
Sex hormone-binding glob	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR[+10.008269]	670.8558++ (heavy)	670.855832	2	23.6	583.343756	y5	1	40.5	41.62		
Sex hormone-binding glob	SHBG	P04278	QAEISASAPTSLR	QAEISASAPTSLR[+10.008269]	670.8558++ (heavy)	670.855832	2	23.6	329.14556	b3	1	40.5	41.62		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER	695.3101++	695.31006	2	24.7	1086.506193	y9	1	24.69	26.88	9.884689927	5.969929916
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER	695.3101++	695.31006	2	24.7	971.47925	y8	1	24.69	26.88		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER	695.3101++	695.31006	2	24.7	631.340966	y5	1	24.69	26.88		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER	695.3101++	695.31006	2	24.7	403.229959	y3	1	24.69	26.88		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER[+10.008269]	700.3142++ (heavy)	700.314194	2	24.7	1096.514462	y9	1	24.69	26.88		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER[+10.008269]	700.3142++ (heavy)	700.314194	2	24.7	981.487519	y8	1	24.69	26.88		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER[+10.008269]	700.3142++ (heavy)	700.314194	2	24.7	641.349235	y5	1	24.69	26.88		
Immunoglobulin J chain	JCHAIN	P01591	SSEDPNEDIVER	SSEDPNEDIVER[+10.008269]	700.3142++ (heavy)	700.314194	2	24.7	413.238228	y3	1	24.69	26.88		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR	469.7927++	469.792726	2	16.3	712.410049	y6	1	45.29	46.42		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR	469.7927++	469.792726	2	16.3	613.341635	y5	1	45.29	46.42		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR	469.7927++	469.792726	2	16.3	516.288871	y4	1	45.29	46.42		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR[+10.008269]	474.7969++ (heavy)	474.796861	2	16.3	722.418318	y6	1	45.29	46.42		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR[+10.008269]	474.7969++ (heavy)	474.796861	2	16.3	623.349904	y5	1	45.29	46.42		
Immunoglobulin J chain	JCHAIN	P01591	IIVPLNNR	IIVPLNNR[+10.008269]	474.7969++ (heavy)	474.796861	2	16.3	526.29714	y4	1	45.29	46.42		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K	427.8814+++	427.881391	3	14.1	735.370552	y6	1	61.77	58.58		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K	427.8814+++	427.881391	3	14.1	622.286488	y5	1	61.77	58.58		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K	427.8814+++	427.881391	3	14.1	420.227516	y3	1	61.77	58.58		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K[+8.014199]	430.5528+++ (heavy)	430.55279	3	14.1	743.384751	y6	1	61.77	58.58		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K[+8.014199]	430.5528+++ (heavy)	430.55279	3	14.1	630.300687	y5	1	61.77	58.58		
Immunoglobulin J chain	JCHAIN	P01591	FVYHLSDLCK	FVYHLSDLC[+57.021464]K[+8.014199]	430.5528+++ (heavy)	430.55279	3	14.1	428.241715	y3	1	61.77	58.58		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK	828.9187++	828.918723	2	29.6	1062.582987	y10	1	70.18	79.62		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK	828.9187++	828.918723	2	29.6	963.514573	y9	1	70.18	79.62		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK	828.9187++	828.918723	2	29.6	425.148932	b3	1	70.18	79.62		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK[+8.014199]	832.9258++ (heavy)	832.925823	2	29.6	1070.597186	y10	1	70.18	79.62		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK[+8.014199]	832.9258++ (heavy)	832.925823	2	29.6	971.528772	y9	1	70.18	79.62		
Immunoglobulin J chain	JCHAIN	P01591	CYTAVVPLVYGGETK	C[+57.021464]YTAVVPLVYGGETK[+8.014199]	832.9258++ (heavy)	832.925823	2	29.6	425.148932	b3	1	70.18	79.62		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK	581.8032++	581.803154	2	20.5	934.488024	y8	1	61.32	78.87	7.778343513	5.029695106
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK	581.8032++	581.803154	2	20.5	700.387582	y6	1	61.32	78.87		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK	581.8032++	581.803154	2	20.5	585.360639	y5	1	61.32	78.87		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK[+8.014199]	585.8103++ (heavy)	585.810253	2	20.5	942.502223	y8	1	61.32	78.87		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK[+8.014199]	585.8103++ (heavy)	585.810253	2	20.5	708.401781	y6	1	61.32	78.87		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EVSFDVELPK	EVSFDVELPK[+8.014199]	585.8103++ (heavy)	585.810253	2	20.5	593.374838	y5	1	61.32	78.87		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR	578.9638+++	578.96383	3	19.5	956.479585	y8	1	50.73	38.77		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR	578.9638+++	578.96383	3	19.5	730.384228	y6	1	50.73	38.77		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR	578.9638+++	578.96383	3	19.5	503.257236	y4	1	50.73	38.77		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR[+10.008269]	582.2999+++ (heavy)	582.29992	3	19.5	966.487854	y8	1	50.73	38.77		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR[+10.008269]	582.2999+++ (heavy)	582.29992	3	19.5	740.392497	y6	1	50.73	38.77		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	EHLVQATPENLQEAR	EHLVQATPENLQEAR[+10.008269]	582.2999+++ (heavy)	582.29992	3	19.5	513.265505	y4	1	50.73	38.77		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER	645.3117++	645.311677	2	22.8	898.441743	y7	1	83.64	85.13		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER	645.3117++	645.311677	2	22.8	751.373329	y6	1	83.64	85.13		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER	645.3117++	645.311677	2	22.8	392.181612	b3	1	83.64	85.13		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER[+10.008269]	650.3158++ (heavy)	650.315812	2	22.8	908.450012	y7	1	83.64	85.13		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER[+10.008269]	650.3158++ (heavy)	650.315812	2	22.8	761.381598	y6	1	83.64	85.13		
Inter-alpha-trypsin inhibito	ITIH3	Q06033	DYIFGNYIER	DYIFGNYIER[+10.008269]	650.3158++ (heavy)	650.315812	2	22.8	392.181612	b3	1	83.64	85.13		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK	626.8141++	626.814053	2	22.1	1025.493838	y8	1	59.62	57.12	6.086944923	3.945221246

Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK	626.8141++	626.814053	2	22.1	765.377745	y6	1	59.62	57.12		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK	626.8141++	626.814053	2	22.1	228.134267	b2	1	59.62	57.12		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK[+8.014199]	630.8212++ (heavy)	630.821152	2	22.1	1033.508037	y8	1	59.62	57.12		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK[+8.014199]	630.8212++ (heavy)	630.821152	2	22.1	773.391944	y6	1	59.62	57.12		
Apolipoprotein A-I	APOA1	P02647	VQPYLDDFQK	VQPYLDDFQK[+8.014199]	630.8212++ (heavy)	630.821152	2	22.1	228.134267	b2	1	59.62	57.12		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR	434.5543+++	434.554331	3	14.3	619.30458	y5	1	53.92	37.9		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR	434.5543+++	434.554331	3	14.3	417.245609	y3	1	53.92	37.9		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR	434.5543+++	434.554331	3	14.3	423.235044	b4	1	53.92	37.9		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR[+10.008269]	437.8904+++ (heavy)	437.890421	3	14.3	629.312849	y5	1	53.92	37.9		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR[+10.008269]	437.8904+++ (heavy)	437.890421	3	14.3	427.253878	y3	1	53.92	37.9		
Apolipoprotein A-I	APOA1	P02647	THLAPYSDELR	THLAPYSDELR[+10.008269]	437.8904+++ (heavy)	437.890421	3	14.3	423.235044	b4	1	53.92	37.9		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK	615.8583++	615.858263	2	21.7	819.461081	y7	1	95.86	108.64		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK	615.8583++	615.858263	2	21.7	623.339903	y5	1	95.86	108.64		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK	615.8583++	615.858263	2	21.7	299.171381	b3	1	95.86	108.64		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK[+8.014199]	619.8654++ (heavy)	619.865363	2	21.7	827.47528	y7	1	95.86	108.64		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK[+8.014199]	619.8654++ (heavy)	619.865363	2	21.7	631.354102	y5	1	95.86	108.64		
Apolipoprotein A-I	APOA1	P02647	QGLLPVLESFK	QGLLPVLESFK[+8.014199]	619.8654++ (heavy)	619.865363	2	21.7	299.171381	b3	1	95.86	108.64		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK	693.8612++	693.8612	2	24.6	940.462203	y8	1	109.44	116.91		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK	693.8612++	693.8612	2	24.6	853.430175	y7	1	109.44	116.91		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK	693.8612++	693.8612	2	24.6	782.393061	y6	1	109.44	116.91		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK[+8.014199]	697.8683++ (heavy)	697.868299	2	24.6	948.476402	y8	1	109.44	116.91		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK[+8.014199]	697.8683++ (heavy)	697.868299	2	24.6	861.444374	y7	1	109.44	116.91		
Apolipoprotein A-I	APOA1	P02647	VSFLSALEEYTK	VSFLSALEEYTK[+8.014199]	697.8683++ (heavy)	697.868299	2	24.6	790.40726	y6	1	109.44	116.91		
Complement component (	C9	P02748	VVEESELAR	VVEESELAR	516.2720++	516.272021	2	18	833.399937	y7	1	20.72	23.94	6.195819262	3.481368134
Complement component (	C9	P02748	VVEESELAR	VVEESELAR	516.2720++	516.272021	2	18	704.357344	y6	1	20.72	23.94		
Complement component (	C9	P02748	VVEESELAR	VVEESELAR	516.2720++	516.272021	2	18	575.314751	y5	1	20.72	23.94		
Complement component (	C9	P02748	VVEESELAR	VVEESELAR[+10.008269]	521.2762++ (heavy)	521.276155	2	18	843.408206	y7	1	20.72	23.94		
Complement component (	C9	P02748	VVEESELAR	VVEESELAR[+10.008269]	521.2762++ (heavy)	521.276155	2	18	714.365613	y6	1	20.72	23.94		
Complement component (	C9	P02748	VVEESELAR	VVEESELAR[+10.008269]	521.2762++ (heavy)	521.276155	2	18	585.32302	y5	1	20.72	23.94		
Complement component (	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK	508.5719+++	508.571939	3	17	607.344989	y5	1	53.21	49.63		
Complement component (	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK	508.5719+++	508.571939	3	17	494.260925	y4	1	53.21	49.63		
Complement component (	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK	508.5719+++	508.571939	3	17	365.218332	y3	1	53.21	49.63		
Complement component (	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK[+8.014199]	511.2433+++ (heavy)	511.243339	3	17	615.359188	y5	1	53.21	49.63		
Complement component (	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK[+8.014199]	511.2433+++ (heavy)	511.243339	3	17	502.275124	y4	1	53.21	49.63		
Complement component (	C9	P02748	TEHYEEQIEAFK	TEHYEEQIEAFK[+8.014199]	511.2433+++ (heavy)	511.243339	3	17	373.23253	y3	1	53.21	49.63		
Complement component (	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK	621.8765++	621.876456	2	21.9	832.492716	y7	1	82.57	90.33		
Complement component (	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK	621.8765++	621.876456	2	21.9	442.302396	y4	1	82.57	90.33		
Complement component (	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK	621.8765++	621.876456	2	21.9	343.233982	y3	1	82.57	90.33		
Complement component (	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK[+8.014199]	625.8836++ (heavy)	625.883555	2	21.9	840.506915	y7	1	82.57	90.33		
Complement component (	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK[+8.014199]	625.8836++ (heavy)	625.883555	2	21.9	450.316595	y4	1	82.57	90.33		
Complement component (	C9	P02748	LSPIYNLVPVK	LSPIYNLVPVK[+8.014199]	625.8836++ (heavy)	625.883555	2	21.9	351.248181	y3	1	82.57	90.33		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK	455.7553++	455.755278	2	15.8	811.434866	y6	1	66.96	68.17	5.603572101	5.707763894
Complement C5	C5	P01031	VFQFLEK	VFQFLEK	455.7553++	455.755278	2	15.8	664.366452	y5	1	66.96	68.17		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK	455.7553++	455.755278	2	15.8	536.307875	y4	1	66.96	68.17		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK[+8.014199]	459.7624++ (heavy)	459.762378	2	15.8	819.449065	y6	1	66.96	68.17		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK[+8.014199]	459.7624++ (heavy)	459.762378	2	15.8	672.380651	y5	1	66.96	68.17		
Complement C5	C5	P01031	VFQFLEK	VFQFLEK[+8.014199]	459.7624++ (heavy)	459.762378	2	15.8	544.322074	y4	1	66.96	68.17		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK	447.7866++	447.786578	2	15.5	684.429053	y6	1	60.46	70.9		

Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK	447.7866++	447.786578	2	15.5	571.344989	y5	1	60.46	70.9		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK	447.7866++	447.786578	2	15.5	244.165568	y2	1	60.46	70.9		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK[+8.014199]	451.7937++ (heavy)	451.793678	2	15.5	692.443252	y6	1	60.46	70.9		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK[+8.014199]	451.7937++ (heavy)	451.793678	2	15.5	579.359188	y5	1	60.46	70.9		
Complement C5	C5	P01031	IPLDLVPK	IPLDLVPK[+8.014199]	451.7937++ (heavy)	451.793678	2	15.5	252.179767	y2	1	60.46	70.9		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK	587.8270++	587.826963	2	20.7	946.535643	y8	1	52.18	62.83		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK	587.8270++	587.826963	2	20.7	669.429387	y6	1	52.18	62.83		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK	587.8270++	587.826963	2	20.7	343.161211	b3	1	52.18	62.83		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK[+8.014199]	591.8341++ (heavy)	591.834063	2	20.7	954.549842	y8	1	52.18	62.83		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK[+8.014199]	591.8341++ (heavy)	591.834063	2	20.7	677.443586	y6	1	52.18	62.83		
Complement C5	C5	P01031	DINYVNPVIK	DINYVNPVIK[+8.014199]	591.8341++ (heavy)	591.834063	2	20.7	343.161211	b3	1	52.18	62.83		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK	946.4391++	946.439063	2	34	1271.590257	y12	1	76.35	77.78	4.411747849	3.454201835
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK	946.4391++	946.439063	2	34	1124.521844	y11	1	76.35	77.78		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK	946.4391++	946.439063	2	34	1053.48473	y10	1	76.35	77.78		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK[+8.014199]	950.4462++ (heavy)	950.446162	2	34	1279.604456	y12	1	76.35	77.78		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK[+8.014199]	950.4462++ (heavy)	950.446162	2	34	1132.536043	y11	1	76.35	77.78		
Alpha-1-antichymotrypsin	SERPINA3	P01011	LYGSEAFATDFQDSAAAK	LYGSEAFATDFQDSAAAK[+8.014199]	950.4462++ (heavy)	950.446162	2	34	1061.498929	y10	1	76.35	77.78		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK	531.2975++	531.297507	2	18.6	633.397024	y5	1	64.34	69.2		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK	531.2975++	531.297507	2	18.6	520.31296	y4	1	64.34	69.2		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK	531.2975++	531.297507	2	18.6	357.249632	y3	1	64.34	69.2		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK[+8.014199]	535.3046++ (heavy)	535.304607	2	18.6	641.411223	y5	1	64.34	69.2		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK[+8.014199]	535.3046++ (heavy)	535.304607	2	18.6	528.327159	y4	1	64.34	69.2		
Alpha-1-antichymotrypsin	SERPINA3	P01011	EIGELYLPK	EIGELYLPK[+8.014199]	535.3046++ (heavy)	535.304607	2	18.6	365.263831	y3	1	64.34	69.2		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR	608.3690++	608.368995	2	21.4	888.514908	y8	1	96.53	103.46		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR	608.3690++	608.368995	2	21.4	775.430844	y7	1	96.53	103.46		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR	608.3690++	608.368995	2	21.4	688.398815	y6	1	96.53	103.46		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR[+10.008269]	613.3731++ (heavy)	613.37313	2	21.4	898.523177	y8	1	96.53	103.46		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR[+10.008269]	613.3731++ (heavy)	613.37313	2	21.4	785.439113	y7	1	96.53	103.46		
Alpha-1-antichymotrypsin	SERPINA3	P01011	ITLLSALVETR	ITLLSALVETR[+10.008269]	613.3731++ (heavy)	613.37313	2	21.4	698.407084	y6	1	96.53	103.46		
Mannose-binding protein (	MBL2	P11226	WLTFSLGK	WLTFSLGK	476.2686++	476.268553	2	16.6	765.450516	y7	1	78.19	92.96	5.870181028	4.008294609
Mannose-binding protein (	MBL2	P11226	WLTFSLGK	WLTFSLGK	476.2686++	476.268553	2	16.6	652.366452	y6	1	78.19	92.96		
Mannose-binding protein (	MBL2	P11226	WLTFSLGK	WLTFSLGK	476.2686++	476.268553	2	16.6	204.134267	y2	1	78.19	92.96		
Mannose-binding protein (	MBL2	P11226	WLTFSLGK	WLTFSLGK[+8.014199]	480.2757++ (heavy)	480.275652	2	16.6	773.464715	y7	1	78.19	92.96		
Mannose-binding protein (	MBL2	P11226	WLTFSLGK	WLTFSLGK[+8.014199]	480.2757++ (heavy)	480.275652	2	16.6	660.380651	y6	1	78.19	92.96		
Mannose-binding protein (	MBL2	P11226	WLTFSLGK	WLTFSLGK[+8.014199]	480.2757++ (heavy)	480.275652	2	16.6	212.148466	y2	1	78.19	92.96		
Mannose-binding protein (	MBL2	P11226	FQASVATPR	FQASVATPR	488.7642++	488.764166	2	17	701.394064	y7	1	20.59	29.2		
Mannose-binding protein (	MBL2	P11226	FQASVATPR	FQASVATPR	488.7642++	488.764166	2	17	630.35695	y6	1	20.59	29.2		
Mannose-binding protein (	MBL2	P11226	FQASVATPR	FQASVATPR	488.7642++	488.764166	2	17	276.134267	b2	1	20.59	29.2		
Mannose-binding protein (	MBL2	P11226	FQASVATPR	FQASVATPR[+10.008269]	493.7683++ (heavy)	493.7683	2	17	711.402333	y7	1	20.59	29.2		
Mannose-binding protein (	MBL2	P11226	FQASVATPR	FQASVATPR[+10.008269]	493.7683++ (heavy)	493.7683	2	17	640.365219	y6	1	20.59	29.2		
Mannose-binding protein (	MBL2	P11226	FQASVATPR	FQASVATPR[+10.008269]	493.7683++ (heavy)	493.7683	2	17	276.134267	b2	1	20.59	29.2		
Mannose-binding protein (	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR	668.8282++	668.828223	2	23.7	921.478856	y8	1	50.44	52.18		
Mannose-binding protein (	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR	668.8282++	668.828223	2	23.7	675.342029	y6	1	50.44	52.18		
Mannose-binding protein (	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR	668.8282++	668.828223	2	23.7	560.315085	y5	1	50.44	52.18		
Mannose-binding protein (	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR	668.8282++	668.828223	2	23.7	447.231021	y4	1	50.44	52.18		
Mannose-binding protein (	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR[+10.008269]	673.8324++ (heavy)	673.832357	2	23.7	931.487125	y8	1	50.44	52.18		
Mannose-binding protein (	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR[+10.008269]	673.8324++ (heavy)	673.832357	2	23.7	685.350298	y6	1	50.44	52.18		
Mannose-binding protein (	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR[+10.008269]	673.8324++ (heavy)	673.832357	2	23.7	570.323354	y5	1	50.44	52.18		

Mannose-binding protein (	MBL2	P11226	TEGQFVDLTGNR	TEGQFVDLTGNR[+10.008269]	673.8324++ (heavy)	673.832357	2	23.7	457.23929	y4	1	50.44	52.18		
Complement component (	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR	605.2967+++	605.296698	3	20.5	774.341694	y6	1	82.62	82.59	2.355204922	8.749827174
Complement component (	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR	605.2967+++	605.296698	3	20.5	659.314751	y5	1	82.62	82.59		
Complement component (	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR	605.2967+++	605.296698	3	20.5	496.251423	y4	1	82.62	82.59		
Complement component (	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR[+10.008269]	608.6328+++ (heavy)	608.632787	3	20.5	784.349963	y6	1	82.62	82.59		
Complement component (	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR[+10.008269]	608.6328+++ (heavy)	608.632787	3	20.5	669.32302	y5	1	82.62	82.59		
Complement component (	C7	P10643	ELSHLPSLYDYSAYR	ELSHLPSLYDYSAYR[+10.008269]	608.6328+++ (heavy)	608.632787	3	20.5	506.259692	y4	1	82.62	82.59		
Complement component (	C7	P10643	VLFYVDSEK	VLFYVDSEK	550.2871++	550.287139	2	19.3	887.414525	y7	1	60.12	60.09		
Complement component (	C7	P10643	VLFYVDSEK	VLFYVDSEK	550.2871++	550.287139	2	19.3	740.346111	y6	1	60.12	60.09		
Complement component (	C7	P10643	VLFYVDSEK	VLFYVDSEK	550.2871++	550.287139	2	19.3	577.282782	y5	1	60.12	60.09		
Complement component (	C7	P10643	VLFYVDSEK	VLFYVDSEK[+8.014199]	554.2942++ (heavy)	554.294239	2	19.3	895.428724	y7	1	60.12	60.09		
Complement component (	C7	P10643	VLFYVDSEK	VLFYVDSEK[+8.014199]	554.2942++ (heavy)	554.294239	2	19.3	748.36031	y6	1	60.12	60.09		
Complement component (	C7	P10643	VLFYVDSEK	VLFYVDSEK[+8.014199]	554.2942++ (heavy)	554.294239	2	19.3	585.296981	y5	1	60.12	60.09		
Complement component (	C7	P10643	LTPLYELVK	LTPLYELVK	538.3235++	538.323525	2	18.9	861.508031	y7	1	83.57	85.42		
Complement component (	C7	P10643	LTPLYELVK	LTPLYELVK	538.3235++	538.323525	2	18.9	764.455267	y6	1	83.57	85.42		
Complement component (	C7	P10643	LTPLYELVK	LTPLYELVK	538.3235++	538.323525	2	18.9	651.371203	y5	1	83.57	85.42		
Complement component (	C7	P10643	LTPLYELVK	LTPLYELVK[+8.014199]	542.3306++ (heavy)	542.330624	2	18.9	869.52223	y7	1	83.57	85.42		
Complement component (	C7	P10643	LTPLYELVK	LTPLYELVK[+8.014199]	542.3306++ (heavy)	542.330624	2	18.9	772.469466	y6	1	83.57	85.42		
Complement component (	C7	P10643	LTPLYELVK	LTPLYELVK[+8.014199]	542.3306++ (heavy)	542.330624	2	18.9	659.385402	y5	1	83.57	85.42		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK	501.7769++	501.776939	2	17.5	731.393395	y6	1	28.75	33	6.572384108	3.406508515
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK	501.7769++	501.776939	2	17.5	603.334818	y5	1	28.75	33		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK	501.7769++	501.776939	2	17.5	474.292225	y4	1	28.75	33		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK[+8.014199]	505.7840++ (heavy)	505.784038	2	17.5	739.407594	y6	1	28.75	33		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK[+8.014199]	505.7840++ (heavy)	505.784038	2	17.5	611.349017	y5	1	28.75	33		
Complement C3	C3	P01024	TGLQEVEVK	TGLQEVEVK[+8.014199]	505.7840++ (heavy)	505.784038	2	17.5	482.306424	y4	1	28.75	33		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR	542.2827++	542.282723	2	19	634.367121	y5	1	46.95	48.54		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR	542.2827++	542.282723	2	19	506.308544	y4	1	46.95	48.54		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR	542.2827++	542.282723	2	19	393.22448	y3	1	46.95	48.54		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR[+10.008269]	547.2869++ (heavy)	547.286857	2	19	644.37539	y5	1	46.95	48.54		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR[+10.008269]	547.2869++ (heavy)	547.286857	2	19	516.316813	y4	1	46.95	48.54		
Complement C3	C3	P01024	GYTQQLAFR	GYTQQLAFR[+10.008269]	547.2869++ (heavy)	547.286857	2	19	403.232748	y3	1	46.95	48.54		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK	471.2869++	471.286942	2	16.4	684.465438	y6	1	50.11	51.64	3.250819754	2.190861941
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK	471.2869++	471.286942	2	16.4	571.381374	y5	1	50.11	51.64		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK	471.2869++	471.286942	2	16.4	470.333696	y4	1	50.11	51.64		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK[+8.014199]	475.2940++ (heavy)	475.294042	2	16.4	692.479637	y6	1	50.11	51.64		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK[+8.014199]	475.2940++ (heavy)	475.294042	2	16.4	579.395573	y5	1	50.11	51.64		
Apolipoprotein A-II	APOA2	P02652	EQLTPLIK	EQLTPLIK[+8.014199]	475.2940++ (heavy)	475.294042	2	16.4	478.347895	y4	1	50.11	51.64		
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK	643.7986++	643.7986	2	22.8	957.431238	y8	1	61.16	65.13	5.044093086	3.149161698
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK	643.7986++	643.7986	2	22.8	870.399209	y7	1	61.16	65.13		
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK	643.7986++	643.7986	2	22.8	620.303852	y5	1	61.16	65.13		
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK[+8.014199]	647.8057++ (heavy)	647.805699	2	22.8	965.445437	y8	1	61.16	65.13		
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK[+8.014199]	647.8057++ (heavy)	647.805699	2	22.8	878.413408	y7	1	61.16	65.13		
Apolipoprotein C-II	APOC2	P02655	ESLSSYWESAK	ESLSSYWESAK[+8.014199]	647.8057++ (heavy)	647.805699	2	22.8	628.318051	y5	1	61.16	65.13		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK	518.2715++	518.271489	2	18.1	771.424696	y7	1	38.01	41.83		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK	518.2715++	518.271489	2	18.1	658.340632	y6	1	38.01	41.83		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK	518.2715++	518.271489	2	18.1	265.118283	b2	1	38.01	41.83		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK[+8.014199]	522.2786++ (heavy)	522.278589	2	18.1	779.438895	y7	1	38.01	41.83		
Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK[+8.014199]	522.2786++ (heavy)	522.278589	2	18.1	666.354831	y6	1	38.01	41.83		

Apolipoprotein C-II	APOC2	P02655	TYLPAVDEK	TYLPAVDEK[+8.014199]	522.2786++ (heavy)	522.278589	2	18.1	265.118283	b2	1	38.01	41.83		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR	858.9292++	858.929196	2	30.7	1144.570525	y10	1	37.28	46.64	6.874210038	3.327132268
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR	858.9292++	858.929196	2	30.7	887.469354	y8	1	37.28	46.64		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR	858.9292++	858.929196	2	30.7	573.310334	y5	1	37.28	46.64		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR[+10.008269]	863.9333++ (heavy)	863.933331	2	30.7	1154.578794	y10	1	37.28	46.64		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR[+10.008269]	863.9333++ (heavy)	863.933331	2	30.7	897.477623	y8	1	37.28	46.64		
Apolipoprotein C-III	APOC3	P02656	DALSSVQESQVAQQAR	DALSSVQESQVAQQAR[+10.008269]	863.9333++ (heavy)	863.933331	2	30.7	583.318603	y5	1	37.28	46.64		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK	598.8009++	598.800945	2	21.1	854.425424	y8	1	72.93	81.29		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK	598.8009++	598.800945	2	21.1	753.377745	y7	1	72.93	81.29		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK	598.8009++	598.800945	2	21.1	244.108053	b2	1	72.93	81.29		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK[+8.014199]	602.8080++ (heavy)	602.808045	2	21.1	862.439623	y8	1	72.93	81.29		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK[+8.014199]	602.8080++ (heavy)	602.808045	2	21.1	761.391944	y7	1	72.93	81.29		
Apolipoprotein C-III	APOC3	P02656	GWVTDGFSSLK	GWVTDGFSSLK[+8.014199]	602.8080++ (heavy)	602.808045	2	21.1	244.108053	b2	1	72.93	81.29		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK	449.7189++	449.718893	2	15.6	620.340238	y5	1	42.7	44.16		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK	449.7189++	449.718893	2	15.6	434.260925	y4	1	42.7	44.16		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK	449.7189++	449.718893	2	15.6	347.228896	y3	1	42.7	44.16		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK[+8.014199]	453.7260++ (heavy)	453.725992	2	15.6	628.354437	y5	1	42.7	44.16		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK[+8.014199]	453.7260++ (heavy)	453.725992	2	15.6	442.275124	y4	1	42.7	44.16		
Apolipoprotein C-III	APOC3	P02656	DYWSTVK	DYWSTVK[+8.014199]	453.7260++ (heavy)	453.725992	2	15.6	355.243095	y3	1	42.7	44.16		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR	536.8035++	536.803488	2	18.8	830.473043	y7	1	54.46	53.92	4.892815806	4.996258139
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR	536.8035++	536.803488	2	18.8	717.388979	y6	1	54.46	53.92		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR	536.8035++	536.803488	2	18.8	588.346386	y5	1	54.46	53.92		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR[+10.008269]	541.8076++ (heavy)	541.807622	2	18.8	840.481312	y7	1	54.46	53.92		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR[+10.008269]	541.8076++ (heavy)	541.807622	2	18.8	727.397248	y6	1	54.46	53.92		
Apolipoprotein C-IV	APOC4	P55056	ELLETVVNR	ELLETVVNR[+10.008269]	541.8076++ (heavy)	541.807622	2	18.8	598.354655	y5	1	54.46	53.92		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK	440.7318++	440.731803	2	15.2	623.339903	y5	1	63.36	67.31		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK	440.7318++	440.731803	2	15.2	476.271489	y4	1	63.36	67.31		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK	440.7318++	440.731803	2	15.2	258.123703	b2	1	63.36	67.31		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK[+8.014199]	444.7389++ (heavy)	444.738903	2	15.2	631.354102	y5	1	63.36	67.31		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK[+8.014199]	444.7389++ (heavy)	444.738903	2	15.2	484.285688	y4	1	63.36	67.31		
Apolipoprotein C-IV	APOC4	P55056	AWFLESK	AWFLESK[+8.014199]	444.7389++ (heavy)	444.738903	2	15.2	258.123703	b2	1	63.36	67.31		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER	815.8996++	815.899573	2	29.1	1301.633185	y12	1	35.65	36	4.530913032	5.97447301
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER	815.8996++	815.899573	2	29.1	1091.496357	y10	1	35.65	36		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER	815.8996++	815.899573	2	29.1	933.427215	y8	1	35.65	36		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER[+10.008269]	820.9037++ (heavy)	820.903708	2	29.1	1311.641454	y12	1	35.65	36		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER[+10.008269]	820.9037++ (heavy)	820.903708	2	29.1	1101.504626	y10	1	35.65	36		
Apolipoprotein L1	APOL1	O14791	VTEPISAESGEQVER	VTEPISAESGEQVER[+10.008269]	820.9037++ (heavy)	820.903708	2	29.1	943.435484	y8	1	35.65	36		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR	637.8241++	637.824094	2	22.5	932.486978	y8	1	56.78	65.34		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR	637.8241++	637.824094	2	22.5	635.318122	y5	1	56.78	65.34		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR	637.8241++	637.824094	2	22.5	522.234058	y4	1	56.78	65.34		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR[+10.008269]	642.8282++ (heavy)	642.828229	2	22.5	942.495247	y8	1	56.78	65.34		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR[+10.008269]	642.8282++ (heavy)	642.828229	2	22.5	645.326391	y5	1	56.78	65.34		
Apolipoprotein L1	APOL1	O14791	VNEPSILEMSR	VNEPSILEMSR[+10.008269]	642.8282++ (heavy)	642.828229	2	22.5	532.242327	y4	1	56.78	65.34		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK	553.3037++	553.303655	2	19.4	765.388979	y6	1	43.15	51.37		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK	553.3037++	553.303655	2	19.4	652.304915	y5	1	43.15	51.37		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK	553.3037++	553.303655	2	19.4	228.134267	b2	1	43.15	51.37		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK[+8.014199]	557.3108++ (heavy)	557.310755	2	19.4	773.403178	y6	1	43.15	51.37		
Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK[+8.014199]	557.3108++ (heavy)	557.310755	2	19.4	660.319114	y5	1	43.15	51.37		

Apolipoprotein L1	APOL1	O14791	LNILNNNYK	LNILNNNYK[+8.014199]	557.3108++ (heavy)	557.310755	2	19.4	228.134267	b2	1	43.15	51.37		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR	687.3352++	687.335161	2	24.4	813.421342	y7	1	59.03	60.24	4.529930849	0.643051853
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR	687.3352++	687.335161	2	24.4	700.337278	y6	1	59.03	60.24		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR	687.3352++	687.335161	2	24.4	571.294684	y5	1	59.03	60.24		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR[+10.008269]	692.3393++ (heavy)	692.339295	2	24.4	823.429611	y7	1	59.03	60.24		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR[+10.008269]	692.3393++ (heavy)	692.339295	2	24.4	710.345547	y6	1	59.03	60.24		
Attractin	ATRN	O75882	CTWLIEGQPNR	C[+57.021464]TWLIEGQPNR[+10.008269]	692.3393++ (heavy)	692.339295	2	24.4	581.302953	y5	1	59.03	60.24		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	914.487647	y9	1	46.12	42.14		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	754.456999	y8	1	46.12	42.14		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	641.372935	y7	1	46.12	42.14		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	570.335821	y6	1	46.12	42.14		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR	636.8219++	636.821886	2	22.5	499.298707	y5	1	46.12	42.14		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	924.495916	y9	1	46.12	42.14		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	764.465268	y8	1	46.12	42.14		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	651.381204	y7	1	46.12	42.14		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	580.34409	y6	1	46.12	42.14		
Attractin	ATRN	O75882	SEAACLAAGPGIR	SEAAC[+57.021464]LAAGPGIR[+10.008269]	641.8260++ (heavy)	641.826021	2	22.5	509.306976	y5	1	46.12	42.14		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR	578.3479++	578.347866	2	20.3	941.556713	y8	1	94.12	100.72		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR	578.3479++	578.347866	2	20.3	828.472649	y7	1	94.12	100.72		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR	578.3479++	578.347866	2	20.3	727.42497	y6	1	94.12	100.72		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR[+10.008269]	583.3520++ (heavy)	583.352	2	20.3	951.564982	y8	1	94.12	100.72		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR[+10.008269]	583.3520++ (heavy)	583.352	2	20.3	838.480918	y7	1	94.12	100.72		
Attractin	ATRN	O75882	LTLTPWVGLR	LTLTPWVGLR[+10.008269]	583.3520++ (heavy)	583.352	2	20.3	737.433239	y6	1	94.12	100.72		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIE	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57.	796.0036+++	796.003585	3	27.3	1005.455738	y8	1	64.84	63.94	5.132881069	2.134835173
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIE	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57.	796.0036+++	796.003585	3	27.3	650.317788	y5	1	64.84	63.94		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIE	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57.	796.0036+++	796.003585	3	27.3	537.233724	y4	1	64.84	63.94		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIE	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57.	798.6750+++ (heavy)	798.674985	3	27.3	1013.469937	y8	1	64.84	63.94		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIE	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57.	798.6750+++ (heavy)	798.674985	3	27.3	658.331987	y5	1	64.84	63.94		
Beta-2-glycoprotein 1	APOH	P02749	ATFGCHDGYSLDGPEEIE	ATFGC[+57.021464]HDGYSLDGPEEIEC[+57.	798.6750+++ (heavy)	798.674985	3	27.3	545.247923	y4	1	64.84	63.94		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGTIE	1043.4588++	1043.458812	2	37.5	743.429781	y7	1	59.45	70.52		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGTIE	1043.4588++	1043.458812	2	37.5	248.069953	b2	1	59.45	70.52		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGTIE	1043.4588++	1043.458812	2	37.5	411.133282	b3	1	59.45	70.52		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGTIE	1047.4659++ (heavy)	1047.465912	2	37.5	751.44398	y7	1	59.45	70.52		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGTIE	1047.4659++ (heavy)	1047.465912	2	37.5	248.069953	b2	1	59.45	70.52		
Beta-2-glycoprotein 1	APOH	P02749	CSYTEDAQCIDGTIEVPK	C[+57.021464]SYTEDAQC[+57.021464]IDGTIE	1047.4659++ (heavy)	1047.465912	2	37.5	411.133282	b3	1	59.45	70.52		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK	552.7773++	552.777273	2	19.4	838.445765	y7	1	60.18	56.45		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK	552.7773++	552.777273	2	19.4	480.260531	y3	1	60.18	56.45		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK	552.7773++	552.777273	2	19.4	267.108781	b2	1	60.18	56.45		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK[+8.014199]	556.7844++ (heavy)	556.784373	2	19.4	846.459964	y7	1	60.18	56.45		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK[+8.014199]	556.7844++ (heavy)	556.784373	2	19.4	488.27473	y3	1	60.18	56.45		
Beta-2-glycoprotein 1	APOH	P02749	EHSSLAFWK	EHSSLAFWK[+8.014199]	556.7844++ (heavy)	556.784373	2	19.4	267.108781	b2	1	60.18	56.45		
C4b-binding protein beta	C4BPB	P20851	ALLAFQESK	ALLAFQESK	503.7820++	503.782024	2	17.6	822.435595	y7	1	48.58	54.25	6.803241971	6.790466134
C4b-binding protein beta	C4BPB	P20851	ALLAFQESK	ALLAFQESK	503.7820++	503.782024	2	17.6	709.351531	y6	1	48.58	54.25		
C4b-binding protein beta	C4BPB	P20851	ALLAFQESK	ALLAFQESK	503.7820++	503.782024	2	17.6	638.314417	y5	1	48.58	54.25		
C4b-binding protein beta	C4BPB	P20851	ALLAFQESK	ALLAFQESK[+8.014199]	507.7891++ (heavy)	507.789124	2	17.6	830.449794	y7	1	48.58	54.25		
C4b-binding protein beta	C4BPB	P20851	ALLAFQESK	ALLAFQESK[+8.014199]	507.7891++ (heavy)	507.789124	2	17.6	717.36573	y6	1	48.58	54.25		
C4b-binding protein beta	C4BPB	P20851	ALLAFQESK	ALLAFQESK[+8.014199]	507.7891++ (heavy)	507.789124	2	17.6	646.328616	y5	1	48.58	54.25		
C4b-binding protein beta	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK	577.7570++	577.757032	2	20.3	750.370217	y6	1	46.12	41.01		

C4b-binding protein beta c	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK	577.7570++	577.757032	2	20.3	649.322539	y5	1	46.12	41.01		
C4b-binding protein beta c	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK	577.7570++	577.757032	2	20.3	518.282054	y4	1	46.12	41.01		
C4b-binding protein beta c	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK[+8.014199]	581.7641++ (heavy)	581.764131	2	20.3	758.384416	y6	1	46.12	41.01		
C4b-binding protein beta c	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK[+8.014199]	581.7641++ (heavy)	581.764131	2	20.3	657.336738	y5	1	46.12	41.01		
C4b-binding protein beta c	C4BPB	P20851	ESGMTMEELK	ESGMTMEELK[+8.014199]	581.7641++ (heavy)	581.764131	2	20.3	526.296253	y4	1	46.12	41.01		
Carboxypeptidase N subu	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK	801.4359++	801.435929	2	28.6	989.541457	y10	1	77.28	87.43	4.598794598	3.229331334
Carboxypeptidase N subu	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK	801.4359++	801.435929	2	28.6	732.403901	y7	1	77.28	87.43		
Carboxypeptidase N subu	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK	801.4359++	801.435929	2	28.6	351.202681	y3	1	77.28	87.43		
Carboxypeptidase N subu	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK[+8.014199]	805.4430++ (heavy)	805.443028	2	28.6	997.555656	y10	1	77.28	87.43		
Carboxypeptidase N subu	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK[+8.014199]	805.4430++ (heavy)	805.443028	2	28.6	740.4181	y7	1	77.28	87.43		
Carboxypeptidase N subu	CPN2	P22792	LSNNALSGLPQGVFGK	LSNNALSGLPQGVFGK[+8.014199]	805.4430++ (heavy)	805.443028	2	28.6	359.21688	y3	1	77.28	87.43		
Carboxypeptidase N subu	CPN2	P22792	LELLSLSK	LELLSLSK	451.7815++	451.781493	2	15.6	789.471646	y7	1	63.55	72.47		
Carboxypeptidase N subu	CPN2	P22792	LELLSLSK	LELLSLSK	451.7815++	451.781493	2	15.6	660.429053	y6	1	63.55	72.47		
Carboxypeptidase N subu	CPN2	P22792	LELLSLSK	LELLSLSK	451.7815++	451.781493	2	15.6	547.344989	y5	1	63.55	72.47		
Carboxypeptidase N subu	CPN2	P22792	LELLSLSK	LELLSLSK	451.7815++	451.781493	2	15.6	243.133933	b2	1	63.55	72.47		
Carboxypeptidase N subu	CPN2	P22792	LELLSLSK	LELLSLSK[+8.014199]	455.7886++ (heavy)	455.788592	2	15.6	797.485845	y7	1	63.55	72.47		
Carboxypeptidase N subu	CPN2	P22792	LELLSLSK	LELLSLSK[+8.014199]	455.7886++ (heavy)	455.788592	2	15.6	668.443252	y6	1	63.55	72.47		
Carboxypeptidase N subu	CPN2	P22792	LELLSLSK	LELLSLSK[+8.014199]	455.7886++ (heavy)	455.788592	2	15.6	555.359188	y5	1	63.55	72.47		
Carboxypeptidase N subu	CPN2	P22792	LELLSLSK	LELLSLSK[+8.014199]	455.7886++ (heavy)	455.788592	2	15.6	243.133933	b2	1	63.55	72.47		
Carboxypeptidase N subu	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER	644.8177++	644.817658	2	22.8	830.436657	y7	1	52.79	56.36		
Carboxypeptidase N subu	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER	644.8177++	644.817658	2	22.8	715.409714	y6	1	52.79	56.36		
Carboxypeptidase N subu	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER	644.8177++	644.817658	2	22.8	602.32565	y5	1	52.79	56.36		
Carboxypeptidase N subu	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER[+10.008269]	649.8218++ (heavy)	649.821792	2	22.8	840.444926	y7	1	52.79	56.36		
Carboxypeptidase N subu	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER[+10.008269]	649.8218++ (heavy)	649.821792	2	22.8	725.417983	y6	1	52.79	56.36		
Carboxypeptidase N subu	CPN2	P22792	AGGSWDLAVQER	AGGSWDLAVQER[+10.008269]	649.8218++ (heavy)	649.821792	2	22.8	612.333919	y5	1	52.79	56.36		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR	760.3750++	760.375006	2	27.1	1059.474165	y8	1	82.13	80.64	4.697400298	4.441388694
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR	760.3750++	760.375006	2	27.1	931.415587	y7	1	82.13	80.64		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR	760.3750++	760.375006	2	27.1	348.191782	b3	1	82.13	80.64		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR[+10.008269]	765.3791++ (heavy)	765.37914	2	27.1	1069.482434	y8	1	82.13	80.64		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR[+10.008269]	765.3791++ (heavy)	765.37914	2	27.1	941.423856	y7	1	82.13	80.64		
Ceruloplasmin	CP	P00450	ALYLQYTDETFR	ALYLQYTDETFR[+10.008269]	765.3791++ (heavy)	765.37914	2	27.1	348.191782	b3	1	82.13	80.64		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR	686.3852++	686.385176	2	24.3	1080.641171	y10	1	76.32	85.33		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR	686.3852++	686.385176	2	24.3	870.504343	y8	1	76.32	85.33		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR	686.3852++	686.385176	2	24.3	541.345657	y5	1	76.32	85.33		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR[+10.008269]	691.3893++ (heavy)	691.389311	2	24.3	1090.64944	y10	1	76.32	85.33		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR[+10.008269]	691.3893++ (heavy)	691.389311	2	24.3	880.512612	y8	1	76.32	85.33		
Ceruloplasmin	CP	P00450	GAYPLSIEPIGVR	GAYPLSIEPIGVR[+10.008269]	691.3893++ (heavy)	691.389311	2	24.3	551.353926	y5	1	76.32	85.33		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK	735.8665++	735.866491	2	26.2	802.412751	y7	1	39.31	50.51		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK	735.8665++	735.866491	2	26.2	687.385808	y6	1	39.31	50.51		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK	735.8665++	735.866491	2	26.2	491.26463	y4	1	39.31	50.51		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK[+8.014199]	739.8736++ (heavy)	739.87359	2	26.2	810.42695	y7	1	39.31	50.51		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK[+8.014199]	739.8736++ (heavy)	739.87359	2	26.2	695.400007	y6	1	39.31	50.51		
Ceruloplasmin	CP	P00450	EVGPTNADPVCLAK	EVGPTNADPVC[+57.021464]LAK[+8.014199]	739.8736++ (heavy)	739.87359	2	26.2	499.278829	y4	1	39.31	50.51		
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR	697.3515++	697.351531	2	24.7	1035.510551	y8	1	87.02	109.62	6.336883435	1.640036723
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR	697.3515++	697.351531	2	24.7	922.426487	y7	1	87.02	109.62		
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR	697.3515++	697.351531	2	24.7	678.35695	y5	1	87.02	109.62		
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR[+10.008269]	702.3557++ (heavy)	702.355665	2	24.7	1045.51882	y8	1	87.02	109.62		
Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR[+10.008269]	702.3557++ (heavy)	702.355665	2	24.7	932.434756	y7	1	87.02	109.62		

Clusterin	CLU	P10909	ASSIIDELFQDR	ASSIIDELFQDR[+10.008269]	702.3557++ (heavy)	702.355665	2	24.7	688.365219	y5	1	87.02	109.62		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR	667.3269+++	667.32688	3	22.7	853.467898	y7	1	79.81	81.45		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR	667.3269+++	667.32688	3	22.7	756.415134	y6	1	79.81	81.45		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR	667.3269+++	667.32688	3	22.7	609.34672	y5	1	79.81	81.45		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR	667.3269+++	667.32688	3	22.7	409.230627	y3	1	79.81	81.45		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR[+10.008269]	670.6630+++ (heavy)	670.662969	3	22.7	863.476167	y7	1	79.81	81.45		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR[+10.008269]	670.6630+++ (heavy)	670.662969	3	22.7	766.423403	y6	1	79.81	81.45		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR[+10.008269]	670.6630+++ (heavy)	670.662969	3	22.7	619.354989	y5	1	79.81	81.45		
Clusterin	CLU	P10909	EPQDTYHYLPFSLPHR	EPQDTYHYLPFSLPHR[+10.008269]	670.6630+++ (heavy)	670.662969	3	22.7	419.238896	y3	1	79.81	81.45		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER	644.8226++	644.822606	2	22.8	715.409714	y6	1	45.06	45.34		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER	644.8226++	644.822606	2	22.8	602.32565	y5	1	45.06	45.34		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER	644.8226++	644.822606	2	22.8	474.267073	y4	1	45.06	45.34		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER[+10.008269]	649.8267++ (heavy)	649.82674	2	22.8	725.417983	y6	1	45.06	45.34		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER[+10.008269]	649.8267++ (heavy)	649.82674	2	22.8	612.333919	y5	1	45.06	45.34		
Clusterin	CLU	P10909	ELDESLQVAER	ELDESLQVAER[+10.008269]	649.8267++ (heavy)	649.82674	2	22.8	484.275342	y4	1	45.06	45.34		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR	937.4989++	937.498923	2	33.6	1296.752178	y12	1	89.49	100.14		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR	937.4989++	937.498923	2	33.6	886.499258	y8	1	89.49	100.14		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR	937.4989++	937.498923	2	33.6	686.383165	y6	1	89.49	100.14		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR[+10.008269]	942.5031++ (heavy)	942.503058	2	33.6	1306.760447	y12	1	89.49	100.14		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR[+10.008269]	942.5031++ (heavy)	942.503058	2	33.6	896.507527	y8	1	89.49	100.14		
Clusterin	CLU	P10909	LFDSDPITVTVPVEVSR	LFDSDPITVTVPVEVSR[+10.008269]	942.5031++ (heavy)	942.503058	2	33.6	696.391434	y6	1	89.49	100.14		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK	683.3105++	683.310494	2	24.2	849.413479	y7	1	40.06	45.61	2.465347685	3.946459171
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK	683.3105++	683.310494	2	24.2	275.080852	b2	1	40.06	45.61		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK	683.3105++	683.310494	2	24.2	404.123445	b3	1	40.06	45.61		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK[+8.0	687.3176++ (heavy)	687.317594	2	24.2	857.427678	y7	1	40.06	45.61		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK[+8.0	687.3176++ (heavy)	687.317594	2	24.2	275.080852	b2	1	40.06	45.61		
Coagulation factor IX	F9	P00740	NCELDVTCNIK	NC[+57.021464]ELDVTC[+57.021464]NIK[+8.0	687.3176++ (heavy)	687.317594	2	24.2	404.123445	b3	1	40.06	45.61		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK	698.3323++	698.332284	2	24.8	963.456407	y9	1	48.06	51.09		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK	698.3323++	698.332284	2	24.8	390.198324	y3	1	48.06	51.09		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK	698.3323++	698.332284	2	24.8	286.139747	b3	1	48.06	51.09		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK[+8.014199]	702.3394++ (heavy)	702.339383	2	24.8	971.470606	y9	1	48.06	51.09		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK[+8.014199]	702.3394++ (heavy)	702.339383	2	24.8	398.212523	y3	1	48.06	51.09		
Coagulation factor IX	F9	P00740	VDAFCGGSIVNEK	VDAFC[+57.021464]GGSIVNEK[+8.014199]	702.3394++ (heavy)	702.339383	2	24.8	286.139747	b3	1	48.06	51.09		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR	531.8189++	531.818941	2	18.6	791.4774	y6	1	75.85	83.35		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR	531.8189++	531.818941	2	18.6	692.408986	y5	1	75.85	83.35		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR	531.8189++	531.818941	2	18.6	579.324922	y4	1	75.85	83.35		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR	531.8189++	531.818941	2	18.6	272.160482	b3	1	75.85	83.35		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR[+10.008269]	536.8231++ (heavy)	536.823076	2	18.6	801.485669	y6	1	75.85	83.35		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR[+10.008269]	536.8231++ (heavy)	536.823076	2	18.6	702.417255	y5	1	75.85	83.35		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR[+10.008269]	536.8231++ (heavy)	536.823076	2	18.6	589.333191	y4	1	75.85	83.35		
Coagulation factor IX	F9	P00740	SALVLQYLR	SALVLQYLR[+10.008269]	536.8231++ (heavy)	536.823076	2	18.6	272.160482	b3	1	75.85	83.35		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK	660.8074++	660.80739	2	23.4	976.455678	y9	1	28.97	43.87	4.8198533	5.792112789
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK	660.8074++	660.80739	2	23.4	778.355236	y7	1	28.97	43.87		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK	660.8074++	660.80739	2	23.4	461.21768	y4	1	28.97	43.87		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK	660.8074++	660.80739	2	23.4	232.075038	b2	1	28.97	43.87		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK[+8.	664.8145++ (heavy)	664.81449	2	23.4	984.469877	y9	1	28.97	43.87		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK[+8.	664.8145++ (heavy)	664.81449	2	23.4	786.369435	y7	1	28.97	43.87		
Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK[+8.	664.8145++ (heavy)	664.81449	2	23.4	469.231879	y4	1	28.97	43.87		

Coagulation factor X	F10	P00742	ACIPTGPYPCGK	AC[+57.021464]IPTGPYPC[+57.021464]GK[+8.	664.8145++ (heavy)	664.81449	2	23.4	232.075038	b2	1	28.97	43.87		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR	671.3379++	671.337892	2	23.8	833.487965	y7	1	88	95.6		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR	671.3379++	671.337892	2	23.8	686.419551	y6	1	88	95.6		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR	671.3379++	671.337892	2	23.8	571.392608	y5	1	88	95.6		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR	671.3379++	671.337892	2	23.8	458.308544	y4	1	88	95.6		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR[+10.008269]	676.3420++ (heavy)	676.342026	2	23.8	843.496234	y7	1	88	95.6		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR[+10.008269]	676.3420++ (heavy)	676.342026	2	23.8	696.42782	y6	1	88	95.6		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR[+10.008269]	676.3420++ (heavy)	676.342026	2	23.8	581.400877	y5	1	88	95.6		
Coagulation factor X	F10	P00742	ETYDFDIAVLR	ETYDFDIAVLR[+10.008269]	676.3420++ (heavy)	676.342026	2	23.8	468.316813	y4	1	88	95.6		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR	561.2866++	561.286616	2	19.7	748.398815	y6	1	58.6	69.59		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR	561.2866++	561.286616	2	19.7	649.330401	y5	1	58.6	69.59		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR	561.2866++	561.286616	2	19.7	374.174418	b3	1	58.6	69.59		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR[+10.008269]	566.2908++ (heavy)	566.290751	2	19.7	758.407084	y6	1	58.6	69.59		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR[+10.008269]	566.2908++ (heavy)	566.290751	2	19.7	659.33867	y5	1	58.6	69.59		
Coagulation factor X	F10	P00742	MLEVPYVDR	MLEVPYVDR[+10.008269]	566.2908++ (heavy)	566.290751	2	19.7	374.174418	b3	1	58.6	69.59		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER	705.3381++	705.338097	2	25	848.447222	y8	1	39.44	34.21	6.549987998	2.014346005
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER	705.3381++	705.338097	2	25	749.378808	y7	1	39.44	34.21		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER	705.3381++	705.338097	2	25	636.294744	y6	1	39.44	34.21		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER[+10.008269]	710.3422++ (heavy)	710.342232	2	25	858.455491	y8	1	39.44	34.21		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER[+10.008269]	710.3422++ (heavy)	710.342232	2	25	759.387077	y7	1	39.44	34.21		
Complement C2	C2	P06681	CSSNLVLTGSSER	C[+57.021464]SSNLVLTGSSER[+10.008269]	710.3422++ (heavy)	710.342232	2	25	646.303013	y6	1	39.44	34.21		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK	625.8426++	625.842613	2	22.1	967.488358	y9	1	80.28	91.01		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK	625.8426++	625.842613	2	22.1	880.45633	y8	1	80.28	91.01		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK	625.8426++	625.842613	2	22.1	783.403566	y7	1	80.28	91.01		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK[+8.014199]	629.8497++ (heavy)	629.849713	2	22.1	975.502558	y9	1	80.28	91.01		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK[+8.014199]	629.8497++ (heavy)	629.849713	2	22.1	888.470529	y8	1	80.28	91.01		
Complement C2	C2	P06681	AVISPGFDVFAK	AVISPGFDVFAK[+8.014199]	629.8497++ (heavy)	629.849713	2	22.1	791.417765	y7	1	80.28	91.01		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER	561.2829++	561.28292	2	19.7	935.494506	y9	1	48.77	46.11		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER	561.2829++	561.28292	2	19.7	663.382437	y5	1	48.77	46.11		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER	561.2829++	561.28292	2	19.7	564.314023	y4	1	48.77	46.11		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER[+10.008269]	566.2871++ (heavy)	566.287054	2	19.7	945.502776	y9	1	48.77	46.11		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER[+10.008269]	566.2871++ (heavy)	566.287054	2	19.7	673.390706	y5	1	48.77	46.11		
Complement C2	C2	P06681	GESGGAVFLER	GESGGAVFLER[+10.008269]	566.2871++ (heavy)	566.287054	2	19.7	574.322292	y4	1	48.77	46.11		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHLGDVLNFLPL	683.3799++	683.379894	2	24.2	877.452642	b8	1	125.95	131.47		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHLGDVLNFLPL	683.3799++	683.379894	2	24.2	1024.521056	b9	1	125.95	131.47		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHLGDVLNFLPL	683.3799++	683.379894	2	24.2	1137.60512	b10	1	125.95	131.47		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHL[+7.017164]GDVLNFLPL	686.8885++ (heavy)	686.888476	2	24.2	884.469806	b8	1	125.95	131.47		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHL[+7.017164]GDVLNFLPL	686.8885++ (heavy)	686.888476	2	24.2	1031.53822	b9	1	125.95	131.47		
Complement C2	C2	P06681	QHLGDVLNFLPL	QHL[+7.017164]GDVLNFLPL	686.8885++ (heavy)	686.888476	2	24.2	1144.622284	b10	1	125.95	131.47		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK	554.8055++	554.805499	2	19.5	846.47198	y7	1	68.39	79.56	4.366580266	5.04089283
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK	554.8055++	554.805499	2	19.5	733.387916	y6	1	68.39	79.56		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK	554.8055++	554.805499	2	19.5	263.139019	b2	1	68.39	79.56		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK[+8.014199]	558.8126++ (heavy)	558.812599	2	19.5	854.486179	y7	1	68.39	79.56		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK[+8.014199]	558.8126++ (heavy)	558.812599	2	19.5	741.402115	y6	1	68.39	79.56		
Complement C4-B	C4B	P0C0L5	YVLPNFEVK	YVLPNFEVK[+8.014199]	558.8126++ (heavy)	558.812599	2	19.5	263.139019	b2	1	68.39	79.56		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK	525.7587++	525.758746	2	18.4	850.430509	y7	1	39.87	39.51		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK	525.7587++	525.758746	2	18.4	703.362095	y6	1	39.87	39.51		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK	525.7587++	525.758746	2	18.4	575.303518	y5	1	39.87	39.51		

Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK[+8.014199]	529.7658++ (heavy)	529.765846	2	18.4	858.444708	y7	1	39.87	39.51		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK[+8.014199]	529.7658++ (heavy)	529.765846	2	18.4	711.376294	y6	1	39.87	39.51		
Complement C4-B	C4B	P0C0L5	AEFQDALEK	AEFQDALEK[+8.014199]	529.7658++ (heavy)	529.765846	2	18.4	583.317717	y5	1	39.87	39.51		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR	557.8144++	557.814387	2	19.6	1015.553084	y9	1	56.9	62		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR	557.8144++	557.814387	2	19.6	742.456999	y6	1	56.9	62		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR	557.8144++	557.814387	2	19.6	629.372935	y5	1	56.9	62		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR[+10.008269]	562.8185++ (heavy)	562.818521	2	19.6	1025.561353	y9	1	56.9	62		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR[+10.008269]	562.8185++ (heavy)	562.818521	2	19.6	752.465268	y6	1	56.9	62		
Complement C4-B	C4B	P0C0L5	VGDTLNLNLR	VGDTLNLNLR[+10.008269]	562.8185++ (heavy)	562.818521	2	19.6	639.381204	y5	1	56.9	62		
Complement component C	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K	748.8561++	748.856123	2	26.6	1098.488435	y10	1	59.31	63.04	4.415944589	4.403072098
Complement component C	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K	748.8561++	748.856123	2	26.6	534.270444	y5	1	59.31	63.04		
Complement component C	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K	748.8561++	748.856123	2	26.6	286.139747	b3	1	59.31	63.04		
Complement component C	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K[+8.014199]	752.8632++ (heavy)	752.863222	2	26.6	1106.502634	y10	1	59.31	63.04		
Complement component C	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K[+8.014199]	752.8632++ (heavy)	752.863222	2	26.6	542.284643	y5	1	59.31	63.04		
Complement component C	C6	P13671	GEVLDNSFTGGICK	GEVLDNSFTGGIC[+57.021464]K[+8.014199]	752.8632++ (heavy)	752.863222	2	26.6	286.139747	b3	1	59.31	63.04		
Complement component C	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR	620.9916+++	620.991608	3	21	609.335487	y5	1	82.87	75.87		
Complement component C	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR	620.9916+++	620.991608	3	21	538.298373	y4	1	82.87	75.87		
Complement component C	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR	620.9916+++	620.991608	3	21	425.214309	y3	1	82.87	75.87		
Complement component C	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR	620.9916+++	620.991608	3	21	549.314357	b5	1	82.87	75.87		
Complement component C	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR[+10.008269]	624.3277+++ (heavy)	624.327698	3	21	619.343756	y5	1	82.87	75.87		
Complement component C	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR[+10.008269]	624.3277+++ (heavy)	624.327698	3	21	548.306642	y4	1	82.87	75.87		
Complement component C	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR[+10.008269]	624.3277+++ (heavy)	624.327698	3	21	435.222578	y3	1	82.87	75.87		
Complement component C	C6	P13671	ALNHLPLEYNSALYSR	ALNHLPLEYNSALYSR[+10.008269]	624.3277+++ (heavy)	624.327698	3	21	549.314357	b5	1	82.87	75.87		
Complement component C	C6	P13671	SEYGAALAWEK	SEYGAALAWEK	612.7984++	612.798403	2	21.6	1008.514908	y9	1	58.81	62		
Complement component C	C6	P13671	SEYGAALAWEK	SEYGAALAWEK	612.7984++	612.798403	2	21.6	845.451579	y8	1	58.81	62		
Complement component C	C6	P13671	SEYGAALAWEK	SEYGAALAWEK	612.7984++	612.798403	2	21.6	717.393001	y6	1	58.81	62		
Complement component C	C6	P13671	SEYGAALAWEK	SEYGAALAWEK[+8.014199]	616.8055++ (heavy)	616.805502	2	21.6	1016.529107	y9	1	58.81	62		
Complement component C	C6	P13671	SEYGAALAWEK	SEYGAALAWEK[+8.014199]	616.8055++ (heavy)	616.805502	2	21.6	853.465778	y8	1	58.81	62		
Complement component C	C6	P13671	SEYGAALAWEK	SEYGAALAWEK[+8.014199]	616.8055++ (heavy)	616.805502	2	21.6	725.4072	y6	1	58.81	62		
Complement component C	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR	638.3399++	638.339912	2	22.6	1061.540805	y9	1	53.9	66.73		
Complement component C	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR	638.3399++	638.339912	2	22.6	947.497878	y8	1	53.9	66.73		
Complement component C	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR	638.3399++	638.339912	2	22.6	834.413814	y7	1	53.9	66.73		
Complement component C	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR[+10.008269]	643.3440++ (heavy)	643.344046	2	22.6	1071.549074	y9	1	53.9	66.73		
Complement component C	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR[+10.008269]	643.3440++ (heavy)	643.344046	2	22.6	957.506147	y8	1	53.9	66.73		
Complement component C	C6	P13671	TLNICEVGTIR	TLNIC[+57.021464]EVGTIR[+10.008269]	643.3440++ (heavy)	643.344046	2	22.6	844.422083	y7	1	53.9	66.73		
Complement component C	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK	968.9333++	968.933287	2	34.8	726.414465	y7	1	39.7	46.98	5.964573054	4.149751869
Complement component C	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK	968.9333++	968.933287	2	34.8	516.277637	y5	1	39.7	46.98		
Complement component C	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK	968.9333++	968.933287	2	34.8	362.20341	y3	1	39.7	46.98		
Complement component C	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK[+8.01419	972.9404++ (heavy)	972.940387	2	34.8	734.428664	y7	1	39.7	46.98		
Complement component C	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK[+8.01419	972.9404++ (heavy)	972.940387	2	34.8	524.291836	y5	1	39.7	46.98		
Complement component C	C8A	P07357	AIDEDCSQYEPIPGSQK	AIDEDC[+57.021464]SQYEPIPGSQK[+8.01419	972.9404++ (heavy)	972.940387	2	34.8	370.217609	y3	1	39.7	46.98		
Complement component C	C8A	P07357	MESLGITSR	MESLGITSR	497.2553++	497.255316	2	17.3	733.420279	y7	1	34.37	38.14		
Complement component C	C8A	P07357	MESLGITSR	MESLGITSR	497.2553++	497.255316	2	17.3	646.38825	y6	1	34.37	38.14		
Complement component C	C8A	P07357	MESLGITSR	MESLGITSR	497.2553++	497.255316	2	17.3	533.304186	y5	1	34.37	38.14		
Complement component C	C8A	P07357	MESLGITSR	MESLGITSR	497.2553++	497.255316	2	17.3	348.122382	b3	1	34.37	38.14		
Complement component C	C8A	P07357	MESLGITSR	MESLGITSR[+10.008269]	502.2595++ (heavy)	502.259451	2	17.3	743.428548	y7	1	34.37	38.14		
Complement component C	C8A	P07357	MESLGITSR	MESLGITSR[+10.008269]	502.2595++ (heavy)	502.259451	2	17.3	656.396519	y6	1	34.37	38.14		
Complement component C	C8A	P07357	MESLGITSR	MESLGITSR[+10.008269]	502.2595++ (heavy)	502.259451	2	17.3	543.312455	y5	1	34.37	38.14		

Complement component (	C8A	P07357	MESLGITSR	MESLGITSR[+10.008269]	502.2595++ (heavy)	502.259451	2	17.3	348.122382	b3	1	34.37	38.14		
Complement component (	C8A	P07357	AMAVEDIISR	AMAVEDIISR	552.7895++	552.789523	2	19.4	902.494172	y8	1	58.42	65.68		
Complement component (	C8A	P07357	AMAVEDIISR	AMAVEDIISR	552.7895++	552.789523	2	19.4	831.457058	y7	1	58.42	65.68		
Complement component (	C8A	P07357	AMAVEDIISR	AMAVEDIISR	552.7895++	552.789523	2	19.4	732.388644	y6	1	58.42	65.68		
Complement component (	C8A	P07357	AMAVEDIISR	AMAVEDIISR[+10.008269]	557.7937++ (heavy)	557.793658	2	19.4	912.502441	y8	1	58.42	65.68		
Complement component (	C8A	P07357	AMAVEDIISR	AMAVEDIISR[+10.008269]	557.7937++ (heavy)	557.793658	2	19.4	841.465327	y7	1	58.42	65.68		
Complement component (	C8A	P07357	AMAVEDIISR	AMAVEDIISR[+10.008269]	557.7937++ (heavy)	557.793658	2	19.4	742.396913	y6	1	58.42	65.68		
Complement component (	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK	860.9122++	860.912158	2	30.8	1350.59542	y13	1	27.98	30.75		
Complement component (	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK	860.9122++	860.912158	2	30.8	1222.536842	y11	1	27.98	30.75		
Complement component (	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK	860.9122++	860.912158	2	30.8	1151.499728	y10	1	27.98	30.75		
Complement component (	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK[+8.0141	864.9193++ (heavy)	864.919257	2	30.8	1358.609618	y13	1	27.98	30.75		
Complement component (	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK[+8.0141	864.9193++ (heavy)	864.919257	2	30.8	1230.551041	y11	1	27.98	30.75		
Complement component (	C8A	P07357	LGSLGAACEQTQTEGAK	LGSLGAAC[+57.021464]EQTQTEGAK[+8.0141	864.9193++ (heavy)	864.919257	2	30.8	1159.513927	y10	1	27.98	30.75		
Complement component (	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR	642.7766++	642.776622	2	22.7	995.472725	y9	1	27.53	28.79	5.170409929	0.765846118
Complement component (	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR	642.7766++	642.776622	2	22.7	791.382848	y7	1	27.53	28.79		
Complement component (	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR	642.7766++	642.776622	2	22.7	692.314434	y6	1	27.53	28.79		
Complement component (	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR[+1	647.7808++ (heavy)	647.780756	2	22.7	1005.480994	y9	1	27.53	28.79		
Complement component (	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR[+1	647.7808++ (heavy)	647.780756	2	22.7	801.391117	y7	1	27.53	28.79		
Complement component (	C8B	P07358	CEGFVCAQTGR	C[+57.021464]EGFVC[+57.021464]AQTGR[+1	647.7808++ (heavy)	647.780756	2	22.7	702.322703	y6	1	27.53	28.79		
Complement component (	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR	695.3379++	695.337892	2	24.7	1179.53168	y9	1	66.47	67.05		
Complement component (	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR	695.3379++	695.337892	2	24.7	1066.447616	y8	1	66.47	67.05		
Complement component (	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR	695.3379++	695.337892	2	24.7	937.405023	y7	1	66.47	67.05		
Complement component (	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR	695.3379++	695.337892	2	24.7	774.341694	y6	1	66.47	67.05		
Complement component (	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR[+10.008269]	700.3420++ (heavy)	700.342026	2	24.7	1189.539949	y9	1	66.47	67.05		
Complement component (	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR[+10.008269]	700.3420++ (heavy)	700.342026	2	24.7	1076.455885	y8	1	66.47	67.05		
Complement component (	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR[+10.008269]	700.3420++ (heavy)	700.342026	2	24.7	947.413292	y7	1	66.47	67.05		
Complement component (	C8B	P07358	LPLEYSYGEYR	LPLEYSYGEYR[+10.008269]	700.3420++ (heavy)	700.342026	2	24.7	784.349963	y6	1	66.47	67.05		
Complement component (	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR	573.7899++	573.789858	2	20.2	748.355905	y5	1	62.79	71.22	3.798720231	7.713830267
Complement component (	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR	573.7899++	573.789858	2	20.2	588.325256	y4	1	62.79	71.22		
Complement component (	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR	573.7899++	573.789858	2	20.2	286.139747	b3	1	62.79	71.22		
Complement component (	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR[+10.008269]	578.7940++ (heavy)	578.793992	2	20.2	758.364174	y5	1	62.79	71.22		
Complement component (	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR[+10.008269]	578.7940++ (heavy)	578.793992	2	20.2	598.333525	y4	1	62.79	71.22		
Complement component (	C8G	P07360	LDGICWQVR	LDGIC[+57.021464]WQVR[+10.008269]	578.7940++ (heavy)	578.793992	2	20.2	286.139747	b3	1	62.79	71.22		
Complement component (	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR	589.8118++	589.811844	2	20.8	937.473771	y9	1	48.57	51.08		
Complement component (	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR	589.8118++	589.811844	2	20.8	774.410442	y8	1	48.57	51.08		
Complement component (	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR	589.8118++	589.811844	2	20.8	602.362036	y6	1	48.57	51.08		
Complement component (	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR	589.8118++	589.811844	2	20.8	345.22448	y3	1	48.57	51.08		
Complement component (	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR[+10.008269]	594.8160++ (heavy)	594.815979	2	20.8	947.48204	y9	1	48.57	51.08		
Complement component (	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR[+10.008269]	594.8160++ (heavy)	594.815979	2	20.8	784.418711	y8	1	48.57	51.08		
Complement component (	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR[+10.008269]	594.8160++ (heavy)	594.815979	2	20.8	612.370305	y6	1	48.57	51.08		
Complement component (	C8G	P07360	QLYGDTGVLGR	QLYGDTGVLGR[+10.008269]	594.8160++ (heavy)	594.815979	2	20.8	355.232748	y3	1	48.57	51.08		
Complement component (	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR	810.9150++	810.915026	2	28.9	1224.585506	y11	1	81.33	88.93		
Complement component (	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR	810.9150++	810.915026	2	28.9	836.426093	y7	1	81.33	88.93		
Complement component (	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR	810.9150++	810.915026	2	28.9	723.342029	y6	1	81.33	88.93		
Complement component (	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR	810.9150++	810.915026	2	28.9	636.31	y5	1	81.33	88.93		
Complement component (	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR[+10.008269]	815.9192++ (heavy)	815.919161	2	28.9	1234.593775	y11	1	81.33	88.93		
Complement component (	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR[+10.008269]	815.9192++ (heavy)	815.919161	2	28.9	846.434362	y7	1	81.33	88.93		
Complement component (	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR[+10.008269]	815.9192++ (heavy)	815.919161	2	28.9	733.350298	y6	1	81.33	88.93		

Complement component (	C8G	P07360	SLPVSDSVLSGFEQR	SLPVSDSVLSGFEQR[+10.008269]	815.9192++ (heavy)	815.919161	2	28.9	646.318269	y5	1	81.33	88.93		
Complement component (	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK	655.6633+++	655.663269	3	22.3	814.449788	y6	1	90.59	87.29		
Complement component (	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK	655.6633+++	655.663269	3	22.3	701.365724	y5	1	90.59	87.29		
Complement component (	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK	655.6633+++	655.663269	3	22.3	554.29731	y4	1	90.59	87.29		
Complement component (	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK	655.6633+++	655.663269	3	22.3	391.233982	y3	1	90.59	87.29		
Complement component (	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK[+8.014199]	658.3347+++ (heavy)	658.334669	3	22.3	822.463987	y6	1	90.59	87.29		
Complement component (	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK[+8.014199]	658.3347+++ (heavy)	658.334669	3	22.3	709.379923	y5	1	90.59	87.29		
Complement component (	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK[+8.014199]	658.3347+++ (heavy)	658.334669	3	22.3	562.311509	y4	1	90.59	87.29		
Complement component (	C8G	P07360	VQEAHLTEDQIFYFPK	VQEAHLTEDQIFYFPK[+8.014199]	658.3347+++ (heavy)	658.334669	3	22.3	399.248181	y3	1	90.59	87.29		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK	638.3346++	638.334621	2	22.6	942.49311	y8	1	66.66	64.9	7.428136166	4.337436473
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK	638.3346++	638.334621	2	22.6	843.424696	y7	1	66.66	64.9		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK	638.3346++	638.334621	2	22.6	334.176132	b3	1	66.66	64.9		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK[+8.014199]	642.3417++ (heavy)	642.34172	2	22.6	950.507309	y8	1	66.66	64.9		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK[+8.014199]	642.3417++ (heavy)	642.34172	2	22.6	851.438895	y7	1	66.66	64.9		
Complement factor B	CFB	P00751	YGLVTYATYPK	YGLVTYATYPK[+8.014199]	642.3417++ (heavy)	642.34172	2	22.6	334.176132	b3	1	66.66	64.9		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK	411.2420++	411.242004	2	14.1	593.365724	y5	1	53.17	60.74		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK	411.2420++	411.242004	2	14.1	480.28166	y4	1	53.17	60.74		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK	411.2420++	411.242004	2	14.1	229.118283	b2	1	53.17	60.74		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK[+8.014199]	415.2491++ (heavy)	415.249103	2	14.1	601.379923	y5	1	53.17	60.74		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK[+8.014199]	415.2491++ (heavy)	415.249103	2	14.1	488.295859	y4	1	53.17	60.74		
Complement factor B	CFB	P00751	DLLYIGK	DLLYIGK[+8.014199]	415.2491++ (heavy)	415.249103	2	14.1	229.118283	b2	1	53.17	60.74		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK	526.2689++	526.268947	2	18.4	867.409439	y7	1	43.01	39.71		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK	526.2689++	526.268947	2	18.4	720.341026	y6	1	43.01	39.71		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK	526.2689++	526.268947	2	18.4	621.272612	y5	1	43.01	39.71		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK[+8.014199]	530.2760++ (heavy)	530.276046	2	18.4	875.423638	y7	1	43.01	39.71		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK[+8.014199]	530.2760++ (heavy)	530.276046	2	18.4	728.355225	y6	1	43.01	39.71		
Complement factor B	CFB	P00751	ALFVSEEEK	ALFVSEEEK[+8.014199]	530.2760++ (heavy)	530.276046	2	18.4	629.286811	y5	1	43.01	39.71		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK	465.9329+++	465.932919	3	15.4	881.509094	y7	1	78.41	73.96	5.194613296	3.025619327
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK	465.9329+++	465.932919	3	15.4	768.42503	y6	1	78.41	73.96		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK	465.9329+++	465.932919	3	15.4	655.340966	y5	1	78.41	73.96		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK[+8.014199]	468.6043+++ (heavy)	468.604319	3	15.4	889.523293	y7	1	78.41	73.96		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK[+8.014199]	468.6043+++ (heavy)	468.604319	3	15.4	776.439229	y6	1	78.41	73.96		
Complement factor H	CFH	P08603	SSNLIILEEHLK	SSNLIILEEHLK[+8.014199]	468.6043+++ (heavy)	468.604319	3	15.4	663.355165	y5	1	78.41	73.96		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR	595.2690++	595.268955	2	21	989.414542	y8	1	43.14	43.45		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR	595.2690++	595.268955	2	21	826.351213	y7	1	43.14	43.45		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR	595.2690++	595.268955	2	21	725.303535	y6	1	43.14	43.45		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR[+10.008269]	600.2731++ (heavy)	600.27309	2	21	999.422811	y8	1	43.14	43.45		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR[+10.008269]	600.2731++ (heavy)	600.27309	2	21	836.359482	y7	1	43.14	43.45		
Complement factor H	CFH	P08603	LSYTCEGGFR	LSYTC[+57.021464]EGGFR[+10.008269]	600.2731++ (heavy)	600.27309	2	21	735.311804	y6	1	43.14	43.45		
Complement factor H-relat	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK	738.3454++	738.345391	2	26.3	901.441408	y8	1	45.27	43.18	5.906252545	5.252912222
Complement factor H-relat	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK	738.3454++	738.345391	2	26.3	772.398815	y7	1	45.27	43.18		
Complement factor H-relat	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK	738.3454++	738.345391	2	26.3	529.298038	y5	1	45.27	43.18		
Complement factor H-relat	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK[+8.014199]	742.3525++ (heavy)	742.352491	2	26.3	909.455607	y8	1	45.27	43.18		
Complement factor H-relat	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK[+8.014199]	742.3525++ (heavy)	742.352491	2	26.3	780.413014	y7	1	45.27	43.18		
Complement factor H-relat	CFHR2	P36980	ITCAEEGWSPTPK	ITC[+57.021464]AEEGWSPTPK[+8.014199]	742.3525++ (heavy)	742.352491	2	26.3	537.312237	y5	1	45.27	43.18		
Complement factor H-relat	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK	562.7683++	562.768257	2	19.8	912.376759	y7	1	24.08	28.1		
Complement factor H-relat	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK	562.7683++	562.768257	2	19.8	749.313431	y6	1	24.08	28.1		
Complement factor H-relat	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK	562.7683++	562.768257	2	19.8	652.260667	y5	1	24.08	28.1		

Complement factor H-relat	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK[+8.014199]	566.7754++ (heavy)	566.775356	2	19.8	920.390958	y7	1	24.08	28.1		
Complement factor H-relat	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK[+8.014199]	566.7754++ (heavy)	566.775356	2	19.8	757.32763	y6	1	24.08	28.1		
Complement factor H-relat	CFHR2	P36980	LVYPSCEEK	LVYPSC[+57.021464]EEK[+8.014199]	566.7754++ (heavy)	566.775356	2	19.8	660.274866	y5	1	24.08	28.1		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK	706.3512++	706.351196	2	25.1	1211.579024	y10	1	39.82	38.45	7.318074262	3.965110851
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK	706.3512++	706.351196	2	25.1	1048.515696	y9	1	39.82	38.45		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK	706.3512++	706.351196	2	25.1	947.468017	y8	1	39.82	38.45		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK[+8.014199]	710.3583++ (heavy)	710.358296	2	25.1	1219.593223	y10	1	39.82	38.45		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK[+8.014199]	710.3583++ (heavy)	710.358296	2	25.1	1056.529895	y9	1	39.82	38.45		
Complement factor I	CFI	P05156	VTYTSQEDLVEK	VTYTSQEDLVEK[+8.014199]	710.3583++ (heavy)	710.358296	2	25.1	955.482216	y8	1	39.82	38.45		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK	728.8530++	728.853049	2	25.9	969.470994	y8	1	60.39	66.83		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK	728.8530++	728.853049	2	25.9	856.38693	y7	1	60.39	66.83		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK	728.8530++	728.853049	2	25.9	785.349816	y6	1	60.39	66.83		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK[+8.014199]	732.8601++ (heavy)	732.860148	2	25.9	977.485193	y8	1	60.39	66.83		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK[+8.014199]	732.8601++ (heavy)	732.860148	2	25.9	864.401129	y7	1	60.39	66.83		
Complement factor I	CFI	P05156	GLETSLAECTFTK	GLETSLAEC[+57.021464]TFTK[+8.014199]	732.8601++ (heavy)	732.860148	2	25.9	793.364015	y6	1	60.39	66.83		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR	503.7820++	503.782024	2	17.6	794.404294	y6	1	49.21	53.29		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR	503.7820++	503.782024	2	17.6	681.32023	y5	1	49.21	53.29		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR	503.7820++	503.782024	2	17.6	552.277637	y4	1	49.21	53.29		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR[+10.008269]	508.7862++ (heavy)	508.786159	2	17.6	804.412563	y6	1	49.21	53.29		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR[+10.008269]	508.7862++ (heavy)	508.786159	2	17.6	691.328499	y5	1	49.21	53.29		
Complement factor I	CFI	P05156	IVIEYVDR	IVIEYVDR[+10.008269]	508.7862++ (heavy)	508.786159	2	17.6	562.285906	y4	1	49.21	53.29		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK	596.8217++	596.821681	2	21	946.499258	y8	1	77.16	87.15		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK	596.8217++	596.821681	2	21	746.383165	y6	1	77.16	87.15		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK	596.8217++	596.821681	2	21	618.324588	y5	1	77.16	87.15		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK[+8.014199]	600.8288++ (heavy)	600.82878	2	21	954.513457	y8	1	77.16	87.15		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK[+8.014199]	600.8288++ (heavy)	600.82878	2	21	754.397364	y6	1	77.16	87.15		
Complement factor I	CFI	P05156	VFSLQWGEVK	VFSLQWGEVK[+8.014199]	600.8288++ (heavy)	600.82878	2	21	626.338787	y5	1	77.16	87.15		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR	557.2774++	557.27744	2	19.6	865.431512	y7	1	52.68	40.7	6.425940703	4.254625556
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR	557.2774++	557.27744	2	19.6	794.394398	y6	1	52.68	40.7		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR	557.2774++	557.27744	2	19.6	657.335487	y5	1	52.68	40.7		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR[+10.008269]	562.2816++ (heavy)	562.281575	2	19.6	875.439781	y7	1	52.68	40.7		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR[+10.008269]	562.2816++ (heavy)	562.281575	2	19.6	804.402667	y6	1	52.68	40.7		
Ficolin-3	FCN3	O75636	TFAHYATFR	TFAHYATFR[+10.008269]	562.2816++ (heavy)	562.281575	2	19.6	667.343756	y5	1	52.68	40.7		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR	512.7460++	512.745973	2	17.9	861.421342	y8	1	50.26	57.08		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR	512.7460++	512.745973	2	17.9	691.315814	y6	1	50.26	57.08		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR	512.7460++	512.745973	2	17.9	390.209558	y4	1	50.26	57.08		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR[+10.008269]	517.7501++ (heavy)	517.750108	2	17.9	871.429611	y8	1	50.26	57.08		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR[+10.008269]	517.7501++ (heavy)	517.750108	2	17.9	701.324083	y6	1	50.26	57.08		
Ficolin-3	FCN3	O75636	YGIDWASGR	YGIDWASGR[+10.008269]	517.7501++ (heavy)	517.750108	2	17.9	400.217827	y4	1	50.26	57.08		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR	425.9104+++	425.910449	3	14	501.314357	y4	1	38.85	30.25	5.539146744	1.776406171
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR	425.9104+++	425.910449	3	14	402.245943	y3	1	38.85	30.25		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR	425.9104+++	425.910449	3	14	676.3413	b6	1	38.85	30.25		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR[+10.008269]	429.2465+++ (heavy)	429.246539	3	14	511.322626	y4	1	38.85	30.25		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR[+10.008269]	429.2465+++ (heavy)	429.246539	3	14	412.254212	y3	1	38.85	30.25		
Gelsolin	GSN	P06396	HVVPNEVVVQR	HVVPNEVVVQR[+10.008269]	429.2465+++ (heavy)	429.246539	3	14	676.3413	b6	1	38.85	30.25		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK	440.8678+++	440.86781	3	14.5	682.38825	y6	1	48.13	42.81		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK	440.8678+++	440.86781	3	14.5	569.304186	y5	1	48.13	42.81		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK	440.8678+++	440.86781	3	14.5	456.220122	y4	1	48.13	42.81		

Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK[+8.014199]	443.5392+++ (heavy)	443.53921	3	14.5	690.402449	y6	1	48.13	42.81		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK[+8.014199]	443.5392+++ (heavy)	443.53921	3	14.5	577.318385	y5	1	48.13	42.81		
Gelsolin	GSN	P06396	SEDCFILDHGK	SEDC[+57.021464]FILDHGK[+8.014199]	443.5392+++ (heavy)	443.53921	3	14.5	464.234321	y4	1	48.13	42.81		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK	915.4858++	915.485816	2	32.8	1187.630666	y11	1	82.81	87.42		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK	915.4858++	915.485816	2	32.8	1074.546602	y10	1	82.81	87.42		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK	915.4858++	915.485816	2	32.8	504.318046	y4	1	82.81	87.42		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK[+8.014199]	919.4929++ (heavy)	919.492915	2	32.8	1195.644865	y11	1	82.81	87.42		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK[+8.014199]	919.4929++ (heavy)	919.492915	2	32.8	1082.560801	y10	1	82.81	87.42		
Gelsolin	GSN	P06396	QTQVSVLPEGGETPLFK	QTQVSVLPEGGETPLFK[+8.014199]	919.4929++ (heavy)	919.492915	2	32.8	512.332245	y4	1	82.81	87.42		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	660.3513++	660.351334	2	23.4	1007.515636	y9	1	64.37	63.98		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	660.3513++	660.351334	2	23.4	893.472708	y8	1	64.37	63.98		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	660.3513++	660.351334	2	23.4	806.44068	y7	1	64.37	63.98		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK	660.3513++	660.351334	2	23.4	692.397753	y6	1	64.37	63.98		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8.014199]	664.3584++ (heavy)	664.358433	2	23.4	1015.529835	y9	1	64.37	63.98		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8.014199]	664.3584++ (heavy)	664.358433	2	23.4	901.486907	y8	1	64.37	63.98		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8.014199]	664.3584++ (heavy)	664.358433	2	23.4	814.454879	y7	1	64.37	63.98		
Gelsolin	GSN	P06396	AGALNSNDAFVLK	AGALNSNDAFVLK[+8.014199]	664.3584++ (heavy)	664.358433	2	23.4	700.411952	y6	1	64.37	63.98		
Haptoglobin-related protei	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK	615.6842+++	615.684227	3	20.8	885.540394	y8	1	82.13	69.77	4.228418192	4.115241803
Haptoglobin-related protei	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK	615.6842+++	615.684227	3	20.8	757.481817	y7	1	82.13	69.77		
Haptoglobin-related protei	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK	615.6842+++	615.684227	3	20.8	543.38646	y5	1	82.13	69.77		
Haptoglobin-related protei	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK	615.6842+++	615.684227	3	20.8	449.28708	b4	1	82.13	69.77		
Haptoglobin-related protei	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK[+8.014199]	618.3556+++ (heavy)	618.355627	3	20.8	893.554593	y8	1	82.13	69.77		
Haptoglobin-related protei	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK[+8.014199]	618.3556+++ (heavy)	618.355627	3	20.8	765.496016	y7	1	82.13	69.77		
Haptoglobin-related protei	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK[+8.014199]	618.3556+++ (heavy)	618.355627	3	20.8	551.400659	y5	1	82.13	69.77		
Haptoglobin-related protei	HPR	P00739	VVLHPNYHQVDIGLIK	VVLHPNYHQVDIGLIK[+8.014199]	618.3556+++ (heavy)	618.355627	3	20.8	449.28708	b4	1	82.13	69.77		
Haptoglobin-related protei	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK	772.3624++	772.36243	2	27.5	1125.495963	y10	1	67.74	65.91		
Haptoglobin-related protei	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK	772.3624++	772.36243	2	27.5	795.363158	y7	1	67.74	65.91		
Haptoglobin-related protei	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK	772.3624++	772.36243	2	27.5	320.160482	b3	1	67.74	65.91		
Haptoglobin-related protei	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK[+8.014199]	776.3695++ (heavy)	776.369529	2	27.5	1133.510162	y10	1	67.74	65.91		
Haptoglobin-related protei	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK[+8.014199]	776.3695++ (heavy)	776.369529	2	27.5	803.377357	y7	1	67.74	65.91		
Haptoglobin-related protei	HPR	P00739	VGYVSGWGQSDNFK	VGYVSGWGQSDNFK[+8.014199]	776.3695++ (heavy)	776.369529	2	27.5	320.160482	b3	1	67.74	65.91		
Haptoglobin-related protei	HPR	P00739	SPVGVQPILNEHTFCVGM	SPVGVQPILNEHTFC[+57.021464]VGMSK	734.0345+++	734.034491	3	25.1	1309.566368	y11	1	89.52	85.36		
Haptoglobin-related protei	HPR	P00739	SPVGVQPILNEHTFCVGM	SPVGVQPILNEHTFC[+57.021464]VGMSK	734.0345+++	734.034491	3	25.1	929.421935	y8	1	89.52	85.36		
Haptoglobin-related protei	HPR	P00739	SPVGVQPILNEHTFCVGM	SPVGVQPILNEHTFC[+57.021464]VGMSK	734.0345+++	734.034491	3	25.1	422.206781	y4	1	89.52	85.36		
Haptoglobin-related protei	HPR	P00739	SPVGVQPILNEHTFCVGM	SPVGVQPILNEHTFC[+57.021464]VGMSK[+8.	736.7059+++ (heavy)	736.705891	3	25.1	1317.580567	y11	1	89.52	85.36		
Haptoglobin-related protei	HPR	P00739	SPVGVQPILNEHTFCVGM	SPVGVQPILNEHTFC[+57.021464]VGMSK[+8.	736.7059+++ (heavy)	736.705891	3	25.1	937.436134	y8	1	89.52	85.36		
Haptoglobin-related protei	HPR	P00739	SPVGVQPILNEHTFCVGM	SPVGVQPILNEHTFC[+57.021464]VGMSK[+8.	736.7059+++ (heavy)	736.705891	3	25.1	430.22098	y4	1	89.52	85.36		
Heparin cofactor 2	SERPIND	P05546	YEITTIHNLFR	YEITTIHNLFR	469.5857+++	469.585743	3	15.6	686.373269	y5	1	85.61	80.38	4.92480748	3.760385426
Heparin cofactor 2	SERPIND	P05546	YEITTIHNLFR	YEITTIHNLFR	469.5857+++	469.585743	3	15.6	549.314357	y4	1	85.61	80.38		
Heparin cofactor 2	SERPIND	P05546	YEITTIHNLFR	YEITTIHNLFR	469.5857+++	469.585743	3	15.6	293.113198	b2	1	85.61	80.38		
Heparin cofactor 2	SERPIND	P05546	YEITTIHNLFR	YEITTIHNLFR[+10.008269]	472.9218+++ (heavy)	472.921832	3	15.6	696.381538	y5	1	85.61	80.38		
Heparin cofactor 2	SERPIND	P05546	YEITTIHNLFR	YEITTIHNLFR[+10.008269]	472.9218+++ (heavy)	472.921832	3	15.6	559.322626	y4	1	85.61	80.38		
Heparin cofactor 2	SERPIND	P05546	YEITTIHNLFR	YEITTIHNLFR[+10.008269]	472.9218+++ (heavy)	472.921832	3	15.6	293.113198	b2	1	85.61	80.38		
Heparin cofactor 2	SERPIND	P05546	SVNDLYIQK	SVNDLYIQK	540.2902++	540.290213	2	18.9	893.472708	y7	1	40.43	38.62		
Heparin cofactor 2	SERPIND	P05546	SVNDLYIQK	SVNDLYIQK	540.2902++	540.290213	2	18.9	551.318774	y4	1	40.43	38.62		
Heparin cofactor 2	SERPIND	P05546	SVNDLYIQK	SVNDLYIQK	540.2902++	540.290213	2	18.9	388.255445	y3	1	40.43	38.62		
Heparin cofactor 2	SERPIND	P05546	SVNDLYIQK	SVNDLYIQK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	901.486907	y7	1	40.43	38.62		
Heparin cofactor 2	SERPIND	P05546	SVNDLYIQK	SVNDLYIQK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	559.332973	y4	1	40.43	38.62		

Heparin cofactor 2	SERPIND	P05546	SVNDLYIQK	SVNDLYIQK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	396.269644	y3	1	40.43	38.62		
Heparin cofactor 2	SERPIND	P05546	QFPILLDFK	QFPILLDFK	560.8237++	560.823692	2	19.7	845.513117	y7	1	93.99	114.06		
Heparin cofactor 2	SERPIND	P05546	QFPILLDFK	QFPILLDFK	560.8237++	560.823692	2	19.7	635.376289	y5	1	93.99	114.06		
Heparin cofactor 2	SERPIND	P05546	QFPILLDFK	QFPILLDFK	560.8237++	560.823692	2	19.7	294.181218	y2	1	93.99	114.06		
Heparin cofactor 2	SERPIND	P05546	QFPILLDFK	QFPILLDFK[+8.014199]	564.8308++ (heavy)	564.830792	2	19.7	853.527316	y7	1	93.99	114.06		
Heparin cofactor 2	SERPIND	P05546	QFPILLDFK	QFPILLDFK[+8.014199]	564.8308++ (heavy)	564.830792	2	19.7	643.390488	y5	1	93.99	114.06		
Heparin cofactor 2	SERPIND	P05546	QFPILLDFK	QFPILLDFK[+8.014199]	564.8308++ (heavy)	564.830792	2	19.7	302.195417	y2	1	93.99	114.06		
Heparin cofactor 2	SERPIND	P05546	NYNLVESLK	NYNLVESLK	540.2902++	540.290213	2	18.9	802.466895	y7	1	52.87	60.67		
Heparin cofactor 2	SERPIND	P05546	NYNLVESLK	NYNLVESLK	540.2902++	540.290213	2	18.9	575.339903	y5	1	52.87	60.67		
Heparin cofactor 2	SERPIND	P05546	NYNLVESLK	NYNLVESLK	540.2902++	540.290213	2	18.9	278.113532	b2	1	52.87	60.67		
Heparin cofactor 2	SERPIND	P05546	NYNLVESLK	NYNLVESLK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	810.481094	y7	1	52.87	60.67		
Heparin cofactor 2	SERPIND	P05546	NYNLVESLK	NYNLVESLK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	583.354102	y5	1	52.87	60.67		
Heparin cofactor 2	SERPIND	P05546	NYNLVESLK	NYNLVESLK[+8.014199]	544.2973++ (heavy)	544.297313	2	18.9	278.113532	b2	1	52.87	60.67		
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR	562.8086++	562.808573	2	19.8	789.498135	y6	1	100.51	111.96	4.33357769	9.278010211
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR	562.8086++	562.808573	2	19.8	676.414071	y5	1	100.51	111.96		
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR	562.8086++	562.808573	2	19.8	336.119011	b3	1	100.51	111.96		
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR[+10.008269]	567.8127++ (heavy)	567.812708	2	19.8	799.506404	y6	1	100.51	111.96		
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR[+10.008269]	567.8127++ (heavy)	567.812708	2	19.8	686.42234	y5	1	100.51	111.96		
Histidine-rich glycoprotein	HRG	P04196	DGYLFQLLR	DGYLFQLLR[+10.008269]	567.8127++ (heavy)	567.812708	2	19.8	336.119011	b3	1	100.51	111.96		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER	841.8990++	841.899042	2	30.1	1171.526595	y9	1	116.14	123.22		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER	841.8990++	841.899042	2	30.1	1058.442531	y8	1	116.14	123.22		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER	841.8990++	841.899042	2	30.1	399.187425	b4	1	116.14	123.22		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER[+10.008269]	846.9032++ (heavy)	846.903176	2	30.1	1181.534864	y9	1	116.14	123.22		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER[+10.008269]	846.9032++ (heavy)	846.903176	2	30.1	1068.4508	y8	1	116.14	123.22		
Histidine-rich glycoprotein	HRG	P04196	DSPVLIDFFEDTER	DSPVLIDFFEDTER[+10.008269]	846.9032++ (heavy)	846.903176	2	30.1	399.187425	b4	1	116.14	123.22		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR	745.8492++	745.849155	2	26.5	1089.536371	y9	1	79.46	86.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR	745.8492++	745.849155	2	26.5	869.451579	y7	1	79.46	86.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR	745.8492++	745.849155	2	26.5	623.314751	y5	1	79.46	86.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR[+10.008269]	750.8533++ (heavy)	750.85329	2	26.5	1099.54464	y9	1	79.46	86.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR[+10.008269]	750.8533++ (heavy)	750.85329	2	26.5	879.459848	y7	1	79.46	86.31		
Histidine-rich glycoprotein	HRG	P04196	GGEGTGYFVDFSVR	GGEGTGYFVDFSVR[+10.008269]	750.8533++ (heavy)	750.85329	2	26.5	633.32302	y5	1	79.46	86.31		
Immunoglobulin heavy cor	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK	770.8675++	770.867545	2	27.5	1111.541851	y10	1	61.59	71.75	5.465909719	0.801207615
Immunoglobulin heavy cor	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK	770.8675++	770.867545	2	27.5	863.425758	y8	1	61.59	71.75		
Immunoglobulin heavy cor	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK	770.8675++	770.867545	2	27.5	475.251088	y5	1	61.59	71.75		
Immunoglobulin heavy cor	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK[+8.014199]	774.8746++ (heavy)	774.874644	2	27.5	1119.55605	y10	1	61.59	71.75		
Immunoglobulin heavy cor	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK[+8.014199]	774.8746++ (heavy)	774.874644	2	27.5	871.439957	y8	1	61.59	71.75		
Immunoglobulin heavy cor	IGHA1	P01876	DASGVTFTWTPSSGK	DASGVTFTWTPSSGK[+8.014199]	774.8746++ (heavy)	774.874644	2	27.5	483.265287	y5	1	61.59	71.75		
Immunoglobulin heavy cor	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK	688.3136++	688.31356	2	24.4	866.425424	y8	1	36.38	34.42		
Immunoglobulin heavy cor	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK	688.3136++	688.31356	2	24.4	765.377745	y7	1	36.38	34.42		
Immunoglobulin heavy cor	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK	688.3136++	688.31356	2	24.4	460.240189	y4	1	36.38	34.42		
Immunoglobulin heavy cor	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK[+8.014199]	692.3207++ (heavy)	692.320659	2	24.4	874.439623	y8	1	36.38	34.42		
Immunoglobulin heavy cor	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK[+8.014199]	692.3207++ (heavy)	692.320659	2	24.4	773.391944	y7	1	36.38	34.42		
Immunoglobulin heavy cor	IGHA1	P01876	TFTCTAAYPESK	TFTC[+57.021464]TAAYPESK[+8.014199]	692.3207++ (heavy)	692.320659	2	24.4	468.254388	y4	1	36.38	34.42		
Immunoglobulin heavy cor	IGHA1	P01876	TPLTATLSK	TPLTATLSK	466.2766++	466.276575	2	16.2	733.445431	y7	1	32.11	35.16		
Immunoglobulin heavy cor	IGHA1	P01876	TPLTATLSK	TPLTATLSK	466.2766++	466.276575	2	16.2	620.361367	y6	1	32.11	35.16		
Immunoglobulin heavy cor	IGHA1	P01876	TPLTATLSK	TPLTATLSK	466.2766++	466.276575	2	16.2	519.313689	y5	1	32.11	35.16		
Immunoglobulin heavy cor	IGHA1	P01876	TPLTATLSK	TPLTATLSK[+8.014199]	470.2837++ (heavy)	470.283674	2	16.2	741.45963	y7	1	32.11	35.16		
Immunoglobulin heavy cor	IGHA1	P01876	TPLTATLSK	TPLTATLSK[+8.014199]	470.2837++ (heavy)	470.283674	2	16.2	628.375566	y6	1	32.11	35.16		

Immunoglobulin heavy cor	IGHA1	P01876	TPLTATLSK	TPLTATLSK[+8.014199]	470.2837++ (heavy)	470.283674	2	16.2	527.327888	y5	1	32.11	35.16		
Immunoglobulin heavy var	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK	645.7872++	645.787178	2	22.8	803.375637	y6	1	21.23	29.77	4.93874881	1.16542966
Immunoglobulin heavy var	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK	645.7872++	645.787178	2	22.8	704.307223	y5	1	21.23	29.77		
Immunoglobulin heavy var	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK	645.7872++	645.787178	2	22.8	541.243895	y4	1	21.23	29.77		
Immunoglobulin heavy var	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK[+8.014199]	649.7943++ (heavy)	649.794277	2	22.8	811.389836	y6	1	21.23	29.77		
Immunoglobulin heavy var	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK[+8.014199]	649.7943++ (heavy)	649.794277	2	22.8	712.321422	y5	1	21.23	29.77		
Immunoglobulin heavy var	IGHV3-23	P01764	AEDTAVYYCAK	AEDTAVYYC[+57.021464]AK[+8.014199]	649.7943++ (heavy)	649.794277	2	22.8	549.258094	y4	1	21.23	29.77		
Insulin-like growth factor-b	IGFALS	P35858	LEYLLLSR	LEYLLLSR	503.8002++	503.800217	2	17.6	764.466501	y6	1	77.62	78.61	4.561318706	3.240351366
Insulin-like growth factor-b	IGFALS	P35858	LEYLLLSR	LEYLLLSR	503.8002++	503.800217	2	17.6	601.403172	y5	1	77.62	78.61		
Insulin-like growth factor-b	IGFALS	P35858	LEYLLLSR	LEYLLLSR	503.8002++	503.800217	2	17.6	488.319108	y4	1	77.62	78.61		
Insulin-like growth factor-b	IGFALS	P35858	LEYLLLSR	LEYLLLSR	503.8002++	503.800217	2	17.6	375.235044	y3	1	77.62	78.61		
Insulin-like growth factor-b	IGFALS	P35858	LEYLLLSR	LEYLLLSR[+10.008269]	508.8044++ (heavy)	508.804351	2	17.6	774.47477	y6	1	77.62	78.61		
Insulin-like growth factor-b	IGFALS	P35858	LEYLLLSR	LEYLLLSR[+10.008269]	508.8044++ (heavy)	508.804351	2	17.6	611.411441	y5	1	77.62	78.61		
Insulin-like growth factor-b	IGFALS	P35858	LEYLLLSR	LEYLLLSR[+10.008269]	508.8044++ (heavy)	508.804351	2	17.6	498.327377	y4	1	77.62	78.61		
Insulin-like growth factor-b	IGFALS	P35858	LEYLLLSR	LEYLLLSR[+10.008269]	508.8044++ (heavy)	508.804351	2	17.6	385.243313	y3	1	77.62	78.61		
Insulin-like growth factor-b	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR	657.8437++	657.843676	2	23.3	740.404963	y7	1	53.29	60.2		
Insulin-like growth factor-b	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR	657.8437++	657.843676	2	23.3	626.362036	y6	1	53.29	60.2		
Insulin-like growth factor-b	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR	657.8437++	657.843676	2	23.3	263.102633	b2	1	53.29	60.2		
Insulin-like growth factor-b	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR	657.8437++	657.843676	2	23.3	334.139747	b3	1	53.29	60.2		
Insulin-like growth factor-b	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR[+10.008269]	662.8478++ (heavy)	662.84781	2	23.3	750.413232	y7	1	53.29	60.2		
Insulin-like growth factor-b	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR[+10.008269]	662.8478++ (heavy)	662.84781	2	23.3	636.370305	y6	1	53.29	60.2		
Insulin-like growth factor-b	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR[+10.008269]	662.8478++ (heavy)	662.84781	2	23.3	263.102633	b2	1	53.29	60.2		
Insulin-like growth factor-b	IGFALS	P35858	DFALQNPSAVPR	DFALQNPSAVPR[+10.008269]	662.8478++ (heavy)	662.84781	2	23.3	334.139747	b3	1	53.29	60.2		
Inter-alpha-trypsin inhibito	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK	580.8135++	580.813521	2	20.4	932.50876	y8	1	76.87	87.97	6.642218584	2.50371549
Inter-alpha-trypsin inhibito	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK	580.8135++	580.813521	2	20.4	714.403232	y6	1	76.87	87.97		
Inter-alpha-trypsin inhibito	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK	580.8135++	580.813521	2	20.4	599.376289	y5	1	76.87	87.97		
Inter-alpha-trypsin inhibito	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK[+8.014199]	584.8206++ (heavy)	584.820621	2	20.4	940.522959	y8	1	76.87	87.97		
Inter-alpha-trypsin inhibito	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK[+8.014199]	584.8206++ (heavy)	584.820621	2	20.4	722.417431	y6	1	76.87	87.97		
Inter-alpha-trypsin inhibito	ITIH1	P19827	EVAFDLEIPK	EVAFDLEIPK[+8.014199]	584.8206++ (heavy)	584.820621	2	20.4	607.390488	y5	1	76.87	87.97		
Inter-alpha-trypsin inhibito	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR	579.3173++	579.317294	2	20.4	902.46902	y9	1	40.12	33.6		
Inter-alpha-trypsin inhibito	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR	579.3173++	579.317294	2	20.4	629.372935	y6	1	40.12	33.6		
Inter-alpha-trypsin inhibito	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR	579.3173++	579.317294	2	20.4	714.341694	b8	1	40.12	33.6		
Inter-alpha-trypsin inhibito	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR[+10.008269]	584.3214++ (heavy)	584.321428	2	20.4	912.477289	y9	1	40.12	33.6		
Inter-alpha-trypsin inhibito	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR[+10.008269]	584.3214++ (heavy)	584.321428	2	20.4	639.381204	y6	1	40.12	33.6		
Inter-alpha-trypsin inhibito	ITIH1	P19827	AAISGENAGLVR	AAISGENAGLVR[+10.008269]	584.3214++ (heavy)	584.321428	2	20.4	714.341694	b8	1	40.12	33.6		
Inter-alpha-trypsin inhibito	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR	735.8648++	735.864805	2	26.2	1179.600428	y11	1	56.39	52.64		
Inter-alpha-trypsin inhibito	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR	735.8648++	735.864805	2	26.2	1016.5371	y10	1	56.39	52.64		
Inter-alpha-trypsin inhibito	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR	735.8648++	735.864805	2	26.2	887.494506	y9	1	56.39	52.64		
Inter-alpha-trypsin inhibito	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR[+10.008269]	740.8689++ (heavy)	740.86894	2	26.2	1189.608697	y11	1	56.39	52.64		
Inter-alpha-trypsin inhibito	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR[+10.008269]	740.8689++ (heavy)	740.86894	2	26.2	1026.545369	y10	1	56.39	52.64		
Inter-alpha-trypsin inhibito	ITIH1	P19827	QYYEGSEIVVAGR	QYYEGSEIVVAGR[+10.008269]	740.8689++ (heavy)	740.86894	2	26.2	897.502776	y9	1	56.39	52.64		
Inter-alpha-trypsin inhibito	ITIH2	P19823	VVNNSPQPQNVVFDVQIP	VVNNSPQPQNVVFDVQIPK	708.0479+++	708.047894	3	24.2	945.540394	y8	1	75.87	90.78	5.654181674	3.252923165
Inter-alpha-trypsin inhibito	ITIH2	P19823	VVNNSPQPQNVVFDVQIP	VVNNSPQPQNVVFDVQIPK	708.0479+++	708.047894	3	24.2	846.47198	y7	1	75.87	90.78		
Inter-alpha-trypsin inhibito	ITIH2	P19823	VVNNSPQPQNVVFDVQIP	VVNNSPQPQNVVFDVQIPK	708.0479+++	708.047894	3	24.2	739.373329	b7	1	75.87	90.78		
Inter-alpha-trypsin inhibito	ITIH2	P19823	VVNNSPQPQNVVFDVQIP	VVNNSPQPQNVVFDVQIPK[+8.014199]	710.7193+++ (heavy)	710.719294	3	24.2	953.554593	y8	1	75.87	90.78		
Inter-alpha-trypsin inhibito	ITIH2	P19823	VVNNSPQPQNVVFDVQIP	VVNNSPQPQNVVFDVQIPK[+8.014199]	710.7193+++ (heavy)	710.719294	3	24.2	854.486179	y7	1	75.87	90.78		
Inter-alpha-trypsin inhibito	ITIH2	P19823	VVNNSPQPQNVVFDVQIP	VVNNSPQPQNVVFDVQIPK[+8.014199]	710.7193+++ (heavy)	710.719294	3	24.2	739.373329	b7	1	75.87	90.78		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FLHVPDTFEGHFDGVPVIS	FLHVPDTFEGHFDGVPVISK	747.7161+++	747.716144	3	25.6	543.350074	y5	1	99.43	96.88		

Inter-alpha-trypsin inhibito	ITIH2	P19823	FLHVPDTFEGHFDGVPVIS	FLHVPDTFEGHFDGVPVISK	747.7161+++	747.716144	3	25.6	398.218666	b3	1	99.43	96.88		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FLHVPDTFEGHFDGVPVIS	FLHVPDTFEGHFDGVPVISK	747.7161+++	747.716144	3	25.6	497.28708	b4	1	99.43	96.88		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FLHVPDTFEGHFDGVPVIS	FLHVPDTFEGHFDGVPVISK[+8.014199]	750.3875+++ (heavy)	750.387544	3	25.6	551.364273	y5	1	99.43	96.88		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FLHVPDTFEGHFDGVPVIS	FLHVPDTFEGHFDGVPVISK[+8.014199]	750.3875+++ (heavy)	750.387544	3	25.6	398.218666	b3	1	99.43	96.88		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FLHVPDTFEGHFDGVPVIS	FLHVPDTFEGHFDGVPVISK[+8.014199]	750.3875+++ (heavy)	750.387544	3	25.6	497.28708	b4	1	99.43	96.88		
Inter-alpha-trypsin inhibito	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR	791.9310++	791.931011	2	28.2	1341.712104	y13	1	64.91	61.6		
Inter-alpha-trypsin inhibito	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR	791.9310++	791.931011	2	28.2	1157.627312	y11	1	64.91	61.6		
Inter-alpha-trypsin inhibito	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR	791.9310++	791.931011	2	28.2	715.409714	y6	1	64.91	61.6		
Inter-alpha-trypsin inhibito	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR[+10.008269]	796.9351++ (heavy)	796.935145	2	28.2	1351.720373	y13	1	64.91	61.6		
Inter-alpha-trypsin inhibito	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR[+10.008269]	796.9351++ (heavy)	796.935145	2	28.2	1167.635581	y11	1	64.91	61.6		
Inter-alpha-trypsin inhibito	ITIH2	P19823	IQPSGGTNINEALLR	IQPSGGTNINEALLR[+10.008269]	796.9351++ (heavy)	796.935145	2	28.2	725.417983	y6	1	64.91	61.6		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR	669.3642++	669.364244	2	23.7	785.487965	y7	1	73.42	70.84		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR	669.3642++	669.364244	2	23.7	686.419551	y6	1	73.42	70.84		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR	669.3642++	669.364244	2	23.7	498.339844	y4	1	73.42	70.84		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR[+10.008269]	674.3684++ (heavy)	674.368379	2	23.7	795.496234	y7	1	73.42	70.84		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR[+10.008269]	674.3684++ (heavy)	674.368379	2	23.7	696.42782	y6	1	73.42	70.84		
Inter-alpha-trypsin inhibito	ITIH2	P19823	FYNQVSTPLLR	FYNQVSTPLLR[+10.008269]	674.3684++ (heavy)	674.368379	2	23.7	508.348113	y4	1	73.42	70.84		
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK	497.7582++	497.758215	2	17.4	794.429447	y6	1	40.39	41.22	9.133958443	10.71110831
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK	497.7582++	497.758215	2	17.4	681.345383	y5	1	40.39	41.22		
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK	497.7582++	497.758215	2	17.4	552.302789	y4	1	40.39	41.22		
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK[+8.014199]	501.7653++ (heavy)	501.765314	2	17.4	802.443646	y6	1	40.39	41.22		
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK[+8.014199]	501.7653++ (heavy)	501.765314	2	17.4	689.359582	y5	1	40.39	41.22		
L-selectin	SELL	P14151	AEIEYLEK	AEIEYLEK[+8.014199]	501.7653++ (heavy)	501.765314	2	17.4	560.316988	y4	1	40.39	41.22		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR	529.2769++	529.276909	2	18.5	807.451185	y6	1	84.78	82.76		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR	529.2769++	529.276909	2	18.5	644.387856	y5	1	84.78	82.76		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR	529.2769++	529.276909	2	18.5	458.308544	y4	1	84.78	82.76		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR[+10.008269]	534.2810++ (heavy)	534.281044	2	18.5	817.459454	y6	1	84.78	82.76		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR[+10.008269]	534.2810++ (heavy)	534.281044	2	18.5	654.396125	y5	1	84.78	82.76		
L-selectin	SELL	P14151	SYYWIGIR	SYYWIGIR[+10.008269]	534.2810++ (heavy)	534.281044	2	18.5	468.316813	y4	1	84.78	82.76		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK	433.2297+++	433.229736	3	14.3	612.346386	y5	1	42.78	41.73	6.830079033	4.624870555
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK	433.2297+++	433.229736	3	14.3	499.262322	y4	1	42.78	41.73		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK	433.2297+++	433.229736	3	14.3	398.214643	y3	1	42.78	41.73		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK[+8.014199]	435.9011+++ (heavy)	435.901136	3	14.3	620.360585	y5	1	42.78	41.73		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK[+8.014199]	435.9011+++ (heavy)	435.901136	3	14.3	507.276521	y4	1	42.78	41.73		
Lumican	LUM	P51884	SLEDLQLTHNK	SLEDLQLTHNK[+8.014199]	435.9011+++ (heavy)	435.901136	3	14.3	406.228842	y3	1	42.78	41.73		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK	613.3086++	613.308603	2	21.6	1112.525866	y9	1	60.76	65.86		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK	613.3086++	613.308603	2	21.6	798.366846	y6	1	60.76	65.86		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK	613.3086++	613.308603	2	21.6	315.166296	b3	1	60.76	65.86		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK[+8.014199]	617.3157++ (heavy)	617.315703	2	21.6	1120.540065	y9	1	60.76	65.86		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK[+8.014199]	617.3157++ (heavy)	617.315703	2	21.6	806.381045	y6	1	60.76	65.86		
Lumican	LUM	P51884	ISNIPDEYFK	ISNIPDEYFK[+8.014199]	617.3157++ (heavy)	617.315703	2	21.6	315.166296	b3	1	60.76	65.86		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK	489.2869++	489.286942	2	17	751.398481	y7	1	48.64	54.56		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK	489.2869++	489.286942	2	17	694.377017	y6	1	48.64	54.56		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK	489.2869++	489.286942	2	17	484.240189	y4	1	48.64	54.56		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK[+8.014199]	493.2940++ (heavy)	493.294042	2	17	759.41268	y7	1	48.64	54.56		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK[+8.014199]	493.2940++ (heavy)	493.294042	2	17	702.391216	y6	1	48.64	54.56		
Lumican	LUM	P51884	ILGPLSYSK	ILGPLSYSK[+8.014199]	493.2940++ (heavy)	493.294042	2	17	492.254388	y4	1	48.64	54.56		
Mannan-binding lectin seri	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR	581.3062++	581.306198	2	20.4	874.478128	y8	1	60.43	69.67	7.151834749	13.79975831

Mannan-binding lectin seri	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR	581.3062++	581.306198	2	20.4	761.394064	y7	1	60.43	69.67		
Mannan-binding lectin seri	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR	581.3062++	581.306198	2	20.4	660.346386	y6	1	60.43	69.67		
Mannan-binding lectin seri	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR	581.3062++	581.306198	2	20.4	589.309272	y5	1	60.43	69.67		
Mannan-binding lectin seri	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR[+10.008269]	586.3103++ (heavy)	586.310332	2	20.4	884.486397	y8	1	60.43	69.67		
Mannan-binding lectin seri	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR[+10.008269]	586.3103++ (heavy)	586.310332	2	20.4	771.402333	y7	1	60.43	69.67		
Mannan-binding lectin seri	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR[+10.008269]	586.3103++ (heavy)	586.310332	2	20.4	670.354655	y6	1	60.43	69.67		
Mannan-binding lectin seri	MASP2	O00187	WTLTAPPGYR	WTLTAPPGYR[+10.008269]	586.3103++ (heavy)	586.310332	2	20.4	599.317541	y5	1	60.43	69.67		
Pigment epithelium-derive	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR	780.3963++	780.396272	2	27.8	1233.589864	y10	1	84.42	86.21	8.672280831	3.603111145
Pigment epithelium-derive	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR	780.3963++	780.396272	2	27.8	1134.52145	y9	1	84.42	86.21		
Pigment epithelium-derive	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR	780.3963++	780.396272	2	27.8	786.37808	y6	1	84.42	86.21		
Pigment epithelium-derive	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR[+10.008269]	785.4004++ (heavy)	785.400407	2	27.8	1243.598133	y10	1	84.42	86.21		
Pigment epithelium-derive	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR[+10.008269]	785.4004++ (heavy)	785.400407	2	27.8	1144.529719	y9	1	84.42	86.21		
Pigment epithelium-derive	SERPINF1	P36955	LAAAVSNFGYDLYR	LAAAVSNFGYDLYR[+10.008269]	785.4004++ (heavy)	785.400407	2	27.8	796.386349	y6	1	84.42	86.21		
Pigment epithelium-derive	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK	652.6632+++	652.663157	3	22.2	1104.532014	y10	1	97.88	86		
Pigment epithelium-derive	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK	652.6632+++	652.663157	3	22.2	930.467957	y8	1	97.88	86		
Pigment epithelium-derive	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK	652.6632+++	652.663157	3	22.2	605.304186	y5	1	97.88	86		
Pigment epithelium-derive	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK[+8.014199]	655.3346+++ (heavy)	655.334557	3	22.2	1112.546213	y10	1	97.88	86		
Pigment epithelium-derive	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK[+8.014199]	655.3346+++ (heavy)	655.334557	3	22.2	938.482156	y8	1	97.88	86		
Pigment epithelium-derive	SERPINF1	P36955	ALYYDLISSPDIHGTYK	ALYYDLISSPDIHGTYK[+8.014199]	655.3346+++ (heavy)	655.334557	3	22.2	613.318385	y5	1	97.88	86		
Pigment epithelium-derive	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK	528.3266++	528.326599	2	18.5	855.529829	y8	1	45.68	52.82		
Pigment epithelium-derive	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK	528.3266++	528.326599	2	18.5	727.471252	y7	1	45.68	52.82		
Pigment epithelium-derive	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK	528.3266++	528.326599	2	18.5	557.365724	y5	1	45.68	52.82		
Pigment epithelium-derive	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK[+8.014199]	532.3337++ (heavy)	532.333698	2	18.5	863.544028	y8	1	45.68	52.82		
Pigment epithelium-derive	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK[+8.014199]	532.3337++ (heavy)	532.333698	2	18.5	735.485451	y7	1	45.68	52.82		
Pigment epithelium-derive	SERPINF1	P36955	TVQAVLTVPK	TVQAVLTVPK[+8.014199]	532.3337++ (heavy)	532.333698	2	18.5	565.379923	y5	1	45.68	52.82		
Pigment epithelium-derive	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK	692.3432++	692.343174	2	24.6	1142.536431	y10	1	78.26	80.8		
Pigment epithelium-derive	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK	692.3432++	692.343174	2	24.6	680.324982	y6	1	78.26	80.8		
Pigment epithelium-derive	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK	692.3432++	692.343174	2	24.6	593.292953	y5	1	78.26	80.8		
Pigment epithelium-derive	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK[+8.014199]	696.3503++ (heavy)	696.350274	2	24.6	1150.55063	y10	1	78.26	80.8		
Pigment epithelium-derive	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK[+8.014199]	696.3503++ (heavy)	696.350274	2	24.6	688.339181	y6	1	78.26	80.8		
Pigment epithelium-derive	SERPINF1	P36955	LQSLFDSPDFSK	LQSLFDSPDFSK[+8.014199]	696.3503++ (heavy)	696.350274	2	24.6	601.307152	y5	1	78.26	80.8		
Plasma protease C1 inhib	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK	632.8428++	632.84281	2	22.3	1049.587738	y9	1	71.35	86.11	4.257128063	5.451469444
Plasma protease C1 inhib	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK	632.8428++	632.84281	2	22.3	936.503674	y8	1	71.35	86.11		
Plasma protease C1 inhib	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK	632.8428++	632.84281	2	22.3	807.461081	y7	1	71.35	86.11		
Plasma protease C1 inhib	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK[+8.014199]	636.8499++ (heavy)	636.84991	2	22.3	1057.601937	y9	1	71.35	86.11		
Plasma protease C1 inhib	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK[+8.014199]	636.8499++ (heavy)	636.84991	2	22.3	944.517873	y8	1	71.35	86.11		
Plasma protease C1 inhib	SERPING1	P05155	TNLESILSYPK	TNLESILSYPK[+8.014199]	636.8499++ (heavy)	636.84991	2	22.3	815.47528	y7	1	71.35	86.11		
Plasma protease C1 inhib	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR	609.6635+++	609.663492	3	20.6	908.494841	y8	1	82.33	91.84		
Plasma protease C1 inhib	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR	609.6635+++	609.663492	3	20.6	771.435929	y7	1	82.33	91.84		
Plasma protease C1 inhib	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR	609.6635+++	609.663492	3	20.6	684.403901	y6	1	82.33	91.84		
Plasma protease C1 inhib	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR	609.6635+++	609.663492	3	20.6	472.324194	y4	1	82.33	91.84		
Plasma protease C1 inhib	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR[+10.008269]	612.9996+++ (heavy)	612.999581	3	20.6	918.50311	y8	1	82.33	91.84		
Plasma protease C1 inhib	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR[+10.008269]	612.9996+++ (heavy)	612.999581	3	20.6	781.444198	y7	1	82.33	91.84		
Plasma protease C1 inhib	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR[+10.008269]	612.9996+++ (heavy)	612.999581	3	20.6	694.41217	y6	1	82.33	91.84		
Plasma protease C1 inhib	SERPING1	P05155	GVTSVSQIFHSPDLAIR	GVTSVSQIFHSPDLAIR[+10.008269]	612.9996+++ (heavy)	612.999581	3	20.6	482.332463	y4	1	82.33	91.84		
Plasma protease C1 inhib	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR	593.3531++	593.353148	2	20.9	910.572029	y8	1	80.89	89.14		
Plasma protease C1 inhib	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR	593.3531++	593.353148	2	20.9	599.387522	y5	1	80.89	89.14		
Plasma protease C1 inhib	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR	593.3531++	593.353148	2	20.9	276.134267	b2	1	80.89	89.14		

Plasma protease C1 inhibi	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR[+10.008269]	598.3573++ (heavy)	598.357283	2	20.9	920.580298	y8	1	80.89	89.14		
Plasma protease C1 inhibi	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR[+10.008269]	598.3573++ (heavy)	598.357283	2	20.9	609.395791	y5	1	80.89	89.14		
Plasma protease C1 inhibi	SERPING1	P05155	FQPTLLTLPR	FQPTLLTLPR[+10.008269]	598.3573++ (heavy)	598.357283	2	20.9	276.134267	b2	1	80.89	89.14		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK	667.3245++	667.324459	2	23.6	1092.499	y11	1	25.73	36.23	5.284822554	0.499595831
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK	667.3245++	667.324459	2	23.6	964.440422	y9	1	25.73	36.23		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK	667.3245++	667.324459	2	23.6	707.302866	y6	1	25.73	36.23		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK[+8.014199]	671.3316++ (heavy)	671.331558	2	23.6	1100.513199	y11	1	25.73	36.23		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK[+8.014199]	671.3316++ (heavy)	671.331558	2	23.6	972.454621	y9	1	25.73	36.23		
Plasminogen	PLG	P00747	QLGAGSIEECAAK	QLGAGSIEEC[+57.021464]AAK[+8.014199]	671.3316++ (heavy)	671.331558	2	23.6	715.317065	y6	1	25.73	36.23		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR	433.5544+++	433.554442	3	14.3	713.357679	y6	1	41.16	33.05		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR	433.5544+++	433.554442	3	14.3	487.262322	y4	1	41.16	33.05		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR	433.5544+++	433.554442	3	14.3	485.250694	b4	1	41.16	33.05		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR[+10.008269]	436.8905+++ (heavy)	436.890532	3	14.3	723.365948	y6	1	41.16	33.05		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR[+10.008269]	436.8905+++ (heavy)	436.890532	3	14.3	497.270591	y4	1	41.16	33.05		
Plasminogen	PLG	P00747	HSIFTPETNPR	HSIFTPETNPR[+10.008269]	436.8905+++ (heavy)	436.890532	3	14.3	485.250694	b4	1	41.16	33.05		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR	953.4129++	953.412856	2	34.2	1308.578982	y11	1	56.68	63.42		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR	953.4129++	953.412856	2	34.2	1194.536054	y9	1	56.68	63.42		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR	953.4129++	953.412856	2	34.2	588.31	y5	1	56.68	63.42		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR[+10.00	958.4170++ (heavy)	958.416991	2	34.2	1318.587251	y11	1	56.68	63.42		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR[+10.00	958.4170++ (heavy)	958.416991	2	34.2	1204.544323	y9	1	56.68	63.42		
Plasminogen	PLG	P00747	NPDGDVGGPWCYTTNPR	NPDGDVGGPWC[+57.021464]YTTNPR[+10.00	958.4170++ (heavy)	958.416991	2	34.2	598.318269	y5	1	56.68	63.42		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK	570.8166++	570.816595	2	20.1	699.403566	y6	1	42.81	46.19		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK	570.8166++	570.816595	2	20.1	503.282388	y4	1	42.81	46.19		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK	570.8166++	570.816595	2	20.1	329.14556	b3	1	42.81	46.19		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK[+8.014199]	574.8237++ (heavy)	574.823695	2	20.1	707.417765	y6	1	42.81	46.19		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK[+8.014199]	574.8237++ (heavy)	574.823695	2	20.1	511.296587	y4	1	42.81	46.19		
Plasminogen	PLG	P00747	EAQLPVIENK	EAQLPVIENK[+8.014199]	574.8237++ (heavy)	574.823695	2	20.1	329.14556	b3	1	42.81	46.19		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK	561.8057++	561.805696	2	19.7	922.488024	y8	1	85.81	90.97	4.757181811	5.995024229
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK	561.8057++	561.805696	2	19.7	775.41961	y7	1	85.81	90.97		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK	561.8057++	561.805696	2	19.7	674.371932	y6	1	85.81	90.97		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK[+8.014199]	565.8128++ (heavy)	565.812796	2	19.7	930.502223	y8	1	85.81	90.97		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK[+8.014199]	565.8128++ (heavy)	565.812796	2	19.7	783.433809	y7	1	85.81	90.97		
Pregnancy zone protein	PZP	P20742	SLFTDLVAEK	SLFTDLVAEK[+8.014199]	565.8128++ (heavy)	565.812796	2	19.7	682.386131	y6	1	85.81	90.97		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK	729.8879++	729.887946	2	25.9	1131.552809	y10	1	70.3	67.47		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK	729.8879++	729.887946	2	25.9	1032.484395	y9	1	70.3	67.47		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK	729.8879++	729.887946	2	25.9	903.441802	y8	1	70.3	67.47		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK	729.8879++	729.887946	2	25.9	703.362095	y6	1	70.3	67.47		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK[+8.014199]	733.8950++ (heavy)	733.895045	2	25.9	1139.567008	y10	1	70.3	67.47		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK[+8.014199]	733.8950++ (heavy)	733.895045	2	25.9	1040.498594	y9	1	70.3	67.47		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK[+8.014199]	733.8950++ (heavy)	733.895045	2	25.9	911.456001	y8	1	70.3	67.47		
Pregnancy zone protein	PZP	P20742	TLLVEAEGIEQEK	TLLVEAEGIEQEK[+8.014199]	733.8950++ (heavy)	733.895045	2	25.9	711.376294	y6	1	70.3	67.47		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR	620.8379++	620.837862	2	21.9	850.478128	y7	1	59.57	62.49		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR	620.8379++	620.837862	2	21.9	737.394064	y6	1	59.57	62.49		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR	620.8379++	620.837862	2	21.9	624.31	y5	1	59.57	62.49		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR	620.8379++	620.837862	2	21.9	523.262322	y4	1	59.57	62.49		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR[+10.008269]	625.8420++ (heavy)	625.841997	2	21.9	860.486397	y7	1	59.57	62.49		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR[+10.008269]	625.8420++ (heavy)	625.841997	2	21.9	747.402333	y6	1	59.57	62.49		
Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR[+10.008269]	625.8420++ (heavy)	625.841997	2	21.9	634.318269	y5	1	59.57	62.49		

Pregnancy zone protein	PZP	P20742	AVGYLITGYQR	AVGYLITGYQR[+10.008269]	625.8420++ (heavy)	625.841997	2	21.9	533.270591	y4	1	59.57	62.49		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK	637.3304++	637.330401	2	22.5	1136.594615	y10	1	65.97	47.12	5.283473353	2.932209531
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK	637.3304++	637.330401	2	22.5	688.36243	y6	1	65.97	47.12		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK	637.3304++	637.330401	2	22.5	225.098216	b2	1	65.97	47.12		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK	637.3304++	637.330401	2	22.5	829.383893	b7	1	65.97	47.12		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK[+8.014199]	641.3375++ (heavy)	641.337501	2	22.5	1144.608814	y10	1	65.97	47.12		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK[+8.014199]	641.3375++ (heavy)	641.337501	2	22.5	696.376629	y6	1	65.97	47.12		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK[+8.014199]	641.3375++ (heavy)	641.337501	2	22.5	225.098216	b2	1	65.97	47.12		
Serotransferrin	TF	P02787	HSTIFENLANK	HSTIFENLANK[+8.014199]	641.3375++ (heavy)	641.337501	2	22.5	829.383893	b7	1	65.97	47.12		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK	426.2155+++	426.215538	3	14	612.31	y6	1	55.5	56.97		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK	426.2155+++	426.215538	3	14	525.277972	y5	1	55.5	56.97		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK	426.2155+++	426.215538	3	14	438.245943	y4	1	55.5	56.97		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK[+8.014199]	428.8869+++ (heavy)	428.886938	3	14	620.324199	y6	1	55.5	56.97		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK[+8.014199]	428.8869+++ (heavy)	428.886938	3	14	533.292171	y5	1	55.5	56.97		
Serotransferrin	TF	P02787	EFQLFSSPHGK	EFQLFSSPHGK[+8.014199]	428.8869+++ (heavy)	428.886938	3	14	446.260142	y4	1	55.5	56.97		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK	500.7529++	500.752932	2	17.5	837.43526	y7	1	43	46.71		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK	500.7529++	500.752932	2	17.5	724.351196	y6	1	43	46.71		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK	500.7529++	500.752932	2	17.5	538.287139	y4	1	43	46.71		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK[+8.014199]	504.7600++ (heavy)	504.760032	2	17.5	845.449459	y7	1	43	46.71		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK[+8.014199]	504.7600++ (heavy)	504.760032	2	17.5	732.365395	y6	1	43	46.71		
Serotransferrin	TF	P02787	YLGEEYVK	YLGEEYVK[+8.014199]	504.7600++ (heavy)	504.760032	2	17.5	546.301338	y4	1	43	46.71		
Serum amyloid A-4 protei	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR	566.7744++	566.774405	2	19.9	819.377762	y8	1	39.01	37.3	5.716127085	1.392780022
Serum amyloid A-4 protei	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR	566.7744++	566.774405	2	19.9	691.319185	y7	1	39.01	37.3		
Serum amyloid A-4 protei	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR	566.7744++	566.774405	2	19.9	535.229307	y5	1	39.01	37.3		
Serum amyloid A-4 protei	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR[+10.008269]	571.7785++ (heavy)	571.778539	2	19.9	829.386031	y8	1	39.01	37.3		
Serum amyloid A-4 protei	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR[+10.008269]	571.7785++ (heavy)	571.778539	2	19.9	701.327454	y7	1	39.01	37.3		
Serum amyloid A-4 protei	SAA4	P35542	EALQGVGDMGR	EALQGVGDMGR[+10.008269]	571.7785++ (heavy)	571.778539	2	19.9	545.237576	y5	1	39.01	37.3		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	1069.513344	y9	1	67.04	75.01		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	956.42928	y8	1	67.04	75.01		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	869.397252	y7	1	67.04	75.01		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	755.354325	y6	1	67.04	75.01		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR	616.9530+++	616.953048	3	20.9	618.295413	y5	1	67.04	75.01		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	1079.521613	y9	1	67.04	75.01		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	966.437549	y8	1	67.04	75.01		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	879.405521	y7	1	67.04	75.01		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	765.362594	y6	1	67.04	75.01		
Serum amyloid A-4 protei	SAA4	P35542	AYWDIMISNHQNSNR	AYWDIMISNHQNSNR[+10.008269]	620.2891+++ (heavy)	620.289138	3	20.9	628.303682	y5	1	67.04	75.01		
Serum amyloid P-compon	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR	703.8386++	703.83859	2	25	972.45337	y8	1	59.44	69.05	6.134262187	4.376157643
Serum amyloid P-compon	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR	703.8386++	703.83859	2	25	825.384956	y7	1	59.44	69.05		
Serum amyloid P-compon	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR	703.8386++	703.83859	2	25	738.352928	y6	1	59.44	69.05		
Serum amyloid P-compon	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR[+10.008269]	708.8427++ (heavy)	708.842725	2	25	982.461639	y8	1	59.44	69.05		
Serum amyloid P-compon	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR[+10.008269]	708.8427++ (heavy)	708.842725	2	25	835.393225	y7	1	59.44	69.05		
Serum amyloid P-compon	APCS	P02743	AYSLFSYNTQGR	AYSLFSYNTQGR[+10.008269]	708.8427++ (heavy)	708.842725	2	25	748.361197	y6	1	59.44	69.05		
Serum amyloid P-compon	APCS	P02743	DNELLVYK	DNELLVYK	497.2662++	497.266207	2	17.3	522.32861	y4	1	52.15	51.49		
Serum amyloid P-compon	APCS	P02743	DNELLVYK	DNELLVYK	497.2662++	497.266207	2	17.3	409.244546	y3	1	52.15	51.49		
Serum amyloid P-compon	APCS	P02743	DNELLVYK	DNELLVYK	497.2662++	497.266207	2	17.3	310.176132	y2	1	52.15	51.49		
Serum amyloid P-compon	APCS	P02743	DNELLVYK	DNELLVYK[+8.014199]	501.2733++ (heavy)	501.273306	2	17.3	530.342809	y4	1	52.15	51.49		
Serum amyloid P-compon	APCS	P02743	DNELLVYK	DNELLVYK[+8.014199]	501.2733++ (heavy)	501.273306	2	17.3	417.258745	y3	1	52.15	51.49		

Serum amyloid P-compon	APCS	P02743	DNELLVYK	DNELLVYK[+8.014199]	501.2733++ (heavy)	501.273306	2	17.3	318.190331	y2	1	52.15	51.49		
Serum amyloid P-compon	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR	578.8035++	578.803488	2	20.3	871.467229	y7	1	60.33	63.17		
Serum amyloid P-compon	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR	578.8035++	578.803488	2	20.3	708.403901	y6	1	60.33	63.17		
Serum amyloid P-compon	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR	578.8035++	578.803488	2	20.3	508.287808	y4	1	60.33	63.17		
Serum amyloid P-compon	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR[+10.008269]	583.8076++ (heavy)	583.807622	2	20.3	881.475498	y7	1	60.33	63.17		
Serum amyloid P-compon	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR[+10.008269]	583.8076++ (heavy)	583.807622	2	20.3	718.41217	y6	1	60.33	63.17		
Serum amyloid P-compon	APCS	P02743	VGEYSLYIGR	VGEYSLYIGR[+10.008269]	583.8076++ (heavy)	583.807622	2	20.3	518.296077	y4	1	60.33	63.17		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK	657.3874++	657.387385	2	23.3	871.524744	y8	1	91.31	96.93	6.427389038	4.069209951
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK	657.3874++	657.387385	2	23.3	800.48763	y7	1	91.31	96.93		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK	657.3874++	657.387385	2	23.3	330.165962	b3	1	91.31	96.93		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK[+8.014199]	661.3945++ (heavy)	661.394484	2	23.3	879.538943	y8	1	91.31	96.93		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK[+8.014199]	661.3945++ (heavy)	661.394484	2	23.3	808.501829	y7	1	91.31	96.93		
Tetranectin	CLEC3B	P05452	LDTLAQEVALLK	LDTLAQEVALLK[+8.014199]	661.3945++ (heavy)	661.394484	2	23.3	330.165962	b3	1	91.31	96.93		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK	659.3452++	659.345194	2	23.3	748.402186	y6	1	46.62	44.51		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK	659.3452++	659.345194	2	23.3	620.343609	y5	1	46.62	44.51		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK	659.3452++	659.345194	2	23.3	420.227516	y3	1	46.62	44.51		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK[+8.014199]	663.3523++ (heavy)	663.352294	2	23.3	756.416385	y6	1	46.62	44.51		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK[+8.014199]	663.3523++ (heavy)	663.352294	2	23.3	628.357808	y5	1	46.62	44.51		
Tetranectin	CLEC3B	P05452	EQQALQTVCLK	EQQALQTVC[+57.021464]LK[+8.014199]	663.3523++ (heavy)	663.352294	2	23.3	428.241715	y3	1	46.62	44.51		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK	558.2813++	558.281334	2	19.6	808.45633	y7	1	58.6	68.03		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK	558.2813++	558.281334	2	19.6	695.372266	y6	1	58.6	68.03		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK	558.2813++	558.281334	2	19.6	624.335152	y5	1	58.6	68.03		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK[+8.014199]	562.2884++ (heavy)	562.288434	2	19.6	816.470529	y7	1	58.6	68.03		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK[+8.014199]	562.2884++ (heavy)	562.288434	2	19.6	703.386465	y6	1	58.6	68.03		
Tetranectin	CLEC3B	P05452	CFLAFTQTK	C[+57.021464]FLAFTQTK[+8.014199]	562.2884++ (heavy)	562.288434	2	19.6	632.349351	y5	1	58.6	68.03		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR	484.5455+++	484.545507	3	16.1	650.292636	y5	1	29.06	22.12		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR	484.5455+++	484.545507	3	16.1	375.235044	y3	1	29.06	22.12		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR	484.5455+++	484.545507	3	16.1	386.18228	b3	1	29.06	22.12		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR[+10.008269]	487.8816+++ (heavy)	487.881597	3	16.1	660.300905	y5	1	29.06	22.12		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR[+10.008269]	487.8816+++ (heavy)	487.881597	3	16.1	385.243313	y3	1	29.06	22.12		
Tetranectin	CLEC3B	P05452	TFHEASEDCISR	TFHEASEDC[+57.021464]ISR[+10.008269]	487.8816+++ (heavy)	487.881597	3	16.1	386.18228	b3	1	29.06	22.12		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK	621.2984++	621.298432	2	21.9	1011.499317	y9	1	53.5	48.98	8.340036463	3.378722094
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK	621.2984++	621.298432	2	21.9	375.223811	y3	1	53.5	48.98		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK	621.2984++	621.298432	2	21.9	231.097548	b2	1	53.5	48.98		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK[+8.014199]	625.3055++ (heavy)	625.305532	2	21.9	1019.513516	y9	1	53.5	48.98		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK[+8.014199]	625.3055++ (heavy)	625.305532	2	21.9	383.23801	y3	1	53.5	48.98		
Thyroxine-binding globulin	SERPINA7	P05543	TEDSSSFLIDK	TEDSSSFLIDK[+8.014199]	625.3055++ (heavy)	625.305532	2	21.9	231.097548	b2	1	53.5	48.98		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK	543.3395++	543.339509	2	19	787.507637	y7	1	95.36	105.58		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK	543.3395++	543.339509	2	19	716.470524	y6	1	95.36	105.58		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK	543.3395++	543.339509	2	19	186.087317	b2	1	95.36	105.58		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK	543.3395++	543.339509	2	19	299.171381	b3	1	95.36	105.58		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK[+8.014199]	547.3466++ (heavy)	547.346609	2	19	795.521836	y7	1	95.36	105.58		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK[+8.014199]	547.3466++ (heavy)	547.346609	2	19	724.484723	y6	1	95.36	105.58		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK[+8.014199]	547.3466++ (heavy)	547.346609	2	19	186.087317	b2	1	95.36	105.58		
Thyroxine-binding globulin	SERPINA7	P05543	NALALFVLPK	NALALFVLPK[+8.014199]	547.3466++ (heavy)	547.346609	2	19	299.171381	b3	1	95.36	105.58		
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK	652.7768++	652.77681	2	23.1	1119.466303	y8	1	36.66	38.1	7.708799169	1.783583157
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK	652.7768++	652.77681	2	23.1	956.402974	y7	1	36.66	38.1		
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK	652.7768++	652.77681	2	23.1	796.372326	y6	1	36.66	38.1		

Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK[+8.014199]	656.7839++ (heavy)	656.78391	2	23.1	1127.480502	y8	1	36.66	38.1
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK[+8.014199]	656.7839++ (heavy)	656.78391	2	23.1	964.417173	y7	1	36.66	38.1
Vitronectin	VTN	P04004	GQYCYELDEK	GQYC[+57.021464]YELDEK[+8.014199]	656.7839++ (heavy)	656.78391	2	23.1	804.386525	y6	1	36.66	38.1
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR	711.8304++	711.830431	2	25.3	875.425758	y7	1	58.85	66.7
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR	711.8304++	711.830431	2	25.3	647.314751	y5	1	58.85	66.7
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR	711.8304++	711.830431	2	25.3	435.235044	y3	1	58.85	66.7
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR[+10.008269]	716.8346++ (heavy)	716.834566	2	25.3	885.434027	y7	1	58.85	66.7
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR[+10.008269]	716.8346++ (heavy)	716.834566	2	25.3	657.32302	y5	1	58.85	66.7
Vitronectin	VTN	P04004	FEDGVLDPDYPR	FEDGVLDPDYPR[+10.008269]	716.8346++ (heavy)	716.834566	2	25.3	445.243313	y3	1	58.85	66.7
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR	556.2633+++	556.263334	3	18.7	691.319185	y7	1	55.45	66.43
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR	556.2633+++	556.263334	3	18.7	505.255128	y5	1	55.45	66.43
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR	556.2633+++	556.263334	3	18.7	595.262322	b5	1	55.45	66.43
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR[+10.008269]	559.5994+++ (heavy)	559.599423	3	18.7	701.327454	y7	1	55.45	66.43
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR[+10.008269]	559.5994+++ (heavy)	559.599423	3	18.7	515.263397	y5	1	55.45	66.43
Vitronectin	VTN	P04004	DWHGVPGQVDAAMAGR	DWHGVPGQVDAAMAGR[+10.008269]	559.5994+++ (heavy)	559.599423	3	18.7	595.262322	b5	1	55.45	66.43
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWLGC[+57.021464]PAPGHL	835.4114++	835.4114	2	29.8	808.377034	y8	1	90.7	101.66
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWLGC[+57.021464]PAPGHL	835.4114++	835.4114	2	29.8	591.324922	y6	1	90.7	101.66
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWLGC[+57.021464]PAPGHL	835.4114++	835.4114	2	29.8	423.235044	y4	1	90.7	101.66
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWL[+7.017164]GC[+57.021464]PAPGHL	838.9200++ (heavy)	838.919982	2	29.8	808.377034	y8	1	90.7	101.66
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWL[+7.017164]GC[+57.021464]PAPGHL	838.9200++ (heavy)	838.919982	2	29.8	591.324922	y6	1	90.7	101.66
Vitronectin	VTN	P04004	SIAQYWLGCPAPGHL	SIAQYWL[+7.017164]GC[+57.021464]PAPGHL	838.9200++ (heavy)	838.919982	2	29.8	423.235044	y4	1	90.7	101.66
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK	644.8590++	644.858991	2	22.8	834.456724	y8	1	49	53.46
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK	644.8590++	644.858991	2	22.8	563.303518	y5	1	49	53.46
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK	644.8590++	644.858991	2	22.8	342.177195	b3	1	49	53.46
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK[+8.014199]	648.8661++ (heavy)	648.866091	2	22.8	842.470923	y8	1	49	53.46
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK[+8.014199]	648.8661++ (heavy)	648.866091	2	22.8	571.317717	y5	1	49	53.46
Enolase 1	ENO1	P00924	VNQIGTLSESIK	VNQIGTLSESIK[+8.014199]	648.8661++ (heavy)	648.866091	2	22.8	342.177195	b3	1	49	53.46

Supplementary Table 3. Differential analysis: isolated ileal ulcers vs endoscopic remission

Gene names	Uniprot accession number	Technology	Mean in patients in endoscopic remission	Mean in patients with isolated ileal ulcers	Fold change	U-statistic	p-value
FCRL6	Q6DN72	PEA (immune response)	3.491081304	2.945783529	0.843802614	96	0.006756694
LTA	P01374	PEA (cytokines)	9.233861739	7.437765882	0.805488115	102	0.010945119
CNTNAP2	Q9UHC6	PEA (immune response)	2.116473043	2.476322941	1.170023379	274	0.032838556
JUN	P05412	PEA (immune response)	1.393068261	1.638775882	1.176378738	272	0.037586815
CLEC4A	Q9UMR7	PEA (immune response)	4.475768696	4.201515882	0.938724981	120	0.040172315
NTF4	P34130	PEA (immune response)	2.005184783	1.681968235	0.838809595	122	0.045797659
TNFSF12	O43508	PEA (cytokines)	915.8643961	812.5678965	0.887214199	125	0.05547025
SERPINA3	P01011	SRM	0.467028294	0.589516084	1.262270598	266	0.05547025
ITGB6	P18564	PEA (immune response)	3.859515652	3.618909412	0.937658955	126	0.059050806
ITM2A	O43736	PEA (immune response)	2.625915652	2.27331	0.865720876	128	0.066788353
APCS	P02743	SRM	0.098026341	0.119237827	1.216385573	263	0.066788353
CLEC4G	Q6UXB4	PEA (immune response)	3.798412174	3.999490588	1.052937492	259	0.084769769
MASP1	P48740	PEA (immune response)	1.55938	1.355677059	0.869369274	132	0.084769769
IL17C	Q9P0M4	PEA (cytokines)	21.94604652	15.44533529	0.703786683	134	0.095129707
CD83	Q01151	PEA (immune response)	3.238728696	3.056053529	0.943596644	134	0.095129707
LY75	O60449	PEA (immune response)	3.313334348	3.150760588	0.950933488	135	0.100677456
C8G	P07360	SRM	0.05966825	0.06849382	1.147910649	256	0.100677456
PIK3AP1	Q6ZUJ8	PEA (immune response)	4.173570435	4.574202353	1.09599261	255	0.106480035
CFB	P00751	SRM	0.102844871	0.132008611	1.283570194	255	0.106480035
IL7	P13232	PEA (cytokines)	5.481498261	6.001769412	1.094914041	253	0.118878261
MGMT	P16455	PEA (immune response)	4.282666522	4.705284118	1.098680949	253	0.118878261
TREM1	Q9NP99	PEA (immune response)	3.15582087	3.500403529	1.10918955	253	0.118878261
CRP	P02741	hsCRP	1.306086957	4.275294118	3.273361009	251.5	0.128826753
LILRB4	Q8NHJ6	PEA (immune response)	2.804328696	2.956582353	1.054292372	251	0.132380652
GSN	P06396	SRM	0.164816491	0.151134603	0.916987141	141	0.139562995
CCL7	P80098	PEA (cytokines)	1.181370435	1.481883529	1.254376685	249	0.14704159
LRG1	P02750	SRM	0.043788874	0.060038421	1.371088486	248	0.154822829
FAM3B	P58499	PEA (immune response)	4.557243913	4.430755294	0.972244492	144	0.162912902
KLRD1	Q13241	PEA (immune response)	7.311702174	7.061404118	0.965767471	144	0.162912902
PRDX1	Q06830	PEA (immune response)	3.407153043	3.790534706	1.112522583	247	0.162912902
ITIH3	Q06033	SRM	0.038473864	0.048166664	1.251932059	247	0.162912902
IL15	P40933	PEA (cytokines)	13.85634696	15.02167176	1.084100435	246	0.171317772
IRAK4	Q9NWZ3	PEA (immune response)	1.939994348	2.254408235	1.162069486	246	0.171317772
APOA4	P06727	SRM	0.133797121	0.105387928	0.787669622	146	0.180043157
C8A	P07357	SRM	0.062497243	0.068917657	1.102731152	245	0.180043157
VTN	P04004	SRM	0.584007932	0.658579408	1.127689151	245	0.180043157
NCR1	O76036	PEA (immune response)	3.740976087	3.492935882	0.933696394	147	0.1890945
C4B	P0C0L5	SRM	0.178384964	0.202476085	1.135051299	244	0.1890945
GALNT3	Q14435	PEA (immune response)	3.134937826	3.021398824	0.963782694	148	0.198476953
IL1B	P01584	PEA (cytokines)	0.561427619	0.240089375	0.427640834	126	0.203279289
IGFALS	P35858	SRM	0.020019684	0.018279474	0.913075016	151	0.228657617
MASP2	O00187	SRM	0.006455162	0.007430511	1.151095944	240	0.228657617
SERPINA7	P05543	SRM	0.102569787	0.121940914	1.18885802	239	0.23940937
FGF2	P09038	PEA (immune response)	2.024343913	2.404930588	1.18800495	238	0.250512805
APOB	P04114	SRM	0.128382075	0.140293997	1.092784929	238	0.250512805
CCL13	Q99616	PEA (cytokines)	168.4364061	179.9763835	1.06851237	237	0.261970844

C9	P02748	SRM	0.081531173	0.097990136	1.201873262	237	0.261970844
FCN3	O75636	SRM	0.044236313	0.047786754	1.080260792	237	0.261970844
IL33	O95760	PEA (cytokines)	0.271942727	1.898675882	6.981896157	227	0.263259039
CFI	P05156	SRM	0.061845356	0.069636024	1.125970142	236	0.273785966
DGKZ	Q13574	PEA (immune response)	0.533401739	0.578589412	1.08471602	235	0.285960183
EGLN1	Q9GZT9	PEA (immune response)	2.25114913	2.280585882	1.013076322	235	0.285960183
TRAF2	Q12933	PEA (immune response)	3.073471304	3.263914706	1.061963618	235	0.285960183
BACH1	O14867	PEA (immune response)	2.843862609	2.943029412	1.034870462	234	0.298495023
SERPING1	P05155	SRM	0.318189405	0.349420053	1.098151126	234	0.298495023
CXADR	P78310	PEA (immune response)	2.551278261	2.705523529	1.060458034	233	0.311391512
DFFA	O00273	PEA (immune response)	4.58491913	4.761051176	1.038415519	233	0.311391512
CLEC3B	P05452	SRM	0.034553696	0.033411506	0.966944481	158	0.311391512
ORM1	P02763	SRM	1.056412122	1.229749741	1.164081437	233	0.311391512
DCTN1	Q14203	PEA (immune response)	4.927415652	5.082721176	1.031518657	232	0.324650155
C2	P06681	SRM	0.025598601	0.028457523	1.111682755	232	0.324650155
PPP1R9B	Q96SB3	PEA (immune response)	2.800640435	2.882118824	1.02909277	231	0.338270925
APOH	P02749	SRM	0.916421112	0.995773026	1.086588919	231	0.338270925
CCL3	P10147	PEA (cytokines)	18.00903	10.08526706	0.560011675	161	0.352253241
CXCL9	Q07325	PEA (cytokines)	95.71045391	62.16168412	0.649476432	161	0.352253241
TANK	Q92844	PEA (immune response)	2.530642174	2.652590588	1.048188723	230	0.352253241
C8B	P07358	SRM	0.03203925	0.034668423	1.082060984	230	0.352253241
IGHV3-23	P01764	SRM	0.438086678	0.438237882	1.000345146	230	0.352253241
MMP12	P39900	PEA (cytokines)	252.2313791	281.5339041	1.116173194	229	0.366595961
OSM	P13725	PEA (cytokines)	12.48392609	13.43516941	1.076197449	229	0.366595961
F9	P00740	SRM	0.018527203	0.019870633	1.072511195	229	0.366595961
TSLP	Q969D9	PEA (cytokines)	0.241723684	0.6715	2.777965271	179	0.38021366
IL17F	Q96PD4	PEA (cytokines)	1.372027826	1.039856471	0.757897508	163	0.381297367
EDAR	Q9UNE0	PEA (immune response)	4.314686957	4.025236471	0.932915067	163	0.381297367
SAA4	P35542	SRM	0.262718834	0.301823826	1.148847309	228	0.381297367
PSIP1	O75475	PEA (immune response)	3.080049565	3.066542353	0.995614612	227	0.396355153
ATRN	O75882	SRM	0.029565962	0.027493549	0.929905435	164	0.396355153
CFH	P08603	SRM	0.415849784	0.448198419	1.077789231	227	0.396355153
HP	P00738	SRM	4.586313261	5.789404297	1.262322037	227	0.396355153
IL17A	Q16552	PEA (cytokines)	0.556373913	0.548704118	0.986214675	226	0.411766419
PRDX3	P30048	PEA (immune response)	0.435637391	0.437128824	1.003423563	226	0.411766419
STC1	P52823	PEA (immune response)	6.187215217	6.348651765	1.026091956	226	0.411766419
SERPIND1	P05546	SRM	0.178502131	0.198154483	1.110095894	226	0.411766419
SHBG	P04278	SRM	0.013850582	0.017194557	1.241432143	226	0.411766419
CCL2	P13500	PEA (cytokines)	521.8414665	576.4048494	1.104559309	225	0.427527661
CCL4	P13236	PEA (cytokines)	167.8779939	138.7197206	0.826312713	166	0.427527661
CSF1	P09603	PEA (cytokines)	131.2414952	138.22435	1.053206151	225	0.427527661
CLEC7A	Q9BXN2	PEA (immune response)	3.857227826	3.996228235	1.036036349	225	0.427527661
GLB1	P16278	PEA (immune response)	3.477088696	3.556624118	1.022874142	225	0.427527661
JCHAIN	P01591	SRM	0.157183253	0.131882171	0.839034496	166	0.427527661
CCL11	P51671	PEA (cytokines)	148.9854835	185.02204	1.241879649	224	0.443634766
IL13	P35225	PEA (cytokines)	0.829182609	5.500594706	6.633755518	167	0.443634766
FN1	P02751	SRM	0.163323621	0.148029954	0.906359733	167	0.443634766
ITIH2	P19823	SRM	0.314934295	0.300420253	0.953914065	167	0.443634766
EIF4G1	Q04637	PEA (immune response)	4.059956522	4.252651176	1.047462246	223	0.460083007
HEXIM1	O94992	PEA (immune response)	3.610026087	3.693134706	1.023021612	223	0.460083007

IRF9	Q00978	PEA (immune response)	3.117368696	3.171858235	1.017479338	223	0.460083007
RIGI	O95786	PEA (immune response)	3.528424783	3.604709412	1.021620024	223	0.460083007
AHSG	P02765	SRM	0.864712795	0.946649657	1.094756158	223	0.460083007
F10	P00742	SRM	0.024306883	0.025881965	1.064799846	223	0.460083007
SELL	P14151	SRM	0.010845342	0.010342909	0.953672903	168	0.460083007
SERPINF1	P36955	SRM	0.034145215	0.032411521	0.949225854	168	0.460083007
THBS1	P07996	SRM	0.02454962	0.025787832	1.050437121	223	0.460083007
EGF	P01133	PEA (cytokines)	597.2157852	612.1311218	1.024974786	221	0.493980911
ICA1	Q05084	PEA (immune response)	1.440737826	1.498471176	1.040072072	221	0.493980911
SH2B3	Q9UQQ2	PEA (immune response)	2.412432174	2.623782941	1.087608999	221	0.493980911
TRIM5	Q9C035	PEA (immune response)	2.954707826	3.136711765	1.061597948	221	0.493980911
MBL2	P11226	SRM	0.007312202	0.007401361	1.012193265	221	0.493980911
CXCL10	P02778	PEA (cytokines)	92.63456739	78.37650471	0.846082698	171	0.51141804
AREG	P15514	PEA (immune response)	4.015142174	3.975053529	0.990015635	171	0.51141804
HSD11B1	P28845	PEA (immune response)	3.459246957	3.39835	0.982395892	171	0.51141804
ITGA6	P23229	PEA (immune response)	2.384212609	2.283352353	0.957696618	171	0.51141804
SRPK2	P78362	PEA (immune response)	1.734883043	1.741542941	1.003838817	220	0.51141804
CD14	P08571	SRM	0.004037904	0.004321157	1.070148394	220	0.51141804
TNF	P01375	PEA (cytokines)	204.4088091	186.7507259	0.913613883	172	0.529171242
DPP10	Q8N608	PEA (immune response)	1.664942174	1.770016471	1.063109878	219	0.529171242
IFNLR1	Q8IU57	PEA (immune response)	3.312180435	3.232962941	0.976082978	172	0.529171242
CSF2	P04141	PEA (cytokines)	0.168212174	0.198461765	1.179829974	218	0.547232721
APOA1	P02647	SRM	8.400184191	7.797136517	0.928210185	173	0.547232721
IL6	P05231	PEA (cytokines)	2.617591304	3.112566471	1.189095664	217	0.565594081
OLR1	P78380	PEA (cytokines)	466.4073978	402.3958447	0.862756137	174	0.565594081
CLEC6A	Q6EIG7	PEA (immune response)	3.937800435	3.804785882	0.966221104	174	0.565594081
IL5	P05113	PEA (immune response)	0.847356522	1.095162941	1.292446465	217	0.565594081
MILR1	Q7Z6M3	PEA (immune response)	4.333724348	4.409155294	1.017405571	217	0.565594081
C3	P01024	SRM	1.47717763	1.558726987	1.055206196	217	0.565594081
FCRL3	Q96P31	PEA (immune response)	2.080829565	1.955538235	0.939787798	175	0.584246336
APOC3	P02656	SRM	1.688279934	1.588942201	0.94116039	175	0.584246336
TPSAB1	Q15661	PEA (immune response)	6.512177826	6.485777059	0.995945939	176	0.603179917
APOA2	P02652	SRM	8.560258309	8.094110726	0.94554515	176	0.603179917
C4BPB	P20851	SRM	0.026518855	0.028112343	1.060088877	215	0.603179917
ITIH1	P19827	SRM	0.257294088	0.251769076	0.978526472	177	0.622384687
MMP1	P03956	PEA (cytokines)	3576.493573	3915.742529	1.094855184	213.5	0.632069469
IL4	P05112	PEA (cytokines)	0.046906522	0.042669412	0.909669065	178	0.641849955
PRKCQ	Q04759	PEA (immune response)	1.968970435	2.066835294	1.04970357	213	0.641849955
SIT1	Q9Y3P8	PEA (immune response)	1.657896522	1.713086471	1.03328914	213	0.641849955
C6	P13671	SRM	0.053151293	0.056679907	1.066388118	213	0.641849955
VEGFA	P15692	PEA (cytokines)	789.6829513	806.7105176	1.021562535	179	0.661564492
EIF5A	P63241	PEA (immune response)	1.224933043	1.278415294	1.043661367	212	0.661564492
CP	P00450	SRM	0.703809983	0.778169677	1.105653083	212	0.661564492
FGB	P02675	SRM	0.005511314	0.004929534	0.89443891	179	0.661564492
CCL8	P80075	PEA (cytokines)	59.67616478	60.62313412	1.015868468	211	0.68151655
IFNG	P01579	PEA (cytokines)	0.40072	0.362278824	0.904069733	211	0.68151655
IL18	Q14116	PEA (cytokines)	308.7232387	324.5592535	1.051295182	211	0.68151655
HCLS1	P14317	PEA (immune response)	4.857825652	4.890164118	1.006656984	211	0.68151655
IRAK1	P51617	PEA (immune response)	2.41485	2.421568824	1.002782294	211	0.68151655
PLXNA4	Q9HCM2	PEA (immune response)	5.918636522	5.857668824	0.98969903	211	0.68151655

SPRY2	O43597	PEA (immune response)	2.71269087	2.482165294	0.915019593	211	0.68151655
TRIM21	P19474	PEA (immune response)	2.441927826	2.425487647	0.993267541	211	0.68151655
APOC2	P02655	SRM	0.337766065	0.315797768	0.934960025	180	0.68151655
HPR	P00739	SRM	0.175636764	0.167631639	0.954422272	180	0.68151655
SAA1	P0DJI8	SRM	0.013219985	0.025467353	1.926428229	211	0.68151655
BIRC2	Q13490	PEA (immune response)	1.131571739	1.173398824	1.036963705	210	0.701693884
DAPP1	Q9UN19	PEA (immune response)	1.804213913	1.699738235	0.94209352	181	0.701693884
APOC4	P55056	SRM	0.026324	0.026120672	0.99227596	181	0.701693884
CFHR2	P36980	SRM	0.019336617	0.020739448	1.072547945	210	0.701693884
IGKV4-1	P06312	SRM	1.052345166	1.008201842	0.958052429	181	0.701693884
PZP	P20742	SRM	0.059241744	0.101105742	1.706663822	210	0.701693884
SERPINA4	P29622	SRM	0.023804911	0.022964821	0.964709419	181	0.701693884
TGFA	P01135	PEA (cytokines)	31.08017609	31.43259471	1.011339016	209	0.722083768
APOL1	O14791	SRM	0.104957319	0.112076104	1.067825529	209	0.722083768
CXCL11	O14625	PEA (cytokines)	70.89079522	58.99136353	0.832144192	183	0.742673026
CDSN	Q15517	PEA (immune response)	4.98525087	4.992081765	1.001370221	183	0.742673026
CLEC4C	Q8WTT0	PEA (immune response)	5.260004348	5.137589412	0.976727218	183	0.742673026
PADI2	Q9Y2J8	PEA (immune response)	1.262778696	1.348273529	1.067703735	183	0.742673026
CNDP1	Q96KN2	SRM	0.009187948	0.009287314	1.010814817	208	0.742673026
ARNT	P27540	PEA (immune response)	2.277862174	2.140638824	0.939757834	207	0.763448049
LAMP3	Q9UQV4	PEA (immune response)	5.606167391	5.757625294	1.0270163	207	0.763448049
AMBP	P02760	SRM	0.144521039	0.138336702	0.957208052	184	0.763448049
LAG3	P18627	PEA (immune response)	2.753544783	2.792931176	1.014303887	206	0.784394831
ZBTB16	Q05516	PEA (immune response)	1.866733478	1.736292941	0.930123642	185	0.784394831
CKAP4	Q07065	PEA (immune response)	5.755657391	5.687685882	0.988190487	205	0.805498989
SH2D1A	O60880	PEA (immune response)	2.037228261	1.977516471	0.970689691	186	0.805498989
C7	P10643	SRM	0.059643154	0.058531609	0.9813634	186	0.805498989
CCL19	Q99731	PEA (cytokines)	119.47341	104.1561306	0.871793402	187	0.826745795
NFATC3	Q12968	PEA (immune response)	1.410978696	1.541432941	1.092456566	204	0.826745795
PRDX5	P30044	PEA (immune response)	6.876787391	6.999168235	1.017796223	204	0.826745795
CLU	P10909	SRM	0.344055864	0.353200622	1.026579282	204	0.826745795
DEFA1	P59665	SRM	0.025952793	0.022026924	0.848730373	187	0.826745795
BTN3A2	P78410	PEA (immune response)	3.842279565	3.889945294	1.012405586	203	0.848120209
CLEC4D	Q8WXI8	PEA (immune response)	5.141724348	5.108998824	0.993635302	203	0.848120209
CPN2	P22792	SRM	0.052445197	0.053946538	1.028626838	203	0.848120209
IGLC6	P0CF74	SRM	21.14815423	20.63537741	0.975753117	188	0.848120209
LUM	P51884	SRM	0.036703146	0.036081536	0.983063851	188	0.848120209
CSF3	P09919	PEA (cytokines)	88.67265957	97.28194059	1.097090592	202	0.869606908
IL27	Q8NEV9_Q14213	PEA (cytokines)	12.16030652	10.97191765	0.902273115	202	0.869606908
ITGA11	Q9UKX5	PEA (immune response)	2.42098087	2.377191176	0.981912417	189	0.869606908
HGF	P14210	PEA (cytokines)	818.3351526	780.8339994	0.954173845	190	0.891190322
IL10	P22301	PEA (cytokines)	6.965966522	6.848469412	0.983132691	190	0.891190322
TNFSF10	P50591	PEA (cytokines)	492.91899	489.3093171	0.992676945	190	0.891190322
TF	P02787	SRM	4.354240524	4.38300874	1.006606942	201	0.891190322
IL12RB1	P42701	PEA (immune response)	2.59720913	2.574598235	0.991294157	191	0.912854663
FLT3LG	P49771	PEA (cytokines)	119.5948861	123.8692524	1.035740377	199	0.934583965
NF2	P35240	PEA (immune response)	-0.439270435	-0.388567647	0.884575005	199	0.934583965
C5	P01031	SRM	0.052438448	0.05502649	1.049353898	199	0.934583965
IGHA1	P01876	SRM	2.827297491	2.881741701	1.019256626	199	0.934583965
PLG	P00747	SRM	0.18695411	0.189437886	1.013285487	192	0.934583965

CD28	P10747	PEA (immune response)	2.283443478	2.275268824	0.996420032	193	0.956362115
FXYD5	Q96DB9	PEA (immune response)	1.20358087	1.227815882	1.020135758	193	0.956362115
HNMT	P50135	PEA (immune response)	9.820934783	9.86165	1.004145758	193	0.956362115
PTH1R	Q03431	PEA (immune response)	3.918386522	3.90016	0.995348463	193	0.956362115
HRG	P04196	SRM	0.24183762	0.24470324	1.011849356	193	0.956362115
CXCL8	P10145	PEA (cytokines)	48.98301652	23.91137118	0.488156363	194	0.978172892
DCBLD2	Q96PD2	PEA (immune response)	8.364280435	8.363280588	0.999880462	197	0.978172892
KPNA1	P52294	PEA (immune response)	1.758508696	1.674208235	0.952061391	197	0.978172892
KRT19	P08727	PEA (immune response)	4.133217391	4.337493529	1.049423033	197	0.978172892
IL2	P60568	PEA (cytokines)	0.018334783	0.013760588	0.750518211	195	1

Supplementary Table 4. Differential analysis: isolated colonic ulcers vs endoscopic remission

Gene names	Uniprot accession number	Technology	Mean in patients in endoscopic remission	Mean in patients with isolated colonic ulcers	Fold change	U-statistic	p-value
CSF3	P09919	PEA (cytokines)	88.67265957	151.3125713	1.706417423	311	0.000304044
IL7	P13232	PEA (cytokines)	5.481498261	8.088996875	1.475690859	289	0.002847996
CRP	P02741	hsCRP	1.306086957	8.185	6.266810919	284	0.004490179
IL10	P22301	PEA (cytokines)	6.965966522	21.081295	3.026327349	282	0.005372264
APCS	P02743	SRM	0.098026341	0.129057271	1.316557052	281	0.005864387
MMP12	P39900	PEA (cytokines)	252.2313791	412.5634513	1.635654742	278	0.007593869
IL6	P05231	PEA (cytokines)	2.617591304	5.652158125	2.15929741	277	0.008264681
VEGFA	P15692	PEA (cytokines)	789.6829513	1306.260754	1.654158485	276	0.00898803
IL17A	Q16552	PEA (cytokines)	0.556373913	1.09925	1.97573965	269	0.015837236
CFB	P00751	SRM	0.102844871	0.128849039	1.252848465	268	0.017121275
MBL2	P11226	SRM	0.007312202	0.010830513	1.481156193	266	0.019965852
TPSAB1	Q15661	PEA (immune response)	6.512177826	5.946403333	0.91312054	97	0.025103644
CLEC3B	P05452	SRM	0.034553696	0.029769907	0.861554927	106	0.026912752
TNFSF12	O43508	PEA (cytokines)	915.8643961	785.0949156	0.857217421	106	0.026912752
GSN	P06396	SRM	0.164816491	0.141606566	0.85917717	107	0.028945431
CLEC4G	Q6UXB4	PEA (immune response)	3.798412174	4.041252	1.063931931	242	0.039339329
CCL19	Q99731	PEA (cytokines)	119.47341	193.5511969	1.620035763	256	0.041204246
CXCL10	P02778	PEA (cytokines)	92.63456739	206.2782213	2.226795321	255	0.044123378
CCL7	P80098	PEA (cytokines)	1.181370435	1.73781375	1.471015101	253	0.050487208
IL5	P05113	PEA (immune response)	0.847356522	1.572436667	1.855696659	238	0.052238442
SERPINA4	P29622	SRM	0.023804911	0.020163199	0.847018475	118	0.061462048
FCRL6	Q6DN72	PEA (immune response)	3.491081304	3.058896	0.876203025	110	0.064087395
HP	P00738	SRM	4.586313261	5.947534341	1.29680072	249	0.065532982
JCHAIN	P01591	SRM	0.157183253	0.124163429	0.789927851	119	0.065532982
IGHV3-23	P01764	SRM	0.438086678	0.491954702	1.122962022	248	0.069823684
ZBTB16	Q05516	PEA (immune response)	1.866733478	1.501156	0.804161932	112	0.073158074
CXCL11	O14625	PEA (cytokines)	70.89079522	244.4896224	3.448820423	247	0.074342333
APOC3	P02656	SRM	1.688279934	1.328264231	0.786755919	123	0.084096438
CCL13	Q99616	PEA (cytokines)	168.4364061	229.2311462	1.360935866	245	0.084096438
CD83	Q01151	PEA (immune response)	3.238728696	3.024216667	0.933766595	115	0.088708304
HRG	P04196	SRM	0.24183762	0.198718552	0.8217024	124	0.089348446
IFNG	P01579	PEA (cytokines)	0.40072	2.321095	5.79231134	243	0.094861466
IGHA1	P01876	SRM	2.827297491	3.627385749	1.282986937	243	0.094861466
NFATC3	Q12968	PEA (immune response)	1.410978696	1.586837333	1.124635927	228	0.100481662
LRG1	P02750	SRM	0.043788874	0.060511643	1.381895398	242	0.100643755
C9	P02748	SRM	0.081531173	0.099713505	1.223010803	241	0.106703522
TF	P02787	SRM	4.354240524	3.92800368	0.902109945	127	0.106703522
PLXNA4	Q9HCM2	PEA (immune response)	5.918636522	5.449997333	0.920819738	118	0.106818623
TNF	P01375	PEA (cytokines)	204.4088091	324.5014187	1.587511909	239	0.119687963
CD28	P10747	PEA (immune response)	2.283443478	2.176054	0.95297038	120	0.120439657
APOA4	P06727	SRM	0.133797121	0.096216246	0.719120456	130	0.126628616
APOA1	P02647	SRM	8.400184191	7.02288822	0.836039789	132	0.141445705
APOC2	P02655	SRM	0.337766065	0.264729465	0.783765727	132	0.141445705
ITIH2	P19823	SRM	0.314934295	0.27463101	0.872026371	132	0.141445705
APOC4	P55056	SRM	0.026324	0.02145327	0.814970004	133	0.149337186
CFH	P08603	SRM	0.415849784	0.459154868	1.104136363	235	0.149337186

F9	P00740	SRM	0.018527203	0.020311081	1.09628427	235	0.149337186
CP	P00450	SRM	0.703809983	0.812544819	1.154494592	234	0.157560305
APOH	P02749	SRM	0.916421112	0.795810862	0.868389926	135	0.166122017
DCBLD2	Q96PD2	PEA (immune response)	8.364280435	8.207181333	0.981217858	126	0.169520391
KRT19	P08727	PEA (immune response)	4.133217391	3.80509	0.920612114	126	0.169520391
CLEC6A	Q6EIG7	PEA (immune response)	3.937800435	4.122990667	1.047028852	218	0.178986399
FAM3B	P58499	PEA (immune response)	4.557243913	4.479656667	0.982974963	127	0.178986399
CCL8	P80075	PEA (cytokines)	59.67616478	81.28679063	1.362131614	231	0.184287624
CFI	P05156	SRM	0.061845356	0.067028617	1.083810031	231	0.184287624
IGFALS	P35858	SRM	0.020019684	0.017520077	0.875142505	137	0.184287624
ORM1	P02763	SRM	1.056412122	1.239807339	1.173601961	231	0.184287624
IL12RB1	P42701	PEA (immune response)	2.59720913	2.476596	0.953560486	128	0.18884001
IGLC6	P0CF74	SRM	21.14815423	24.47084772	1.157115058	230	0.193903935
IL17F	Q96PD4	PEA (cytokines)	1.372027826	0.95472625	0.695850501	138	0.193903935
FCN3	O75636	SRM	0.044236313	0.047501017	1.07380146	229	0.20388361
LY75	O60449	PEA (immune response)	3.313334348	3.132436667	0.945403131	130	0.20973651
SERPINA3	P01011	SRM	0.467028294	0.523624779	1.121184275	228	0.214231941
CLEC4A	Q9UMR7	PEA (immune response)	4.475768696	4.283634667	0.957072395	131	0.220791475
ITGA6	P23229	PEA (immune response)	2.384212609	2.264950667	0.949978479	131	0.220791475
C7	P10643	SRM	0.059643154	0.055025195	0.922573529	141	0.224953803
GALNT3	Q14435	PEA (immune response)	3.134937826	3.046073333	0.971653507	132	0.23225813
C3	P01024	SRM	1.47717763	1.623971334	1.099374443	226	0.236053626
C8G	P07360	SRM	0.05966825	0.063264712	1.060274303	226	0.236053626
OSM	P13725	PEA (cytokines)	12.48392609	15.05392063	1.205864287	225	0.247535372
HSD11B1	P28845	PEA (immune response)	3.459246957	3.636666	1.051288343	211	0.256444845
PRDX3	P30048	PEA (immune response)	0.435637391	0.60282	1.383765517	211	0.256444845
PSIP1	O75475	PEA (immune response)	3.080049565	3.208862	1.041821546	211	0.256444845
CNDP1	Q96KN2	SRM	0.009187948	0.007706927	0.838808365	144	0.259402503
SAA1	P0DJI8	SRM	0.013219985	0.030610727	2.315488703	224	0.259402503
SERPINF1	P36955	SRM	0.034145215	0.031158581	0.912531402	144	0.259402503
TREM1	Q9NP99	PEA (immune response)	3.15582087	3.337752667	1.057649596	210	0.269172579
F10	P00742	SRM	0.024306883	0.025668008	1.055997484	222	0.28430414
CSF1	P09603	PEA (cytokines)	131.2414952	143.5355706	1.093675216	221	0.297342864
LUM	P51884	SRM	0.036703146	0.032911625	0.896697651	147	0.297342864
MASP2	O00187	SRM	0.006455162	0.006932127	1.073888899	221	0.297342864
IGKV4-1	P06312	SRM	1.052345166	1.137251072	1.080682564	220	0.310775363
JUN	P05412	PEA (immune response)	1.393068261	1.506205333	1.081214306	206	0.324371754
C4B	P0C0L5	SRM	0.178384964	0.190667758	1.068855545	218	0.338823521
C4BPB	P20851	SRM	0.026518855	0.028832896	1.087260235	218	0.338823521
CXCL9	Q07325	PEA (cytokines)	95.71045391	266.4507162	2.783924903	218	0.338823521
VTN	P04004	SRM	0.584007932	0.623411966	1.067471745	218	0.338823521
EGLN1	Q9GZT9	PEA (immune response)	2.25114913	2.297540667	1.020607936	205	0.339249218
OLR1	P78380	PEA (cytokines)	466.4073978	401.0616819	0.859895627	151	0.353438491
ITM2A	O43736	PEA (immune response)	2.625915652	2.418401333	0.920974492	141	0.354557363
C2	P06681	SRM	0.025598601	0.027656465	1.080389733	216	0.368445827
IL17C	Q9P0M4	PEA (cytokines)	21.94604652	25.9759875	1.183629474	216	0.368445827
FLT3LG	P49771	PEA (cytokines)	119.5948861	102.945705	0.860786848	153	0.383843505
CXADR	P78310	PEA (immune response)	2.551278261	2.692141333	1.055212744	202	0.386458583
EDAR	Q9UNE0	PEA (immune response)	4.314686957	4.024526	0.932750404	143	0.386458583
EIF4G1	Q04637	PEA (immune response)	4.059956522	3.784746	0.932213431	143	0.386458583

IRAK4	Q9NWZ3	PEA (immune response)	1.939994348	2.051378667	1.057414765	202	0.386458583
CLEC7A	Q9BXN2	PEA (immune response)	3.857227826	4.064436667	1.053719627	201	0.403046037
TRIM5	Q9C035	PEA (immune response)	2.954707826	2.775921333	0.939490974	144	0.403046037
IL1B	P01584	PEA (cytokines)	0.561427619	0.267783333	0.476968578	131	0.404127549
ATRN	O75882	SRM	0.029565962	0.027152735	0.918378187	155	0.415798301
ITIH3	Q06033	SRM	0.038473864	0.043604272	1.133347868	213	0.415798301
NTF4	P34130	PEA (immune response)	2.005184783	1.807068667	0.901198075	145	0.420052899
IL2	P60568	PEA (cytokines)	0.018334783	0.317584375	17.32141481	212	0.432301252
C5	P01031	SRM	0.052438448	0.054001743	1.029812012	212	0.432347846
CCL2	P13500	PEA (cytokines)	521.8414665	658.8880087	1.262621028	212	0.432347846
CLU	P10909	SRM	0.344055864	0.323066837	0.938995292	156	0.432347846
CPN2	P22792	SRM	0.052445197	0.054013851	1.029910344	212	0.432347846
CSF2	P04141	PEA (cytokines)	0.168212174	0.202293125	1.202606924	212	0.432347846
TNFSF10	P50591	PEA (cytokines)	492.91899	548.7727031	1.113312155	211	0.44927257
CLEC4C	Q8WTT0	PEA (immune response)	5.260004348	5.105887333	0.970700212	147	0.455304223
CCL11	P51671	PEA (cytokines)	148.9854835	167.3459981	1.123236937	210	0.466566877
IRAK1	P51617	PEA (immune response)	2.41485	2.213055333	0.916435942	148	0.473536199
PIK3AP1	Q6ZUJ8	PEA (immune response)	4.173570435	4.368780667	1.046772957	197	0.473536199
IL4	P05112	PEA (cytokines)	0.046906522	0.045983125	0.980314108	209.5	0.475328332
SERPIND1	P05546	SRM	0.178502131	0.190074576	1.06483085	209	0.484224435
THBS1	P07996	SRM	0.02454962	0.022400962	0.91247691	159	0.484224435
RIGI	O95786	PEA (immune response)	3.528424783	3.599411333	1.020118482	196	0.4921626
MMP1	P03956	PEA (cytokines)	3576.493573	4114.664206	1.150474375	208	0.502151636
APOA2	P02652	SRM	8.560258309	7.734353898	0.903518751	160	0.502238187
TGFA	P01135	PEA (cytokines)	31.08017609	35.00223438	1.126191637	208	0.502238187
BTN3A2	P78410	PEA (immune response)	3.842279565	3.762669333	0.979280469	150	0.511174999
FGF2	P09038	PEA (immune response)	2.024343913	1.882293333	0.929828831	150	0.511174999
IFNLR1	Q8IU57	PEA (immune response)	3.312180435	3.394898	1.02497375	195	0.511174999
ITGA11	Q9UKX5	PEA (immune response)	2.42098087	2.287139333	0.944715988	151	0.530564095
KPNA1	P52294	PEA (immune response)	1.758508696	1.781073333	1.01283169	151	0.530564095
TRAF2	Q12933	PEA (immune response)	3.073471304	3.134756667	1.019940112	194	0.530564095
EGF	P01133	PEA (cytokines)	597.2157852	525.1363225	0.879307506	162	0.539302387
ITIH1	P19827	SRM	0.257294088	0.237549282	0.923259774	162	0.539302387
LTA	P01374	PEA (cytokines)	9.233861739	8.554943125	0.926475116	162	0.539302387
IL33	O95760	PEA (cytokines)	0.271942727	0.18856625	0.693404276	155	0.544451534
EIF5A	P63241	PEA (immune response)	1.224933043	1.281404	1.04610126	193	0.550319725
PRDX5	P30044	PEA (immune response)	6.876787391	6.724877333	0.977909735	152	0.550319725
SH2D1A	O60880	PEA (immune response)	2.037228261	2.149569333	1.055144077	193	0.550319725
LAMP3	Q9UQV4	PEA (immune response)	5.606167391	5.469440667	0.975611373	153	0.570430876
NCR1	O76036	PEA (immune response)	3.740976087	3.743176	1.000588059	192	0.570430876
STC1	P52823	PEA (immune response)	6.187215217	6.053908	0.978454408	153	0.570430876
C6	P13671	SRM	0.053151293	0.051230799	0.963867425	164	0.577688523
DAPP1	Q9UN19	PEA (immune response)	1.804213913	1.898428667	1.052219281	191	0.590885696
ICA1	Q05084	PEA (immune response)	1.440737826	1.442268667	1.001062539	191	0.590885696
SRPK2	P78362	PEA (immune response)	1.734883043	1.660739333	0.957262992	191	0.590885696
AHSG	P02765	SRM	0.864712795	0.820704261	0.949106184	165	0.597352047
SAA4	P35542	SRM	0.262718834	0.277257909	1.055340815	203	0.597352047
TSLP	Q969D9	PEA (cytokines)	0.241723684	0.216934	0.897446192	127	0.602878203
PADI2	Q9Y2J8	PEA (immune response)	1.262778696	1.131234	0.895829177	155	0.611671513
PPP1R9B	Q96SB3	PEA (immune response)	2.800640435	2.611376	0.932421016	155	0.611671513

KLRD1	Q13241	PEA (immune response)	7.311702174	7.125642	0.974553097	156	0.632774855
APOB	P04114	SRM	0.128382075	0.127323992	0.991758327	201	0.637563471
CCL3	P10147	PEA (cytokines)	18.00903	12.25617625	0.680557268	167	0.637563471
IL15	P40933	PEA (cytokines)	13.85634696	13.72178938	0.990289101	167	0.637563471
ARNT	P27540	PEA (immune response)	2.277862174	2.345505333	1.029695897	157	0.654181473
MILR1	Q7Z6M3	PEA (immune response)	4.333724348	4.229502	0.975950859	157	0.654181473
C8A	P07357	SRM	0.062497243	0.064069124	1.025151207	200	0.658086781
BIRC2	Q13490	PEA (immune response)	1.131571739	1.162020667	1.026908526	187	0.67587637
ITGB6	P18564	PEA (immune response)	3.859515652	3.800292667	0.984655332	158	0.67587637
MGMT	P16455	PEA (immune response)	4.282666522	4.422714	1.032701	187	0.67587637
HGF	P14210	PEA (cytokines)	818.3351526	853.2927012	1.042717887	199	0.67887105
IL27	8NEV9_Q1421	PEA (cytokines)	12.16030652	21.18949625	1.742513333	169	0.67887105
SPRY2	O43597	PEA (immune response)	2.71269087	2.262863333	0.834176632	159	0.697843828
CXCL8	P10145	PEA (cytokines)	48.98301652	50.41954937	1.029327162	198	0.699902442
IL13	P35225	PEA (cytokines)	0.829182609	0.510166875	0.615264804	170	0.699902442
SELL	P14151	SRM	0.010845342	0.010666254	0.983487038	170	0.699902442
DEFA1	P59665	SRM	0.025952793	0.020901482	0.805365397	171	0.721166557
CLEC4D	Q8WXI8	PEA (immune response)	5.141724348	5.244288667	1.019947456	184	0.742530166
DGKZ	Q13574	PEA (immune response)	0.533401739	0.52462	0.983536351	184	0.742530166
CD14	P08571	SRM	0.004037904	0.004174212	1.033757061	196	0.742648451
C8B	P07358	SRM	0.03203925	0.033198948	1.03619614	195	0.76433267
FXYD5	Q96DB9	PEA (immune response)	1.20358087	1.297330667	1.077892395	183	0.765214325
HCLS1	P14317	PEA (immune response)	4.857825652	4.775295333	0.983010852	183	0.765214325
LILRB4	Q8NHJ6	PEA (immune response)	2.804328696	2.876936667	1.025891391	183	0.765214325
HEXIM1	O94992	PEA (immune response)	3.610026087	3.402435333	0.942496052	163	0.788101685
PTH1R	Q03431	PEA (immune response)	3.918386522	3.87335	0.988506361	163	0.788101685
CFHR2	P36980	SRM	0.019336617	0.018561977	0.959939216	175	0.808243926
FGB	P02675	SRM	0.005511314	0.005456459	0.990046914	175	0.808243926
CKAP4	Q07065	PEA (immune response)	5.755657391	5.667034	0.984602386	164	0.811173481
DFFA	O00273	PEA (immune response)	4.58491913	4.542708667	0.99079363	164	0.811173481
FCRL3	Q96P31	PEA (immune response)	2.080829565	1.962726667	0.943242397	164	0.811173481
FN1	P02751	SRM	0.163323621	0.172146501	1.054020843	192	0.830437813
BACH1	O14867	PEA (immune response)	2.843862609	2.753668	0.96828447	180	0.834410469
SIT1	Q9Y3P8	PEA (immune response)	1.657896522	1.623001333	0.978952131	165	0.834410469
AMBP	P02760	SRM	0.144521039	0.14288552	0.988683177	177	0.852767803
DPP10	Q8N608	PEA (immune response)	1.664942174	1.660803333	0.997514124	179	0.857792969
GLB1	P16278	PEA (immune response)	3.477088696	3.351816667	0.96397215	166	0.857792969
LAG3	P18627	PEA (immune response)	2.753544783	2.786654667	1.012024458	179	0.857792969
PRDX1	Q06830	PEA (immune response)	3.407153043	3.355534667	0.984849998	166	0.857792969
SH2B3	Q9UQQ2	PEA (immune response)	2.412432174	2.309679333	0.957406952	166	0.857792969
PZP	P20742	SRM	0.059241744	0.073878609	1.247070111	190	0.875216424
HNMT	P50135	PEA (immune response)	9.820934783	9.689986	0.986666363	167	0.881300919
SHBG	P04278	SRM	0.013850582	0.014358351	1.036660483	179	0.897765917
CNTNAP2	Q9UHC6	PEA (immune response)	2.116473043	2.079787333	0.982666583	168	0.904913924
TANK	Q92844	PEA (immune response)	2.530642174	2.493234667	0.985218176	168	0.904913924
TRIM21	P19474	PEA (immune response)	2.441927826	2.321523333	0.950692854	168	0.904913924
IL18	Q14116	PEA (cytokines)	308.7232387	311.5943213	1.009299859	188	0.920398278
SERPINA7	P05543	SRM	0.102569787	0.107908905	1.052053515	180	0.920398278
DCTN1	Q14203	PEA (immune response)	4.927415652	4.889236667	0.992251722	176	0.928611312
PRKCQ	Q04759	PEA (immune response)	1.968970435	1.938952	0.984754248	169	0.928611312

APOL1	O14791	SRM	0.104957319	0.103215541	0.983404898	181	0.943095303
CCL4	P13236	PEA (cytokines)	167.8779939	172.4951069	1.027502789	187	0.943095303
PLG	P00747	SRM	0.18695411	0.187129769	1.000939582	186	0.965838629
SERPING1	P05155	SRM	0.318189405	0.306194568	0.96230284	182	0.965838629
AREG	P15514	PEA (immune response)	4.015142174	4.047795333	1.008132504	174	0.976175473
CDSN	Q15517	PEA (immune response)	4.98525087	4.970204667	0.996981856	174	0.976175473
MASP1	P48740	PEA (immune response)	1.55938	1.59273	1.021386705	171	0.976175473
HPR	P00739	SRM	0.175636764	0.17404984	0.990964738	185	0.988609782
IRF9	Q00978	PEA (immune response)	3.117368696	3.075879333	0.986690903	173	1
NF2	P35240	PEA (immune response)	-0.439270435	-0.433970667	0.987935068	173	1