Nasal protein profiles in work-related asthma caused by different exposures

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Short title: Nasal protein profiles in work-related asthma

Key words: exposure, isocyanate, proteomics, work-related asthma, welding

Word count: 3561

This work was supported by grant from the Finnish Work Environment Fund (project No. 109365).

Abstract

Background The mechanisms of work-related asthma are incompletely delineated. Nasal cell samples may be informative about processes in the lower airways. Our aim was to determine the nasal protein expression profiles of work-related asthma caused by different kind of exposures.

Methods We collected nasal brush samples from 82 non-smoking participants, including healthy controls and work-related asthma patients exposed to 1) protein allergens, 2) isocyanates, and 3) welding fumes the day after relevant exposure. The proteome changes in samples were analysed by two-dimensional difference gel electrophoresis and the differentially regulated proteins found were identified by mass spectrometry. Immunological comparison was carried out using Western blot.

Results We detected an average of 2500 spots per protein gel. Altogether 228 protein spots were chosen for identification, yielding 77 different proteins. Compared to the controls exposure to protein allergens had the largest effects on the proteome. Hierarchical clustering revealed that protein allergen and isocyanate related asthma had similar profiles, whereas asthma related to welding fumes differed. The highly overrepresented functional categories in the asthma groups were defence response, protease inhibitor activity, inflammatory and calcium signalling, complement activation, and cellular response to oxidative stress. Immunological analysis confirmed the found abundance differences in Galectin 10 and Protein S100-A9 between the groups.

Conclusions Work-related asthma patients exposed to protein allergens and isocyanates elicit similar nasal proteome responses and the profiles of welders and healthy controls were alike. Revealed biological activities of the protein expression changes are associated with allergic inflammation and asthma.

Introduction

Occupational exposure can initiate or trigger asthma, leading to the development of different types of work-related asthma (WRA) (1). Protein allergens at workplaces cause asthma via Immunoglobulin E (IgE)-associated mechanisms, which are similar to allergic asthma unrelated to work (2). Asthma associated with isocyanate exposure is often IgE-independent, but the mechanisms are incompletely delineated. Welding fumes and aerosols composed of potentially hazardous metals and gases are also common exposures among WRA patients (3, 4). These fumes diminish functionality of local and circulating immune cells but the mechanisms in airway diseases are poorly understood (5).

Asthma and rhinitis commonly coexist and this is also true in WRA. Up to 90% of WRA patients report work-related rhinitis symptoms (6). Nasal epithelium provides an important physico-chemical and immunological barrier against the different factors targeting lower airways, but the mechanisms explaining the correlations between these diseases are not fully understood. According to the united airway concept, both diseases could be secondary to the same disease mechanisms occurring throughout the respiratory tract (7).

Proteomic approaches offer great potential for the systematic analysis of complex biological airway samples and have the advantage of assessing the presence and abundance of gene products (i.e., proteins), which are functionally relevant to the clinical phenotypes of airway diseases (8). A nasal brush sample (NBS) is a relatively non-invasive specimen containing proteins secreted from epithelial and inflammatory cells (9). Induced sputum and nasal lavage fluid (NLF), have been applied to characterize proteomic changes in airway diseases (10, 11). The identified proteins in these samples have been mostly identical (12) suggesting that also NBS may be useful in the research of upper airway epithelia and as a surrogate of lower airways.

We assessed the NBS proteome in patients with WRA who were exposed to protein allergens, isocyanates or welding fumes, and in healthy subjects. Our aim was to determine whether the proteomics method could reveal differences between the protein expressions of these groups and to investigate potential reaction mechanisms. Our premise was that nasal samples could reflect the protein profile of the entire airways.

Materials and methods

Study design and population

The study population included WRA patients examined at the Finnish Institute of Occupational Health during 2009-2012 (Figure 1). Their asthma diagnosis was confirmed by demonstrating reversible airway obstruction or bronchial hyperresponsiveness. They were exposed at work to 1) protein allergens, 2) isocyanates, or 3) welding fumes. Their asthma symptoms emerged while they were exposed to the occupational agent, and worsened during exposure. The control group comprised healthy men who carried out their military service 1986-1990 and participated in a follow-up study in 2009 (13). Current smokers were excluded. A subset of samples were used in the proteomic analysis and few found differences were compared both in the whole population and in those excluded from proteomic analysis. In order to analyse representative and homogeneous groups, NBS from eight participants in each group were selected based on clinical symptoms to represent their groups, outliers were not included. The clinical characteristics of these groups are presented in Table S1. The study was

approved by the ethics committee of Helsinki University Central Hospital (approval number 284/13/03/00/08, 125/13/03/00/09). All participants signed their informed consent.

Methods of clinical tests, controlled exposure to occupational agent as well as induced sputum and nasal brush sample preparation are described in Supplementary material 1.

Two-dimensional differential gel electrophoresis and gel spot protein identification

For proteomics analysis, 2 ml of NBS supernatant was concentrated. Protein samples were prepared and two-dimensional differential gel electrophoresis (2D-DIGE) was performed, as previously described (12). For protein identification, in-gel digestion was conducted for the chosen gel spots and the resulting peptides were extracted (12) and dried in a vacuum centrifuge. Each peptide mixture was analysed by an automated EASY nanoLC 1000 (Proxeon, Thermo Fisher Scientific Inc., USA) coupled to an electrospray ionization quadrupole orpitrap mass spectrometer (QExactive, Thermo Fisher Scientific Inc., USA). Reverse-phase separation of peptides was carried out using a 75 µm × 15 cm Acclaim PepMap100 C18 column (Dionex, Thermo Fisher Scientific Inc., USA) at a flow rate of 300 nL /min. Peptides were eluted from the column with a linear gradient of 5–35% solvent B (0.1% formic acid in 95% acetonitrile) in 80 minutes. Solvent A was 0.1% formic acid in 5% acetonitrile. We searched for the mass fragment spectra obtained in the SwissProt database (www.uniprot.org) against human entries using Proteome Discoverer 1.4 (Thermo Fisher Scientific Inc., USA).

Immunological comparison

Abundances of Glutathione S-transferase 1 (GSTP1), Galectin 10 (LEG10), Protein S100-A9 (S10A9), and Calcyphosin (CAYP1) were compared by Western blotting in the whole study population using precast 26-well 12% Criterion TGX gels (BioRad), as previously described (12). The gel lane was loaded with 10 µl of untreated NBS. Primary antibody dilutions were 1:100 for S10A9 (Abcam 24111), 1:10000 for LEG10 (Abcam 157475), 1:2000 for GSTP1 (Abcam 47709) and 1:4400 for CAYP1 (Abcam 188470). Immunoblots were stained with anti-rabbit or anti-mouse peroxidase-conjugated immunoglobulins (1:2000) (Dako Cytomaton) and chemiluminescent HRP-substrate ECL detection reagent (Perkin Elmer). They were visualized by an Image Quant LAS 4000 mini quantitative imager (GE Healthcare Biosciences). ImageQuant TL (GE Healthcare Biosciences) was used to calculate the intensities of the protein bands, which were normalized to the band intensity of a pool containing all samples.

Statistical and bioinformatical analyses

Continuous variables were expressed as means (± standard deviation) or median (interquartile range) depending on their distribution and categorical values as percentages. Logaritmic transformation was used to attain normal distribution of continuous variables. The differences between the groups were analysed using Student's *t*-test or Anova and Fisher's LSD test for post hoc comparisons. Mann-Whitney U-test or Kruskal-Wallis test or was used when normal distribution was not attained after logarithmic transformation, and Chi-square test for categorical values. We computed Spearman's correlation between continuous values. A p-value of <0.05 was considered statistically

significant. IBM SPSS Statistics for Windows, Version 20.0 (Armonk, NY: IBM Corp.) software was used for analysing the clinical parameters and for correlations. Principal component analysis (PCA) and hierarchical clustering of the identified differentially abundant proteins were performed with DeCyder Extended Data Analysis software (Version 7.0, GE Healthcare), using average linkage and the Euclidean metric as a distance measure. Western blot intensities were statistically analysed using GraphPad Prism 5 software (GraphPad Software). Ingenuity Pathway Analysis (IPA) (Qiagen), String (string-db.org) and Enrichr (amp.pharm.mssm.edu/Enrichr) were used to investigate interactions, functions and pathways of relevance in the identified proteins.

Results

Study population

Table 1 presents the characteristics of 82 participants. Work-exacerbated rhinitis symptoms were reported by 27 (93%) of the WRA patients in the protein allergen group, 12 (100%) in the isocyanate group, and 11 (79%) in the welding group (p= 0.139). Nonspecific bronchial hyperresponsiveness was detected in 17 (59%), 4 (33%), 7 (54%) of the patients of the above groups, respectively (p=0.333) (n=54). Nasal steroid was withdrawn at least three days before sample collection; 12 (22%) of the WRA patients had used a nasal steroid during the previous four weeks. Positive skin prick tests (SPT) to common environmental allergens were detected more often in the protein allergen group (82%) than in the isocyanate (42%), welding (43%) or control (30%) groups (Table 1). Positive SPT to the occupational allergen of controlled exposure was found in 26 of 27 tested participants in the protein allergen group, but none in the isocyanate or welding group reacted to the isocyanate-albumin conjugate or metal suspension. Similarly, specific IgE to the occupational allergen was detected in 21 of 28 tested participants in the protein allergen group, but in none of the 10 tested in the isocyanate group. Fractional exhaled nitric oxide (FeNO) was highest in the protein allergen group, whereas nasal eosinophil count was biggest in the isocyanate group.

Two-dimensional differential gel electrophoresis (2D-DIGE) differences in protein abundances

DeCyder software matched on average 2500 spots per DIGE gel, no significant difference was observed between the total number of protein spots of the study groups. 228 protein spots with changed intensity from statistical analysis (Student's t –test <0.05, a fold change of \leq -1.5 or \geq 1.5) between groups were identified (Table S2, Figure S1) revealing altogether 77 different proteins (Table 2), as several proteins were identified from multiple gel spots. As many as 95% of the proteins found are known to have an extracellular location (Gene Ontology (GO):0070062, GO:0005615). In addition to plasma-derived proteins, various nasal epithelium proteins were detectable. Of the identified molecules, 32 were involved in inflammatory responses, 36 in cellular movement, 20 in free radical scavenging, 42 in cell death and survival, and 18 in allergy (Table S3). Calcium binding proteins were also enriched among the proteins identified. Three up-regulated and seven downregulated proteins were common to all the WRA groups.

Clustering analyses revealed similar protein regulation patterns in protein allergen and isocyanate groups

Unsupervised classification analyses were applied to the data to obtain an overview of protein abundance patterns. Hierarchical clustering analysis (Figure 2A), in which proteins with similar manifestation profiles are clustered together, showed that the protein patterns from participants with protein and isocyanate WRA resembled each other, and that the patterns in the welding group differed from the other WRA groups. When PCA was applied to the set of all the proteins identified in the nasal epithelium, the groups were positioned into separate quadrants, implying that different types of occupational exposures appear to perturb the global variability of nasal epithelial protein levels (Figure 2B). The PCA of identified protein spots (Figure 2C) showed clear separation of the spots to two abundance clusters, similarly to the abundance differences in Figure 2A.

Group-specific differently abundant proteins

The largest effects on the proteome of nasal epithelium were in the protein allergen group (Tables 2 and S1, Figures 2A and S2), in which 20 proteins were up-regulated and 43 down-regulated in comparison to the healthy controls. Exposure to isocyanates showed changes in 32 proteins and welding in 19 proteins. When WRA groups were compared with each other, the largest proteome differences observed were between the protein allergen and welding groups (45 different proteins). Welding-specific changes were decreased levels of heat shock cognate 71 kDa protein spots, and increased amounts of pyruvate kinase isozymes M1/M2 and Fatty acid binding protein.

Protein S100-A9 abundance was increased in all WRA groups, but protein S100-A8 (S10A8) was identified only for the protein allergen group. Other calcium binding proteins, calcyphosin (CAYP1) and annexins A1 and A2 (ANXA1, 2) had decreased protein levels in the protein allergen and isocyanate groups. The protein allergen group seemed to also contain low levels of annexins 3 and 5.

We identified several proteins involved in the detoxification of reactive oxygen species (Table 2). The catalase level was increased, whereas the levels of glutathione (GSH) synthesis-linked proteins s-formylglutathione hydrolase, glutathione synthetase and adenosylhomocysteinase were diminished, as was the GSH conjugation catalysing enzyme, GSTP1. Peroxiredoxins 1, 2 and 5 (PRDXs) levels were lower in the protein allergen group, and superoxide dismutase (SODC) levels decreased in the protein allergen and isocyanate groups. Changes in the abundancies of thioredoxin and protein disulphide-isomerase, which also belongs to the thioredoxin superfamily, were specific to isocyanate exposure.

Pathways and networks of proteins

Figure S2 shows the protein association networks of the proteins identified in each WRA group. Mitogen-activated protein kinases (MAPKs) and nuclear factor kappa B (NFκB)-signalling pathways consistently emerged in network searches, including single protein fishes, and were thus added to Figure S3 networks.

Pathways and diseases linked to the observed proteomic changes of the nasal mucosa in the IPA search are presented in Table 3. The reported ethanol degradation pathway, common to the protein allergen and isocyanate groups, is most likely connected to the aldehyde dehydrogenases involved in the metabolism of corticosteroids. The nuclear factor erythroid 2-related, factor 2 (Nrf2)-mediated oxidative stress response pathway is common to protein allergen and isocyanate WRA groups. Nrf2 is a key transcription factor that regulates antioxidant defence in macrophages and epithelial cells (14), and is a component of the GSTP1 interactome (15). Protein-allergen and

Isocyanate exposed asthma patients experienced more severe nasal symptoms and had a suggestive increase in nasal and sputum eosinophils which may be linked to inflammatory response in Table 3.

Immunological comparison of nasal brush samples

Several of the identified proteins are associated with allergic reaction mechanisms, among them GSTP1, LEG10 and S100A9, which were selected for further analysis as high quality commercial antibodies were also available for them. The unfamiliar fourth analyte, calcium binding protein CAYP1, may play a role in cellular signaling events. The Western blot analysis revealed similar abundance differences in a few proteins in the whole study population (Figure 3) and in 50 subjects who were excluded from proteomic analysis (Table S4). The levels of the calcium binding protein S10A9 and T cell proliferation suppressor protein LEG10 were up-regulated in all asthma groups. The oxidative stress defence protein GSTP1 showed a trend of reduction in the protein allergen group in comparison to the control group, whereas there was tendency for decreased levels of CAYP1 in all WRA groups compared to the controls. Abundances of the GSTP1 and CAYP1 proteoforms might vary in opposite directions, and together with the statistically relatively small study population, they could be the underlying causes for the lack of clear group differences.

Associations between protein abundances and clinical parameters

Protein abundances of GSTP1, LEG10, S10A9 or CAYP1 did not correlate with age, sputum eosinophils, FeNO, nNO or total IgE, whereas moderate correlation was seen between LEG10 and blood eosinophils (r=0.536, p=0.008) as well as S10A9 and FEV₁/FVC (r=0.438, p=0.017). GSTP1 was higher in men (p=0.016), but no significant gender difference was found in Western blot intensities of GSTP1 (p=0.242) or other protein abundances.

Discussion

Proteomic analysis of NBS is a relatively non-invasive way to evaluate airway inflammation. Hierarchical clustering analysis of the protein abundance patterns of NBS indicated that the nasal protein profile in protein-allergen- and isocyanate-related asthma groups are similar, and differ from those of healthy controls, whereas the welding group pattern bore more resemblance to that of the controls.

Clinical tests targeted to show causal relationship with asthma and occupational exposure (e.g. specific IgE, specific inhalation challenge) may select patients based on disease mechanisms. To avoid this preselection, we studied WRA patients. The vast majority of our WRA patients had concurrent work-aggravated rhinitis symptoms, as others have reported (6). The use of nasal steroids among the three WRA groups (p=0.75) during the four previous weeks did not significantly differ, suggesting that steroids had no significant effect on the protein abundances of these groups. Highest FeNO level reflecting Th2-derived inflammation in protein-allergen-related asthma group was similar to pervious findings (16). Isocyanate-related asthma patients had more nasal, but not sputum, eosinophils than other groups. Raulf-Heimsoth et al. detected an increase in sputum eosinophils but not in NLF after a positive isocyanate challenge (17).

Few studies have reported the proteome of work-related airway diseases. Mörtstedt et al. performed targeted proteomic analyses of NLF before and after a persulfate challenge among hairdressers with bleaching powder-associated rhinitis as compared to healthy hairdressers and atopic subjects (18). They detected changes in proteins related to inflammatory responses and oxidative stress, but the changes were not specific to rhinitis patients. Studies of nasal proteome in seasonal allergic rhinitis have shown a perennial inflammatory response in nasal mucus and lack of adequate reaction to allergens in season (19-21).

Proteomic changes in airway diseases have been characterized from induced sputum and NLF (10, 11). The most abundant proteins observed in these biofluids are plasma proteins, which are presumably derived from diffusion across the blood-air barrier (e.g. albumin, transferrins, immunoglobulins, alpha-1-antitrypsin), and interfere with the detection of less abundant proteins (12). NBS has rarely been used to investigate the proteome of patients with respiratory disorders (22). In this study, NBS provided good quality material, which was not distracted by blood derived high abundance proteins.

Protein abundance patterns analysed by hierarchical clustering were similar in protein allergen- and isocyanate-related WRA. IgE-mediated sensitization to isocyanates was not detected, while it was seen to occupational protein allergens in all but one case. This suggests that protein-allergen- and isocyanate-related WRA share non-IgE mediated immunological mechanisms. The welders' profile differed from that of the other WRA groups and controls, proposing different underlying mechanisms.

Our results indicate that the nasal epithelial proteome of the WRA patients is highly enriched in processes related to inflammatory and calcium signalling, free radical scavenging and oxidative stress response, and metabolism. The most relevant signalling networks were through the pathways associated with redox sensitive transcription factors, NFκB and Nfr2, and with MAPKs, which differentially regulate pro-inflammatory cytokine genes and protective antioxidant genes (23-25). Nrf2-deficient mice have a heightened susceptibility to asthma, including elevated oxidative stress, inflammation, mucus, and airway hyperresponsiveness (26). Airway inflammation and remodelling in asthma involves degradation of the extracellular matrix. Among the identified proteases and their inhibitors was Serpin B3, which inhibits inflammation and promotes epithelial proliferation with increased transforming growth factor-beta secretion (27). Several inflammatory defence proteins with both increased and decreased abundance were detected in subjects exposed to protein allergens and isocyanates.

LEG10 (aka Charcot-Leyden Crystal (CLC) protein, Eosinophil lysophospholipase) has been associated with eosinophilic inflammation in allergic diseases (28, 29) and with the function of regulatory T-cells (30). LEG10 is mainly released from eosinophil granules, but it is also expressed by basophils and some T cells (30). It belongs to the galectin superfamily of lectins (31), although its physiologically relevant carbohydrate ligand is unknown. Further knowledge of this would help us understand its role in inflammatory reactions.

Oxidative stress is important for the pathogenesis of lung damage and for the development of lung fibrosis. Among the various enzymatic and non-enzymatic mechanisms that protect cells and tissues from oxidants, GSH, SODs and PRDXs play a key protective role, especially in the lungs (32, 33). A lower level of GSH synthesis enzymes, SODs and PRDXs might induce continuous oxidative stress in the airways. In this study, a decreased abundance of all these proteins was observed in the participants with symptoms on exposure to protein allergens and isocyanates, but not in the welding group, suggesting that the impairment of protection from oxidative stress might play a key role in the pathogenesis of WRA. GSTP1 plays a significant role in detoxification processes that regulate inflammatory responses stimulated by xenobiotic and oxidative compounds, and is important in determining susceptibility to asthma. GSTP1 conjugates reduce GSH to electrophilic species, and adduct formation with xenobiotics promotes their elimination, whereas binding to protein thiols causes a reversible posttranslational modification, S-glutathionylation, which protects proteins from irreversible oxidations and can modulate their function (34). GSTP1 gene activation is mainly regulated by Nrf2 (35), and the functional association between GSTP and Nrf2 proteins supports the regulatory role of GSTP in the adaption response to cellular stresses produced in the course of inflammatory and oxidative reactions (15). As in the present study, GSTP was decreased in NLF after the persulphate challenge (18).

Ca²⁺ signals are important in inflammatory signalling and in the pathophysiology of airway diseases. Calcium-modulated S100 protein family members S10A9 and S10A8 are both among the most abundant proteins in airway cells during chronic inflammation. They may form a calprotectin complex which can induce cell proliferation, apoptosis, inflammation, collagen synthesis, and cell migration. S10A9 alone mediates fibroblast proliferation, increases mucin production, and is involved in NFkB network and inflammasome activation (36), whereas the protective role of S10A8 in allergic inflammation is to modulate mast cell activation and eosinophil recruitment, and scavenge the oxidants generated by activated leukocytes (37). Synthesis and activation of CAYP1 is induced by the cAMP cascade (protein kinase A) and CAYP1 may regulate cell proliferation and differentiation (38, 39). Interestingly, String DB predicts as functional partners for CAYP1 several MAP kinases, which are activated in response to inflammatory and oxidative stress signals (24). Glucocorticoid regulated annexins interact with cell membrane phospholipids, and are involved in various cellular processes, including endocytosis, exocytosis, membrane-cytoskeletal organization, and migration through the association of partner proteins, including members of the S100 family. ANXA1 is an antiinflammatory protein that plays a critical regulatory role in the development of asthma (40, 41), whereas ANXA2 promotes fibrinolysis (42). The roles of ANXA3 and 5 in asthma are largely unknown, but their amounts were reduced in the protein allergen exposure groups.

Conclusions

Proteome analysis of NBS provides preliminary results regarding the mechanisms of work-related airway diseases in patients exposed to protein allergens, isocyanates and welding fumes. WRA patients exposed to protein allergens and isocyanates showed similar nasal proteome responses, although the specific IgE was found only among patients exposed to protein allergens. The proteome of patients exposed to welding fumes resembled healthy controls. The identified changes in protein expressions of asthma patients reveal biological activities related to airway inflammation, oxidation reduction, tissue matrix turnover, and inflammatory signalling. Our findings provide new possibilities to biomarker research and the development of diagnostic methods of work-related airway diseases.

Acknowledgements

We warmly thank Risto Voutilainen, Liisa Airaksinen, Sauli Savukoski, Niina Ahonen, Sari Tillander, Outi Fisher, and the nurses for their valuable work. The Finnish Work Environment Fund supported the study.

Authors' contributions

All authors participated in conception, design and interpretation of data and approved the final version. HS, AP and IL acquired data, HS

and AP analysed data and drafted the article which IL and HW reviewed.

Conflict of interest

The authors declare no conflict of interest.

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Table 1 Characteristics of 82 participants. Continuous variables were expressed as means (± standard deviation) or median (interquartile range) depending on their distribution and categorical values as percentages. Logaritmic transformation was used to attain normal distribution of continuous variables. The differences between the groups were analysed using the ANOVA, Kruskal-Wallis test (when normal distribution was not attained after logarithmic transformation) or Chi-square test.

	Healthy		Asthma related to		
	controls (n=27)	protein allergen (n=29)	isocyanate (n=12)	welding (n=14)	р
Age, mean (SD)	43.2 (1.9)	42.7 (10.3)	41.0 (10.9)	43.4 (9.9)	0.880
Sex, male, n (%)	27 (100.0)	10 (34.5)	9 (75.0)	12 (85.7)	<0.001
Duration of work exposure, years, median $(Q_1-Q_3)^{\#}$	NA	9.0 (5.0-27.0)	4.0 (2.3-9.5)	15.5 (8.8-25.3)	0.014
Duration of asthma symptoms, years, median $(Q_1-Q_3)^{\mu}$	NA	2.0 (2.0-3.5)	1.0 (0.6-2.0)	2.0 (1.8-9.0)	0.006
VAS rhinitis, mm, median (Q ₁ -Q ₃) [#]	12.0 (3.0-25.0)	30.0 (7.5-54.5)	30.0 (2.0-50.0)	10.0 (2.5-45.5)	0.123
VAS nasal congestion, mm, median (Q_1 - Q_3) [#]	12.0 (0.0-22.5)	40.0 (14.0-57.3)	50.0 (9.0-80.0)	30.0 (8.5-71.5)	0.003
VAS nasal itching, mm , median $(Q_1-Q_3)^{\#}$	1.0 (0.0-11.5)	20.5 (3.3-38.0)	50.0 (2.0-80.0)	14.0 (2.5-45.0)	0.001
Nasal steroid during 4 weeks, n (%)	0 (0.0)	6 (20.7)	2 (16.7)	4 (28.6)	0.053
Inhaled steroid during 4 weeks, n (%)	0.0 (0.0)	17 (58.6)	7 (58.3)	14 (100.0)	<0.001
≥1 SPT positive to common environmental allergen*	8 (29.6)	22 (81.5)	5 (41.7)	6 (42.9)	<0.001
Positive SPT to exposed occupational allergen, n (%)*	NA	26 (96.3)	0 (0.0)	0 (0.0)	<0.001
Total IgE, kU/l, median (Q₁-Q₃) [¤]	34.0 (13.0-73.0)	187 (51.5-309.5)	46.0 (26.3- 70.0)	61.5 (29.3-132.5)	<0.001
Blood eosinophils 10 ⁶ /l, mean (SD)	129.3 (65.3)	206.6 (155.0)	148.3 (147.4)	182.5 (130.5)	0.137
FVC % predicted, mean (SD)	96.9 (10.2)	99.4 (10.9)	97.9 (12.4)	95.7 (8.8)	0.706
FEV ₁ % predicted, mean (SD)	95.8 (12.7)	91.0 (10.8)	92.9 (7.3)	88.9 (11.5)	0.239
FeNO, ppb, median $(Q_1 - Q_3)^{\times}$	13.2 (11.9-16.9)	23.2 (12.8-37.9)	17.0 (10.4-26.9)	23.0 (13.7-32.9)	0.004
nNO, ppb, mean (SD)	836.2 (272.7)	929.5 (351.1)	760.6 (233.8)	896.1 (339.8)	0.400
Sputum eosinophil %, median (Q₁-Q₃), n=57 [#]	0.0 (0.0-0.25)	1.0 (0.0-4.0)	1.0 (0.0-1.5)	0.5 (0.0-1.0)	0.044
Nasal eosinophil %, median (Q1-Q3) [#]	0.0 (0.0-0.0)	0.0 (0.0-1.0)	1.0 (0.0-1.0)	0.0 (0.0-0.0)	0.009

*Kruskal-Wallis test was used; Logaritmic transformation was used; *two participants with negative control wheal ≥ 2 mm were excluded from analysis; *VAS*, Visual analogue scale of nasal symptoms within a week; *SPT*, skin prick test; *IgE*, Immunoglobulin E; *FVC*, forced vital capacity; *FEV*₁, Forced expiratory volume in one second; FeNO, exhaled nitric oxide; nNO, nasal nitric oxide.

Table 2 Relationships between differently abundant proteins in study groups. Average ratios (\geq |1.5| fold change in abundance) of statistically significant (Student's T-test p-value \leq 0.05) up- and down-regulated nasal mucosa proteins are presented for the protein allergen, isocyanate and welding exposed asthma groups in comparison to the control group.

Protein Name	UniProt AC	Gene ID	Protein allergen vs Control	Isocyanate vs Control	Welding vs Control
	504022		Av. ratio	Av. ratio	Av. ratio
Alpha-2-macroglobulin (A2MG)	P01023	A2M	1,83		
Complement C3 (CO3)	P01024	C3	1,82	4.00	
Complement factor B (CFAB)	P00751	CFB	1,88	1,88	4.05
Alpha-actinin-4 (ACTN4)	043707	ACTN4	2.47	-1,77	-1,95
Serum albumin (ALBU) Polymeric immunoglobulin receptor	P02768	ALB	3,17	2,81	2,36
(PIGR) Protein-glutamine gamma-	P01833	PIGR	1,85		
glutamyltransferase (TGM3)	Q08188	TGM3	2		
Lactotransferrin (TRFL)	P02788	TRFL	5,43	4,95	2,87
Ig mu chain C region (IGHM)	P01871	IGHM	1,89		
Serotransferrin (TRFE)	P02787	TF	1,75		
Heat shock cognate 71 kDa protein					
(HSP7C)	P11142	HSPA8			-2,49
Protein disulfide-isomerase (PDIA1)	P07237	P4HB		1,67	
Histidine ammonia-lyase (HUTH) Glucose-6-phosphatate isomerase	P42357	HAL		1,74	
(G6PI)	P06744	GPI			2,09
Pyruvate kinase isozymes M1/M2					
(KPYM)	P14618	PKM			2,45
Ig alpha-1 chain C region (IGHA1)	P01876	IGHA1	2,04		
Alpha-1-antitrypsin (A1AT) HistidinetRNA ligase; cytoplasmic	P01009	SERPINA1	2,15		
(SYHC) Tryptophan-tRNA ligase; cytoplasmic	P12081	HARS	-1,57		
(SYWC)	P23381	WARS	-1,67		
Aldehyde dehydrogenase (AL3A1)	P30838	ALDH3A1	-2,76	-3,4	-2,19
Selenium-binding protein 1 (SBP1)	Q13228	SELENBP1	-2,05	-1,58	
Glutathione synthetase (GSHB)	P48637	GSS	-2,08		
Retinal dehydrogenase 1 (AL1A1)	P00352	ALDH1A1	-2,25		
Rab GDP dissociation inhibitor beta					
(GDIB)	P50395	GDI2	-2,51	-2	-1,71
Glyceraldehyde-3-phosphate dehydrogenase (G3P)	P04406	GAPDH	-1,51	-1,55	
6-phosphogluconate dehydrogenase	104400	GAI DIT	1,51	1,55	
(6PGD)	P52209	PGD		2,32	2
Catalase (CATA)	P04040	CAT	1,77	2,87	
Zinc-alpha-2-glycoprotein (ZA2G)	P25311	AZGP1	,	1,63	
Serpin B3 (SPB3)	P29508	SERPINB3	-2,02	-1,92	-1,72
26S proteasome non-ATPase			,	,	,
regulatory subunit 11 (PSD11)	O00231	PSMD11	-1,58		
Haptoglobin (HPT)	P00738	HP	2,02		
Isocitrate deheydrogenase [NADP];					
cytoplasmic (IDHC)	075874	IDH1	-2,74		
Arginosuccinate synthase (ASSY)	P00966	ASS1	-2,79		
Creatine kinase B-type (KCRB) Fructose-bisphosphate aldolase A	P12277	СКВ	1,71		
(ALDOA)	P04075	ALDOA	-2,53		
Leukocyte elastase inhibitor (ILEU)	P30740	SERPINB1	-1,56		
GDP-L-fucose synthase (FLC) Plasminogen activator inhibitor 2	Q13630	TSTA3	-1,97		
(PAI2)	P05120	SERPINB2	-1,8		
Alcohol dehydrogenase [NADP(+)]	P14550	AK1A1	-3,06		

	504000				
Annexin A1 (ANXA1)	P04083	ANXA1	-3,78	-5,05	
Annexin A2 (ANXA2)	P07355	ANXA2	-4,59	-5,75	
Annexin A3 (ANXA3)	P12429	ANXA3	-1,9		
Annexin A5 (ANXA5)	P08758	ANXA5	-2,59		
S-formylglutathione hydrolase (ESTD)	P10768	ESD	-2,18		
Tropomyosin alpha-1 chain (TPM1)	P09493	TMP1	-1,9		
Tropomyosin alpha-4 chain (TPM4)	P67936	TMP4			
Actin; cytoplasmic 1 (ACTB)	P60709	ACTB	-1,68		
Chloride intracellular channel protein1					
(CLIC1)	000299	CLIC1	-1,8		-1,56
14-3-3 protein sigma (1433S)	P31947	SFN	-1,88		
14-3-3 protein zeta/delta (1433Z)	P63104	YWHAZ	-2,14	-1,58	-1,85
14-3-3 protein epsilon (1433E)	P62258	YWHAE	-2,63	-2,27	-1,9
Serum amyloid P-component (SAMP)	P02743	APCS	1,75	2,01	
Proteasome subunit alpha type-5					
(PSA5)	P28066	PSMA5	-1,96		
Kallikrein-7 (KLK7)	P49862	KLK7	-2,75	-2,34	-1,89
Glutathione S-transferase P (GSTP1)	P09211	GSTP1	-2,6	-1,93	
Complement C1q subcomponent					
subunit C (C1QC)	P02747	C1QC		1,6	
Heat shock protein beta-1 (HSPB1)	P04792	HSPB1	1,75	1,85	
BPI fold-containing family A member 1					
(BPIA1)	Q9NP55	BPIFA1		-1,96	
Translationally-controlled tumour					
protein (TCTP)	P13693	TPT1	-1,95	-1,9	-1,59
Peroxiredoxin-2 (PRDX2)	P32119	PRDX2	-2,5		
Peroxiredoxin-1 (PRDX1)	Q06830	PRDX1	-3,6		
Phosphatidylethanolamine-binding					
protein 1 (PEBP1)	P30086	PEBP1	-2,18		
Adenine phosphoribosyltransferase					
(APT)	P07741	APRT	-3,11		
Calcyphosin (CAYP1)	Q13938	CAPS	-4,76	-5,15	
Nucleoside diphosphatate kinase A					
(NDKA)	P15531	NME1		-1,58	
Thioredoxin (THIO)	P10599	THIO		-2,16	
Superoxide dismutase [Cu-Zn] (SODC)	P00441	SOD1	-1,98	-2,21	
Cofilin-1 (COF1)	P23528	CFL1	-2,13	-2,13	
Nucleoside diphosphatate kinase B					
(NDKB)	P22392	NME2	-2,26		
Prolactin-inducible protein (PIP)	P12273	PIP	2,22		
Peroxiredoxin 5 (PRDX5)	P30044	PRDX5	-2,85		
Peptidyl-prolyl cis-trans isomerase A					
(PPIA)	P62937	PPIA	-2,86		
Fatty acid binding protein, epidermal					
(FABP5)	Q01469	FABP5			2,69
Galectin 10 (LEG10)	Q05315	CLC	4,04		
Haemoglobin subunit beta (HBB)	P68871	HBB			-2,27
Protein S100-A9 (S10A9)	P06702	S100A9	2,2	7,11	8,71
Protein S100-A8 (S10A8)	P05109	S100A8	2,43		
LINGHI 2100-40 (21040)	L0210A	3100A0	2,43		

Table 3 Pathways and diseases linked to the observed proteomic changes in the nasal mucosa after exposure to protein allergen, isocyanate and welding fume.

Canonical pathways

Protein allergen	Isocyanate	Welding
Acute Phase Response Signalling	Superoxide Radicals Degradation	Glycolysis I

NRF2-mediated Oxidative Stress Response	NRF2-mediated Oxidative Stress Response	Cell Cycle: DNA Damage Checkpoint Regulation
Tryptophan Degradation X	Ethanol Degradation IV	Myc Mediated Apoptosis Signalling
LXR/RXR Activation	Aryl Hydrocarbon Receptor Signalling	ERK5 Signalling
Ethanol Degradation IV	Complement System	HIPPO signalling

Diseases and Disorders

Protein allergen	Isocyanate	Welding
Inflammatory Response	Inflammatory Response	Dermatological Diseases and Conditions
Immunological Disease	Dermatological Diseases and Conditions	Immunological Disease
Dermatological Diseases and Conditions	Immunological Disease	Neurological Disease
Haematological Disease	Neurological Disease	Psychological Disorders
Inflammatory Disease	Skeletal and Muscular Disorders	Cancer

The top five canonical pathways and disease-associated functions from the Ingenuity Pathway Analysis of the affected protein levels in protein allergen, isocyanate and welding challenged groups compared to the control group. The p-values of likelihoods for the protein list of each study group were calculated using the Fisher Exact test. The top five p-values were for protein allergens from E-21 to E-08, for isocyanate from E-11 to E-07 and for the welding group with the shortest identified protein list from E-11 to E-05.

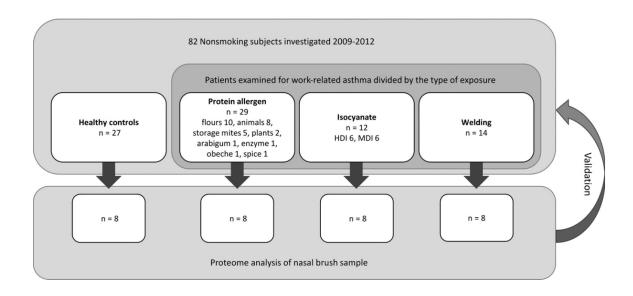
Figure legends

Figure 1 Study flow chart. HDI, Hexamethylene diisocyanate; MDI, Methylene diphenyl diisocyanate.

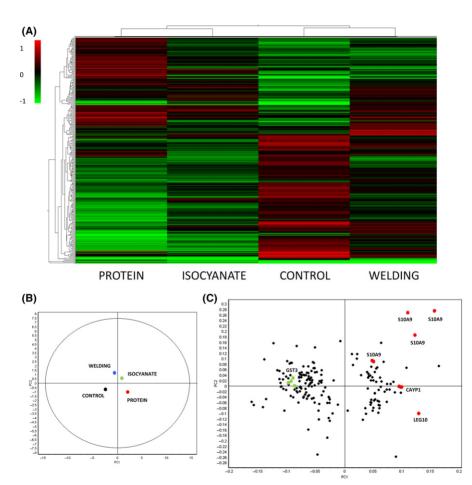
Figure 2 Clustering analyses of the differentially abundant proteins between study groups. A heat map of hierarchical clustering (A), on which nasal epithelial proteins with decreased abundance are marked in green and those with increased abundance in red; and Principal Component Analysis (B-C), in which spheres correspond to a study group (Fig. 2B) or to an identified gel spot (Fig. 2C). In the Fig. 2C the further apart from the origo a spot is, the clearer the separation between the groups, and the more suitable the finding would be as a biomarker. All figures indicate differences between the protein allergen (Protein) and isocyanate (Isocyanate) groups and the healthy controls (Control), whereas the welding group (Welding) shows the least up- or down-regulation to healthy persons. Immunoblot analysed gel spots are highlighted in Fig. 2C.

Figure 3 Comparison of protein abundance by Western blotting. 2D-DIGE gel spot intensities for Glutathione S-transferase 1 (GSTP1, mean of several spots/gel), Galectin 10 (LEG10, one gel spot), Protein S100-A9 (S10A9, mean of several spots/gel) and Calcyphosin (CAYP1, one gel spot) of the 32 nasal brush samples (NBS) are on the left. The corresponding protein levels in the Western blot analysis for 82 NBS are on the right. Bars indicate means. Logaritmic transformation was used to attain normal distribution of the variables. The differences between the groups were analysed using the Anova and Fisher's LSD test for post hoc comparisons. Control = healthy persons, Protein= protein allergens group; Isocyanate= isocyanate group; Welding= welding group.

Figure 1.







Supplementary data

Supplementary material 1 Methods

Skin prick tests and IgE measurements

The skin prick test (SPT) panel for common environmental allergens included a negative control, a positive control (histamine), and 11 standardized environmental antigens (ALK-Abello, Hørsholm, Denmark). Occupational protein allergens were tested with commercial extracts, as is, or as an in-house extract in potassium phosphate, depending on the agent. Isocyanates were conjugated with human serum albumin (1), and metals (CoCl₂, NiSO₄, K₂CrO₄, CrCl₂) were diluted in aqua. The results were regarded as positive if the mean wheal diameter was \geq 3 mm, and the negative control wheal was < 2 mm. Serum total and specific (protein allergens and isocyanates) IgE were measured using the Phadia UniCAP System (Phadia, Uppsala, Sweden). A specific IgE of < 0.35 kU/l was considered normal.

Lung function, exhaled and nasal nitric oxide

Flow-volume spirometry was performed using a standard spirometer (Spirostar USB Medikro, Finland), and the predicted values of the Finnish population. Nonspecific airway hyperresponsiveness was measured using the histamine challenge (2). Exhaled (FeNO) and nasal (nNO) nitric oxide were measured using an online chemiluminescence analyser (NIOX, Aerocrine AB, Solna, Sweden) in compliance with recommendations (3).

Controlled exposure to occupational agent

The WRA patients were exposed to the relevant occupational agent for 15–30 minutes approximately 24 h before sample collection, by mimicking work tasks in a 6 m³ challenge chamber or by nebulizing allergen extracts (animal dander, storage mites), in-house solutions (Methylene diphenyl diisocyanate) or occupational agents (Hexamethylene diisocyanate) (4).

Nasal brush and induced sputum samples

The NBS was taken from the nasal cavity's middle meatus. The brush was dipped into 5 mL of cold PBS, mixed gently and centrifuged at 500g. Supernatant was filtered through a 0.45 μ m membrane, divided into aliquots and frozen to -70°C for further use. Sputum was induced with hypertonic saline, in accordance with the guidelines (5). The number of eosinophils /200 cells were counted in the sputum and the NBS smear samples.

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- 3 Ats/Ers. ATS/ERS recommendations for standardized procedures for the online and offline measurement of exhaled lower respiratory nitric oxide and nasal nitric oxide, 2005. *Am J Respir Crit Care Med* 2005: **171**: 912-30.
- Vandenplas O, Suojalehto H, Aasen T B, Baur X, Burge P S, De Blay F, Fishwick D, Hoyle J, Maestrelli P, Munoz X,
 Moscato G, Sastre J, Sigsgaard T, Suuronen K, Walusiak-Skorupa J, Cullinan P. Specific inhalation challenge in
 the diagnosis of occupational asthma: consensus statement. *Eur Respir J* 2014: 43: 1573-87.
- 5 Djukanovic R, Sterk P J, Fahy J V, Hargreave F E. Standardised methodology of sputum induction and processing. *Eur Respir J Suppl* 2002: **37**: 1s-2s.

Table S1. Characteristics of 32 participants whose nasal brush samples were included in proteomic analysis. Continuous variables were expressed as means (± standard deviation) or median (interquartile range) depending on their distribution and categorical values as percentages. Logaritmic transformation was used to attain normal distribution of continuous variables. The differences between the groups were analysed using the ANOVA, Kruskal-Wallis test (when normal distribution was not attained after logarithmic transformation) or Chi-square test.

	Healthy		Asthma related to		
	controls (n=8)	protein allergen (n=8)	isocyanate (n=8)	welding (n=8)	р
Age	43.8 (2.1)	35.6 (12.3)	41.7 (11.4)	43.3 (10.4)	0.349
Sex, male, n (%)	8 (100.0)	1 (12.5)	6 (75.0)	6 (75.0)	0.002
Duration of work exposure, years, median $(Q_1-Q_3)^{\#}$	NA	7.5 (5.3-25.5)	6.5 (2.3-13.8)	21.5 (6.3-25.8)	0.265
Duration of asthma symptoms, years, median $(Q_1-Q_3)^{lpha}$	NA	3.0 (2.3-4.0)	1.0 (0.7-2.8)	3.5 (1.3-9.8)	0.032
VAS rhinitis, mm, median (Q ₁ -Q ₃) [#]	10.5 (0.0-16.3)	57.5 (11.8-66.8)	20.0 (0.0-50.0)	7.5 (0.0-38.5)	0.083
VAS nasal congestion, mm, median (Q_1 - Q_3) #	5.0 (0.0-20.5)	49.5 (30.3-71.3)	80.0 (30.0-84.0)	14.5 (2.3-45.5)	0.021
VAS nasal itching, mm, median (Q ₁ -Q ₃) *	0.0 (0.0-0.0)	45.0 (16.8-59.8)	60.0 (0.0-80.0)	4.5 (0.3-16.3)	0.002
Nasal steroid during 4 weeks, n (%)	0 (0.0)	1 (12.5)	1 (12.5)	2 (25.0)	0.515
Inhaled steroid during 4 weeks, n (%)	0 (0.0)	3 (37.5)	5 (62.5)	8 (100.0)	0.001
≥1 positive SPT to common environmental allergen, n (%)	0 (0.0)	7 (87.5)	3 (37.5)	4 (50.0)	0.005
Positive SPT to occupational allergen, n (%)	NA	8 (100.0)	0 (0.0)	0 (0.0)	<0.001
Total IgE, kU/l, median (Q₁-Q₃) [⊭]	16.5 (8.8-23.3)	143.0 (42.8-301.8)	40.0 (17.5-63.5)	95.5 (32.8-203.0)	0.007
Blood eosinophils 10 ⁶ /l, mean (SD)	128.8 (86.8)	255.0 (166.2)	183.8 (172.5)	207.5 (129.9)	0.374
FVC % predicted, mean (SD)	98.6 (8.1)	99.9 (10.1)	97.3 (14.1)	94.9 (10.7)	0.821
FEV1 % predicted, mean (SD)	97.9 (9.8)	92.6 (9.5)	92.5 (8.5)	91.0 (12.9)	0.573
FeNO, ppb, median $(Q_1-Q_3)^{k}$	12.8 (11.1-16.9)	32.3 (18.5-69.4)	15.8 (10.4-25.1)	18.8 (10.5-39.9)	0.009
nNO, ppb, mean (SD)	858.7 (263.4)	1006.7 (358.1)	694.4 (233.6)	927.1 (370.0)	0.249
Sputum eosinophil %, median (Q₁-Q₃), n=20 [#]	0.0 (0.0-0.3)	3.0 (0.5-6.5)	1.0 (0.0-2.0)	0.5 (0.0-1.0)	0.080
Nasal eosinophil %, median (Q ₁ -Q ₃) [#]	0.0 (0.0-0.0)	0.5 (0.0-1.75)	1.0 (0.0-4.0)	0.0 (0.0-0.0)	0.056

*Kruskal-Wallis test was used; *Logaritmic transformation was used; VAS, Visual analogue scale of nasal symptoms within a week; SPT, skin prick test; IgE, Immunoglobulin E; FVC, forced vital capacity; FEV1, Forced expiratory volume in one second; FeNO, exhaled nitric oxide; nNO, nasal nitric oxide.

Table S2

Table S2. List of identified proteins from 2D-DIGE analysis of nasal brush samples. Proteins were identified from the picked 228 gel spots by tandem mass spectrometry with subsequent database searches using Proteome Discover software. Student's t-test and the Average (Av.) Ratio (with significance levels of < 0.05 and Av. Ratio ≥ |1.5|, respectively) for comparing inhalation challenged protein, isocyanate and welding groups and healthy controls to one another were obtained from DeCyder software. Isocyanate vs Protein vs Welding vs Protein+Isocyanate Welding vs Contro Welding vs cyanate Contro Contro Contro Protein UniProt UniProt Mascot Sequest Sequence MW Coverage %^{b)} Peptides^{c)} (kDa)^{d)} pl^{e)} Gel spot # Accession Identification T-test T-test T-test Av. Rati Av.Ratio T-test Av.Ratio T-test Av. Rati Av. Rat Entry Name score score a) P01023 P01023 P08603 Alpha-2-macroglobulin Alpha-2-macroglobulin Complement factor H A2MG A2MG CFAH 6,72 1,29 9,10 3,37 163,1879 163,1879 138,9787 6,46 6,46 6,62 27,61 9 2 0.0079 3 9 134,75 1,83 0,0043 0,023 1,62 53 9 66 P01024 Complement C3; alpha-chain CO3 17,53 6 111,5 6,40 0,041 Complement C3; alpha-chain Alpha-2-macroglobulin Complement C3; alpha-chain CO3 A2MG CO3 1,62 25,85 20,32 3 28 27 111,5 163,1879 111,5 85,47853 6,40 6,46 6,40 0,031 0,038 103 P01024 122,61 0,036 1,82 P01023 P01024 91,67 54,64 108 0,005 2,11 159 P00751 Complement factor B CFAB 1,82 7,20 4 7,06 0,027 1,88 0,033 1,88 0,01 1,75 PIGR UBA1 PIGR ACTN4 538,18 292,64 595,07 557,60 19,37 8,98 15,71 12,84 P01833 P22314 Polymeric immunoglobulin receptor Ubiquitin-like modifier-activating enzyme 1 11 83,23166 5,74 5,76 185 0,024 1,55 282 83,23166 5,74 P01833 Polymeric immunoglobulin receptor Alpha-actinin-4 11 0,042 -2,43 0,033 -2,47 0,018 043707 11 104,7885 5,44 353 P01023 P02787 Alpha-2-macroglobulin Serotransferrin A2MG TRFE 279,60 589,26 6,51 35,67 163,1879 77.01 6,46 7,12 8 20 0,048 3,1 0,035 1,84 0,0087 1,63 0,02 2,18 354 13 76,58359 Q08188 Protein-glutamine gamma-glutamyltransferase TGM3 521,24 20,78 5,86

lsocyanate vs Welding

T-test

0,027 1,58

-1,85 -1,93

-1,75

-1,71

-2,01

Isocyanate vs

-1,83 0,02

0,0034 -1,98

0,0053 -2,19

Protei

T-test Av. Ratio

	00100	Froten-grutanine ganna-grutaniyitransierase	1GIVI3	521,24		20,78	15	70,38333	5,60														
382	P15311	Ezrin	EZRI	588,67		17,24	13	69,36974	6,27											0,029	-1,94	0,023	-1,96
399	O43707	Alpha-actinin-4	ACTN4	757,34		14,05	10	104,7885	5,44			0,026	-1,77	0,024	-1,95	0,026	-1,59						
400	P02768	Serum albumin	ALBU	503,77		15,44	8	69,3215	6,28	0,0035	3,17	0,0071	2,81	0,022	2,36	0,00016	2,8						
						,				0,0000	0,27	0,0071	2,01	0,022	2,00	0,00010	2,0				-		
464	P15311	Ezrin	EZRI	1165,71		20,82	13	69,36974	6,27													0,0017	-1,67
484	P01833	Polymeric immunoglobulin receptor	PIGR	89,92		3,40	3	83,23166	5,74	0,0077	1,85							0,0078	-2,18				
513	P01833	Polymeric immunoglobulin receptor	PIGR	1085,85		24.35	15	83,23166	5,74									0,02	-2,11				
							3														-		
514	P02768	Serum albumin	ALBU	256,71		4,60		69,3215	6,28									0,027	-2,07				
537	P02788	Lactotransferrin	TRFL	65,43	8,02	2,25	2	78,13192	8,12	0,018	2,53							0,047	-1,94				
543	P02788	Lactotransferrin	TRFL	2620,00		47,89	31	78,13192	8,12	0.009	2,22					0,023	2,01						
547	P02768	Serum albumin	ALBU	972.85		14.94			6.28	-/						0,010	2,02				-		
547							11	69,3215		0,018	1,82											0,02	-1,64
	P01833	Polymeric immunoglobulin receptor	PIGR	227,52		5,24	4	83,23166	5,74														
552	Q08188	Protein-glutamine gamma-glutamyltransferase	TGM3	521,24		20,78	13	76,58359	5,86	0,042	2												
											-						4.05				-		
553	P02788	Lactotransferrin	TRFL	2916,33		44,37	29	78,13192	8,12	0,018	2,52					0,01	1,95						
588	P02768	Serum albumin	ALBU	198,65		7,22	5	69,3215	6,28									0,0015	-1,7				
592	P02768	Serum albumin	ALBU	3758,28		46,14	30	69.32	6,28					0,044	1,54	0,022	1,57						
														0,044	2,34						-		
602	P02787	Serotransferrin	TRFE	983,48		34,10	23	77,01363	7,12	0,0088	2,3					0,038	1,67	0,016	-2				
	P01871	Ig mu chain C region	IGHM	626,10		23,45	9	(49.3)	6,77														
	P16050	Arachidonate 15-lipoxygenase	LOX15	316,44		13,90	9	74,75652	6.58														
							-		-,												-		
603	P02788	Lactotransferrin	TRFL	257,69		6,48	4	78,13192	8,12	0,023	2,06					0,011	1,73	0,035	-1,7				
608	P02788	Lactotransferrin	TRFL	9208,64		70,14	52	78,13192	8,12	0,00096	5,43	0,012	4,95	0,018	2,87	0,00013	4,51	0,0035	-1,89				
624	P02787	Serotransferrin	TRFE	3446.42		40,54	31	77,01363	7.12	0,022	2.01							0,022	-1,93				
			IGHM							0,011	2,02							0,011	2,50		-		
	P01871	Ig mu chain C region		1057,51		26,33	10	(49.3)	6,77														
	P16050	Arachidonate 15-lipoxygenase	LOX15	513,01		22,66	15	74,75652	6,58														
629	P02788	Lactotransferrin	TRFL	3986,27		34,96	23	78,13192	8,12	0,011	2,04							0,016	-1,97				
						,											-				1 1		
630	P01871	Ig mu chain C region	IGHM	176,98		5,97	3	(49.3)	6,77	0,014	1,89	L						0,04	-1,68			L	
633	P02787	Serotransferrin	TRFE	737,05		31,23	21	77,01363	7,12	0,013	1,73							0,012	-1,76				
	P01871	Ig mu chain C region	IGHM	230,18		9,29	4	(49.3)	6,77														
600											4.00										1		
637	P02787	Serotransferrin	TRFE	15912,88		69,63	64	77,01363	7,12	0,034	1,75							0,032	-1,71				
638	P02768	Serum albumin	ALBU	2671,67		30,38	19	69,3215	6,28	0,045	1,58							0,002	-1,78			0,0076	-1,6
660	P02768	Serum albumin	ALBU	1327,98		18,56	13	69,3215	6,28									0,029	-1,64				
						,												0,025	4,04				
	P11142	Heat shock cognate 71 kDa protein	HSP7C	684,85		18,58	11	70,85423	5,52														
665	P11142	Heat shock cognate 71 kDa protein	HSP7C	4584,98		34,83	24	70,85423	5,52					0,025	-1,84								
668	P02768	Serum albumin	ALBU	2832,91		23,15	16	69,3215	6,28									0,024	-1,67				
000																		0,024	-1,07		-		
	P02790	Hemopexin	HEMO	117,65		4,76	2	51,64328	7,02														
689	P11142	Heat shock cognate 71 kDa protein	HSP7C	17471,84		45,51	33	70,85423	5,52					0,025	-1,84	0,007	-1,94						1
692	P11142	Heat shock cognate 71 kDa protein	HSP7C	5313,46		39,47	27	70,85423	5,52					0,0058	-2,49								
						,																	
728	P11142	Heat shock cognate 71 kDa protein	HSP7C	2054,24		33,75	24	70,85423	5,52					0,024	-2,15	0,02	-1,82						
	P02768	Serum albumin	ALBU	2018,43		39,74	26	69,3215	6,28														1
735	P01024	Complement C3; beta chain	CO3	5760,72		21,47	38	(187,03)	6,40	0.02	1.69					0.012	1.6						
										0,02	1,09					0,012	1,6				-		
738	P01024	Complement C3;beta chain	CO3	3595,60		23,99	33	(187,03)	6,40									0,016	-1,89				
790	P07237	Protein disulfide-isomerase	PDIA1	620,17		13,58	6	57,08068	4,87											0,0052	2,07		1
801	P07237	Protein disulfide-isomerase	PDIA1	2699,54		25,79	14	57.08068	4.87			0,0073	1,67										
												0,0075	1,07										
810	P36871	Phosphoglucomutase-1	PGM1	320,71		17,97	9	61,41053	6,76	0,045	1,67												
	P00751	Complement factor B	CFAB	296,29		5,37	4	85,47853	7,06														
813	P42357	Histidine ammonia-lyase	HUTH	365.92		19,94	10	72,65183	6.95			0,029	1,74										
												0,029	1,74										
842	P14618	Pyruvate kinase isozymes M1/M2	KPYM	3398,92		40,30	21	57,90003	7,84									0,0029	1,9	0,023	-1,55		
851	P06744	Glucose-6-phosphate isomerase	G6PI	970,34		28,85	13	63,10725	8,32					0,024	2,09	0,027	1,57						
852	P14618	Pyruvate kinase isozymes M1/M2	KPYM	94,91		7,16	3	57,90003	7.84					0,011	2,45					0,023	-2,02		
														0,011	2,45					0,025	-2,02		
865	P01857	lg gamma-1 chain C	IGHG1	1098,75		26,06	8	(36,08)	8,19													0,025	-1,54
882	P01876	Ig alpha-1 chain C region	IGHA1	646,88		14,45	4	(37,63)	6,51	0,0035	2,04												1
916	P01009	Alpha-1-antitrypsin	A1AT	1668,40		28,47	11	46,70702	5,59	0,042	2,15							0,035	-2,12				
																		0,035	-2,12				
929	P23381	TryptophantRNA ligase, cytoplasmic	SYWC	1060,52		39,28	17	53,13161	6,23	0,013	-2,18					0,011	-1,8						
	P30838	Aldehyde dehydrogenase	AL3A1	856,43		28,70	11	50,36285	6,54														
	Q13228	Colonium binding protein 1	SBP1	708,88		41,95	18	52,35763	6,37														
		Selenium-binding protein 1																-					
932	P05091	Aldehyde dehydrogenase, mitochondrial	ALDH2	583,59		19,15	11	56,34563	7,05					0,012	-1,68								
	Q13228	Selenium-binding protein 1	SBP1	423,81		21,19	10	52,35763	6,37														
936	P12081	HistidinetRNA ligase, cytoplasmic	SYHC	867.12		34,38	16	57.37422	5.88	0.038	-1,57							0,017	1				
												L						0,017	1,55		+		
941	P23381	TryptophantRNA ligase, cytoplasmic	SYWC	1122,89		32,70	14	53,13161	6,23	0,008	-1,67												
942	Q13228	Selenium-binding protein 1	SBP1	3077,83		35,38	17	52,35763	6,37	0,011	-1,93												
943	P30838	Aldehyde dehydrogenase	AL3A1	3003,11		36,42	14	50,36285	6,54	0.0033	-2.76	6,40E-05	-3,4	0.015	-2,19	0.00062	-2.7						
														0,015	-6,13						<u> </u>		
946	Q13228	Selenium-binding protein 1	SBP1	356,58		12,92	5	52,35763	6,37	0,00023	-2,05	0,013	-1,58			0,011	-1,51	0,012	1,84			L	
949	P68371	Tubulin beta-4B	TBB4B	1019,53		24,27	10	49,799	4,89													0,038	-1,69
951	P30838	Aldehyde dehydrogenase	AL3A1	6555,53		43,05	18	50,36285	6,54	0,023	-2,21	0,036	-2,33			0,022	-1,92						
551										0,020	-4,41	0,000	-2,33			0,022	-1,72						
	Q13228	Selenium-binding protein 1	SBP1	3491,67		65,25	29	52,35763	6,37														
	P00352	Retinal dehydrogenase 1	AL1A1	2463,28		47,90	21	54,82695	6,73														
953	P48637	Glutathione synthetase	GSHB	312,03		8,02	5	52,35226	5,92	0,0063	-2,08					0,043	-1,53						
													-								+ I		
955	P30838	Aldehyde dehydrogenase	AL3A1	340,27		10,38	5	50,36285	6,54	0,0013	-2,74	0,014	-2,28			0,0041	-2,04	0,038	1,87				
956	P02768	Serum albumin	ALBU	2744,40		29,23	22	69,3215	6,28	0.0006	-4,75					0.013	-2.17	0,0051	3.62			0,015	2,12
	P30838		AL3A1	1287.45		41.72	19	50,36285	6,54	-,						-,540	-,	-,	-,0%		1	-,	
		Aldehyde dehydrogenase										L						<u> </u>					
959	P68104	Elongation factor 1-alpha 1	EF1A1	550,07		12,12	2	50,10911	9,01	0,03	-1,94					0,048	-1,51						
	P04406	Glyceraldehyde-3-phosphate dehydrogenase	G3P	402,13		18,51	2	36,0304	8,46														
																		-			+		
960	P04406	Glyceraldehyde-3-phosphate dehydrogenase	G3P	1037,57		18,51	2	36,0304	8,46	0,026	-1,43	0,03	-1,5										
	P68104	Elongation factor 1-alpha 1	EF1A1	918,53		17,10	4	50,10911	9,01														
964	P00352	Retinal dehydrogenase 1	AL1A1	5359,22		48,10	28	54,82695	6,73	0.032	-2.25							0.0097	1.01	0.042	.1.57		
										0,022	-2,25	l						0,0087	1,91	0,042	-1,57		
975	P00352	Retinal dehydrogenase 1	AL1A1	1013,50		11,18	6	54,82695	6,73	0,043	-2,27							0,03	1,89				
987	P48637	Glutathione synthetase	GSHB	2496,22		41,77	16	52,35226	5,92	0,032	-1,69							0,00072	1,98	0,02	-1,67		
993	P02679		FIBG	1971.19		40.40	15	51,47887	5.62	,	/								,	/	,		
		Fibrinogen gamma chain																0,017	1,53				
998	Q13867	Bleomycin hydrolase	BLMH	672,78		30,11	15	52,52802	6,27	0,037	-1,86					0,0096	-1,79						
	P50395	Rab GDP dissociation inhibitor beta	GDIB	635,21		58,43	21	50,63088	6,47														
	P04040	Catalase	CATA	591,11		32,64	16	59,71876	7,39														
																	l						
1004	P50395	Rab GDP dissociation inhibitor beta	GDIB	1563,65		68,54	28	50,63088	6,47	0,0013	-2,51	0,018	-2	0,019	-1,71	0,0023	-2,02						
1008	P02679	Fibrinogen gamma chain	FIBG	1742,41		18,32	9	51,47887	5,62									0,003	1,71	0,032	-1,56		
							-		-,	• • •		• • •						-,500	-,**	-,002	-100		
1008	P020/9	riurinogen gamma chain	FIBG	1/42,41	ļ	10,32	9	31,4/88/	3,82		ļ							0,003	1,71	0,032	-1,55	ļ	

| 1019 | P00738 | Haptoglobin | HPT
 | 461,47 | | 26,11

 | 9 | (45,18) | 6,58 | |
 | | | | | |
 | | | 0,007 |
--	--	---
--
---|--
---|--|--|--|--
--|------------------------|---------------------------------|---|---|---------|--------------|-------|
| 1024 | P04406
P50395 | Glyceraldehyde-3-phosphate dehydrogenase
Rab GDP dissociation inhibitor beta | G3P
GDIB
 | 588,61
133.39 | | 46,87

 | 11
6 | 36,0304
50.63088 | 8,46
6.47 | 0,034
0,01 | -1,51
-1,89
 | 0,0088
0,015 | -1,55 | | | 0,011 | -1,6
 | | | |
| 1028 | P52209 | 6-phosphogluconate dehydrogenase | 6PGD
 | 220,86 | | 12,84

 | 5 | 53,10596 | 7,23 | |
 | 0,03 | 2,32 | 0,024 | 2 | 0,0074 | 2,11
 | | | |
| 1031 | P26641
P06733 | Elongation factor 1-gamma
Alpha-enolase | EF1G
ENOA
 | 343,48
287,04 | | 18,76
14,75

 | 7 | 50,08714
47,13932 | 6,67
7,39 | 0,013 | -2,11
 | | | | | |
 | 0,022 | 1,67 | |
| 1033 | P06733 | Alpha-enolase | ENOA
 | 1559,68 | | 48,39

 | 16 | 47,13932 | 7,39 | | |
 | | | | | |
 | | | 0,031 |
| 1037 | P04040
P25311 | Catalase
Zinc-alpha-2-glycoprotein | CATA
ZA2G
 | 257,31
688,74 | | 12,90
33,56

 | 6
11 | 59,71876
34,23711 | 7,39
6,05 | 0,022 0,067 | 1,77
1,56
 | 0,046
0,013 | 2,87
1,63 | | | 0,005 | 2,35
 | | | |
| 1040 | P29508 | Serpin B3 | SPB3
SAHH
 | 113,08 | | 7,44

 | 3 | 44,53655 | 6,81 | 0,0021 | -2,02
 | 0,039 | -1,92 | 0,017 | -1,72 | 0,0032 | -1,88
 | | | |
| 1062 | P23526
P50395 | Adenosylhomocysteinase
Rab GDP dissociation inhibitor beta | GDIB
 | 274,84
197,84 | | 23,15
26,52

 | 10 | 47,68521
50,63088 | 6,34
6,47 | 0,004 | -1,91
 | 0,032 | -1,7 | 0,017 | -1,76 | 0,0019 | -1,79
 | | | |
| 1065
1081 | P23526
000231 | Adenosylhomocysteinase
6S proteasome non-ATPase regulatory subunit 11 | SAHH
PSD11
 | 1382,91
1098,05 | | 24,54
51,90

 | 10
20 | 47,68521
47,43404 | 6,34
6,48 | 0,0081 | 1.50
 | | | | | |
 | 0,033 | 1,56 | 0,008 |
| 1081 | P25311 | Zinc-alpha-2-glycoprotein | ZA2G
 | 787,74 | | 24,83

 | 7 | 34,23711 | 6,05 | 0,0081 | -1,58
2,27
 | | | | | 0,015 | 1,77
 | 0,045 | -1,59 | |
| 1087 | P00738
P25311 | Haptoglobin
Zinc-alpha-2-glycoprotein | HPT
ZA2G
 | 371,21
795,44 | | 12,81
42,62

 | 6
15 | (45,18)
34,23711 | 6,58
6,05 | |
 | | | | | 0,023 | 1,8
 | | | |
| | P00738 | Haptoglobin | HPT
 | 315,12 | | 25,12

 | 10 | (45,18) | 6,58 | |
 | | | | | 0,023 | 1,0
 | | | |
| 1104 | P00738
P25311 | Haptoglobin
Zinc-alpha-2-glycoprotein | HPT
ZA2G
 | 1314,18
994,76 | | 29,80
54,03

 | 11 | (45,18)
34,23711 | 6,58
6,05 | 0,022 | 2,02
 | | | | | |
 | | | |
| 1116 | 075874 | Isocitrate dehydrogenase | IDHC
 | 643,12 | | 26,33

 | 11 | 46,62952 | 7,01 | 0,014 | -2,74
 | | | | | |
 | 0,00065 | 2,6 | |
| 1118 | P00738
P25311 | Haptoglobin
Zinc-alpha-2-glycoprotein | HPT
ZA2G
 | 347,65
296,59 | | 17,49

 | 9 | (45,18)
34,23711 | 6,58
6,05 | 0,007 | 1,83
 | | | | | |
 | 0,041 | -1,53 | |
| 1120 | P00966 | Argininosuccinate synthase | ASSY
 | 100,16 | | 5,58

 | 3 | 46,50097 | 8,02 | 0,013 | -2,79
 | | | | | |
 | 0,036 | 3,19 | |
| 1126 | P29508
P12277 | Serpin B3
Creatine kinase B-type | SPB3
KCRB
 | 87,53
3000,36 | | 4,87 65,35

 | 2 | 44,53655
42,61732 | 6,81
5,59 | 0,02 | 1,71
 | | | | | |
 | 0,0021 | -2,09 | |
| 1173
1188 | P04075
P29508 | Fructose-bisphosphate aldolase A | ALDOA
SPB3
 | 560,17
1648.09 | | 24,45

 | 9 | 39,39531 | 8,09 | 0,00014 | -2,53
 | | | | | 0,0087 | -1,73
 | 0,047 | 1,81 | |
| 1188 | P29508
P06733 | Serpin B3
Alpha-enolase | ENOA
 | 270,99 | | 48,72
20,74

 | 20
8 | 44,53655
47,13932 | 6,81
7,39 | 0,038
0,031 | -1,94
-1,85
 | | | | | |
 | 0,0088 | 1,79
2,67 | |
| 1196 | P29508
P30740 | Serpin B3
Leukocyte elastase inhibitor | SPB3
ILEU
 | 105,87
4670,93 | | 8,46
46,97

 | 4 | 44,53655
42,7147 | 6,81
6,28 | 0,023 | -1,56
 | | | | | |
 | | | |
| 1199 | P29508 | Serpin B3 | SPB3
 | 363,00 | | 14,00

 | 5 | 44,53655 | 6,81 | 0,023 | -1,56
 | | | | | |
 | 0,0037 | 4,49 | |
| 1217
1229 | P01009
P04075 | Alpha-1-antitrypsin
Fructose-bisphosphate aldolase A | A1AT
ALDOA
 | 1520,36
1022,93 | | 13,40
43,96

 | 5
12 | 46,70702
39,39531 | 5,59
8,09 | 0,04 | -2,36
 | | | | | |
 | 0,05 | 2,09 | |
| 1244 | P04075 | Fructose-bisphosphate aldolase A | ALDOA
 | 1298,78 | | 46,43

 | 13 | 39,39531 | 8,09 | 0,14 | -1,76
 | | | | | |
 | | ,- | |
| 1251 | P07355
P04075 | Annexin A2
Fructose-bisphosphate aldolase A | ANXA2
ALDOA
 | 389,76
2210,09 | | 28,91
71,98

 | 10
20 | 38,57982
39,39531 | 7,75
8,09 | 0,0027 | -2,57
 | | | | | 0,011 | -1,92
 | | | |
| 1253 | Q9NR45 | Sialic acid synthase | SIAS
ANXA2
 | 1127,70 | | 39,00
31,56

 | 8 | 40,28146 | 6,74 | | |
 | | | | | |
 | 0,022 | 2 | |
| 1259 | P07355
P04406 | Annexin A2
Glyseraldehyde-3-phosphate dehydrogenase | ANXA2
GAPDH
 | 219,41
211,44 | | 31,56
31,64

 | 9 | 36 | 7,75
8,50 | 0,037 | -1,77
 | | | | | |
 | 0,035 | 2,12 | |
| 1264 | Q13630
P29508 | GDP-L-fucose synthase
Serpin B3 | FCL
SPB3
 | 228,42
197.84 | | 26,79
21.03

 | 7 | 35,86996
44,53655 | 6,60
6.81 | 0,091 | -2,76
 | | | | | |
 | 0,025 | 4,05 | |
| 1268 | P29508 | Serpin B3 | SPB3
 | 5631,00 | | 54,10

 | 28 | 44,53655 | 6,81 | | |
 | | | | | |
 | 0,049 | 3,33 | |
| 1269
1274 | P14324
P04083 | Farnesyl pyrophosphate synthase
Annexin A1 | FPPS
ANXA1
 | 193,36
151,43 | | 12,41
16,76

 | 4 | 48,24463
38,68998 | 6,15
7,02 | |
 | 0,03 | -2,4 | | | 0,048 | -1,5
 | | | |
| 1288 | P04075 | Fructose-bisphosphate aldolase A | ALDOA
 | 267,83 | | 23,90

 | 6 | 39,39531 | 8,09 | 0,011 | -2,3
 | | | | | |
 | 0,041 | 1,82 | |
| 1297
1316 | Q13630
P05120 | GDP-L-fucose synthase
Plasminogen activator inhibitor 2 | FCL
PAI2
 | 1109,54
608,47 | | 34,58
31,81

 | 10
11 | 35,86996
46,56615 | 6,60
5,63 | 0,048
0,032 | -1,97
-1,8
 | | | | | |
 | | | |
| 1318 | P37837
P04083 | Transaldolase
Annexin A1 | TALDO
ANXA1
 | 675,14
651,81 | | 37,39
41,04

 | 12 | 37,51646
38,68998 | 6,81
7,02 | 0,0022 | -2,25
 | | | | | |
 | | | |
| 1320 | P14550 | Alcohol dehydrogenase [NADP(+)] | AK1A1
 | 4263,42 | | 59,38

 | 20 | 36,54986 | 6,79 | 0,023 | -3,06
 | | | | | |
 | | | |
| 1334 | P37837
P04083 | Transaldolase
Annexin A1 | TALDO
ANXA1
 | 1451,16
701,44 | | 40,95 46,24

 | 13 | 37,51646
38,68998 | 6,81
7,02 | 0,008 | -2,43
 | | | | | |
 | | | |
| 1344 | P07355 | Annexin A2 | ANXA2
 | 1471,42 | 1.00 | 39,23

 | 14 | 38,57982 | 7,75 | 0,011 | -2,81
 | | | | | |
 | 0,024 | 2,93 | |
| 1346
1347 | P04083
P04083 | Annexin A1
Annexin A1 | ANXA1
ANXA1
 | 86,32
740,72 | 1,89 | 8,09
50,87

 | 3 | 38,68998
38,68998 | 7,02 | 0,032 | -3,16
 | | | | | 0,043 | -2,1
 | | | |
| 1351 | P07355
P04083 | Annexin A2
Annexin A1 | ANXA2
ANXA1
 | 951,28
748,59 | | 37,17
36,13

 | 12
14 | 38,57982 | 7,75 | |
 | | | | | 0,024 | -2,05
 | | | |
| 1001 | 104000 | |
 | | |

 | | | 7.02 | 0.0060 | |
 | | | | | |
 | | | |
| 1364 | P07355 | Annexin A2 | ANXA2
 | 3958,43 | | 50,44

 | 20 | 38,68998
38,57982 | 7,02 | 0,0069
0,01 | -2,89
-3,3
 | 0,045 | -2,27 | | | 0,024 | -2,39
 | | | |
| 1374 | P04083 | Annexin A1 | ANXA2
ANXA1
 | 3958,43
2987,28 | 6,94 | 50,44
57,51

 | | 38,57982
38,68998 | 7,75
7,02 | 0,01
0,014 | -3,3
-3,02
 | 0,045
0,029 | -2,27
-2,72 | | | 0,013
0,022 | -2,39
-2,2
 | 0.033 | 1.91 | |
| 1374
1380
1381 | P04083
P04083
P04406 | Annexin A1
Annexin A1
Glyceraldehyde-3-phosphate dehydrogenase | ANXA2
ANXA1
ANXA1
G3P
 | 3958,43
2987,28
562,96
729,16 | 6,94 | 50,44
57,51
24,86
49,25

 | 20
18
7
12 | 38,57982
38,68998
38,68998
36,0304 | 7,75
7,02
7,02
8,46 | 0,01
0,014
0,006
0,027 | -3,3
-3,02
-3,27
-2,78
 | 0,029 | -2,72 | | | 0,013
0,022
0,015
0,032 | -2,39
-2,2
-2,36
-2,02
 | 0,033 | 1,91 | |
| 1374
1380 | P04083
P04083 | Annexin A1
Annexin A1 | ANXA2
ANXA1
ANXA1
 | 3958,43
2987,28
562,96 | 6,94 | 50,44
57,51
24,86

 | 20
18
7 | 38,57982
38,68998
38,68998 | 7,75
7,02
7,02 | 0,01
0,014
0,006 | -3,3
-3,02
-3,27
 | | | | | 0,013
0,022
0,015 | -2,39
-2,2
-2,36
 | 0,033 | 1,91 | 0,04 |
| 1374
1380
1381
1384
1386 | P04083
P04083
P04406
P04083
P07355
P04083 | Annexin A1
Annexin A1
Glyceraldehyde-3-phosphate dehydrogenase
Annexin A1
Annexin A2
Annexin A1 | ANXA2
ANXA1
ANXA1
G3P
ANXA1
ANXA2
ANXA2
 | 3958,43
2987,28
562,96
729,16
1283,34
628,34
892,71 | 6,94 | 50,44
57,51
24,86
49,25
56,36
41,89
46,82

 | 20
18
7
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15
13 | 38,57982
38,68998
38,68998
36,0304
38,68998
38,57982
38,68998 | 7,75
7,02
7,02
8,46
7,02
7,75
7,02 | 0,01
0,014
0,006
0,027
0,045
0,013 | -3,3
-3,02
-3,27
-2,78
-3,78
-3,15
 | 0,029 | -2,72 | | | 0,013
0,022
0,015
0,032 | -2,39
-2,2
-2,36
-2,02
 | 0,033 | 1,91 | 0,04 |
| 1374
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1384 | P04083
P04083
P04406
P04083
P07355 | Annexin A1
Annexin A1
Giyceraldehyde-3-phosphate dehydrogenase
Annexin A1
Annexin A2 | ANXA2
ANXA1
ANXA1
G3P
ANXA1
ANXA2
 | 3958,43
2987,28
562,96
729,16
1283,34
628,34 | 6,94 | 50,44
57,51
24,86
49,25
56,36
41,89

 | 20
18
7
12
18
15 | 38,57982
38,68998
38,68998
36,0304
38,68998
38,57982 | 7,75
7,02
7,02
8,46
7,02
7,75 | 0,01
0,014
0,006
0,027
0,045 | -3,3
-3,02
-3,27
-2,78
-3,78
 | 0,029 | -2,72 | | | 0,013
0,022
0,015
0,032 | -2,39
-2,2
-2,36
-2,02
 | 0,033 | 1,91 | |
| 1374
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1387 | P04083
P04083
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P04083 | Annexin A1
Annexin A1
Giyceraldehyde-3-phosphate dehydrogenase
Annexin A1
Annexin A1
Annexin A1
Annexin A1
Annexin A1
Annexin A1
Annexin A2 | ANXA2
ANXA1
ANXA1
G3P
ANXA1
ANXA2
ANXA1
ANXA1
 | 3958,43
2987,28
562,96
729,16
1283,34
628,34
892,71
21054,62
811,37
349,95 | 6,94 | 50,44
57,51
24,86
49,25
56,36
41,89
46,82
74,28
29,48
27,14

 | 20
18
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12
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12
8 | 38,57982
38,68998
36,0304
38,68998
38,68998
38,57982
38,68998
38,68998
38,68998
38,68998
38,57982 | 7,75
7,02
7,02
8,46
7,02
7,75
7,02
7,02
7,02
7,02
7,02
7,75 | 0,01
0,014
0,006
0,027
0,045
0,013
0,022
0,011 | -3,3
-3,02
-3,27
-2,78
-3,78
-3,15
-2,22
-4,59
 | 0,029 | -2,72 | | | 0,013
0,022
0,015
0,032
0,024
0,024 | -2,39
-2,2
-2,36
-2,02
-3,22
-3,22
-3,44
 | 0,033 | 1,91 | |
| 1374
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P04406
P04083
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P07355
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P04083 | Annexin A1
Annexin A1
Glyceraldehyde-3-phosphate dehydrogenase
Annexin A1
Annexin A2
Annexin A1
Annexin A1
Annexin A1
Glyseraldehyde-3-phosphate dehydrogenase
Annexin A1 | ANXA2
ANXA1
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ANXA1
 | 3958,43
2987,28
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1283,34
628,34
892,71
21054,62
811,37
349,95
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1809,38 | 6,94 | 50,44
57,51
24,86
49,25
56,36
41,89
46,82
74,28
29,48
27,14
42,00
47,69

 | 20
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15
17 | 38,57982
38,68998
36,0304
38,68998
38,57982
38,68998
38,68998
38,68998
38,57982
36
38,68998 | 7,75
7,02
7,02
8,46
7,02
7,75
7,02
7,02
7,02
7,02
7,75
8,50
7,02 | 0,01
0,014
0,006
0,027
0,045
0,013
0,022
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0,0011
0,0014 | -3,3
-3,02
-3,27
-2,78
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-3,15
-2,22
-4,59
-2,52
-2,52
-2,36
 | 0,029 0,018 0,0021 0,005 | -2,72
-5,05
-5,75
-3,99 | | | 0,013
0,022
0,015
0,032
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0,0049
0,0049 | -2,39
-2,2
-2,36
-2,02
-3,22
-3,22
-3,44
-3,44
-1,72
-1,87
 | 0,033 | 1,91 | 0,036 |
| 1374
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P04406 | Annexin A1
Annexin A1
Giyceraidehyde-3-phosphate dehydrogenase
Annexin A2
Annexin A2
Annexin A1
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Giyseraidehyde-3-phosphate dehydrogenase | ANXA2
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 | 3958,43
2987,28
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1283,34
628,34
892,71
21054,62
811,37
349,95
1009,00 | 6,94 | 50,44
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24,86
49,25
56,36
41,89
46,82
74,28
29,48
27,14
42,00

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8
15 | 38,57982
38,68998
36,0304
38,68998
38,57982
38,68998
38,68998
38,68998
38,68998
38,57982
36 | 7,75
7,02
8,46
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7,75
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7,75
8,50 | 0,01
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0,027
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0,0011 | -3,3
-3,02
-3,27
-2,78
-3,78
-3,15
-2,22
-4,59
-2,52
 | 0,029 | -2,72
-5,05
-5,75 | | | 0,013
0,022
0,015
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0,024
0,0049 | -2,39
-2,2
-2,36
-2,02
-3,22
-3,22
-3,44
-1,72
 | 0,033 | 1,91 | 0,036 |
| 1374
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Annexin A1
Glyceraldehyde-3-phosphate dehydrogenase
Annexin A1
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Annexin A1
Glyseraldehyde-3-phosphate dehydrogenase
Annexin A2
Ghyseraldehyde-3-phosphate dehydrogenase
Annexin A1
Annexin A1
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Annexin A1 | ANXA2
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 | 3958,43
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628,34
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21054,62
811,37
349,95
1009,00
1809,38
1106,05
272,92
204,37 | 6,94 | 50,44
57,51
24,86
49,25
56,36
41,89
46,82
74,28
29,48
27,14
42,00
47,69
36,71
25,72
21,83

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6 | 38,57982
38,68998
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38,57982
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38,68998
38,68998
38,68998
38,68998
38,68998 | 7,75
7,02
8,46
7,02
7,02
7,02
7,02
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7,05
8,50
7,02
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7,02 | 0,01
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0,0072 | -3,3
-3,02
-3,27
-2,78
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-3,15
-2,22
-4,59
-2,52
-2,36
-3,86
-3,1
 | 0,029 0,018 0,0021 0,015 | -2,72
-5,05
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-3,99 | | | 0,013
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-2,2
-2,36
-2,02
-3,22
-3,22
-3,44
-1,72
-1,87
-2,97
 | | | 0,036 |
| 1374
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P04083 | Annexin A1
Annexin A1
Glyceraldehyde-3-phosphate dehydrogenase
Annexin A2
Annexin A1
Annexin A1
Annexin A1
Annexin A1
Annexin A2
Glyseraldehyde-3-phosphate dehydrogenase
Annexin A1
Annexin A1
Annexin A1
Annexin A1
Annexin A3
Annexin A3
Annexin A3 | ANXA2
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ANXA3
 | 3958,43
2987,28
562,96
729,16
1283,34
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21054,62
811,37
349,95
1009,00
1809,38
1106,05
272,92
204,37
799,75
1633,11 | 6,94 | 50,44
57,51
24,86
49,25
56,36
41,89
46,82
29,48
27,14
42,00
47,69
36,71
25,72
21,83
41,18
20,52

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7 | 38,57982
38,68998
36,0304
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38,58998
38,57982 | 7,75
7,02
8,46
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7,02 | 0,01
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-3,27
-2,78
-3,78
-3,78
-3,15
-2,22
-4,59
-2,52
-2,36
-3,86
-3,11
-1,9
 | 0,029 0,018 0,0021 0,015 | -2,72
-5,05
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-3,99 | | | 0,013
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-2,2
-2,36
-2,02
-3,22
-3,22
-3,44
-1,72
-1,87
-2,97
 | 0,033 | 1,91
 | 0,036 |
| 1374
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P04083
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P04083 | Annexin A1
Annexin A1
Giyceraidehyde-3-phosphate dehydrogenase
Annexin A1
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Annexin A1
Giyseraidehyde-3-phosphate dehydrogenase
Annexin A1
Annexin A1
Annexin A1
Annexin A1
Annexin A2
Annexin A2 | ANXA2
ANXA1
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ANXA3
 | 3958,43
2987,28
562,96
729,16
1283,34
628,34
892,71
21054,62
811,37
349,95
1009,00
1809,38
1106,05
272,92
2204,37
799,75 | 6,94 | 50,44
57,51
24,86
49,25
56,36
41,89
46,82
74,28
29,48
29,48
27,14
42,00
47,69
36,71
25,72
21,83
41,18

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12 | 38,57982
38,68998
36,0304
38,68998
38,57982
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38,68998 | 7,75
7,02
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8,46
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0,013
0,022
0,011
0,0011
0,0011
0,014
0,025
0,0072 | -3,3
-3,02
-3,27
-2,78
-3,78
-3,15
-2,22
-4,59
-2,52
-2,36
-3,86
-3,1
 | 0,029 0,018 0,0021 0,015 | -2,72
-5,05
-5,75
-3,99 | | | 0,013
0,022
0,015
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0,024
0,024
0,024
0,012
0,012
0,012 | -2,39
-2,2
-2,36
-2,02
-3,22
-3,22
-3,44
-1,72
-1,87
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L-lactate dehydrogenase A chain
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1374 1374 1380 1381 1384 1384 1384 1387 1388 1391 1392 1393 1393 1393 1401 1433 1401 1433 1401 1433 1434 1437 1457 1480 1513 1553 1554 1553 1555 1577 1573 1553 1555 1577 1583 1601 1686 1686	P04083 P04083 P04066 P04066 P04068 P04083 P07355 P04083 P0408 P0408 P0408 P0408 P0408 P0408 P0408 P0408 P0408 P0408 P040	Annexin A1 Annexin A2 Glyseraldehyde-3-phosphate dehydrogenase Annexin A2 Annexin A2 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 LiJactate dehydrogenase Achain Retinal dehydrogenase Achain Retinal dehydrogenase 1 Complement C4-& gamma chain Annexin A5 Retinal dehydrogenase 1 S-formýlgiutathione hydrolase 14-3-9 protein esolion Tropomyosin alpha-1 chain Tropomyosin alpha-1 chain	ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1	3958,43 2987,28 562,96 729,16 1283,34 628,34 892,71 21034,62 811,37 349,95 1009,00 1809,38 1106,05 1272,92 204,37 7799,72 204,37 272,92 204,37 272,92 204,37 272,92 204,37 272,92 204,37 272,92 204,37 272,92 204,37 1153,351 1000,35 492,14 511,00 272,16 698,21 492,14 511,00 355,50 352,52 355,50 352,52 355,50 352,52 352,52 355,50 352,52 355,50 352,52 352,52 352,52 352,50 352	58,87	50,44 57,51 24,86 49,25 56,36 41,89 45,82 29,48 27,14 47,628 29,48 27,14 47,69 36,71 25,72 21,83 41,18 20,52 42,49 29,40 23,57 42,49 29,40 23,52 42,49 29,40 23,52 42,49 29,40 23,52 42,49 29,40 23,52 25,87 11,98 30,98 35,54 26,52 25,87 17,45 25,72 25,87 17,45 26,27 31,54 12,53 26,27 35,54 12,53 26,27 35,54 12,55 25,97 35,71 25,72 25,97 35,74 25,72 25,97 35,74 25,77 25,97 36,71 25,72 25,97 36,71 25,72 25,97 36,71 25,72 25,97 36,71 25,72 25,97 36,71 25,72 25,97 36,71 25,72 25,97 36,71 25,72 25,97 36,71 25,72 25,97 36,71 25,72 25,97 36,71 25,72 25,97 36,71 25,72 25,97 35,74 25,72 25,97 25,72 25,87 7,45 25,97 35,74 25,97 35,74 25,97 35,74 25,97 25,97 35,74 25,97 35,74 25,97 35,74 25,97 35,74 25,97 35,74 25,97 35,74 25,97 35,74 25,77 25,97 35,74 25,77 25,97 35,74 25,77 25,97 35,74 25,777 25,777 25,777 25,777 25,777 25,777 25,777 25,777 2	20 18 7 12 18 15 13 15 17 13 15 17 13 8 6 12 7 14 8 6 12 7 14 8 8 5 4 4 5 8 8 7 7 14 8 8 5 15 17 17 18 8 15 15 15 15 17 17 18 15 15 17 17 18 19 19 19 19 19 19 19 19 19 19	38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,57982 38,68998 38,5986 29,555 26,9055 26,9055 26,9055 26,9055 27,72773 27,72768 28,0449 32,72773 27,72773 27,72773 27,72773 27,72773 28,5447 38,6449 38,64995 37,72773 32,7273 32,7273 32,7273 32,72773 32,72773 32,72773 32,72773 32,7277	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,006 0,027 0,045 0,013 0,027 0,045 0,022 0,011 0,014 0,014 0,011 0,014 0,001 0,0017 0,0077 0,063 0,0047 0,063 0,0047 0,068 0,003 0,0031 0,0044 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0031 0,0042 0,005 0,0	-3,3 -3,2 -3,27 -2,78 -3,78 -3,78 -2,27 -2,78 -3,78 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -3,8 -1,9 -1,9 -1,9 -1,9 -1,9 -2,29 -2,19 -2,29 -2,18 -1,9 -1,9 -1,9 -1,9 -2,29 -2,18 -1,9 -1,9 -1,9 -1,9 -1,9 -1,9 -1,9 -1,9	0,029 0,018 0,0021 0,015 0,032 0,014 0,014	-2,72 -5,05 -5,75 -3,99 -2,6	0,017 0,03	-1,56	0,013 0,022 0,015 0,032 0,024 0,024 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,012 0,019 0,012 0,014 0,014 0,039 0,023 0,014	-2,39 -2,2 -2,36 -2,2,6 -2,02 -3,22 -3,22 -3,24 -1,72 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,24 -1,84 -3,444 -3,44	0,029	2,1	0,036
1374 1380 1381 1384 1384 1384 1385 1387 1388 1392 1393 1392 1393 1393 1398 1433 1433 1434 1434 1434 1437 1437 1437 1437 1437 1437 1538 1550 1555 1575 1577 1583 1601 1619 1666 1666	P04083 P04083 P0406 P0406 P04083 P055 P04083 P04083 P055 P04083 P055 P04083 P055 P04083 P055 P04083 P055 P04083 P055 P055 P04083 P055 P055 P055 P055 P055 P055 P055 P05	Amenin A1 Annexin A1 Glyceraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A2 Annexin A1 Annexin A2 Annexin A1 Annexin A1 Annexin A1 Annexin A2 Glyseraldehyde-3-phosphate dehydrogenase Annexin A2 Glyseraldehyde-3-phosphate dehydrogenase Annexin A2 Annexin A2 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A4 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A4 Annexin A5 Retinal dehydrogenase 1 Complement C4-A; gamma chain Tropomysin alpha-3 chain Tropomysin alpha-4 chain Tropomy	ANXA2 ANXA1	3958,43 2987,28 562,96 729,16 1283,34 628,34 628,34 892,71 21054,62 811,37 349,95 1009,00 1809,38 1106,05 272,92 204,37 799,75 1633,11 1000,38 1106,05 272,92 204,37 799,75 1633,11 1000,35 492,14 492,14 511,00 272,16 698,21 1153,95 276,98 1004,36 484,82 314,18 993,399 2104,36 214,18 993,392 214,18 214,18 314,1	58,87	50,44 57,51 24,86 49,25 56,36 41,89 41,89 44,82 29,48 27,14 42,00 47,69 36,71 25,72 21,83 42,94 25,72 21,83 42,90 25,72 21,83 42,14 25,72 21,83 42,14 25,72 21,83 42,14 25,72 21,83 42,14 25,72 21,83 42,14 25,72 25,22 9,40 25,22 9,40 29,28 42,19 29,28 42,49 29,28 44,183 20,52 2	20 18 7 12 18 15 13 15 13 12 8 5 17 13 8 6 12 7 14 8 5 12 7 14 8 5 12 15 15 15 15 15 15 15 15 15 15	38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998 38,6998	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,007 0,045 0,013 0,022 0,011 0,014 0,022 0,011 0,014 0,022 0,011 0,014 0,022 0,017 0,017 0,026 0,0072 0,017 0,026 0,004 0,004 0,005 0,004 0,005 0,002 0,002 0,002 0,002 0,002 0,002 0,0008 0,0008	-3,3 -3,02 -3,27 -3,78 -3,78 -3,78 -3,78 -3,78 -3,78 -2,22 -4,59 -2,22 -4,59 -2,23 -3,86 -3,11 -1,91 -1,43 -1,43 -1,54 -2,59 -2,38 -1,64 -2,59 -2,21 -1,64 -2,218 -2,218 -2,228 -2,2	0,029 0,018 0,0021 0,015 0,032 0,015 0,032 0,014 0,014 0,014	-2,72 -5,05 -5,75 -3,99 -2,6 	0,017 0,03 0,042	-1,56 -1,67 1,62	0,013 0,022 0,015 0,032 0,024 0,024 0,012 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,018 0,038	-2,39 -2,2 -2,36 -2,02 -3,22 -3,24 -1,72 -2,27 -2,27 -2,27 -2,27 -2,52 -1,84 -1,59 -2,27 -1,59 -2,24 -1,59 -2,24 -1,87 -1,71 -1,59 -2,24 -1,87 -1,71 -1,59 -2,24 -1,87 -1,59 -2,24 -1,59 -2,25 -2,26 -2,27 -2,26 -2,26 -2,27 -2,26 -2,27 -2,26 -2,27 -	0,029	2,1	0,036
1374 1374 1380 1381 1384 1384 1384 1387 1388 1391 1392 1393 1393 1393 1393 1393 1393	P04083 P04083 P0406 P0406 P0406 P04083 P0408 P04083 P04083 P0408 P0408 P0408 P0408 P0408 P0408 P0408 P0408	Amexin A1 Annexin A1 Glyceraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A1 Clyseraldehydrogenase Achain Retinal dehydrogenase Achain Retinal dehydrogenase Achain Retinal dehydrogenase 1 S-formylgutathione hydrolase 14-3-3 protein esolion Tropomyosin alpha-3 chain Tropomyosin alpha-1 chain Tropomyosin alpha-1 chain Tropomyosin alpha-1 chain Annexin A2 Actin, cytoplasmic 1 14-3-3 protein esolion 14-3-3 protein seta/delta 14-3-3 protein seta/delta	ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1	3958,43 2987,28 562,96 729,16 1283,34 628,34 892,71 21034,62 811,37 349,95 1009,00 1809,38 1106,05 272,92 204,37 799,75 272,92 204,37 11009,00 1809,38 1106,05 272,95 272,92 204,37 11009,35 11000,35 482,14 11100,35 492,14 511,00 277,16 698,21 1153,95 245,40 710,436 492,14 1153,95 245,40 710,436 484,82 355,50 355,50 352,25 276,98 1004,36 484,82 314,18 923,99 1004,36 419,92 314,18 923,99 1004,36 419,25 216,46 217,021 217,021 216,46 217,021 217,0	58,87	50,44 57,51 24,86 49,25 56,36 41,89 42,86 42,86 42,86 42,86 42,86 42,86 41,89 27,14 42,86 47,69 36,71 25,72 21,83 41,18 20,52 9,40 23,51 99,38 19,90 30,98 30,98 35,48 29,84 29,84 29,84 29,85 30,98 30,98 30,98 26,25 25,87 17,65 26,27 31,54 12,03 38,71 65,27 98,77 48,11 39,38	20 18 7 12 18 15 13 15 15 17 13 8 6 12 2 7 14 4 5 5 4 11 6 5 8 5 4 11 6 5 8 5 7 7 14 8 5 7 7 14 8 5 15 15 15 15 15 15 15 15 15	38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,57982 36 38,68998 39,6895 29,555 20,7277 32,5269 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,72773 28,50449 37,5075 37,72773 28,50449 37,5075 37,72773 28,50449 37,5075 37,72773 28,50449 37,5075 37,72773 28,50449 38,50449	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,007 0,045 0,013 0,027 0,045 0,013 0,027 0,011 0,014 0,021 0,011 0,014 0,022 0,017 0,017 0,017 0,017 0,017 0,026 0,0047 0,005 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0088 0,0071 0,0077 0,0052 0,0057 0,0050 0,00000000	-3,3 -3,2 -3,27 -2,78 -3,78 -3,78 -3,78 -2,22 -2,38 -3,38 -2,52 -2,38 -3,38 -1,9 -1,9 -1,9 -1,43 -1,43 -1,9 -1,9 -2,03 -2,18 -1,9 -2,22 -2,18 -2,21 -2,22 -2,25 -2	0,029 0,018 0,0021 0,015 0,032 0,015 0,032 0,014 0,014 0,014	-2,72 -5,05 -5,75 -3,99 -2,6 	0,017 0,03 0,042	-1,56 -1,67 1,62	0,013 0,022 0,015 0,032 0,024 0,024 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,018 0,018 0,018 0,014 0,014 0,014 0,0059 0,023 0,021 0,0059 0,021 0,0059 0,021 0,0059 0,021 0,038	-2,39 -2,2 -2,36 -2,2,6 -2,02 -3,22 -3,22 -3,24 -3,44 -1,72 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -1,84 -2,18 -2,18 -2,18 -2,18 -2,18 -2,18 -2,18 -2,27 -2,27	0,029	2,1	0,036
1374 1374 1380 1381 1384 1384 1384 1387 1388 1389 1391 1392 1393 1393 1393 1401 1433 1434 1437 1453 1434 1437 1453 1513 1513 1550 1553 1554 1555 1555 1555 1555 1555 1555	P04083 P04083 P04086 P04066 P04086 P04083 P07355 P04083 P0555 P0575	Annexin A1 Annexin A1 Annexin A1 Glyceraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A2 Glyseraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Li-lactate dehydrogenase Achain Retinal dehydrogenase 1 Complement C4-& gamma chain Retinal dehydrogenase 1 S-formylgiutathione hydrolase 14-3-3 protein esplon Tropomyosin alpha-1 chain Tropomyosin alpha-3 protein pagion 14-3-3 protein pagion 14-3-5 protein seta/delta 14-3-5 protein seta/delta 14-3-5 protein seta/delta 14-3-5 protein seta/delta Serum amyloid P-component I gkapa chain C region I gkapa chain C region	ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1	3958,43 2987,28 562,96 729,16 1283,34 628,34 892,71 21034,62 811,37 349,95 11060,00 1809,88 11060,00 1809,88 11060,00 1809,88 11060,00 1809,88 11060,05 11009,00 1809,88 11060,05 11009,00 1809,88 11060,05 11009,00 1809,88 11060,05 11000,05 100	58,87	50,44 57,51 24,86 49,25 56,36 41,89 45,82 29,48 27,14 42,20 42,20 42,20 42,29 42,20 42,20 42,49 25,72 21,18 20,52 42,49 29,40 23,57 21,183 41,83 42,49 29,40 23,52 42,49 29,40 23,52 29,40 23,52 29,40 23,52 20,52 42,49 29,40 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,40 29,52 29,52 29,40 29,52 29,40 29,52 29,40 29,52 20,52 29,52 20,52 29,52 20,52 2	20 18 7 12 18 15 15 15 17 13 8 6 12 15 17 13 8 6 17 13 8 6 17 13 8 5 14 8 5 8 15 15 15 15 15 15 15 15 15 15	38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,57982 38,68998 38,6898 38,5984 29,15542 29,15542 27,72773 27,727569 27,72773 28,04433 (11.6) 27,72773 25,37113 25,37113	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,027 0,045 0,013 0,027 0,045 0,022 0,011 0,022 0,011 0,014 0,025 0,0011 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,011 0,004 0,005 0,0088 0,043 0,05 0,0065 0,011	-3,3 -3,27 -3,27 -3,27 -3,78 -3,78 -3,78 -3,78 -3,27 -2,28 -3,28 -2,28 -3,28 -2,28 -3,28 -2,29 -2,28 -3,28 -2,29 -	0,029 0,018 0,0021 0,015 0,032 0,015 0,032 0,014 0,014 0,014	-2,72 -5,05 -5,75 -3,99 -2,6 	0,017 0,03 0,042	-1,56 -1,67 1,62	0,013 0,022 0,015 0,032 0,024 0,024 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,014 0,039 0,038 0,038 0,0059 0,023 0,013	-2,39 -2,2 -2,36 -2,26 -2,26 -2,02 -3,22 -3,22 -3,24 -1,87 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,24 -1,84 -1,59 -2,24 -1,87 -1,71 -2,86 -2,24 -1,87 -1,84 -1,51 -1,51 -1,55 -	0,029	2,1	0,036
1374 1374 1380 1381 1384 1384 1384 1387 1388 1391 1392 1393 1393 1393 1393 1393 1393	P04083 P04083 P0406 P0406 P04083 P0408 P0408 P04083 P0408 P0408 P0408 P04083 P0408 P0408 P0408 P040	Annexin A1 Annexin A1 Annexin A1 Glyceraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A2 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A2 Glyseraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A2 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A4 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A4 Annexin A5 Retinal dehydrogenase A chain Retinal dehydrogenase 1 Complement C4-A; gamma chain Annexin A5 Retinal dehydrogenase 1 S-formylglutathione hydrolase 14-3-3 protein epsilon Tropomyosin alpha-4 chain Tropomyosin alpha-4 chain Tropomyosin alpha-4 chain Annexin A2 Atheraelluar channel protein 1 14-3-3 protein epsilon Chloride intracellular channel protein 1 14-3-3 protein atel/delta 14-3-3 protein in atel/delta	ANXA2 ANXA1	3958,43 2987,28 562,96 729,16 1283,34 628,34 628,34 892,71 21034,62 811,37 394,95 1009,00 1809,38 1106,05 272,92 204,37 799,75 1653,11 1000,30 492,14 494,10 272,16 100,35 100,36 484,82 100,36 484,82 1106,35 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 41,192 100,36 1106,07 100,36 100,0000 100,0000 100,0000 100,0000 100,00000000	58,87	50,44 57,51 24,86 49,25 56,36 41,89 41,89 44,82 27,14 42,00 47,69 25,72 21,83 42,20 25,72 21,83 41,18 20,52 42,49 29,22 9,40 29,22 29,22 9,40 29,22 29,22 9,40 29,22 29,22 9,40 29,22 29,22 29,22 29,22 29,22 29,22 29,22 29,22 29,22 29,22 29,22 29,22 29,22 29,22 29,22 20,2	20 18 7 12 18 15 13 15 13 12 8 15 13 15 17 13 8 6 12 7 14 8 5 12 7 14 8 8 7 15 15 15 17 13 18 15 19 19 19 19 19 19 19 19 19 19	38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,6998 38,6998 38,7982 32,79773 38,06483 31,116,116,116,116,116,116,116,116,116,1	7,75 7,02 8,46 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,007 0,045 0,013 0,027 0,045 0,013 0,027 0,011 0,014 0,021 0,011 0,014 0,022 0,017 0,017 0,017 0,017 0,026 0,0047 0,005 0,0088 0,0071 0,0077 0,00077 0,00077 0,00077 0,00770 0,000770 0,0077000000	-3,3 -3,2 -3,27 -2,78 -3,78 -3,78 -3,78 -2,22 -2,38 -3,38 -2,52 -2,38 -3,38 -1,9 -1,9 -1,9 -1,43 -1,43 -1,9 -1,9 -2,03 -2,18 -1,9 -2,22 -2,18 -2,21 -2,22 -2,25 -2	0,029 0,018 0,0021 0,015 0,032 0,015 0,032 0,014 0,014 0,014	-2,72 -5,05 -5,75 -3,99 -2,6 	0,017 0,03 0,042	-1,56 -1,67 1,62	0,013 0,022 0,015 0,032 0,024 0,024 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,018 0,018 0,018 0,014 0,014 0,014 0,0059 0,023 0,021 0,0059 0,021 0,0059 0,021 0,0059 0,021 0,038	-2,39 -2,2 -2,36 -2,2,6 -2,02 -3,22 -3,22 -3,24 -3,44 -1,72 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -1,84 -3,44 -2,55 -2,55 -2,56 -2,56 -2,02 -3,22 -3,22 -3,24 -3,27 -2,25 -2,25 -3,22 -2,25 -3,22 -2,25 -2,25 -2,25 -2,27	0,029	2,1	0,036
1374 1374 1380 1381 1384 1384 1384 1385 1389 1391 1392 1393 1393 1401 1433 1401 1433 1401 1433 1434 1437 1457 1480 1513 1553 1553 1553 1553 1553 1553 155	P04083 P04083 P04066 P04066 P04066 P04083 P07355 P04083 P0555 P0555 P0555 P0555 P0555 P05755	Annexin A1 Annexin A2 Glyseraldehyde-3-phosphate dehydrogenase Annexin A2 Annexin A2 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Lilactate dehydrogenase Achain Retinal dehydrogenase Achain Retinal dehydrogenase Achain Retinal dehydrogenase 1 Complement C4-kg gamma chain Annexin A5 Retinal dehydrogenase 1 S-formýlgiutathione hydrolase 14-3-3 protein esolion Tropomyosin alpha-1 chain Tropomyosin alpha-2 chain Tropomyosin alpha-1 c	ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2	3958,43 2997,28 562,96 729,16 1283,34 628,34 892,71 21034,62 811,37 349,95 1006,62 1106,93 1106,93 1106,93 1106,05 272,92 204,37 799,75 1633,11 1000,35 492,14 511,00 272,92 204,37 799,75 1633,11 1000,35 492,14 511,00 272,16 698,21 1153,95 245,60 710,62 276,98 204,83 710,62 276,98 276,98 104,35 484,82 72,41 106,59 444,83 776,03 265,63 106,76	58,87	50,44 57,51 24,86 49,25 56,36 41,89 45,82 29,48 27,14 47,69 36,71 25,72 21,83 41,18 20,52 20	20 18 7 12 18 15 13 15 17 13 8 6 12 17 13 8 6 12 7 14 8 5 14 8 5 4 11 6 5 8 8 7 7 14 8 8 5 15 15 15 15 15 15 15 15 15	38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,57982 38,68998 38,57982 29,5542 37,72773 27,7275 28,9443 31,727773 27,72773 27,72773 27,72773 27,72773 27,72773 27,72773 27,72773 28,5449 30,727773 28,5449 30,7277773 28,5449 30,7277773 28,5449 30,7277773 28,5449 30,727773 28,5449 30,727773 28,5449 30,727773 28,5449 30,727773 28,5449 30,727773 28,5449 30,727773 28,5449 30,727773 28,5449 30,727773 28,5449 30,727773 20,72773 20,72773 20,72773 20,72773 20,72773 20,72773 20,72773 20,72773 20,72773 20,72773 20,72773 20,72773 20,727773 20,727773 20,727773 20,727773 20,72773 20,72773 20,7277	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,027 0,045 0,013 0,027 0,045 0,022 0,011 0,022 0,011 0,011 0,014 0,025 0,0071 0,007 0,0077 0,063 0,0047 0,063 0,0047 0,063 0,0047 0,008 0,0031 0,0044 0,0024 0,0012 0,0012 0,0008 0,0024 0,0012 0,0008 0,0071 0,0008 0,0008 0,005 0,	-3,3 -3,27 -3,27 -3,27 -3,27 -3,28 -3,27 -2,28 -3,28 -2,28 -2,29 -2,29 -2,29 -2,29 -2,29 -2,29 -2,29 -3,86 -1,99 -1,99 -1,99 -2,20 -2,18 -1,99 -2,21 -1,88 -2,21 -1,75 -1,28 -2,21 -1,78 -1,28 -2,21 -1,78 -1,29 -2,21 -1,78 -1,29 -2,21 -1,29 -2,21 -1,29 -2,21 -1,29 -2,21 -2,21 -2,21 -2,21 -2,21 -2,22 -2,25 -	0,029 0,018 0,0021 0,015 0,032 0,015 0,032 0,014 0,014 0,014	-2,72 -5,05 -5,75 -3,99 -2,6 	0,017 0,03 0,042	-1,56 -1,67 1,62	0,013 0,022 0,015 0,032 0,024 0,024 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,014 0,039 0,038 0,038 0,0059 0,023 0,013	-2,39 -2,2 -2,36 -2,2,6 -2,2,6 -2,02 -3,22 -3,22 -3,24 -1,87 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,24 -1,84 -1,59 -2,24 -1,87 -1,71 -2,86 -1,87 -1,87 -1,84 -1,51 -1,51 -1,55	0,029	2,1	0,036
1374 1380 1381 1384 1384 1384 1385 1387 1389 1392 1393 1392 1393 1393 1393 1398 1433 1433 1433 1434 1434 1437 1437 1437 1437 1437 1437 1437 1437 1538 1550 1551 1555 1555 1555 1555 1555 1555 1555 1555 1557 1558 1601 1619 1660 1666 1667 1662 1704 1709 1711 1715 1716	P04083 P04083 P04086 P04066 P04086 P04085 P04083 P0	Amenin A1 Annexin A1 Glyceraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A2 Annexin A1 Annexin A2 Annexin A1 Annexin A1 Annexin A1 Annexin A2 Glyseraldehyde-3-phosphate dehydrogenase Annexin A2 Glyseraldehyde-3-phosphate dehydrogenase Annexin A2 Annexin A2 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A4 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A4 Annexin A5 Retinal dehydrogenase A chain Retinal dehydrogenase 1 Complement C4-A; gamma chain Annexin A5 Retinal dehydrogenase 1 S-formylglutathione hydrolase 14-3-3 protein epsilon Tropomycsin alpha-4 chain Tropomycsin alpha-4 chain Tropomycsin alpha-4 chain Annexin A2 Actin, cytoplasmic 1 14-3-3 protein epsilon 14-3-3 protein epsilon 14-3-3 protein epsilon 14-3-3 protein epsilon 14-3-3 protein seta/delta 14-3-3 protein seta/delta	ANXA2 ANXA1 ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA2 ANXA1 ANXA2	3958,43 2987,28 562,96 729,16 1283,34 628,34 892,71 21034,62 811,37 349,95 1106,05 811,37 349,95 1106,05 11009,00 1809,38 1106,05 272,92 204,37 799,75 1633,11 1000,05 492,14 492,14 492,14 492,14 492,14 492,14 511,00 277,16 698,21 770,62 771,162 772,16 770,05 77	58,87	50,44 57,51 24,86 49,25 56,36 41,89 41,89 44,86 29,48 27,14 42,00 47,62 29,48 27,14 42,00 42,72 21,83 41,89 25,72 21,83 42,49 20,52 42,49 29,40 2,35 30,98 35,48 20,52 9,40 2,35 30,98 30,98 35,48 8,45 16,53 26,25 26,27 31,54 26,27 31,54 26,27 31,54 26,27 31,54 26,27 31,57 38,78 38,78 38,78	20 18 7 12 18 15 13 15 13 15 13 15 17 13 8 5 17 13 8 5 12 7 14 8 5 12 7 14 8 5 12 15 15 15 15 15 15 15 15 15 15	38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,68988 38,6998 38,6998 38,6998 38,6998 38,6998 38,5998 38,5998 38,5998 38	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,027 0,045 0,013 0,027 0,045 0,022 0,011 0,022 0,011 0,014 0,025 0,0011 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,011 0,004 0,005 0,0088 0,043 0,05 0,0065 0,011	-3,3 -3,27 -3,27 -3,27 -3,78 -3,78 -3,78 -3,78 -3,27 -2,28 -3,28 -2,28 -3,28 -2,28 -3,28 -2,29 -2,28 -3,28 -2,29 -	0,029	-2,72 -5,05 -5,75 -3,99 -2,6 	0,017 0,03 0,042	-1,56 -1,67 1,62	0,013 0,022 0,015 0,032 0,032 0,024 0,012 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,018 0,039 0,018 0,038 0,038	-2,39 -2,2 -2,36 -2,26 -2,02 -3,22 -3,24 -1,87 -2,27 -2,27 -2,27 -2,27 -2,52 -1,84 -1,87 -2,97 -2,52 -2,52 -1,84 -1,59 -2,24 -1,59 -1,85 -1,59 -	0,029	2,1	0,036
1374 1380 1381 1384 1384 1384 1384 1385 1387 1389 1393 1393 1393 1393 1393 1393 1393 1401 1433 1434 1437 1457 1450 1513 1513 1553 1555 1575 1577 1573 1554 1555 1575 1577 1573 1601 1660 1660 1666 1667 1662 1704 1704 1715 1716 1778	P04083 P04083 P0406 P0406 P0406 P04083 P0408 P0408 P0408 P0408 P0408 P0408 P0408 P0408 P0408	Amexin A1 Annexin A1 Giveraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A1 Annexin A2 Annexin A1 Annexin A1 Cilectate dehydrogenase Achain Retinal dehydrogenase Achain Retinal dehydrogenase 1 Complement C4-kg gamma chain Annexin A5 Retinal dehydrogenase 1 S-formylglutathione hydrolase 14-3-3 protein epsilon Tropomyosin alpha-4 chain Tropomyosin alpha-1 chain Tropomyosin alpha-1 chain Tropomyosin alpha-1 chain Tropomyosin alpha-1 chain Tropomyosin alpha-1 chain Tropomyosin alpha-3 chain Tropomyosin alpha-3 chain Tropomyosin alpha-1 chain Tropomyosin alpha-1 chain Tropomyosin alpha-4 chain Annexin A2 Actin, cytoplasmic 1 14-3-3 protein epsilon Chloride intracellular channel protein 1 4-3-3 protein epsilon 14-3-3 protein seta/delta 14-3-3 protein seta/delta 14-3-3 protein seta/delta 14-3-3 protein i gama 14-3-3 protein i gama 14-3-3 protein seta/delta 14-3-3 protein i ata/alpha gi kappa chain C region gi gi kappa chain C region	ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1 ANXA1 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1	3958,43 2987,28 562,96 729,16 1283,34 628,34 892,71 21034,62 811,37 349,95 1009,38 1106,052 272,92 204,37 799,75 1033,11 103,35 492,14 511,00 272,92 273,92 274,92 274,91 285,50 355,50 352,52 272,92 272,92 204,37 799,71 2153,95 245,40 710,62 276,98 1004,36 484,82 314,18 923,99 1004,36 484,82 314,18 923,99 188,83 619,61 106,591 346,621 1070,11	58,87	50,44 57,51 24,86 49,25 56,36 41,89 42,82 29,48 27,14 42,86 47,628 29,48 27,14 41,89 36,71 25,72 21,83 41,18 25,72 21,83 41,18 25,72 9,40 235 30,98 30,98 35,98 26,25 25,87 17,65 26,27 31,54 12,03 38,71 26,27 31,54 12,03 88,71 25,97 35,89 38,71 49,19 51,89 38,71 42,27 44,19 52,28 14,80 25,35 <td>20 18 7 12 18 15 13 15 15 17 13 8 6 12 2 7 14 8 6 12 7 14 8 6 12 7 14 8 6 12 15 15 15 15 15 15 15 15 15 15</td> <td>38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,57982 38,68998 32,68868 29,1554 29,15542 29,15542 29,15542 29,15542 29,15542 29,57773 27,727373 27,72773 27,72773 27,72773 27,72773 27,72773 27,72773 27,</td> <td>7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02</td> <td>0,01 0,014 0,006 0,027 0,045 0,027 0,045 0,027 0,045 0,011 0,011 0,014 0,021 0,011 0,014 0,022 0,017 0,017 0,017 0,017 0,017 0,025 0,0047 0,005 0,0047 0,008 0,003 0,003 0,0012 0,008 0,0071 0,008 0,0071 0,008 0,0071 0,008 0,0071 0,008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0</td> <td>-3,3 -3,27 -3,27 -2,28 -3,27 -2,28 -3,28 -2,28 -2,28 -2,28 -2,28 -2,28 -2,28 -2,28 -2,28 -2,28 -3,86 -1,91 -1,9 -1,9 -1,9 -2,22 -2,14 -1,91 -1,95 -2,21 -2,18 -1,95 -2,21 -2,21 -2,21 -2,21 -1,95 -2,22 -2,18 -1,75 -2,22 -2,18 -2,21 -2,21 -2,21 -2,21 -2,21 -2,21 -2,21 -2,21 -2,21 -2,22 -2,25 -2,218 -2,25 -2,218 -2,25 -2,218 -2,25 -2,218 -2,25 -2,218 -2,218 -2,218 -2,218 -2,222 -2,218 -2,219</td> <td>0,029 0,018 0,0021 0,015 0,032 0,032 0,014 0,014 0,014</td> <td>-2,72 -5,05 -5,75 -3,99 -2,6 </td> <td>0,017 0,03 0,042</td> <td>-1,56 -1,67 1,62</td> <td>0,013 0,022 0,015 0,032 0,024 0,024 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,010 0,019 0,019 0,019 0,019 0,019 0,010 0,019 0,019 0,010 0,019 0,010 0,003 0,00000000</td> <td>-2,39 -2,2 -2,36 -2,02 -3,22 -3,24 -1,72 -1,87 -2,27 -2,27 -2,27 -2,27 -1,88 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,59 -1,71 -1,59 -1,71 -1,59 -1,71 -1,71 -1,71 -1,71 -1,71 -1,71 -1,71 -1,71 -1,71 -1,71 -1,71 -1,71 -1,71 -1,71 -1,72 -1,59 -1,79 -1,59 -1,79 -1,79 -1,79 -1,59 -</td> <td>0,029</td> <td>2,1</td> <td>0,036</td>	20 18 7 12 18 15 13 15 15 17 13 8 6 12 2 7 14 8 6 12 7 14 8 6 12 7 14 8 6 12 15 15 15 15 15 15 15 15 15 15	38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,57982 38,68998 32,68868 29,1554 29,15542 29,15542 29,15542 29,15542 29,15542 29,57773 27,727373 27,72773 27,72773 27,72773 27,72773 27,72773 27,72773 27,	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,027 0,045 0,027 0,045 0,027 0,045 0,011 0,011 0,014 0,021 0,011 0,014 0,022 0,017 0,017 0,017 0,017 0,017 0,025 0,0047 0,005 0,0047 0,008 0,003 0,003 0,0012 0,008 0,0071 0,008 0,0071 0,008 0,0071 0,008 0,0071 0,008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0,0008 0,005 0	-3,3 -3,27 -3,27 -2,28 -3,27 -2,28 -3,28 -2,28 -2,28 -2,28 -2,28 -2,28 -2,28 -2,28 -2,28 -2,28 -3,86 -1,91 -1,9 -1,9 -1,9 -2,22 -2,14 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1874 1874 1880 1381 1384 1384 1384 1385 1389 1393 1393 1393 1393 1393 1393 1493 1493 1493 1493 1493 1493 1493 1493 1493 1493 1493 1494 1497 1490 1510 1513 1513 1555 1575 1577 1577 1578 1687 1692 1711 1716 1778 1778 1778 1788 1844	P04083 P04083 P04086 P04066 P04068 P04083 P0	Annexin A1 Annexin A2 Glyseraldehyde-3-phosphate dehydrogenase Annexin A2 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Annexin A1 Clattate dehydrogenase Achain Retinal dehydrogenase Achain Retinal dehydrogenase 1 Complement C4-k gamma chain Annexin A5 Retinal dehydrogenase 1 S-formýlgiutathione hydrolase 14-3-3 protein esolion Tropomyosin alpha-3 chain Tropomyosin alpha-3 chain Tropomyosin alpha-3 chain Tropomyosin alpha-3 chain Tropomyosin alpha-3 chain Tropomyosin alpha-4 chain Tropomyosin alpha-4 chain Tropomyosin alpha-3 chain Annexin A2 Actin, cytoplasmic 1 14-3-3 protein esolion 14-3-3 protein esolion 14-3-3 protein esolion 14-3-3 protein atel/delta Cathepsin D 14-3-3 protein seta/delta 14-3-3 protein seta/delta	ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA1 ANXA1 ANXA1 ANXA1 ANXA2 ANXA1 ANXA1 ANXA2 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2	9958,43 2997,28 562,96 729,16 1283,34 628,34 811,37 349,95 11060,00 1809,88 11060,00 1809,88 11060,00 1809,88 11060,00 1809,88 11060,00 1809,88 11060,00 1809,88 11060,05 492,14 511,00 7272,16 688,21 688,21 688,21 688,21 688,21 688,21 688,21 688,21 688,21 688,21 688,21 688,21 688,21 710,62 776,98 1004,35 776,98 1006,23 619,61 346,65	58,87	50,44 57,51 24,86 49,25 56,36 41,89 45,82 29,48 27,14 42,20 47,69 36,71 25,72 21,83 41,83 20,52 42,49 29,40 2,85 20,52 42,49 29,20 39,38 11,98 19,50 80,98 35,48 8,45 16,53 26,27 31,54 12,03 7,45 26,27 31,54 12,03 7,45 26,27 31,54 12,03 7,45 26,27 31,54 12,03 7,45 26,27 31,54 12,03 7,45 26,27 31,54 12,03 7,45 26,27 31,54 12,03 7,45 26,27 35,10 35,	20 18 7 12 18 15 15 15 17 13 15 17 13 15 17 13 8 6 12 17 13 8 6 12 17 13 8 5 17 13 8 5 17 14 8 5 15 17 15 15 15 15 17 17 13 18 15 15 17 17 13 18 15 17 17 13 18 15 17 17 13 18 15 17 17 13 18 15 17 17 13 18 15 17 17 13 18 15 17 17 13 18 15 17 17 13 18 18 19 19 19 19 19 19 19 19 19 19	38,57982 38,68998 38,68998 38,68998 38,67982 38,68998 38,57982 38,68998 38,4998 38,5798 29,5542 32,72773 32,537113 52,537114 52,537115 52,	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,027 0,045 0,013 0,022 0,011 0,022 0,011 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,017 0,007 0,007 0,008 0,031 0,0071 0,008 0,003 0,008 0,003 0,0071 0,008 0,008 0,008 0,005 0,000	-3,3 -3,27 -3,27 -3,27 -3,27 -3,27 -3,28 -3,27 -2,28 -3,26 -2,25 -2,25 -2,25 -3,86 -1,9 -1,9 -1,9 -1,9 -1,43 -1,19 -1,9 -1,43 -1,19 -1,19 -2,20 -2,20 -2,20 -2,20 -2,20 -2,20 -1,19	0,029 0,018 0,0021 0,015 0,032 0,032 0,032 0,014 0,014 0,014 0,014 0,034 0,039	-2,72 -5,05 -5,75 -3,99 -2,6 -3,99 -2,75 -3,99 -2,6 -3,99 -2,6 -3,99 -2,6 -3,99 -2,6 -3,99 -2,6 -3,99 -2,75 -3,99 -2,6 -2,75 -3,99 -2,75 -3,99 -2,75 -2,75 -3,99 -2,75 -2,75 -3,99 -2,75 -2,75 -3,99 -2,75 -2	0,017 0,03 0,042 0,016	-1,56 -1,67 1,62 -1,85	0,013 0,022 0,015 0,032 0,024 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,018 0,0094 0,0059 0,023 0,013 0,0059 0,023 0,013 0,0059 0,023 0,013 0,004 0,012 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,014 0,013 0,014 0,013 0,014 0,013 0,014 0,013 0,014 0,013 0,014 0,013 0,013 0,014 0,013 0,013 0,013 0,013 0,013 0,013 0,013 0,013 0,013 0,013 0,013 0,013 0,013 0,014 0,013 0,013 0,013 0,013 0,013 0,013 0,014 0,014 0,014 0,014 0,014 0,014 0,000 0,013 0,000 0,013 0,000000	-2,39 -2,2 -2,36 -2,2,6 -2,2,6 -2,02 -3,22 -3,22 -3,24 -1,87 -2,97 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,24 -1,84 -1,59 -1,59 -1,51 1,79 -1,79	0,029	2,1	0,036
1374 1380 1381 1384 1384 1384 1384 1387 1389 1392 1393 1393 1393 1393 1393 1433 1433 1433 1433 1437 1457 1457 1457 1457 1457 1513 1523 1554 1555 1575 1577 1553 1555 1577 1577 1583 1601 1619 1620 1660 1686 1687 1692 1602 1602 1602 1602 1602 1602 1776 1777 1828 1828	P04083 P04083 P04063 P04064 P04083 P07355 P04083 P0	Amenin A1 Annexin A1 Glyceraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A2 Annexin A1 Annexin A2 Annexin A2 Annexin A3 Annexin A3 Annexin A1 Annexin A1 Annexin A1 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A4 Annexin A5 Annexin A5 Annexin A5 Annexin A5 Annexin A6 Annexin A6 Annexin A7 Annexin A7 Annexin A8 Annexin A8 Annexin A9 Annexin A9 Annexin A9 Annexin A1 Annexin A1 Annexin A2 Annexin A2 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A4 Annexin A5 Annexin A5 Annexin A2 Annexin A5 Annexin A2 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A3 Annexin A4 Annexin A5 Annexin A7 Annexin A7 Anne	ANXA2 ANXA1	3958,43 2987,28 562,96 729,16 1283,34 628,34 628,34 892,71 21054,62 811,37 349,95 1009,00 1809,38 1106,05 272,92 204,37 799,75 1653,11 1000,38 1106,05 272,92 204,37 799,75 1653,11 1000,38 492,14 1105,05 272,16 835,50 332,25 276,98 1000,36 448,82 724,11 100,36 448,83 72,41 1100,36 448,83 72,41 1100,36 448,82 72,51,68 1106,57 12551,68 1160,77 12551,68 1160,77 12551,68 1160,77 12551,29 325,29 346,62 170,11 242,91 243,83 464,51 170,11 243,83 1160,77 12551,29 325,29 341,47 325,52 12551,29 321,900	58,87	50,44 57,51 24,86 49,25 56,36 41,89 41,89 44,86 27,14 42,9,00 47,62 29,48 27,14 42,00 42,01 25,72 21,83 41,18 20,52 9,40 29,22 9,40 29,23 99,38 19,50 30,98 55,80 26,25 29,84 8,45 16,53 26,25 29,84 8,45 12,03 7,45 25,27 31,54 12,03 7,45 25,10 38,78 23,54 16,85 14,85 16,85 14,85 14,85 28,71	20 18 7 12 18 15 13 15 13 12 8 17 13 8 6 12 7 14 8 5 12 7 14 8 5 4 11 6 5 8 12 7 14 8 5 15 17 13 8 12 12 13 12 12 12 13 12 12 13 12 12 13 12 12 13 12 12 13 12 12 13 13 12 12 13 13 12 12 13 13 12 12 13 13 13 12 12 13 13 12 13 13 13 12 13 13 13 12 13 13 13 12 13 13 13 13 13 13 13 13 13 13	38,57982 38,68998 38,68998 38,68998 38,68998 38,57982 38,68998 38,6998 38,6998 38,5798 32,72773 32,00683 35,37113 35,24793 35,24998 35,27114 35,24993 35,27114 35,24993 35,27114 35,249	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,027 0,045 0,013 0,022 0,011 0,014 0,022 0,011 0,014 0,022 0,011 0,014 0,0072 0,017 0,0072 0,017 0,0072 0,017 0,0044 0,0042 0,0047 0,0050 0,0071 0,0044 0,0020 0,0047 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,0071 0,0050 0,00000000	-3,3 -3,27 -3,27 -3,78 -3,78 -3,78 -3,78 -3,78 -3,27 -2,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -3,28 -2,28 -2,21 -2,21 -2,21 -2,21 -1,99 -2,23 -2,21 -	0,029 0,018 0,0021 0,015 0,032 0,032 0,014 0,014 0,014	-2,72 -5,05 -5,75 -3,99 -2,6 	0,017 0,03 0,042	-1,56 -1,67 1,62	0,013 0,022 0,015 0,032 0,024 0,024 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,019 0,018 0,039 0,039 0,038 0,038 0,0059 0,023 0,013 0,013 0,015 0,003 0,00000000	-2,39 -2,2 -2,36 -2,26 -2,26 -2,27 -3,22 -3,22 -3,44 -1,72 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,52 -2,52 -2,52 -2,52 -2,52 -2,54 -2,24 -1,87 -2,27 -	0,029	2,1	0,036
1974 1974 1980 1981 1984 1984 1984 1984 1987 1993 1995 1975 1977 1983 1960 1660 1660 1666 1667 1699 1717 1717 1717 1717 1717 1717 1717 1776 1878	P04083 P04083 P0406 P0406 P0406 P04083 P07355 P04083 P0552 P04083 P0755 P04083 P0755 P04083 P0755 P04083 P0755 P	Amexin A1 Annexin A1 Annexin A1 Giveraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A2 Giyseraldehyde-3-phosphate dehydrogenase Annexin A1 Annexin A2 Annexin A1 Annexin A1 Annexin A2 Annexin A3 Annexin A3 Annexin A3 Annexin A1 Complement C4-A; gamma chain Retinal dehydrogenase 1 Complement C4-A; gamma chain Annexin A5 Retinal dehydrogenase 1 S-formylgiutathione hydrolase 14-3-8 protein epsilon Tropomyosin alpha-3 chain Tropomyosin alpha-4 chain Annexin A2 Actin, cytoplasmic 1 14-3-3 protein epsilon Chloride intracellular channel protein 1 Chloride intracellular channel protein 1 14-3-3 protein seta/delta 14-3-3 protein seta/delta	ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA2 ANXA1 ANXA2 ANXA2 ANXA2 ANXA2 ANXA2 ANXA2 ANXA2 ANXA1 ANXA2	9958,43 2987,28 562,96 729,16 1283,34 628,34 628,34 892,71 21054,62 811,37 1009,00 1809,38 11106,05 272,92 204,37 7799,75 204,37 799,75 1633,11 1000,35 272,92 204,37 799,75 1633,11 1000,38 1106,05 272,92 204,37 799,75 1633,11 1000,38 1106,05 272,92 204,37 799,75 1633,11 1000,38 1106,05 272,92 204,37 799,75 1633,11 1000,35 272,92 204,37 710,62 272,16 698,21 1153,95 272,98 1004,36 272,98 1004,36 272,98 1006,35 1006,35 1006,35 1006,37 1006,39 1106,59 1106,59 1106,59 1106,59 1106,59 1106,59 1106,59 1106,59 1106,59 1106,59 1106,59 1106,59 1106,59 1106,59 12551,68 1106,77 2551,68 1106,77 2551,68 1106,77 2551,58 1009,77 2551,58 1009,77 2551,58 1009,77 22551,58 1009,77 22551,58 1009,77 22551,58 1009,77 22551,58 1009,77 22551,58 1009,77 22551,58 1009,77 22551,58 1009,77 22551,58 1009,77 22551,58 1009,77 22551,58 1009,77 2259,29 244,40 161,74 2259,29 244,40 161,74 2259,29 244,40 161,74 2259,29 244,40 161,74 2259,29 245,40	58,87	50,44 57,51 24,86 49,25 55,36 41,89 46,82 74,28 29,48 42,00 47,69 25,72 21,83 42,00 47,69 25,72 21,83 42,00 47,69 25,72 21,83 42,00 47,69 25,72 21,83 42,10 25,72 21,83 42,12 25,72 21,83 43,18 20,52 25,27 39,38 11,98 29,38 11,95 20,52 29,84 29,84 29,84 29,84 29,84 29,84 29,84 29,84 20,55 20,57	20 18 7 12 18 15 15 15 17 12 8 15 17 17 18 8 6 12 7 14 8 5 4 11 16 5 8 4 11 16 5 8 7 7 14 8 5 8 7 7 14 8 8 7 7 14 8 8 7 7 14 8 8 7 7 14 8 8 12 7 15 15 15 15 15 15 15 15 15 15	38,57982 38,68998 38,68998 38,68998 38,57982 38,68998 38,57982 38,68998 39,68998 39,68998 39,77,7569 37,7773 32,06483 4,11,69 22,77849 32,07898 32,079898	7,75 7,02 8,46 7,02 7,75 7,02 7,75 7,02 7,75 7,02 7,02 7,02 7,02 7,02 7,02 7,02 7,02	0,01 0,014 0,006 0,027 0,045 0,013 0,022 0,011 0,011 0,011 0,011 0,012 0,022 0,017 0,025 0,0072 0,017 0,025 0,0072 0,017 0,025 0,0072 0,0047 0,0047 0,0047 0,004 0,003 0,0047 0,004 0,003 0,004 0,003 0,004 0,003 0,004 0,003 0,004 0,0024 0,003 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,0024 0,003 0,0024 0,003 0,0024 0,003 0,0024 0,003 0,004 0,003 0,004 0,003 0,004 0,005 0,004 0,005 0,004 0,005 0,004 0,005 0,007 0,004 0,005 0,004 0,005 0,004 0,005 0,004 0,005 0,007 0,004 0,005 0,007 0,004 0,005 0,007 0,004 0,005 0,007 0,00700000000	-3,3 -3,02 -3,27 -2,78 -3,78 -3,78 -2,28 -3,78 -2,22 -4,59 -2,22 -4,59 -2,22 -4,59 -2,23 -3,88 -3,88 -3,88 -3,88 -3,88 -3,38 -1,9 -1,9 -1,9 -1,9 -1,9 -1,9 -1,9 -1,9	0,029 0,018 0,0021 0,015 0,032 0,032 0,032 0,014 0,014 0,014	-2,72 -5,05 -5,75 -3,99 -2,6 	0,017 0,03 0,042 0,016	-1,56 -1,67 1,62 -1,85	0,013 0,022 0,015 0,032 0,024 0,024 0,012 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,012 0,019 0,019 0,019 0,019 0,019 0,019 0,018 0,038 0,038 0,038 0,0059 0,023 0,013 0,013 0,014 0,015 0,0005 0,015 0,00000000	-2,39 -2,2 -2,36 -2,26 -2,26 -2,27 -3,22 -3,24 -1,87 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,27 -2,24 -1,88 -1,59 -2,24 -1,87 -1,59 -2,24 -1,87 -1,59 -2,24 -1,59 -1,59 -1,59 -1,51 -1,72 -1,72 -1,72 -1,72 -1,72 -1,72 -1,72 -1,72 -2,25 -2,27 -	0,029	2,1	0,036

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1865	P04792	Heat shock protein beta-1	HSPB1	543,80		29,76	5	22,76849	6,40			0,037	1,85							
1868	P09211	Glutathione S-transferase P	GSTP1	1445,67		35,71	5	23,34102	5,64	0,016	-2,85					0,031	-1,99			
1874	Q06830	Peroxiredoxin-1	PRDX1	108,39		25,63	5	22,09628	8,13	0,036	-1,97									
	P13693	Translationally-controlled tumor protein	TCTP	83,17		15,70	2	19,58258	4,93											
1890 1892	Q9NP55 Q06830	BPI fold-containing family A member 1	BPIA1 PRDX1	150,04 468,34		21,09 55,78	4	26,69593	5,76			0,034	-1,96							
1892	Q06830 P13693	Peroxiredoxin-1	TCTP	468,34		24,42	10	22,09628 19,58258	8,13 4,93	0,036	-2,21	0.014	10	0.045		0.0014				
1908	P13693 Q06830	Translationally-controlled tumor protein Peroxiredoxin-1	PRDX1	123,90		67,34	4	22,09628	4,93	0,0022	-1,95 -3,46	0,011	-1,9	0,045	-1,59	0,0011	-1,8			
1914	P32119	Peroxiredoxin-1 Peroxiredoxin-2	PRDX1 PRDX2	560.07		32.32	8	21,87824	5.97	0,025	-3,46				-1,59	0,0021	-2			
1920	P30085	UMP-CMP kinase	KCY	556,65		53,06	8	22,20828	5,57	0,0027	-2,5					0,0021	-2			
1933	Q06830	Peroxiredoxin-1	PRDX1	3490,46		87,94	18	22,09628	8,13							<u> </u>		0,019	3,74	
1939	006830	Peroxiredoxin-1	PRDX1	98,63		13.07	3	22,09628	8,13	0,024	-3,6					0,04	-2,2	0,015	2,15	
1963	P30086	Phosphatidylethanolamine-binding protein 1	PEBP1	1586,33		50,27	8	21,04367	7,53	0.033	-2.18					0,01		0,010	2,25	
1971	P07741	Adenine phosphoribosyltransferase	APT	364,82		28,33	4	19,59543	6,02	0,048	-3,11									
1976	Q13938	Calcyphosin	CAYP1	364,21		35,45	7	20,95428	4,89	-/	-,	0,031	-2,09			0,045	-1,74			
1978	Q13938	Calcyphosin	CAYP1	1739,67		51,32	13	20,95428	4,89	0,029	-4,76	0,029	-5,15			0,014	-3,72			
1998	P06702	Protein S100-A9	\$10A9	1155,94		48,25	6	13,23351	6,13			0,049	-2,98							
	P05109	Protein S100-A8	\$10A8	952,00		58,06	8	10,8	6,1											
2013	P12273	Prolactin-inducible protein	PIP	506,38		47,95	6	16,5618	8,05											0,014
2032	P12273	Prolactin-inducible protein	PIP	306,84		66,44	10	16,5618	8,05			0,017	-4,34	0,029						
	P30626	Sorcin	SORCN	276,07		27,27	6	21,66236	5,59											
2036	P00738	Haptoglobin	HPT	177,13		6,16	2	(45.18)	6,58						-2,64			0,014	-2,91	
2037	P00738	Haptoglobin	HPT	334,72		6,90	4	(45.18)	6,58									0,04	-2,03	i – – – – – – –
2043	P15531	Nucleoside diphosphate kinase A	NDKA	1086,01		63,82	9	17,13767	6,19			0,029	-1,58				-			i – – I
2052	P00738	Haptoglobin	HPT HPT	285,01		7,39	6	(45.18)	6,58									0.000		
2052	P00738	Haptoglobin Thioredoxin	THIO	259,32		8,37 12.38	4	(45.18)	6,58 4 92			0.033	2.16					0,027	-2,48	
2064	P10599 P00441	Thioredoxin Superoxide dismutase [Cu-Zn]	SODC	114,96		12,38 9,09	1	11,72974	4,92			0,033	-2,16			0.012	-2.06			i
2076	P00441 P00441	Superoxide dismutase [Cu-2n] Superoxide dismutase [Cu-Zn]	SODC	101,62		27,92	4	15,9259	6,13			0,013	-2,63			0,012	-2,06			i — †
2078	P00441 P00441	Superoxide dismutase [Cu-Zn] Superoxide dismutase [Cu-Zn]	SODC	1869,73		9,09	4	15,9259	6,13	0,013	-1,98	0,027	-2,32			0,0053	-1,85			
2080	P23528	Cofilin-1	COF1	80.03		6,63	1	18,49066	8.09	0,013	-1,50	0,0008	-2,21			0,045	-2,14			+
2085	P23528	Cofilin-1	COF1	119,46		18,67	2	18,49066	8.09	0,012	-2.89					0,014	2,24			i – †
2087	P23528	Cofilin-1	COF1	329,14		35,54	8	18,49066	8,09	E_Hits, E_Isc	-,					0,023	-2,34			
2095	P37802	Transgelin-2	TAGL2	371,89		24,62	4	22,37717	8,25	0,0038	-3,16	0,042	-2,39			0,035	-1,93	0,00021	2,71	0,019
	P05090	Apolipoprotein D	APOD	405,37		21,16	4	21,26176	5,15							, i	,			
	P00441	Superoxide dismutase [Cu-Zn]	SODC	213,66		13,64	2	15,9259	6,13											
2098	P23528	Cofilin-1	COF1	121,84		27,11	3	18,49066	8,09	0,0035	-2,13	0,0054	-2,13			0,0064	-1,74			
2108	P00441	Superoxide dismutase [Cu-Zn]	SODC	37,74		23,38	1	15,9259	6,13			0,033	-1,61							$ \longrightarrow $
2113	P00441	Superoxide dismutase [Cu-Zn]	SODC	24,61		9,09	1	15,9259	6,13	0,0069	-1,6	0,0025	-1,71							0,039
2128	P00441	Superoxide dismutase [Cu-Zn]	SODC	44,21		9,09	1	15,9259	6,13											0,045
2155	P22392	Nucleoside diphosphate kinase B	NDKB	1035,06		48,68	8	17,28694	8,41	0,025	-2,26							0,046	1,78	
2164	P30044	Peroxiredoxin-5	PRDX5	332,87		37,38	7	22,07255	8,70	0,045	-2,01									i
2168	P12273 P30044	Prolactin-inducible protein Peroxiredoxin-5	PIP PRDX5	1447,58 346.33		66,44 36.92	9	16,5618	8,05 8,70	0,05	2,22					0,023	1,85			i
2173	P30044 P30044	Peroxiredoxin-5 Peroxiredoxin-5	PRDX5 PRDX5	556,23		36,92 37,85	7	22,07255	8,70	0,027	-2,85							0,038	2,07	
21/4	P50044 P62937	Peptidyl-prolyl cis-trans isomerase A	PRUX5	410,21		60,00	,	18,00089	7,81	0,013	-2,07					<u> </u>				
2185	P62937	Peptidyl-prolyl cis-trans isomerase A	PPIA	69,14		17,58	2	18,00089	7,81	0,021	-2,86					0,017	-2,23			i
2192	P63241	Eukaryotic translation initiation factor 5A-1	IF5A1	201.06		7.79	1	16.82141	5.24	0,011	-2,00					0,017	-2,20	0.018	3.57	i — †
2216	P63241	Eukaryotic translation initiation factor 5A-1	IF5A1	122,63		26,62	3	16,82141	5,24									0.035	3.7	
2279	P07355	Annexin A2	ANXA2	185.98		20.65	6	38.57982	7.75									0.0088	-2.39	
2282	Q01469	Fatty acid-binding protein 5	FABP5	648,31		37,78	7	15,15455	7,01					0,038	2,69			0,037	2,58	
2298	Q05315	Galectin 10 (Eosinophil lysophospholipase)	LEG10		31,30	4,23	1 (3)	16,44222	7,37	0,029	4,04							0,037	-3,53	
2303	P68871	Hemoglobin subunit beta	HBB	779,66		82,31	10	15,98829	7,28									0,0098	-5,34	
2314	P07737	Profilin-1	PROF1	1155,02		61,43	9	15,04456	8,27									0,016	-1,82	
2318	P06702	Protein S100-A9	\$10A9	29,64		11,40	1	13,23351	6,13									0,041	2,13	0,039
	Q01469	Fatty acid-binding protein 5	FABP5	26,53		14,81	2	15,15455	7,01											
2361	P68871	Hemoglobin subunit beta	HBB	296,82		40,14	5	15,98829	7,28							L	-	0,044	-5,64	⊢ →
	P01037	Cystatin-SN	CYTN	233,53		33,33	3	16,37734	7,21							I				i – – I
2362	P68871	Hemoglobin subunit beta	HBB	1402,12		82,99	10	15,98829	7,28			0.000		0,043	-2,27			0,021	-6,08	i – – – – –
2371 2387	P06702 P06702	Protein S100-A9 Protein S100-A9	\$10A9 \$10A9	230,90 1537,93		26,32 49,12	2	13,23351 13,23351	6,13 6,13			0,026	5,9	0,0016	5,26	0,017	4,47			i — – †
2387	P06702 P06702	Protein S100-A9 Protein S100-A9	\$10A9 \$10A9	1537,93 296.37		49,12	6	13,23351	6,13			0,047	7,11	0,00023	8,71	0,005	7,01			
2397	P06702 P06702	Protein S100-A9 Protein S100-A9	\$10A9 \$10A9	296,37		44,74	-4	13,23351	6,13					0,017	2,13 4,92	0,026	1,89			
2405	P06702	Protein S100-A9 Protein S100-A9	\$10A9 \$10A9	296,37		105,23	13	13,23351	6,13			0,0084	4,1	0,00018	4,92	0,023	4,27			
2411	P01040	Cystatin-A	CYTA	238,22		76,53	6	10,99966	5,50	0,015	2,2	0,0004	-1,2			0,0018	4,27			+
	P06702	Protein S100-A9	\$10A9	178,22		24,56	2	13,23351	6,13	0,010	-,-					0,020	-,/ +			
2437	P06702	Protein S100-A9	\$10A9	6190,53		71,05	14	13,23351	6,13					0,0097	2,14	0,033	1,88			$ \rightarrow $
2463	P06702	Protein S100-A9	\$10A9	33,48		11,40	1	13,23351	6,13									0,0098	-3,81	
2509	P05109	Protein S100-A8	\$10A8	1716		70	6	10,8	6,1	0,0075	2,43					0,011	1,96	0,015	-1,93	
2528	P02768	Serum albumin	ALBU	7890,68		70,94	46	69,3215	6,28									0,039	-1,8	
	P54652	Heat shock-related 70 kDa protein 2	HSP72	704,29		18,15	11	69,97787	5,74											
2532	P02768	Serum albumin	ALBU	9339,81		59,93	44	69,3215	6,28									0,021	-1,55	
	P02790	Hemopexin	HEMO	1229,12		34,42	16	51,64328	7,02											
		netry data was searched for protein identific				rograms runn	ing in Prot	eome Disco	overy. For	some of th	e gel spot	ts Mascot da	ta search o	did not pro	ide any	protein ide	entificatio	on, wherea	s Sequest	search pro
		e % is how much of the protein sequence w																		
		number of high confidence peptides identif																		
		(MW) is in parenthesis, when it is not the siz	e of the obs	onuod one on	the gol This c	an he due to c	loowage to		inc or prot	oolygig Eg	r immuno	globing Swi	reDrot date	abaco givor	only the	constant r		M lacking th	ao yariahl	

d) Molecular weight (MW) is in parenthesis, when it is not the size of the observed one on the gel. This can be due to cleavage to active chains or proteolysis. For immunoglobins SwissProt database gives only the constant region MW lacking the variable region. e) pl is the theoretical isoelectric point of the protein.

Table S3

t analysis of Top	5 functional categories of the identified 7	77 proteins	
Function	Function Annotation	p-value	Molecules
inflammation	inflammation of organ	6.90E-21	A2M, ACTB, ALB, ALDOA, ANXA1, ANXA3, ANXA5, APCS, APRT, C3, CAT, CFB, CFL1, CKB, GAPDH, GS
			IGKC, KLK7, LTF, PIP, PPIA, PRDX1, S100A8, SELENBP1, SERPINB1, SERPINB3, SFN, SOD1, TF, TGM3
cell movement	cell movement	6.63E-17	A2M, ACTB, ALB, ALDOA, ANXA1, ANXA2, ANXA3, ANXA5, APCS, C3, CAT, CFB, CFL1, GAPDH, HARS, H
			IDH1, IGHM, LTF, NME2, CFL1, GAPDH, HARS, HSPB1, IDH1, IGHM, LTF, NME2, PEBP1, PIGR, PPIA, PR
			S100A8, SELENBP1, SERPINA1, SERPINB1, SERPINB2, SERPINB3, SFN, SOD1, TPT1, WARS, YWHAE,
metabolism	metabolism of reactive oxygen species	3.08E-16	ACTB, ALB, ANXA1, APCS, C3, CAT, CFB, CLIC1, GSTP1, HSPB1, IDH1, LTF, PPIA,
			PRDX1, PRDX5, S100A8, SERPINA1, SOD1, TF, YWHAZ
cell death	cell death	1.39E-15	A2M, ACTB, ALB, ALDH1A1, ALDH3A1, ALDOA, ANXA1, ANXA2, ANXA5, APCS, APRT, C3, CAT, CFB, CFI
			GAPDH, GSS, GSTP1, HSPB1, IGHM, IGKC, LTF, NME2, PEBP1, PIGR, PIP, PPIA, PRDX1, PRDX5, S100A8
			SELENBP1, SERPINA1, SERPINB2, SERPINB3, SFN, SOD1, TF, TGM3, TPT1, TSTA3, YWHAE, YWHAZ
allergy	allergy	1.43E-15	ACTB, ALB, ALDOA, ANXA1, ANXA3, ANXA5, C3, CAT, CFL1, GAPDH, IGHM, KLK7, PPIA,
	0,		PRDX1, S100A8, SELENBP1, SERPINB3, TGM3
	Function inflammation cell movement metabolism cell death	Function Function Annotation inflammation inflammation of organ cell movement cell movement metabolism metabolism of reactive oxygen species cell death cell death	inflammation inflammation of organ 6.90E-21 cell movement cell movement 6.63E-17 metabolism metabolism of reactive oxygen species 3.08E-16 cell death cell death 1.39E-15

Table S4. Western blot analysis of nasal brush samples from 50 subjects who were excluded from proteomic analysis. The protein levels of Glutathione S-transferase 1 (GSTP1), Galectin 10 (LEG10), Protein S100-A9 (S10A9) and Calcyphosin (CAYP1) were assessed. Logarithmic transformation was used to attain normal distribution of the variables. The differences between the groups were analysed using the ANOVA and Fisher's LSD test for post hoc comparisons.

	po	st noc com	iparisons.									Control =
	Control , mean, median (Q ₁ -Q ₃) n= 19	Protein allerge n, mean, median (Q_1-Q_3) n= 21	lsocyan a te, mean, median (Q_1-Q_3) n=4	Weldin g, mean, median (Q ₁ -Q ₃) n=6	P- value ANO VA	P- value Contr ol vs Protei n allerg en	P- value Contr ol vs Isocy anate	P- value Contr ol vs Weldi ng	P- value Protei n allerg en vs Isocy anate	P- value Protei n allerg en vs Weldi ng	P- value Isocy anate vs Weldi ng	healthy persons; Protein= protein allergen group; Isocyanate= isocyanate group;
GSTP 1	289414 7, 170730 7 (30261 7- 392298 9)	156538 0, 970775 (18219 1- 211234 3)	445912 9, 350318 3 (10263 84- 884782 1)	304747 2, 528945 (13210 3- 484621 1)	0.72 8	NT	NT	NT	NT	NT	NT	Welding= welding group; Q ₁ -
LEG1 0	131978 , 48965 (33515- 111336)	234375 3, 432626 (15369 7- 202555 7)	108700 8, 511138 (20851 6- 254137 1)	225335 8, 381704 (38876- 447394 1)	0.00 1	<0.00 1	0.015	0.018	0.859	0.757	0.710	
S10A 9	518310 , 241829 (62877- 338919)	182793 2, 539315 (12710 4- 233302 4)	269198 8, 125442 1 (48019 7- 634134 7)	269613 9, 445668 (20230 2- 456006 2)	0.03 7	0.031	0.020	0.065	0.259	0.693	0.500	
CAYP 1	132029 34, 464328 5 (12303 31- 262818 78)	392414 3, 281068 7 (12114 75- 670278 7)	141750 95, 608024 1 (10847 16- 353603 27)	120813 20, 144542 8 (38333 3- 186223 23)	0.20 7	NT	NT	NT	NT	NT	NT	

Q₃=interquartile range; NT= not tested

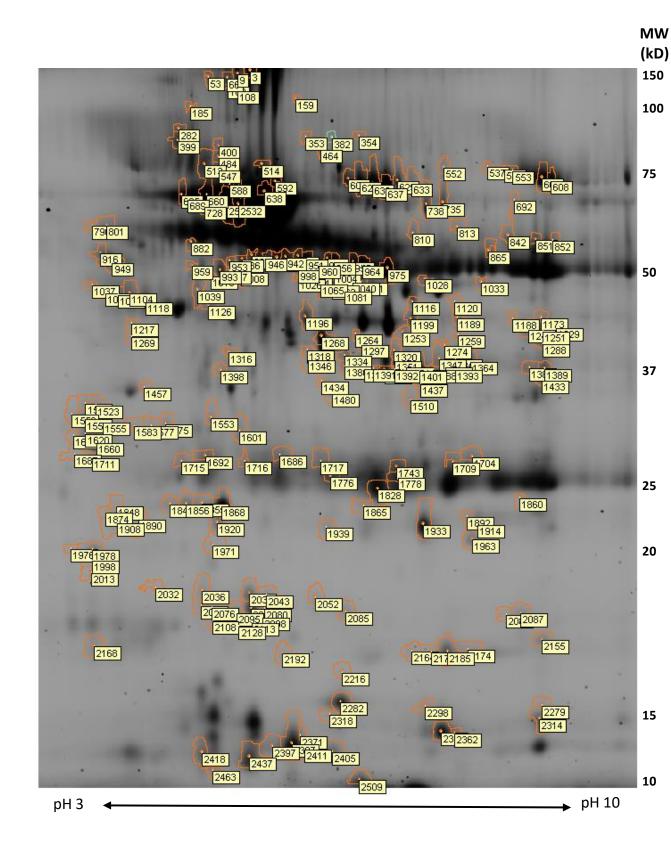


Figure S1 False colour two-dimensional differential gel electrophoresis (2D-DIGE) image of the identific protein spots in the nasal brush samples. Spot numbers are marked on the gel image and protein identifications are listed in Supplementary file Table S2 according to the spot number.

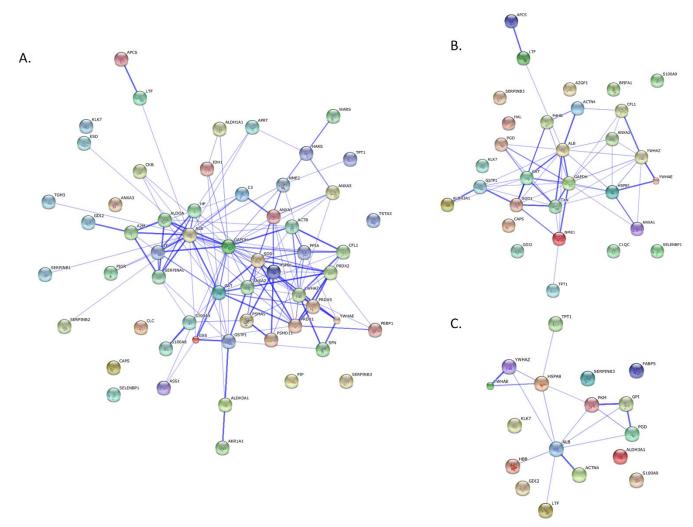


Figure S2 Protein association networks of the work-related asthma groups. Blue lines are confidence-based associations from the Stridatabase for the identified proteins (Table 2) in the protein allergen (A), isocyanate (B) and welding (C) groups. Stronger association presented as thicker lines. Minimum required interaction score was 0,4 and all available STRING data sources were applied in the se

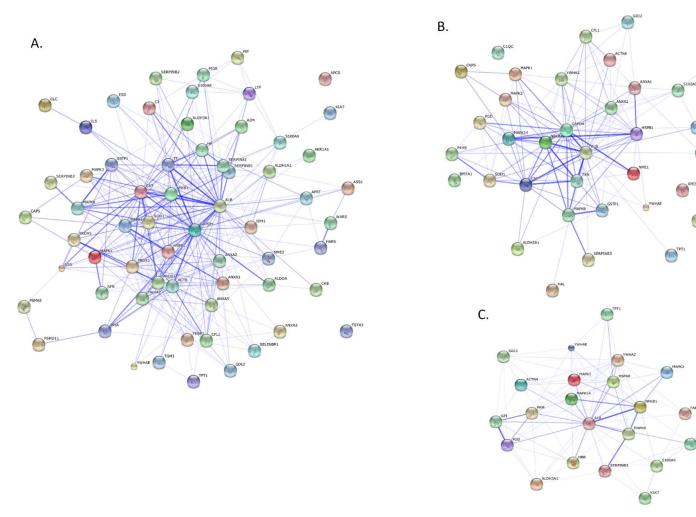


Figure S3 Protein association networks of the work-related asthma groups. Blue lines are confidence-based associations from the Strin database for the identified proteins (Table 2) in the protein allergen (A), isocyanate (B) and welding (C) groups. Stronger associations ar presented as thicker lines. Minimum required interaction score was 0,4 and all available STRING data sources were applied in the searc Mitogen-activated protein kinases (MAPK 1, 3, 8, 14), Nuclear factor kappa B (NFkB) and Interleukin-5 (IL-5) are included in the networ as they came up in individual protein network searches of the identified proteins and in IPA network searches (data not shown).

