Exploration of the shared gene signatures and molecular mechanisms between atherosclerosis and rheumatoid arthritis via multi-microarray data analyses

Hongjun You¹, Qianqian Zhao², Qiling Gou¹, Mengya Dong¹^

¹Department of Cardiovascular Medicine, Shaanxi Provincial People's Hospital, Xi'an, China; ²Department of Clinical Immunology, The First Affiliated Hospital, Air Force Military Medical University, Xi'an, China

Contributions: (I) Conception and design: H You, Q Zhao, Q Gou, M Dong; (II) Administrative support: Q Gou, M Dong; (III) Provision of study materials or patients: H You, Q Zhao, Q Gou; (IV) Collection and assembly of data: H You, Q Zhao, Q Gou; (V) Data analysis and interpretation: H You, Q Zhao, M Dong; (VI) Manuscript writing: All authors; (VII) Final approval of manuscript: All authors.

Correspondence to: Mengya Dong. Department of Cardiovascular Medicine, Shaanxi Provincial People's Hospital, Xi'an, China. Email: 405895903@qq.com.

Background: Accumulating evidence indicates the inflammatory state of rheumatoid arthritis (RA) predisposes to the acceleration of atherosclerosis (AS). Nevertheless, the potential mechanisms of accelerating AS in RA have not been fully elucidated. Our current study was to probe the problem via multimicroarray data analyses.

Methods: The transcriptional profiling of synovial tissues from RA (GSE55235 and GSE55457) and that of atherosclerotic plaques from AS (GSE28829 and GSE41571) were downloaded from the Gene Expression Omnibus database. Bioinformatics analyses procedures included identifying common differentially expressed genes (DEGs), constructing protein-protein interaction network, key modules analysis and identifying hub genes, validating hub genes by using external datasets (GSE77298 and GSE163154), Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses, constructing transcription factor (TF)-miRNA coregulatory network and exploiting candidate drugs targeting hub genes.

Results: A total of 67 common DEGs were identified for downstream analyses. GO and KEGG analyses of these genes expounded a critical role of inflammatory mediators and reactions in the comorbidities. Sixteen hub genes were identified, and their functional analyses further highlighted a complicated inflammatory micro-environment and signaling pathways involving RA and AS. Six TFs and four miRNAs interacted with hub genes, and the candidate drugs targeting them were simvastatin, 5-azacytidine, bisindolylmaleimide, retinoic acid, and verteporfin, etc.

Conclusions: Our comprehensive bioinformatics analyses provided a novel view regarding the potential pathogenesis of AS in RA. Furthermore, exploitation of candidate drugs might hold great promise in the future fight against the comorbidities.

Keywords: Rheumatoid arthritis (RA); atherosclerosis (AS); pathogenesis; bioinformatics

Submitted Sep 14, 2022. Accepted for publication Oct 25, 2022. doi: 10.21037/atm-22-4934 View this article at: https://dx.doi.org/10.21037/atm-22-4934

^ ORCID: 0000-0001-6453-6822.

Page 2 of 17

Introduction

Atherosclerosis (AS) is recognized as a slow, aggressive nonbacterial inflammatory disorder within the arterial wall, involving endothelial dysfunction, vascular smooth muscle cells, macrophage migration, phenotypic transformation, lipid deposit, plaque rupture, and consequential acute ischemic vascular events. Rheumatoid arthritis (RA) is a chronic systemic autoimmune inflammatory disease which contributes an augmented risk of cardiovascular diseases (CVD), including myocardial infarction and stroke (1), and represents a tremendous socioeconomic burden worldwide. Accumulating evidence indicates the RA inflammatory state predisposes to the acceleration of AS (2,3). Not only are shared their risk factors between RA and AS, such as smoking, diabetes mellitus, obesity, and genetic risk factors, the two disorders share many overlapping immune environmental factors, including inflammatory cytokines/chemokines, and local and systemic immune reactions involved signaling pathways. Multi-aspects of the pathophysiological process of AS can be mirrored in diseased RA synovium, including distinct immune cell infiltration, extracellular matrix remodeling, and neovascularization. Nevertheless, the potential mechanisms of accelerating AS in RA have not been fully elucidated.

The small sample size and lack of clinical significance of previous studies produced the present study. In this study, a comprehensive bioinformatics analysis was implemented to probe the underlying relevance of the pathogenesis of RA complicated with AS. Firstly, we integrated transcriptional profiling of synovial tissues from both RA and atherosclerotic plaques from AS, and identified their common differentially expressed genes (DEGs) and hub genes. Secondly, we probed their function and involved molecular mechanisms to investigate whether and how RA plays a causative role in AS progression. Finally, exploitation of candidate drugs targeting hub genes was conducted, which may hold great promise in the future fight against the comorbidities. To our knowledge, few comprehensive analyses of RA and AS via multi-microarray data analyses have been reported. We present the following article in accordance with the STREGA reporting checklist (available at https://atm.amegroups.com/article/view/10.21037/atm-22-4934/rc).

Methods

Datasets collection

The GSE55235 and GSE55457 datasets expound the transcriptional profiling of synovial tissues in patients with RA compared with healthy individuals, and the GSE28829 and GSE41571 datasets elucidate the specifical transcriptional signatures of advanced atherosclerotic plaques compared with early AS. The mRNA expression of hub genes subsequently identified were verified in the GSE77298 and GSE163154 datasets, respectively. The flowchart for the current research is shown in Figure 1. All datasets were extracted from the GEO database of the National Center for Biotechnology Information platform (https://www.ncbi.nlm.nih.gov/geo) (4,5), and information on the platform, sample, source tissue, contributors, and attributions for the six datasets is listed in Table 1. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013).

Identification of DEGs and common DEGs between RA and AS

The original files (cel format) downloaded from the GEO database were pre-processed and normalized by the Robust Multiarray Average (RMA) method based on the R software (version 3.6.3) Affy package (6). Probe sets with no corresponding gene symbol or genes with more than one probe set were removed or averaged, respectively, and the ComBat function of the SVA package in R was used to remove the batch effect. After background correction, quality control, standardization, and ID transformation from probes to gene symbols, we used GEO2R to identify the DEGs between the different groups by comparing their gene expression profile. GEO2R (7) (https://www.ncbi.nlm. nih.gov/geo/ge2r) is a web-accessible analysis tool based on two R packages, namely GEOquery (8) and limma (9), the former to read data, and the latter to calculate the differential expression multiple. The cut-off criteria for statistical significance to identify DEGs was set as adjusted P value <0.05 and |logfold change (FC)|≥1. The DEGs were fully visualized in a volcano plot and partially in a heat map using the R package 'ggplot2' (https://cran.r-project.



Figure 1 Flowchart for the current study. The DEGs for GSE55235 and GSE55457 datasets of RA and GSE28829 and GSE41571 datasets of AS were identified using the GEO2R, respectively. Common DEGs of the two diseases were obtained via the 'VennDiagram'. GO and KEGG analyses were conducted for all common DEGs by the R programming language. From all common DEGs, a PPI network was created, and key modules and candidate hub genes were screened, followed by validation of hub genes in the external datasets GSE77298 (RA) and GSE163154 (AS). Following this, hub genes enrichment analysis using R, TF-miRNA coregulatory network analysis by NetworkAnalyst and candidate drugs identification via DSigDB were conducted. RA, rheumatoid arthritis; AS, atherosclerosis; DEGs, differentially expressed genes; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; PPI, protein-protein interaction; MCC, maximum correlation criterion; TF, transcription factor.

Table T information for selected introarialy datasets									
GEO accession	Platform	Samples [number]	Source tissue	Contributors	Attribute				
GSE55235	GPL96	Rheumatoid arthritis [10]; healthy control [10]	Human synovium	Woetzel D, Huber R, Kupfer P, <i>et al.</i>	Test set				
GSE55457	GPL96	Rheumatoid arthritis [13]; healthy control [10]	Human synovium	Woetzel D, Huber R, Kupfer P, <i>et al.</i>	Test set				
GSE28829	GPL570	Advanced atherosclerotic plaque [16]; early atherosclerotic plaque [13]	Human carotid atheroma	Manca M, Biessen E, Daemen M	Test set				
GSE41571	GPL570	Unstable atheromatous lesions [ruptured, 5]; stable atheromatous lesions [unruptured, 6]	Human carotid atheroma	Lee K, Santibanez-Koref M, Polvikoski T, <i>et al.</i>	Test set				
GSE77298	GPL570	Rheumatoid arthritis [16]; healthy control [7]	Human synovium	Broeren MG	Validation set				
GSE163154	GPL6104	High-risk atherosclerotic lesion [intraplaque haemorrhage, 27]; low-risk atherosclerotic lesion [non-intraplaque haemorrhage, 16]	Human carotid atheroma	Jin H, Biessen E	Validation set				

Table 1 Information for selected microarray datasets

GPL96, (HG-U133A) Affymetrix Human Genome U133A Array; GPL570, (HG-U133_Plus_2) Affymetrix Human Genome U133 Plus 2.0 Array; GPL6104, Illumina humanRef-8 v2.0 expression beadchip.

Page 4 of 17

org/web/packages/ggplot2/) and 'complexHeatmap' (10), respectively. The identification of common DEGs between RA and AS was acquired by the R programming language and visualized through the 'VennDiagram' (https://cran. r-project.org/web/packages/VennDiagram/).

Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses

GO (11,12) and KEGG (13,14) pathway enrichment analyses of common DEGs or hub genes were performed by the R package 'clusterProfiler' (http://www.bioconductor. org/packages/release/bioc/html/clusterProfiler.html) (15). The enrichment analysis results of GO categories included biological process (BP), cellular component (CC), and molecular function (MF) (16). To illustrate and understand the metabolic or signaling pathways which the DEGs might be involved in, KEGG pathway enrichment analysis was simultaneously implemented, and the significance threshold was adjusted P value <0.05.

Protein-protein interactions (PPI) network and key module construction

PPI networks can provide abundant information on the functional interactions between proteins in cellular biology studies (17,18). The common DEGs were input into Search Tool for the Retrieval of Interacting Genes (STRING) (https://string-db.org/) online for creating a PPI network (19). STRING transmits experimental and predictive interaction-founded information and the interaction defined with 3-dimensional structures, auxiliary biomedical information, and confidence score (20). The confidence score in the current study was set as 0.400, a middle value utilizing the STRING platform. Subsequently, the acquired PPIs network was reimported into Cytoscape for further analysis (https://cytoscape.org/) (21,22), and Cytoscape's plug-in molecular complex detection technology (MCODE) was applied to probe key functional modules. The selection criteria weres set as: K-core =2, degree cutoff =2, max depth =100, and node score cutoff =0.2.

Candidate bub gene identification

The Cytoscape software plugin cytoHubba uses multiple scoring methods to dissect the PPIs network. The top 20 genes chosen by the topological algorithm of maximum correlation criterion (MCC) were overlapped with genes in

You et al. Molecular link of atherosclerosis and rheumatoid arthritis

the key modules, and the overlapped genes were identified as candidate hub genes.

Validation of bub gene expression in external datasets and enrichment analyses

The mRNA expression level of candidate hub genes was verified in the GSE77298 and GSE163154 datasets, respectively. The GSE77298 dataset included 16 RA and seven healthy controls, while the GSE163154 dataset contained 27 high-risk atherosclerotic lesion (intraplaque haemorrhage) and 16 low-risk atherosclerotic lesion (nonintraplaque haemorrhage), which indicated the different stages of AS progression. Student's t-test was used for group comparisons of continuous variables distributed normally, while the Mann-Whitney U-test was used for variables with an abnormal distribution. The significance threshold was P value <0.05. The aforementioned candidate hub genes that were simultaneously differentially expressed in the GSE77298 and GSE163154 datasets were confirmed as hub genes. Thereafter the GO and KEGG pathway analyses of confirmed hub genes were executed via R package 'clusterProfiler'.

Transcription factor (TF)-miRNA coregulatory network

The reciprocity of TFs and miRNAs with the hub genes may play a vital role in regulating the expression of hub genes. The TF-miRNA coregulatory network for hub genes was established using NetworkAnalyst (https://www. networkanalyst.ca/), a powerful online-based platform for comprehensive analyses, systematic interpretation, and deciphering of gene expression (23,24) and RegNetwork repository, a synthetical database of transcriptional and post-transcriptional regulating networks (25).

Identification of candidate drugs

The identification of candidate drugs for treating RA combined with AS focused on the aforementioned confirmed hub genes. The user-friendly web-based enrichment analysis platform Enrichr (26) furnishes free access to the Drug Signatures database (DSigDB, http://biotechlab.fudan.edu.cn/database/drugsig/). DSigDB (27) is an absolute drug response gene signature database assembling drug response microarray data and annotated drug and target information derived from public databases and scientific documentation and was established by singling

out the top 500 upregulated and downregulated genes as drug signatures. Current DrugSig includes more than 1,300 drugs, 7,000 microarrays, and 800 targets, enabling computational drug repositioning to exploit neoteric drugs that may target hub genes. The cut-off criterion was P-adjusted <0.05.

Results

Identification of DEGs

Following standardization there was a fundamentally same average gene expression value for each sample, and the differences between groups were examined with principal component analysis (PCA), indicating the sample data were credible. The data pre-processing is presented in Figure S1. After comprehensive analysis of RA-related datasets GSE55235 and GSE55457, 418 DEGs were upregulated and 268 were downregulated, while for the AS-related datasets GSE28829 and GSE41571, 162 DEGs were upregulated and 79 downregulated. The expression profiling for the two diseases is visualized in a volcano plot (Figure 2A,2B), respectively, and that of the top 20 genes with high and low expression level is visualized in a heat map (Figure 2C,2D), respectively. As shown in Figure 2E, following overlap of these DEGs there were 63 common upregulated and four common downregulated DEGs between RA and AS.

GO and KEGG pathway enrichment analyses of common DEGs

GO and KEGG pathway enrichment analyses were conducted to probe the biological functions and pathways involved in RA and AS of the 67 common DEGs, and the top 10 terms of each category (BP, CC and MF) are visualized in the bubble diagram (Figure 3A). KEGG analysis is shown in Figure 3B, and GO and KEGG analyses information are presented in Table S1 in detail. The BP subset indicated common DEGs were highly enhanced in leukocyte migration, regulation of lymphocyte activation, neutrophil activation, and phagocytosis, and the CC subsection mainly manifested external side of plasma membrane, tertiary granule, secretory granule membrane, and endocytic vesicle membrane. The MF part expounded antigen binding, MHC class II protein complex, and immunoglobulin receptor binding and chemokine activity. KEGG pathway enrichment analyses showed common

DEGs were significantly involved in phagosome, viral myocarditis, tuberculosis, intestinal immune network for IgA production, hematopoietic cell lineage, cell adhesion molecules, rheumatoid arthritis, leukocyte transendothelial migration, the chemokine signaling pathway, the NF- κ B signaling pathway, the Toll-like receptor signaling pathway, apoptosis, and Th1 and Th2 cell differentiation.

PPI network and key module construction

A PPI network was established for further analysis including module analysis, hub genes identification, and TF-miRNA coregulatory network construction, and the network contained 52 nodes and 229 edges. To probe key functional modules, MCODE was applied, and two modules were generated (*Figure 4A*). Detail information is listed in Table S2.

Candidate bub gene identification

CytoHubba was applied, and the top 20 genes based on MCC scoring are shown and highlighted in a sub-network with 46 nodes and 220 edges (*Figure 4B*). To obtain candidate hub genes, the 20 genes were overlapped with those in the key modules. The overlapped genes were identified as candidate hub genes, namely *PTPRC*, *ITGB2*, *CD86*, *CSF1R*, *CTSS*, *TLR8*, *CD14*, *MMP9*, *S100A9*, *CD48*, *FCGR2B*, *CSF2RB*, *LCP1*, *DOCK2*, *RAC2*, *EVI2B*, *CD52*, *HLA-DRA*, *CD300A*, and *NCKAP1L*, and the details are presented in *Table 2*.

Validation of bub gene expression in external datasets and enrichment analyses

The mRNA expression level of 20 hub genes were verified in the RA-related dataset GSE77298 and AS-related dataset GSE163154, respectively. Compared with normal synovial tissues, most hub genes were significantly upregulated in the synovium of RA except for four genes, namely *CTSS*, *CD14*, *CD48*, and *FCGR2B* (*Figure 5*). Although the four genes had an ascending tendency in RA, they were excluded from hub genes. Similarly, the expression of all hub genes in high-risk atherosclerotic lesions with intraplaque haemorrhage was also higher than in low-risk atherosclerotic lesions without intraplaque haemorrhage (*Figure 6*). Accordingly, 16 hub genes were confirmed and subject to further analysis. GO enrichment analyses illustrated hub genes were significantly Page 6 of 17

You et al. Molecular link of atherosclerosis and rheumatoid arthritis



Figure 2 Identification of the DEGs for RA and AS respectively and the common DEGs for them. (A) Volcano plot of the distributions of all DEGs for GSE55235 and GSE55457 of RA compared with healthy controls, mapping 418 upregulated genes (red dots) and 268 downregulated genes (blue dots) and genes without significant changes (grey dots). |Log₂FC|>1 and P-adjusted <0.05 were the cut-off criteria. (B) Volcano plot of the distributions of all DEGs for GSE28829 and GSE41571 of AAP compared with EAP, mapping 162 upregulated genes (red dots) and 79 downregulated genes (blue dots) and genes without significant changes (grey dots). |Log₂FC|>1 and P-adjusted <0.05 were the cut-off criteria. (C) Heat map of the top 40 DEGs in RA and healthy controls. (D) Heat map of the top 40 DEGs in AAP and EAP. (E) Venn diagram. The four datasets for the two diseases showed an overlap of 67 common DEGs; 63 upregulated and four downregulated. HC, healthy controls; RA, rheumatoid arthritis; AAP, advanced atherosclerotic plaque; EAP, early atherosclerotic plaque; AS, atherosclerosis; DEGs, differentially expressed genes; FC, fold change.

Page 7 of 17



Figure 3 Enrichment analysis of the common DEGs. (A) Partial visualization of GO enrichment analysis for all common DEGs; (B) partial visualization of KEGG pathway enrichment analysis for all common DEGs. BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes; DEGs, differentially expressed genes; GO, Gene Ontology.



Figure 4 Key modules and genes identification. (A) Identification of key modules with DEGs. (B) Identification of candidate hub genes from the PPI network of common differentially expressed genes. The top 20 genes ranked by their topological MCC value were highlighted and identified as candidate hub genes, namely *PTPRC*, *ITGB2*, *CD86*, *CSF1R*, *CTSS*, *TLR8*, *CD14*, *MMP9*, *S100A9*, *CD48*, *FCGR2B*, *CSF2RB*, *LCP1*, *DOCK2*, *RAC2*, *EVI2B*, *CD52*, *HLA-DRA*, *CD300A*, and *NCKAP1L*. The network has 46 nodes and 220 edges. DEGs, differentially expressed genes; PPI, protein-protein interaction; MCC, maximum correlation criterion.

Page 8 of 17

Table 2 Details of the 20 candidate hub ge	nes
--	-----

No.	Gene symbol	Full name of protein	Main function
1	PTPRC	Receptor-type tyrosine-protein phosphatase C	Protein tyrosine-protein phosphatase required for T-cell activation through the antigen receptor; acts as a positive regulator of T-cell coactivation upon binding to DPP4
2	ITGB2	Integrin beta-2	Integrin ITGAL/ITGB2 is a receptor for ICAMs and the secreted form of ubiquitin-like protein ISG15; the interaction is mediated by ITGA; receptors for the iC3b fragment of the third complement component and for fibrinogen; integrin ITGAX/ITGB2 recognizes the sequence G-P-R in fibrinogen alpha-chain; integrin ITGAD/ITGB2 is a receptor for ICAM3 and VCAM1, contributes to natural killer cell cytotoxicity; involved in leukocyte adhesion and transmigration of leukocytes; integrin ITGAL/ITGB2 in association with ICAM3 contributes to apoptotic neutrophil phagocytosis by macrophages
3	CD86	T-lymphocyte activation antigen CD86	Receptor involved in the costimulatory signal essential for T-lymphocyte proliferation and interleukin-2 production; plays a critical role in the early events of T-cell activation and costimulation of naive T-cells; involved in the regulation of B cells function and plays a role in regulating the level of IgG1 produced; upon CD40 engagement, activates NF-kappa-B signaling pathway via phospholipase C and protein kinase C activation
4	CSF1R	Macrophage colony- stimulating factor 1 receptor	Tyrosine-protein kinase that acts as cell-surface receptor for CSF1 and IL34 and plays an essential role in the regulation of survival, proliferation, and differentiation of hematopoietic precursor cells, especially mononuclear phagocytes, such as macrophages and monocytes; promotes the release of proinflammatory chemokines in response to IL34 and CSF1 in innate immunity; promotes reorganization of the actin cytoskeleton, regulates formation of membrane ruffles, cell adhesion, and cell migration, and promotes cancer cell invasion; activates several signaling pathways in response to ligand binding, including the ERK1/2 and the JNK pathway
5	CTSS	Cathepsin S	Thiol protease, key protease responsible for the removal of the invariant chain from MHC class II molecules and MHC class II antigen presentation; the bond-specificity of this proteinase is in part similar to the specificities of cathepsin L
6	TLR8	Toll-like receptor 8	Endosomal receptor that plays a key role in innate and adaptive immunity; controls host immune response against pathogens through recognition of RNA degradation products specific to microorganisms; recognizes GU-rich single-stranded RNA derived from SARS-CoV-2, SARS-CoV-1, and HIV-1 viruses; upon binding to agonists, undergoes dimerization that brings TIR domains from the two molecules into direct contact, leading to the recruitment of TIR-containing downstream adapter MYD88 through homotypic interaction; in turn, the Myddosome signaling complex is formed involving IRAK4, IRAK1, TRAF6, and TRAF3 leading to activation of downstream transcription factors NF-kappa-B and IRF7 to induce proinflammatory cytokines and interferons, respectively
7	CD14	Monocyte differentiation antigen CD14	Coreceptor for bacterial lipopolysaccharide; mediates the innate immune response to bacterial lipopolysaccharide; acts via MyD88, TIRAP, and TRAF6, leading to NF-kappa-B activation, cytokine secretion, and the inflammatory response; binds electronegative LDL and mediates the cytokine release
8	MMP9	Matrix metalloproteinase-9	Matrix metalloproteinase that plays an essential role in local proteolysis of the extracellular matrix and in leukocyte migration; cleaves type IV and type V collagen into large C-terminal three quarter fragments and shorter N-terminal one quarter fragments; degrades fibronectin
9	S100A9	Protein S100-A9	Regulates neutrophil number and apoptosis by an anti-apoptotic effect; regulates cell survival via ITGAM/ITGB and TLR4 and a signaling mechanism involving MEK-ERK
10	CD48	CD48 antigen	Ligand for CD2; might facilitate interaction between activated lymphocytes; probably involved in regulating T-cell activation

Table 2 (continued)

Tabl	e 2	(continued)
------	-----	-------------

No.	Gene symbol	Full name of protein	Main function
11	FCGR2B	Low affinity immunoglobulin gamma Fc region receptor II-b	Receptor for the Fc region of complexed or aggregated gamma immunoglobulins; involved in a variety of effector and regulatory functions such as phagocytosis of immune complexes and modulation of antibody production by B-cells; binds to this receptor results in down-modulation of previous state of cell activation triggered via antigen receptors on B-cells (BCR), T-cells (TCR), or via another Fc receptor
12	CSF2RB	Cytokine receptor common subunit beta	High affinity receptor for interleukin-3, interleukin-5, and granulocyte-macrophage colony- stimulating factor
13	LCP1	Plastin-2	Actin-binding protein; plays a role in the activation of T-cells in response to costimulation through TCR/CD3 and CD2 or CD28; modulates the cell surface expression of IL2RA/CD25 and CD69
14	DOCK2	Dedicator of cytokinesis protein 2	Involved in cytoskeletal rearrangements required for lymphocyte migration in response to chemokines; activates RAC1 and RAC2 by functioning as a guanine nucleotide exchange factor; participates in IL2 transcriptional activation via the activation of RAC2
15	RAC2	Ras-related C3 botulinum toxin substrate 2	Plasma membrane-associated small GTPase which cycles between an active GTP-bound and inactive GDP-bound state; in the active state binds to a variety of effector proteins to regulate cellular responses, such as secretory processes, phagocytose of apoptotic cells, and epithelial cell polarization; augments the production of ROS by NADPH oxidase
16	EVI2B	Protein EVI2B	Required for granulocyte differentiation and functionality of hematopoietic progenitor cells through the control of cell cycle progression and survival of hematopoietic progenitor cells
17	CD52	CAMPATH-1 antigen	May play a role in carrying and orienting carbohydrate, as well as having a more specific role.
18	HLA-DRA	HLA class II histocompatibility antigen, DR alpha chain	An alpha chain of antigen-presenting MHC II molecule; in complex with the beta chain HLA-DRB, displays antigenic peptides on professional APCs for recognition by TCR on HLA-DR-restricted CD4-positive T cells; guides antigen-specific T-helper effector functions; presents peptides derived from intracellular proteins that are trapped in autolysosomes after macroautophagy
19	CD300A	CMRF35-like molecule 8	Inhibitory receptor which may contribute to the downregulation of cytolytic activity in natural killer cells, and to the downregulation of mast cell degranulation; negatively regulates the TLR signaling mediated by MYD88 but not TRIF through activation of PTPN6
20	NCKAP1L	Nck-associated protein 1-like	Essential hematopoietic-specific regulator of the actin cytoskeleton; controls lymphocyte development, activation, proliferation, and homeostasis, erythrocyte membrane stability, as well as phagocytosis and migration by neutrophils and macrophages; required for efficient T-lymphocyte and neutrophil migration; involved in mechanisms WAVE-independent to regulate myosin and actin polymerization during neutrophil chemotaxis

LDL, low-density lipoprotein; GTP, guanosine triphosphate; GDP, guanosine diphosphate; ROS, reactive oxygen species; NADPH, nicotinamide adenine dinucleotide phosphate; APCs, antigen-presenting cells.

involved in leukocyte proliferation, leukocyte cell-cell adhesion, T cell activation, secretory granule membrane, external side of plasma membrane, focal adhesion, Rac GTPase binding, integrin binding, and MHC class II receptor activity, while KEGG pathway enrichment analysis revealed hub gens were significantly involved in viral myocarditis, cell adhesion molecules, rheumatoid arthritis, leukocyte transendothelial migration, the Rap1 signaling pathway, regulation of actin cytoskeleton, IL-17 signaling pathway, Fc gamma R-mediated phagocytosis, and the Tolllike receptor signaling pathway. GO and KEGG analyses outcomes are partially visualized in a bubble diagram (*Figure 7A*,7*B*), and Table S3 displays the analyses in detail.

TF-miRNA coregulatory network

The TF-miRNA coregulatory network is shown in *Figure 8*, constituting 176 nodes (15 hub genes included) and 214



Figure 5 Expression level validation of candidate hub genes in RA. Validation of the expression level of 20 candidate hub genes in the external dataset GSE77298 (RA compared with healthy controls). *P<0.05; **P<0.01; ***P<0.001; ns, no significance. HC, healthy controls; RA, rheumatoid arthritis.



Figure 6 Expression level validation of candidate hub genes in AS. Validation of the expression level of 20 candidate hub genes in the external dataset GSE163154 (high-risk atherosclerotic lesion with intraplaque haemorrhage compared with low-risk atherosclerotic lesion with non-intraplaque haemorrhage). *P<0.05; **P<0.01; ***P<0.001. IPH, intraplaque haemorrhage; AS, atherosclerosis.

edges and includes abundant interactions between TFs, miRNAs, and hub genes. TFs, namely *SPI1*, *MYC*, *JUN*, *TFAP2A*, *SP1*, and *CTCF* interacted with 11, 5, 4, 4, 4, and 4 hub genes, respectively. Hsa-miR-204, hsa-miR-377, hsa-miR-493, and hsa-miR-525-5p respectively interacted with two hub genes simultaneously.

Identification of candidate drugs

Candidate drugs are depicted in *Table 3*, namely simvastatin, 5-azacytidine, bisindolylmaleimide, retinoic acid, and verteporfin.

Discussion

A growing body of research has demonstrated inflammation

builds a bridge between RA and AS. However, the underlying mechanisms of the pathogenesis of AS in RA patients remains unclear. In the present study, we analyzed several microarray data by a series of bioinformatics methods and attempted to comprehensively demonstrate the pathogenesis involved and provide new therapeutic targets for AS in RA.

Firstly, we identified 67 common DEGs between RA and AS and explored biological functions of these genes through GO and KEGG pathway enrichment analyses. The GO analysis results were concentrated at inflammatory cells-mediated inflammatory immune responses, which indicated inflammation played an essential role in the initial period of AS in RA. RA is recognized as a chronic autoimmune disease characterized by progressive systemic inflammation. Various immune cells are involved in the

Page 11 of 17



Figure 7 Enrichment analysis of hub genes. (A) Partial visualization of GO enrichment analysis for hub genes; (B) partial visualization of KEGG pathway enrichment analysis for hub genes. BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes; GO, Gene Ontology.



Figure 8 The TF-miRNA coregulatory network. The network constitutes of 176 nodes and 214 edges, including 15 hub genes. The nodes in red or orange are the hub genes, a blue node represents a miRNA, and green nodes indicate TF genes. TF, transcription factor.

Page 12 of 17

Term	P value	Adjusted P value	Genes
Simvastatin CTD 00007319	8.27E-08	7.00E-05	CD86; ITGB2; RAC2; HLA-DRA; MMP9; S100A9
5-azacytidine CTD 00005455	6.11E-06	0.00103537	PTPRC; ITGB2; HLA-DRA; MMP9; S100A9
BisindolyImaleimide i CTD 00002749	1.62E-05	0.001501768	CD86; ITGB2; MMP9
Retinoic acid CTD 00006918	5.99E-05	0.003227657	CD86; CSF1R; CD52; PTPRC; CD300A; ITGB2; RAC2; HLA-DRA; EVI2B; MMP9; S100A9
Verteporfin HL60 DOWN	6.25E-05	0.003227657	PTPRC; CD300A; ITGB2; CSF2RB

Table 3 Screening of candidate drugs targeting hub genes

pathomechanism of RA, such as DCs, T cells, B cells, and macrophages, through releasing pro-inflammatory cytokines, secreting autoantibodies, and triggering the complement cascade, which promotes the establishment and maintenance of an inflammatory state (28). Coincidentally, these immune cells and inflammatory processes also take part in the pathogenesis of AS (29,30). This evidence lends support to the hypothesis that auto immune and inflammation result in the initiation and progression of atherosclerotic plaque in patients with RA. KEGG analysis also drew our attention to cytokine-cytokine receptor interactions. Many kinds of cytokines have been proven to participate in the establishment of inflammation in RA, such as tumor necrosis factor- α , interleukin-17A, and interferon- γ (IFN- γ) (31). These cytokines can cause cartilage and bone pathological damage through enhancing antigen presentation and macrophage activation, inducing inflammatory cells differentiation and recruitment, other inflammatory cytokines, and chemokine production (28). These cytokines and associated signaling pathways are also part of the pathogenesis of AS (32) and include IFN- γ , which aggravated neointimal hyperplasia and cholesterol accumulation by inducing endoplasmic reticulum stress and apoptosis, which accelerated AS (33,34). Cytokine-cytokine receptor interaction probably takes part in the development of AS in RA patients. In addition, cell adhesion molecules are indicated as an important pathway in the relationship between RA and AS. Adhesion molecules have been shown be highly expressed in RA synovial tissue cells, especially junctional adhesion molecule (JAM), intracellular adhesion molecule (ICAM), and vascular cell adhesion molecular (VCAM) (35). Recent studies have reported JAM-C was increased in an AS mouse model, and decreasing its expression could attenuate atherogenesis through reducing neointimal hyperplasia and monocyte recruitment (36-38). These results indicate JAM-C might provide a novel molecular target in AS, and treatment with anti-JAM-C

antibody might ameliorate AS in RA patients. In addition, the Toll-like receptor signaling pathway has been reported to be a potential link between RA and AS (39), and our results also found it increased risk the risk of AS in RA patients. These pathways might account for the relationship between RA and AS and could be studied subsequently.

Secondly, to investigate the pathogenesis of AS in RA, we identified 20 hub genes based on common DEGs through PPI network and key module construction. Moreover, we successfully verified 16 hub genes in other datasets to improve the credibility and universality of our results. The reason why the four hub genes were not validated may be because of the relatively small sample size of the external RA dataset. CD86 is a co-stimulatory molecule in the cell membrane of dendritic cells (DCs) and plays an important immunomodulatory function in T cell activation (40,41). It has been reported that the differentiation and maturation of DCs with the upregulation of CD86 might accelerate RA, and importantly, researchers have found low-density lipoprotein (LDL) and oxidized LDL (oxLDL), which trigger the development of AS, could induce the expression of CD86 (42). On the contrary, reducing the level of CD86 and subsequent DCs maturation could be a therapeutic target for both RA and AS (43). In our current study, CD86 was upregulated in these diseases, which is consistent with previous studies (42,43) and indicated it was probably a key molecule linking the two. MMP9 is considered an enhancer of extracellular matrix destruction, and its level is higher in unstable plaques. It has been reported that MMP9 levels were up-regulated in RA, which partly explains the AS burden and plaque vulnerability in the disease (44-46). Nevertheless, drugs that reduce its expression level have the therapeutic potential to prevent AS in RA patients (47,48). In addition, TLR8 and S100A9 have been indicated as mediators between RA and AS (49,50), and other hub genes related with either have been reported, although further research is required to explore their role in the pathogenesis. These genes might be involved in the development of AS in RA and could become preventive and therapeutic targets. Similarly, we performed GO and KEGG pathway enrichment analyses of the 16 hub genes mentioned previously, and the results were the same as those found with common DEGs. In addition to the previously mentioned pathways, the Rap1 signaling pathway was one of the top items in enrichment analyses. Recent studies have indicated suppression of Rap1 might contribute to the pathogenesis of RA (51-53), and the Rap1 signaling pathway offers protection against AS progression through stimulating nitric oxide (NO) release and restricting proinflammatory signaling (54). However, a previous study has found the activity of Rap1 was up-regulated in AS (55), and the role of the Rap1 signaling pathway in RA-induced AS requires further study.

Targeting the regulatory elements of common and hub genes is also a therapeutic option. Therefore, we constructed a TF-miRNA coregulatory network to investigate upstream molecules of hub genes. MYC is an important transcription factor that tightly correlates to cell proliferation (56), and many researchers have found its level is up-regulated in RA and that drug treatment could inhibit its expression (57,58). Consistent with this trend, the expression of MYC was increased in AS lesions, and decreasing its level could reduce the pathogenesis of AS (59,60). These results indicated targeted therapy to MYC might prevent AS in RA patients. Although other transcription factors or miRNAs have not been related to both RA and AS yet, our study could provide a direction for further research. For instance, hsa-miR-204 was downregulated in RA as a target of long non-coding RNA NEAT1, and decreasing its expression level was related to the promotion of cell proliferation, inflammatory cytokine production, and the attenuation of cell apoptosis (61,62). Several pathological processes of AS have been reported as being influenced by hsa-miR-204, including vascular and valves calcification, ageing, foam cell formation, inflammation, apoptosis, endothelial cell dysfunction, and vascular smooth muscle cell proliferation and migration (63-67). These and other results suggest hsa-miR-204 probably acts as a key molecule in the development of AS in RA and deserves further study. In addition, hsa-miR-377, hsa-miR-493, and hsa-miR-525-5p have been reported in either RA or AS (68-73), and whether these miRNAs take part in the other disease is also worthy of further investigation.

Lastly, we identified candidate drugs based on hub genes by bioinformatic methods to treat patients with RA and AS. Apart from classical anti-atherosclerotic drugs, such as simvastatin, several newfound therapeutic options attracted our attention, including 5-azacytidine, a DNA methyltransferase-1 inhibitor, which could exert a protective effect from AS through promoting the maintenance of vascular smooth muscle cells, reducing pathological vascular remodeling, and decreasing inflammatory cytokine expression (74). Another study also reported 5-azacytidine reduced disturbed flow-induced endothelial inflammation and the development of AS in a mouse model (75), and this beneficial effect could also be achieved by suppressing macrophage inflammation (76). DNA hypermethylation also plays an essential role in the pathogenesis of RA, and 5-azacytidine could ameliorate its progression (77,78). Therefore, treatment of RA with 5-azacytidine might not only improve RA but also slow the development of AS in RA patients. Retinoic acid exhibited its beneficial effect on RA through inhibiting the inflammatory response, suppressing cell motility, migration, and invasiveness, and inducing apoptosis (79,80), and the retinoic acid signaling pathway is dysregulated in AS (81,82). To sum up, these candidate drugs could be therapeutic for patients with RA and AS.

Recently, several researches attempted to explore the influence of coronary artery disease and subclinical AS related polymorphisms on the risk of AS in RA, yet most of these studies draw negative results. However, Kisiel *et al.* reported that similar genetic factors played a pathogenic role in RA patients with early subclinical AS. But the role might decrease with the prolongation of the AS course, which might be resulted from the effect of anti-rheumatic drugs (83). These inconsistent conclusions remind us that our results also need to be verified in other AS population. To sum up, identified DEGs and hub genes, enriched GO and KEGG pathways, gotten TFs and miRNAs, especially suggested candidate drugs could become therapeutic for RA patients with clinical and subclinical AS, which deserved further experimental research and clinical study.

The novelty of our study is mainly featured in following aspects compared with previous researches. Firstly, four study datasets and two validation datasets were used in our study, the results of which were more convincing. Secondly, candidate drugs were identified in our study, which could be therapeutic for patients with RA and AS.

The leading limitation of the current study is its lack of basic and clinical experimental verification. Although we have verified primary results in external datasets, further experiments would provide more powerful evidence for the transformation and application of our findings in

Page 14 of 17

You et al. Molecular link of atherosclerosis and rheumatoid arthritis

clinical work. In addition, though previous studies have reported genetic associations of AS plaques with RA (84,85), enrichment of common genetic factors for RA and AS in these DEGs requires verification.

In conclusion, our comprehensive bioinformatics analyses of transcriptional profiling provides a novel view regarding the potential pathogenesis of AS in RA. Furthermore, exploitation of candidate drugs targeting hub genes might hold great promise in the future fight against the comorbidities.

Acknowledgments

Funding: None.

Footnote

Reporting Checklist: The authors have completed the STREGA reporting checklist. Available at https://atm. amegroups.com/article/view/10.21037/atm-22-4934/rc

Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at https://atm. amegroups.com/article/view/10.21037/atm-22-4934/coif). The authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013.

Open Access Statement: This is an Open Access article distributed in accordance with the Creative Commons Attribution-NonCommercial-NoDerivs 4.0 International License (CC BY-NC-ND 4.0), which permits the non-commercial replication and distribution of the article with the strict proviso that no changes or edits are made and the original work is properly cited (including links to both the formal publication through the relevant DOI and the license). See: https://creativecommons.org/licenses/by-nc-nd/4.0/.

References

 Castañeda S, Nurmohamed MT, González-Gay MA. Cardiovascular disease in inflammatory rheumatic diseases. Best Pract Res Clin Rheumatol 2016;30:851-69.

- Nurmohamed MT, Heslinga M, Kitas GD. Cardiovascular comorbidity in rheumatic diseases. Nat Rev Rheumatol 2015;11:693-704.
- Fransen J, Kazemi-Bajestani SM, Bredie SJ, et al. Rheumatoid Arthritis Disadvantages Younger Patients for Cardiovascular Diseases: A Meta-Analysis. PLoS One 2016;11:e0157360.
- Edgar R, Domrachev M, Lash AE. Gene Expression Omnibus: NCBI gene expression and hybridization array data repository. Nucleic Acids Res 2002;30:207-10.
- Clough E, Barrett T. The Gene Expression Omnibus Database. Methods Mol Biol 2016;1418:93-110.
- Gautier L, Cope L, Bolstad BM, et al. affy--analysis of Affymetrix GeneChip data at the probe level. Bioinformatics 2004;20:307-15.
- Barrett T, Wilhite SE, Ledoux P, et al. NCBI GEO: archive for functional genomics data sets--update. Nucleic Acids Res 2013;41:D991-5.
- Davis S, Meltzer PS. GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor. Bioinformatics 2007;23:1846-7.
- Ritchie ME, Phipson B, Wu D, et al. limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Res 2015;43:e47.
- Gu Z, Eils R, Schlesner M. Complex heatmaps reveal patterns and correlations in multidimensional genomic data. Bioinformatics 2016;32:2847-9.
- The Gene Ontology Consortium. The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Res 2019;47:D330-8.
- Ashburner M, Ball CA, Blake JA, et al. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. Nat Genet 2000;25:25-9.
- Kanehisa M, Furumichi M, Tanabe M, et al. KEGG: new perspectives on genomes, pathways, diseases and drugs. Nucleic Acids Res 2017;45:D353-61.
- 14. Kanehisa M, Goto S. KEGG: kyoto encyclopedia of genes and genomes. Nucleic Acids Res 2000;28:27-30.
- 15. Yu G, Wang LG, Han Y, et al. clusterProfiler: an R package for comparing biological themes among gene clusters. OMICS 2012;16:284-7.
- Doms A, Schroeder M. GoPubMed: exploring PubMed with the Gene Ontology. Nucleic Acids Res 2005;33:W783-6.
- Ben-Hur A, Noble WS. Kernel methods for predicting protein-protein interactions. Bioinformatics 2005;21 Suppl 1:i38-46.
- 18. Ewing RM, Chu P, Elisma F, et al. Large-scale mapping of

human protein-protein interactions by mass spectrometry. Mol Syst Biol 2007;3:89.

- Szklarczyk D, Franceschini A, Wyder S, et al. STRING v10: protein-protein interaction networks, integrated over the tree of life. Nucleic Acids Res 2015;43:D447-52.
- Szklarczyk D, Franceschini A, Kuhn M, et al. The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. Nucleic Acids Res 2011;39:D561-8.
- Shannon P, Markiel A, Ozier O, et al. Cytoscape: a software environment for integrated models of biomolecular interaction networks. Genome Res 2003;13:2498-504.
- 22. Chin CH, Chen SH, Wu HH, et al. cytoHubba: identifying hub objects and sub-networks from complex interactome. BMC Syst Biol 2014;8 Suppl 4:S11.
- Xia J, Gill EE, Hancock RE. NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data. Nat Protoc 2015;10:823-44.
- Zhou G, Soufan O, Ewald J, et al. NetworkAnalyst
 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. Nucleic Acids Res 2019;47:W234-41.
- Liu ZP, Wu C, Miao H, et al. RegNetwork: an integrated database of transcriptional and post-transcriptional regulatory networks in human and mouse. Database (Oxford) 2015;2015:bav095.
- Chen EY, Tan CM, Kou Y, et al. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. BMC Bioinformatics 2013;14:128.
- 27. Wu H, Huang J, Zhong Y, et al. DrugSig: A resource for computational drug repositioning utilizing gene expression signatures. PLoS One 2017;12:e0177743.
- Lin YJ, Anzaghe M, Schülke S. Update on the Pathomechanism, Diagnosis, and Treatment Options for Rheumatoid Arthritis. Cells 2020;9:880.
- Zhu Y, Xian X, Wang Z, et al. Research Progress on the Relationship between Atherosclerosis and Inflammation. Biomolecules 2018;8:80.
- 30. Wolf D, Ley K. Immunity and Inflammation in Atherosclerosis. Circ Res 2019;124:315-27.
- Smolen JS, Aletaha D, McInnes IB. Rheumatoid arthritis. Lancet 2016;388:2023-38.
- Tedgui A, Mallat Z. Cytokines in atherosclerosis: pathogenic and regulatory pathways. Physiol Rev 2006;86:515-81.
- Zhao Q, Zhou D, You H, et al. IFN-γ aggravates neointimal hyperplasia by inducing endoplasmic reticulum

stress and apoptosis in macrophages by promoting ubiquitin-dependent liver X receptor- α degradation. FASEB J 2017;31:5321-31.

- 34. Dong M, Zhang Y, Xu C, et al. Interferon-γ decreases ATP-binding cassette subfamily G member 1-mediated cholesterol efflux through small ubiquitin-like modifier/ ubiquitin-dependent liver X receptor-α degradation in macrophages. Biotechnol Appl Biochem 2021;68:1412-20.
- Elshabrawy HA, Chen Z, Volin MV, et al. The pathogenic role of angiogenesis in rheumatoid arthritis. Angiogenesis 2015;18:433-48.
- 36. Shagdarsuren E, Djalali-Talab Y, Aurrand-Lions M, et al. Importance of junctional adhesion molecule-C for neointimal hyperplasia and monocyte recruitment in atherosclerosis-prone mice-brief report. Arterioscler Thromb Vasc Biol 2009;29:1161-3.
- Keiper T, Al-Fakhri N, Chavakis E, et al. The role of junctional adhesion molecule-C (JAM-C) in oxidized LDL-mediated leukocyte recruitment. FASEB J 2005;19:2078-80.
- Bradfield PF, Menon A, Miljkovic-Licina M, et al. Divergent JAM-C Expression Accelerates Monocyte-Derived Cell Exit from Atherosclerotic Plaques. PLoS One 2016;11:e0159679.
- Huang Q, Pope RM. Toll-like receptor signaling: a potential link among rheumatoid arthritis, systemic lupus, and atherosclerosis. J Leukoc Biol 2010;88:253-62.
- 40. Bourque J, Hawiger D. Immunomodulatory Bonds of the Partnership between Dendritic Cells and T Cells. Crit Rev Immunol 2018;38:379-401.
- Gardner JK, Cornwall SMJ, Musk AW, et al. Elderly dendritic cells respond to LPS/IFN-γ and CD40L stimulation despite incomplete maturation. PLoS One 2018;13:e0195313.
- 42. Zaguri R, Verbovetski I, Atallah M, et al. 'Danger' effect of low-density lipoprotein (LDL) and oxidized LDL on human immature dendritic cells. Clin Exp Immunol 2007;149:543-52.
- 43. Xiao Y, Shi M, Qiu Q, et al. Piperlongumine Suppresses Dendritic Cell Maturation by Reducing Production of Reactive Oxygen Species and Has Therapeutic Potential for Rheumatoid Arthritis. J Immunol 2016;196:4925-34.
- 44. Gunter S, Solomon A, Tsang L, et al. Apelin concentrations are associated with altered atherosclerotic plaque stability mediator levels and atherosclerosis in rheumatoid arthritis. Atherosclerosis 2017;256:75-81.
- 45. Ram M, Sherer Y, Shoenfeld Y. Matrix metalloproteinase-9 and autoimmune diseases. J Clin

You et al. Molecular link of atherosclerosis and rheumatoid arthritis

Page 16 of 17

Immunol 2006;26:299-307.

- 46. Ibrahem EM, El-Gendi SS, Mahmoud AA, et al. Predictors of Cardiovascular Affection in Patients with Active Rheumatoid Arthritis: Secondary Analysis of a Randomized Controlled Trial. Curr Rheumatol Rev 2021;17:258-66.
- Otto M, Dorn B, Grasmik T, et al. Apremilast effectively inhibits TNFα-induced vascular inflammation in human endothelial cells. J Eur Acad Dermatol Venereol 2022;36:237-46.
- Rudra DS, Pal U, Maiti NC, et al. Melatonin inhibits matrix metalloproteinase-9 activity by binding to its active site. J Pineal Res 2013;54:398-405.
- 49. Crump KE, Sahingur SE. Microbial Nucleic Acid Sensing in Oral and Systemic Diseases. J Dent Res 2016;95:17-25.
- Lim SY, Raftery MJ, Goyette J, et al. Oxidative modifications of S100 proteins: functional regulation by redox. J Leukoc Biol 2009;86:577-87.
- 51. Abreu JR, Krausz S, Dontje W, et al. Sustained T cell Rap1 signaling is protective in the collagen-induced arthritis model of rheumatoid arthritis. Arthritis Rheum 2010;62:3289-99.
- 52. Kojima F, Kapoor M, Kawai S, et al. Prostaglandin E2 activates Rap1 via EP2/EP4 receptors and cAMPsignaling in rheumatoid synovial fibroblasts: involvement of Epac1 and PKA. Prostaglandins Other Lipid Mediat 2009;89:26-33.
- 53. Remans PH, Wijbrandts CA, Sanders ME, et al. CTLA-4IG suppresses reactive oxygen species by preventing synovial adherent cell-induced inactivation of Rap1, a Ras family GTPASE mediator of oxidative stress in rheumatoid arthritis T cells. Arthritis Rheum 2006;54:3135-43.
- 54. Singh B, Kosuru R, Lakshmikanthan S, et al. Endothelial Rap1 (Ras-Association Proximate 1) Restricts Inflammatory Signaling to Protect From the Progression of Atherosclerosis. Arterioscler Thromb Vasc Biol 2021;41:638-50.
- 55. Cai Y, Sukhova GK, Wong HK, et al. Rap1 induces cytokine production in pro-inflammatory macrophages through NFκB signaling and is highly expressed in human atherosclerotic lesions. Cell Cycle 2015;14:3580-92.
- 56. Bretones G, Delgado MD, León J. Myc and cell cycle control. Biochim Biophys Acta 2015;1849:506-16.
- 57. Lee YZ, Guo HC, Zhao GH, et al. Tylophorine-based compounds are therapeutic in rheumatoid arthritis by targeting the caprin-1 ribonucleoprotein complex and inhibiting expression of associated c-Myc and HIF-1α. Pharmacol Res 2020;152:104581.

- 58. Pap T, Nawrath M, Heinrich J, et al. Cooperation of Rasand c-Myc-dependent pathways in regulating the growth and invasiveness of synovial fibroblasts in rheumatoid arthritis. Arthritis Rheum 2004;50:2794-802.
- 59. Xu L, Hao H, Hao Y, et al. Aberrant MFN2 transcription facilitates homocysteine-induced VSMCs proliferation via the increased binding of c-Myc to DNMT1 in atherosclerosis. J Cell Mol Med 2019;23:4611-26.
- 60. Khanna A. Concerted effect of transforming growth factor-beta, cyclin inhibitor p21, and c-myc on smooth muscle cell proliferation. Am J Physiol Heart Circ Physiol 2004;286:H1133-40.
- Xiao J, Wang R, Zhou W, et al. LncRNA NEAT1 regulates the proliferation and production of the inflammatory cytokines in rheumatoid arthritis fibroblastlike synoviocytes by targeting miR-204-5p. Hum Cell 2021;34:372-82.
- 62. Chen J, Luo X, Liu M, et al. Silencing long non-coding RNA NEAT1 attenuates rheumatoid arthritis via the MAPK/ERK signalling pathway by downregulating microRNA-129 and microRNA-204. RNA Biol 2021;18:657-68.
- 63. Xu F, Zhong JY, Lin X, et al. Melatonin alleviates vascular calcification and ageing through exosomal miR-204/ miR-211 cluster in a paracrine manner. J Pineal Res 2020;68:e12631.
- 64. Liu X, Guo JW, Lin XC, et al. Macrophage NFATc3 prevents foam cell formation and atherosclerosis: evidence and mechanisms. Eur Heart J 2021;42:4847-61.
- 65. Yu C, Li L, Xie F, et al. LncRNA TUG1 sponges miR-204-5p to promote osteoblast differentiation through upregulating Runx2 in aortic valve calcification. Cardiovasc Res 2018;114:168-79.
- 66. Wang Z, Zhang M, Wang Z, et al. Cyanidin-3-Oglucoside attenuates endothelial cell dysfunction by modulating miR-204-5p/SIRT1-mediated inflammation and apoptosis. Biofactors 2020;46:803-12.
- 67. Ghasempour G, Mohammadi A, Zamani-Garmsiri F, et al. miRNAs through β -ARR2/p-ERK1/2 pathway regulate the VSMC proliferation and migration. Life Sci 2021;279:119703.
- Wang H, Wei Z, Li H, et al. MiR-377-3p inhibits atherosclerosis-associated vascular smooth muscle cell proliferation and migration via targeting neuropilin2. Biosci Rep 2020;40:BSR20193425.
- 69. Guo Y, Huang S, Ma Y, et al. MiR-377 mediates the expression of Syk to attenuate atherosclerosis lesion development in ApoE-/- mice. Biomed Pharmacother

2019;118:109332.

- Zhang P, Wang W, Li M. Circ_0010283/miR-377-3p/Cyclin D1 Axis Is Associated With Proliferation, Apoptosis, Migration, and Inflammation of Oxidized Lowdensity Lipoprotein-Stimulated Vascular Smooth Muscle Cells. J Cardiovasc Pharmacol 2021;78:437-47.
- 71. Chen LY, Xia XD, Zhao ZW, et al. MicroRNA-377 Inhibits Atherosclerosis by Regulating Triglyceride Metabolism Through the DNA Methyltransferase 1 in Apolipoprotein E-Knockout Mice. Circ J 2018;82:2861-71.
- 72. Niu M, Li H, Li X, et al. Circulating Exosomal miRNAs as Novel Biomarkers Perform Superior Diagnostic Efficiency Compared With Plasma miRNAs for Large-Artery Atherosclerosis Stroke. Front Pharmacol 2021;12:791644.
- 73. Chang TK, Zhong YH, Liu SC, et al. Apelin Promotes Endothelial Progenitor Cell Angiogenesis in Rheumatoid Arthritis Disease via the miR-525-5p/Angiopoietin-1 Pathway. Front Immunol 2021;12:737990.
- 74. Strand KA, Lu S, Mutryn MF, et al. High Throughput Screen Identifies the DNMT1 (DNA Methyltransferase-1) Inhibitor, 5-Azacytidine, as a Potent Inducer of PTEN (Phosphatase and Tensin Homolog): Central Role for PTEN in 5-Azacytidine Protection Against Pathological Vascular Remodeling. Arterioscler Thromb Vasc Biol 2020;40:1854-69.
- 75. Dunn J, Simmons R, Thabet S, et al. The role of epigenetics in the endothelial cell shear stress response and atherosclerosis. Int J Biochem Cell Biol 2015;67:167-76.
- 76. Cao Q, Wang X, Jia L, et al. Inhibiting DNA Methylation by 5-Aza-2'-deoxycytidine ameliorates atherosclerosis through suppressing macrophage inflammation. Endocrinology 2014;155:4925-38.
- 77. Tóth DM, Ocskó T, Balog A, et al. Amelioration of Autoimmune Arthritis in Mice Treated With the DNA Methyltransferase Inhibitor 5'-Azacytidine. Arthritis Rheumatol 2019;71:1265-75.
- 78. Li XF, Wu S, Yan Q, et al. PTEN Methylation Promotes

Cite this article as: You H, Zhao Q, Gou Q, Dong M. Exploration of the shared gene signatures and molecular mechanisms between atherosclerosis and rheumatoid arthritis via multi-microarray data analyses. Ann Transl Med 2022;10(21):1164. doi: 10.21037/atm-22-4934 Inflammation and Activation of Fibroblast-Like Synoviocytes in Rheumatoid Arthritis. Front Pharmacol 2021;12:700373.

- Mosquera N, Rodriguez-Trillo A, Blanco FJ, et al. All-Trans Retinoic Acid Inhibits Migration and Invasiveness of Rheumatoid Fibroblast-Like Synoviocytes. J Pharmacol Exp Ther 2020;372:185-92.
- Cui Z, Lin Y, Liu Y, et al. Retinoic Acid-Platinum (II) Complex [RT-Pt(II)] Protects Against Rheumatoid Arthritis in Mice via MEK/Nuclear Factor kappa B (NF-κB) Pathway Downregulation. Med Sci Monit 2020;26:e924787.
- Pan H, Xue C, Auerbach BJ, et al. Single-Cell Genomics Reveals a Novel Cell State During Smooth Muscle Cell Phenotypic Switching and Potential Therapeutic Targets for Atherosclerosis in Mouse and Human. Circulation 2020;142:2060-75.
- Krivospitskaya O, Elmabsout AA, Sundman E, et al. A CYP26B1 polymorphism enhances retinoic acid catabolism and may aggravate atherosclerosis. Mol Med 2012;18:712-8.
- Kisiel B, Kruszewski R, Juszkiewicz A, et al. Common atherosclerosis genetic risk factors and subclinical atherosclerosis in rheumatoid arthritis: the relevance of disease duration. Rheumatol Int 2019;39:327-36.
- Arya R, Escalante A, Farook VS, et al. A genetic association study of carotid intima-media thickness (CIMT) and plaque in Mexican Americans and European Americans with rheumatoid arthritis. Atherosclerosis 2018;271:92-101.
- 85. López-Mejías R, Genre F, García-Bermúdez M, et al. The ZC3HC1 rs11556924 polymorphism is associated with increased carotid intima-media thickness in patients with rheumatoid arthritis. Arthritis Res Ther 2013;15:R152.

(English Language Editor: B. Draper)

Supplementary



Figure S1 Data preprocessing. (A) Pre-normalization for GSE55235 and GSE55457. (B) Post-normalization for GSE55235 and GSE55457. (C-D) Principal component analysis (PCA) for GSE55235 and GSE55457. (E) Pre-normalization for GSE28829 and GSE41571. (F) Post-normalization for GSE28829 and GSE41571. (G-H) PCA for GSE28829 and GSE41571. HC, healthy controls; RA, rheumatoid arthritis; EAP, early atherosclerotic plaque; AAP, advanced atherosclerotic plaque.

Table S1 Gene Ontology and Kyoto	Encyclopedia of Genes and	Genomes pathway enrichment a	analyses of common different	ially expressed genes

|
 | Ontology and Ky
 | roto Encyclopedia of Genes and Genomes pathway enrichment | analyses of commo
 | on differentially
 | expressed genes. | |
 | | |

--
--
--|---
--|--|--|
| BP
 | ID
GO:0050900
 | Description | Gene Ratio
 | BgRatio
 | P value | p.adjust | qvalue
 | genelD
CD48/NCKAP1I /IGHM/IGKC/IGI C1/ITGB2/BAC2/S100A9/CCI 13/CCI 18/CCI 19/CXCB4/PI A2G7/COBO1A/ | Count |
| Ы
 | 00.0000000
 | | 17/00
 | 433/10070
 | 1.000002 10 | 0.2000+L 10 | 2.022002 10
 | CD300A/IGLV1-44/SLAMF8 | 17 |
| BP
 | GO:0051249
 | regulation of lymphocyte activation | 16/60
 | 485/18670
 | 1.75971E-12 | 1.52661E-09 | 9.53674E-10
 | CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5 | 16 |
| BP
 | GO:0042119
 | neutrophil activation | 16/60
 | 498/18670
 | 2.62606E-12 | 1.52661E-09 | 9.53674E-10
 | ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A | 16 |
| BP
 | GO:0006909
 | phagocytosis | 14/60
 | 369/18670
 | 8.27003E-12 | 3.60573E-09 | 2.25249E-09
 | CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/ | 14 |
| BP
 | GO:0050864
 | regulation of B cell activation | 11/60
 | 184/18670
 | 1.42121E-11 | 4.9572E-09 | 3.09675E-09
 | IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5 | 11 |
| BP
 | GO:0043312
 | neutrophil degranulation | 15/60
 | 485/18670
 | 2.43026E-11 | 6.60473E-09 | 4.12596E-09
 | ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ | 15 |
| BP
 | GO:0002283
 | neutrophil activation involved in immune response | 15/60
 | 488/18670
 | 2.65098E-11 | 6.60473E-09 | 4.12596E-09
 | ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ | 15 |
| BP
 | GO:0002446
 | neutrophil mediated immunity | 15/60
 | 499/18670
 | 3.62817E-11 | 7.9094F-09 | 4.94099F-09
 | VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ | 15 |
|
 |
 | · · · · · · · · · · · · |
 |
 | | |
 | VAMP8/CD300A | |
| BP
 | GO:0030595
GO:0002697
 | leukocyte chemotaxis regulation of immune effector process | 11/60
14/60
 | 224/18670
458/18670
 | 1.18654E-10
1.45234E-10 | 2.29925E-08
2.45605E-08 | 1.43634E-08
1.53429E-08
 | NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8
CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/ | 11
14 |
|
 | 00 000007
 | | 11/00
 | 000/10717
 | 4 470005 00 | 0.075005.00 | 0.000755.00
 | SLAMF8 | |
| CC
 | GO:0009897
GO:0070820
 | external side of plasma membrane
tertiary granule | 7/63
 | 393/19717
164/19717
 | 4.17226E-08
9.06323E-07 | 6.67562E-06
7.25059E-05 | 3.90875E-06
4.24541E-05
 | CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A | 11
7 |
| CC
 | GO:0101002
 | ficolin-1-rich granule | 7/63
 | 185/19717
 | 2.02926E-06 | 0.000108227 | 6.33699E-05
 | ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A | 7 |
| CC
 | GO:0030667
 | secretory granule membrane | 8/63
 | 298/19717
 | 4.66784E-06 | 0.000186714 | 0.000109326
 | CD14/CYBA/NCKAP1L/ITGB2/PTPRC/SLC2A5/VAMP8/CD300A | 8 |
| cc
 | GO:0030666
GO:0042613
 | MHC class II protein complex | 3/63
 | 16/19717
 | 1.69005E-05 | 0.000450681 | 0.000263885
 | HLA-DMA/HLA-DMB/HLA-DRA | 3 |
| CC
 | GO:0042611
 | MHC protein complex | 3/63
 | 25/19717
 | 6.80025E-05 | 0.001552276 | 0.000908899
 | HLA-DMA/HLA-DMB/HLA-DRA | 3 |
| CC
 | GO:0042571
 | immunoglobulin complex, circulating | 4/63
 | 72/19717
 | 8.27284E-05 | 0.001552276 | 0.000908899
 | IGHM/IGKC/IGLC1/IGLL5 | 4 |
| CC
 | GO:0030670
 | phagocytic vesicle membrane | 4/63
 | 76/19717
 | 0.000102188 | 0.001635005 | 0.000957338
 | CYBA/RAC2/VAMP8/CORO1A | 4 |
| MF
 | GO:0003823
 | antigen binding | 7/59
 | 160/17697
 | 9.95363E-07 | 0.000230924 | 0.000183356
 | CD48/HLA-DRA/IGHM/IGKC/IGLC1/IGLV1-44/IGLL5 | 7 |
| MF
MF
 | GO:0023026
GO:0023023
 | MHC class II protein complex binding | 3/59
3/59
 | 16/17697
25/17697
 | 1.91121E-05
7.68384E-05 | 0.002217009 | 0.001760329
 | HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA | 3
3 |
| MF
 | GO:0034987
 | immunoglobulin receptor binding | 4/59
 | 76/17697
 | 0.000119512 | 0.006931719 | 0.00550386
 | IGHM/IGKC/IGLC1/IGLL5 | 4 |
| MF
 | GO:0048020
 | CCR chemokine receptor binding | 3/59
 | 43/17697
 | 0.000395083 | 0.018331851 | 0.014555689
 | CCL13/CCL18/CCL19 | 3 |
| MF
MF
 | GO:0008009
GO:0019864
 | chemokine activity | 3/59
2/59
 | 49/17697
11/17697
 | 0.000581514 | 0.019537216 | 0.015512762
 | CCL13/CCL18/CCL19
FCGR1B/FCGR2B | 3
2 |
| MF
 | GO:0005178
 | integrin binding | 4/59
 | 132/17697
 | 0.000979876 | 0.02841641 | 0.022562939
 | ITGB2/LCP1/SPP1/ITGBL1 | 4 |
| MF
 | GO:0042379
 | chemokine receptor binding | 3/59
 | 66/17697
 | 0.00138748 | 0.033384871 | 0.026507951
 | CCL13/CCL18/CCL19 | 3 |
| IVII
 | JUJUDU064
 | acceptor | 2/39
 | ואיזאאפאזייזי
 | J.JU1439003 | J.JJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJ | v.vzvoU/951
 | | ۷ |
| KEGG
KEGG
 | hsa04145
hsa05416
 | Phagosome
Viral mvocarditis | 9/42
6/42
 | 152/8076
60/8076
 | 6.13591E-08
5.55121F-07 | 7.42445E-06
3.35848E-05 | 5.29626E-06
2.39578F-05
 | CD14/CTSS/CYBA/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/CORO1A
CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/RAC2 | 9
6 |
| KEGG
 | hsa05152
 | Tuberculosis | 8/42
 | 180/8076
 | 3.21921E-06 | 0.000129841 | 9.26229E-05
 | CD14/CTSS/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/CORO1A | 8 |
| KEGG
 | hsa04672
 | Intestinal immune network for IgA production | 5/42
 | 49/8076
 | 4.7939E-06 | 0.000145016 | 0.000103447
 | CD86/HLA-DMA/HLA-DMB/HLA-DRA/CXCR4 | 5 |
| KEGG
 | nsa04640
hsa05330
 | Allograft rejection | 0/42
4/42
 | ອອ/8076
38/8076
 | 1.00974E-05
4.10371E-05 | 0.000258877
0.000771375 | 0.000184671
 | CD86/HLA-DMA/HLA-DMB/HLA-DRA | о
4 |
| KEGG
 | hsa05140
 | Leishmaniasis | 5/42
 | 77/8076
 | 4.4625E-05 | 0.000771375 | 0.000550263
 | CYBA/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2 | 5 |
| KEGG
 | hsa05332
 | Graft-versus-host disease | 4/42
4/42
 | 42/8076
 | 6.12967E-05 | 0.000905209 | 0.000645734
 | CD86/HLA-DMA/HLA-DMB/HLA-DRA | 4
4 |
| KEGG
 | hsa04514
 | Cell adhesion molecules | 6/42
 | 149/8076
 | 0.000108131 | 0.001214553 | 0.000866406
 | CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/PTPRC | ,
6 |
| KEGG
 | hsa05323
 | Rheumatoid arthritis | 5/42
 | 93/8076
 | 0.000110414 | 0.001214553 | 0.000866406
 | CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2 | 5 |
| KEGG
KEGG
 | hsa05150
hsa05320
 | Staphylococcus aureus infection
Autoimmune thyroid disease | 5/42
4/42
 | 96/8076
53/8076
 | 0.000128378
0.000153857 | 0.001294476
0.001345905 | 0.000923419
 | FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2
CD86/HLA-DMA/HLA-DMB/HLA-DRA | 5
4 |
| KEGG
 | hsa04061
 | Viral protein interaction with cytokine and cytokine recepto | or 5/42
 | 100/8076
 | 0.000155725 | 0.001345905 | 0.000960106
 | CSF1R/CCL13/CCL18/CCL19/CXCR4 | 5 |
| KEGG
 | hsa04670
 | Leukocyte transendothelial migration | 5/42
 | 114/8076
 | 0.00028782 | 0.002321749 | 0.001656228
 | CYBA/ITGB2/MMP9/RAC2/CXCR4 | 5 |
| KEGG
 | hsa04062
hsa05310
 | Chemokine signaling pathway
Asthma | 6/42
3/42
 | 192/8076
31/8076
 | 0.000429397 | 0.003247314 | 0.002316483
 | HLA-DMA/HLA-DMB/HLA-DRA | 6
3 |
| KEGG
 | hsa04612
 | Antigen processing and presentation | 4/42
 | 78/8076
 | 0.000682249 | 0.00458623 | 0.003271604
 | CTSS/HLA-DMA/HLA-DMB/HLA-DRA | 4 |
| KEGG
 | hsa04064
 | NF-kappa B signaling pathway | 4/42
 | 104/8076
 | 0.001994807 | 0.012068582 | 0.008609167
 | BCL2A1/CD14/CCL13/CCL19 | 4 |
| KEGG
 | hsa05145
 | Toxoplasmosis | 4/42
 | 112/8076
 | 0.002614852 | 0.015066527 | 0.010747762
 | ALOX5/HLA-DMA/HLA-DMB/HLA-DRA | 4 |
| KEGG
 | hsa05202
 | Transcriptional misregulation in cancer | 5/42
 | 192/8076
 | 0.003002662 | 0.016514642 | 0.01178078
 | BCL2A1/CD14/CD86/CSF1R/MMP9 | 5 |
| KEGG
KEGG
 | hsa04060
hsa05321
 | Cytokine-cytokine receptor interaction | 6/42
3/42
 | 295/8076
65/8076
 | 0.00390778 | 0.02055832 | 0.014665353
 | CSF1R/CSF2RB/CCL13/CCL18/CCL19/CXCR4
HLA-DMA/HLA-DMB/HLA-DRA | 6
3 |
| KEGG
 | hsa05221
 | Acute myeloid leukemia | 3/42
 | 67/8076
 | 0.004973176 | 0.023513674 | 0.016773565
 | BCL2A1/CD14/CSF1R | 3 |
| KEGG
 | hsa04210
 | Apoptosis
Systemic lunus erythematosus | 4/42
4/42
 | 136/8076
136/8076
 | 0.005246853 | 0.023513674 | 0.016773565
 | BCL2A1/CTSC/CSF2RB/CTSS | 4
4 |
| KEGG
 | hsa04662
 | B cell receptor signaling pathway | 3/42
 | 82/8076
 | 0.008711718 | 0.037647067 | 0.026855672
 | CD72/FCGR2B/RAC2 | 3 |
| KEGG
 | hsa04658
 | Th1 and Th2 cell differentiation | 3/42
 | 92/8076
 | 0.011918685 | 0.049729685 | 0.035474852
 | HLA-DMA/HLA-DMB/HLA-DRA | 3 |
| ONTOLOGY
 |
 | Description |
 |
 | P value | p.adjust | qvalue
 | geneID | Count |
| BP
 | ID
GO:0050900
 | leukocyte migration | Gene Ratio
 | BgRatio
499/18670
 | 1.85598E-13 | 3.23684E-10 | 2.02205E-10
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/ | 17 |
| BP
 | ID
GO:0050900
 | | Gene Ratio
17/60
 | BgRatio
499/18670
 | 1.85598E-13 | 3.23684E-10 | 2.02205E-10
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8 | 17 |
| BP
BP
 | ID
GO:0050900
GO:0051249
 | leukocyte migration
regulation of lymphocyte activation | Gene Ratio
17/60
16/60
 | BgRatio
499/18670
485/18670
 | 1.85598E-13
1.75971E-12 | 3.23684E-10
1.52661E-09 | 2.02205E-10
9.53674E-10
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5 | 17
16 |
| BP
BP
BP
 | ID
GO:0050900
GO:0051249
GO:0042119
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation | Gene Ratio
17/60
16/60
16/60
 | BgRatio
499/18670
485/18670
498/18670
 | 1.85598E-13
1.75971E-12
2.62606E-12 | 3.23684E-10
1.52661E-09
1.52661E-09 | 2.02205E-10
9.53674E-10
9.53674E-10
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A | 17
16
16 |
| BP
BP
BP
BP
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis | Gene Ratio
17/60
16/60
16/60
14/60
 | BgRatio
499/18670
485/18670
498/18670
369/18670
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5 | 17
16
16
14 |
| BP
BP
BP
BP
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation | Gene Ratio
17/60
16/60
16/60
14/60
11/60
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12
1.42121E-11 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5 | 17
16
16
14
11 |
| BP
BP
BP
BP
BP
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12
1.42121E-11
2.43026E-11 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A | 17
16
16
14
11
15 |
| BP
BP
BP
BP
BP
BP
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
GO:0002283
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
488/18670
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12
1.42121E-11
2.43026E-11
2.65098E-11 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A | 17
16
16
14
11
15
15 |
| BP
BP
BP
BP
BP
BP
BP
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
GO:0002283
GO:00022446
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
488/18670
499/18670
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12
1.42121E-11
2.43026E-11
2.65098E-11
3.62817E-11 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
4.94099E-09
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/ILA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A | 17
16
14
11
15
15 |
| BP
BP
BP
BP
BP
BP
BP
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
GO:0002283
GO:00022446
GO:0030595
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immune response | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
488/18670
499/18670
224/18670
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12
1.42121E-11
2.43026E-11
2.65098E-11
3.62817E-11
1.18654E-10 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A | 17
16
16
14
11
15
15
15
15 |
| BP
BP
BP
BP
BP
BP
BP
BP
BP
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
GO:0002283
GO:0002283
GO:00022446
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
11/60
14/60
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
488/18670
224/18670
458/18670
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12
1.42121E-11
2.43026E-11
2.65098E-11
3.62817E-11
1.18654E-10
1.45234E-10 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
1.53429E-08
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8
CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8 | 17
16
14
11
15
15
11
14 |
| BP
BP
BP
BP
BP
BP
BP
BP
BP
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:00050864
GO:0002283
GO:0002283
GO:00022446
GO:0002697
GO:0009897
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
488/18670
499/18670
224/18670
458/18670
393/19717
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12
1.42121E-11
2.43026E-11
2.65098E-11
3.62817E-11
1.18654E-10
1.45234E-10
4.17226E-08 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
6.67562E-06 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
1.53429E-08
3.90875E-06
 | CD88/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8 CD86/FCGR2B/NCKAP1L/ILA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5 ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5 FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5 ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8 CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8 CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5 | 17
16
14
11
15
15
15
11
14
11 |
| BP
BP
BP
BP
BP
BP
BP
BP
CC
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0002283
GO:0002283
GO:0002283
GO:0002283
GO:0002697
GO:0009897
GO:0009897
GO:0070820
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector processs
external side of plasma membrane
tertiary granule | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
488/18670
499/18670
224/18670
458/18670
393/19717
164/19717
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12
1.42121E-11
2.43026E-11
2.65098E-11
3.62817E-11
1.18654E-10
1.45234E-10
4.17226E-08
9.06323E-07 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8
CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5 | 17
16
14
11
15
15
15
11
14
11
7 |
| BP
BP
BP
BP
BP
BP
BP
BP
CC
CC
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0002283
GO:0002283
GO:0002283
GO:0002283
GO:0002697
GO:0009897
GO:0009897
GO:0070820
GO:0101002
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
7/63
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
488/18670
499/18670
224/18670
458/18670
393/19717
164/19717
185/19717
 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 3.62817E-11 1.18654E-10 1.45234E-10 4.17226E-08 9.06323E-07 2.02926E-06 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000108227 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8
CD86/FCGR2B/ILA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/ILA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/ILA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/ILA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/ILA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/ILA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/ILA-DMB/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A | 17
16
14
11
15
15
15
11
14
11
7
~ |
| BP
BP
BP
BP
BP
BP
BP
BP
CC
CC
CC
CC
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:00050864
GO:0002283
GO:0002283
GO:0002283
GO:0002446
GO:0002697
GO:0009897
GO:0009897
GO:0070820
GO:0070820
GO:0101002
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
7/63
8/63
6/63
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
485/18670
488/18670
499/18670
224/18670
224/18670
393/19717
164/19717
185/19717
167/19717
 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 3.62817E-111 1.18654E-10 1.45234E-10 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/COR01A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8
CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A
ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A
ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A | 17
16
14
11
15
15
15
11
14
11
7
8
6 |
| BP
BP
BP
BP
BP
BP
BP
BP
CC
CC
CC
CC
CC
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
GO:0002283
GO:0002283
GO:0002283
GO:0002697
GO:0002697
GO:0009897
GO:0070820
GO:0101002
GO:0101002
GO:0030667
GO:0030667
GO:0030666
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
MHC class II protein complex | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
7/63
8/63
6/63
3/63
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
485/18670
499/18670
224/18670
224/18670
393/19717
164/19717
167/19717
16/19717
 | 1.85598E-13
1.75971E-12
2.62606E-12
8.27003E-12
1.42121E-11
2.43026E-11
2.65098E-11
3.62817E-11
1.18654E-10
1.45234E-10
4.17226E-08
9.06323E-07
2.02926E-06
4.66784E-06
1.5378E-05
1.69005E-05 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
 | CD48/NCKAP1L/IGHIM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/IHLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/COR01A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8
CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A | 17 16 14 11 15 15 11 14 11 7 8 6 3 |
| BP
BP
BP
BP
BP
BP
BP
BP
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
GO:0002283
GO:0002283
GO:0002283
GO:0002697
GO:0002697
GO:0009897
GO:0009897
GO:0009897
GO:0002697
GO:0002697
GO:0002697
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
MHC class II protein complex | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
11/60
11/60
11/63
7/63
7/63
8/63
6/63
3/63
3/63
3/63
 | BgRatio
499/18670
485/18670
498/18670
369/18670
485/18670
485/18670
488/18670
499/18670
224/18670
224/18670
393/19717
164/19717
185/19717
167/19717
16/19717
25/19717
 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 3.62817E-11 1.18654E-10 1.45234E-10 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.001552276 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
0.000908899
0.000908899
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/TSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8
CD86/FCGR2B/IHA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A
ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CVBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/PTPRC/SLC2A5/VAMP8/CD300A
CVBA/FCGR1B/HLA-DRA/RAC2/VAMP8/CORO1A
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA | 17 16 14 11 15 15 11 14 11 7 8 6 3 3 4 |
| BP
BP
BP
BP
BP
BP
BP
BP
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0002283
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0009897
GO:0009897
GO:0009897
GO:0002697
GO:0002697
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
MHC class II protein complex
MHC protein complex | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
8/63
6/63
3/63
3/63
3/63
4/63
 | BgRatio
499/18670
485/18670
498/18670
369/18670
485/18670
485/18670
488/18670
499/18670
224/18670
224/18670
393/19717
164/19717
185/19717
167/19717
16/19717
25/19717
72/19717
 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 3.62817E-11 1.18654E-10 1.45234E-10 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 8.27284E-05 8.73155E-05 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.001552276
0.001552276 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
0.000908899
0.000908899
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/ILA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALCX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/NAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/COR01A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALCX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALCX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALCX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALCX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8
CD64/FCGR2B/IGLAM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
ALCX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CYBA/FCGR1B/HLA-DRA/RAC2/VAMP8/COR01A
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA | 17 16 14 11 15 15 15 11 14 11 7 8 6 3 4 4 |
| BP
BP
BP
BP
BP
BP
BP
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
GO:0002283
GO:0002283
GO:0002283
GO:0002697
GO:0002697
GO:0009897
GO:0009897
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002697
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
MHC class II protein complex
MHC protein complex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
8/63
6/63
3/63
3/63
3/63
4/63
4/63
 | BgRatio
499/18670
485/18670
369/18670
369/18670
485/18670
485/18670
488/18670
488/18670
499/18670
224/18670
458/18670
393/19717
164/19717
167/19717
16/19717
72/19717
73/19717
 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 3.62817E-111 1.18654E-10 1.45234E-10 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 8.27284E-05 8.73155E-05 0.000102188 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.94099E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
0.000908899
0.000908899
0.000908899
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/COR01A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A
ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/FLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CYBA/FCGR1B/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
IGHM/IGKC/IGLC1/IGLL5
CYBA/NCKAP1L/IGB2/VAMP8/COR01A
HLA-DMA/HLA-DMB/B/HLA-DRA
IGHM/IGKC/IGLC1/IGLL5
CYBA/NCKAP8/COR01A
CYBA/RAC2/VAMP8/COR01A | 17
16
14
11
15
15
15
11
14
11
7
8
6
3
3
4
4
4
4 |
| BP
BP
BP
BP
BP
BP
BP
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0002283
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0009897
GO:0009897
GO:0009897
GO:0009897
GO:0000821
GO:0030667
GO:0030667
GO:0042611
GO:0042611
GO:0042611
GO:0042611
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
dHC class II protein complex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
antigen binding | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
7/63
8/63
6/63
3/63
3/63
3/63
4/63
4/63
4/63
4
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
485/18670
488/18670
499/18670
224/18670
458/18670
393/19717
164/19717
167/19717
16/19717
72/19717
73/19717
76/19717
160/17697
 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 3.62817E-111 1.45234E-10 1.45234E-10 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.000450681
0.0001552276
0.001552276
0.001552276
0.001635005
0.000230924
0.002217009 |
2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
4.12596E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
0.000263885
0.000908899
0.000908899
0.000908899
0.000957338
0.000183356
0.000183356 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/COR01A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8
CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CYBA/FCGR1B/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
IGHM/IGKC/IGLC1/IGLS
CYBA/ITGB2/VAMP8/CD300A
CYBA/RAC2/VAMP8/COR01A
CYBA/RAC2/VAMP8/COR01A
CYBA/RAC2/VAMP8/COR01A
CD48/HLA-DMA/IGKC/IGLC1/IGL1-44/IGLL5
HLA-DMA/HLA-DMB/HLA-DRA | 17 16 14 11 15 15 15 11 14 11 7 8 6 3 4 4 4 7 3 |
| BP
BP
BP
BP
BP
BP
BP
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
GO:0002283
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:00070820
GO:00070820
GO:0030667
GO:0030667
GO:0042611
GO:0042611
GO:0042611
GO:0042611
GO:0042611
GO:0042611
GO:0042611
GO:0042611
GO:0042611
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
MHC class II protein complex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
antigen binding
MHC class II protein complex binding | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
7/63
8/63
6/63
3/63
3/63
3/63
4/63
4/63
4/63
4
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
488/18670
489/18670
499/18670
224/18670
393/19717
164/19717
185/19717
16/19717
16/19717
72/19717
73/19717
76/19717
160/17697
25/17697
 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-10 1.45234E-10 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.000450681
0.000450681
0.0001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276 |
2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.12596E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
0.000263885
0.000263885
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000957338
0.0001760329
0.0001760329
0.0001760329 | CD48/NCKAP1L/IGH//IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/C0R01A/
CD300A/IGLV1-44/SLAMF8
CD68/FCGR28/NCKAP1L/ILA-DM8/IGH//IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR28/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC28/AVMP8/CD300A
CD14/CYBA/DOCK2/FCGR28/NCKAP1L/IGH//IGKC/IGLC1/ITGB2/PTPRC/COR01A/CD300A/IGLV1-44/
IGLL5
FCGR28/NCKAP1L/IGH//IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8
CD56/FCGR2B/ILA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/AMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGH/M/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/RCAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/RCAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/RCAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/RCAP1L/ITGB2/MMP9/SERPINA1/CD300A
CYBA/FCGR1B/HLA-DRA/RAC2/VAMP8/COR01A
HLA-DMA/HLA-DMB/HLA-DRA
IGHM/IGKC/IGLC1/IGLS
CYBA/TGB12/AMP8/CD300A
CYBA/FAC2/VAMP8/COR01A
CYBA/FAC2/VAMP8/COR01A
CYBA/FAC2/VAMP8/COR01A
CYBA/FAC2/VAMP8/COR01A
CYBA/FAC2/VAMP8/COR01A
CYBA/FAC2/VAMP8/COR01A
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA | 17
16
14
11
15
15
15
11
14
11
7
8
6
3
4
4
4
4
7
3
3 |
| BP BP BP BP BP BP BP BP CC MF MF MF MF MF MF MF MF MF
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0002283
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002611
GO:00101002
GO:0023026
GO:0023026
GO:0023026
GO:0023026
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
ficoline unoplex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
antigen binding
MHC class II protein complex binding
MHC protein complex binding
MHC protein complex binding | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
7/63
8/63
3/63
3/63
3/63
3/63
3/63
4/63
4/63
4
 | BgRatio
499/18670
485/18670
498/18670
369/18670
485/18670
485/18670
485/18670
499/18670
224/18670
224/18670
393/19717
164/19717
185/19717
167/19717
167/19717
72/19717
72/19717
73/19717
76/19717
160/17697
16/17697
25/17697
76/17697
 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-10 1.45234E-10 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000119512 0.000385025 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.000450681
0.000450681
0.000450681
0.0001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001230924
0.00230924
0.00594217 |
2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.12596E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.00026385
0.00026385
0.00026385
0.00026385
0.00026385
0.00026385
0.000265
0.0005
0.0005
0.0005
0.0005
0.0005 | CD48/NCKAP1L/IGH//IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/C0R01A/
CD300A/IGLV1-44/SLAMF8
CD88/FCGR28/NCKAP1L/HLA-DM8/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2AS/VAMP8/CD300A
CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGH//IGKC/IGLC1/ITGB2/PTPRC/COR01A/CD300A/IGLV1-44/
IGLL5
FCGR2B/NCKAP1L/IGH//IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOXS/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CYBA/FCGR1B/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA
HLA-DMA/HLA-DM8/HLA-DRA | 17 16 14 11 15 15 15 11 14 11 7 8 6 3 4 4 7 3 4 4 7 3 4 4 7 3 4 3 4 3 4 3 4 4 |
| BP BP BP BP BP BP BP CC MF
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0002283
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002697
GO:0002607
GO:00030670
GO:0042611
GO:0042613
GO:0042613
GO:0042613
GO:0023026
GO:0023026
GO:0023026
GO:0023026
GO:0023026
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
MHC class II protein complex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
antigen binding
MHC class II protein complex binding
MHC protein complex binding
MHC protein complex binding
immunoglobulin receptor binding
immunoglobulin receptor binding | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
8/63
3/63
3/63
3/63
3/63
4/63
4/63
4/63
4
 | BgRatio
499/18670
485/18670
369/18670
369/18670
485/18670
485/18670
488/18670
488/18670
499/18670
224/18670
458/18670
393/19717
164/19717
165/19717
167/19717
16/19717
72/19717
72/19717
73/19717
76/19717
160/17697
16/17697
43/17697 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 3.62817E-111 3.62817E-111 1.18654E-100 1.45234E-100
4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000119512 0.000395083 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.000450681
0.0001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.0015 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.12596E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000908899
0.000908899
0.000908899
0.000908899
0.000957338
0.000183356
0.001760329
0.0004718148
0.00550386
0.014555689
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/ CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/M2B1/ SLAMF8/GSAMSN1/IGLL5 ALCX5/C014/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/ SLC2A5/VAMP8/CD300A CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1//TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5 ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VAMP8/CD300A NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8 CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/PLA2G7/COR01A/SLAMF8 CD86/FCGR2B/IB/ILA-DMB/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5 CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5 CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/ | 17 16 14 11 15 15 15 11 14 11 7 8 6 3 4 4 7 3 4 3 3 4 3 3 4 3 3 |
| BP BP BP BP BP BP BP CC MF
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:006909
GO:0050864
GO:0050864
GO:0002283
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0009897
GO:0009897
GO:0002697
GO:0002607
GO:00191002
GO:00191002
GO:0019864
GO:0023026
GO:0023026
GO:0023026
GO:0023026
GO:0023026
GO:0023026
GO:0023026
GO:0023026
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
dHC class II protein complex
MHC protein complex
tertiary granule membrane
antigen binding
MHC class II protein complex binding
MHC class II protein complex binding
MHC class II protein complex binding
immunoglobulin receptor binding
MHC protein complex binding
MHC protein complex binding
immunoglobulin receptor binding | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
8/63
3/63
3/63
3/63
3/63
3/63
3/63
3
 | BgRatio
499/18670
485/18670
369/18670
369/18670
485/18670
485/18670
488/18670
499/18670
224/18670
458/18670
393/19717
164/19717
164/19717
167/19717
16/19717
16/19717
72/19717
73/19717
75/19717
160/17697
16/17697
43/17697
49/17697 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 3.62817E-111 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000581514 0.000581514
 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.000450681
0.000450681
0.000450681
0.000450681
0.0001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.0015 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.12596E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000263885
0.000908899
0.000908899
0.000908899
0.000957338
0.000183356
0.001760329
0.0004718148
0.0015512762
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXGR4/PLA2G7/CORO1A/
CD300A/IGLV1-44/SLAMF8
CD86/FCGR28/NCKAP1L/ILA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/M2B1/
SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR28/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A
CD14/CYSA/DOCK2/FCGR28/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/
IGLL5
FCGR28/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/M2B1/SLAMF8/SAMSN1/IGLL5
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A
NCKAP1L/ITGB2/RAC2/S100A9/CC13/CC119/CXCR4/PLA2G7/CORO1A/SLAMF8
CD86/FCGR28/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5
CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A
CD14/CYBA/NCKAP1L/ITGB2/MMP9/CORO1A
HLA-DMA/HLA-DMB/HLA-DRA
IGHM/IGKC/IGLC1/IGLS
CYBA/FCGR1B/HLA-DRA/RAC2/VAMP8/CORO1A
HLA-DMA/HLA-DMB/HLA-DRA
IGHM/IGKC/IGLC1/IGLS
CYBA/FCGR1B/HLA-DRA/RAC2/VAMP8/CORO1A
HLA-DMA/HLA-DMB/HLA-DRA
IGHM/IGKC/IGLC1/IGLS
CYBA/FCGR1B/HLA-DRA/HA-DRA
IGHM/IGKC/IGLC1/IGLS
CCL13/CCL18/CCL19
CCL13/CCL18/CCL19
CCL13/CCL18/CCL19
CCL13/CCL18/CCL19
CCL13/CCL18/CCL19
CCL13/CCL18/CCL19
CCL13/CCL18/CCL19 | 17
16
14
11
15
15
15
11
14
11
7
8
6
3
4
4
4
4
7
3
4
4
4
7
3
4
3
4
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
3
3
4
5
5
5
5 |
| BP BP BP BP BP BP BP BP CC MF
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:006909
GO:0050864
GO:0043312
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:00070820
GO:0070820
GO:0070820
GO:0042611
GO:0042611
GO:0042611
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:004261
GO:0003823
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
mHC class II protein complex
MHC protein complex
immunoglobulin complex, circulating
tertiary granule membrane
antigen binding
MHC class II protein complex binding
MHC protein complex binding
immunoglobulin receptor binding
chemokine activity
IgG binding
integrin binding | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/63
7/63
7/63
7/63
7/63
7/63
3/63
4/63
4/63
4/63
4/63
4/63
4/63
4
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
485/18670
488/18670
499/18670
224/18670
458/18670
393/19717
164/19717
167/19717
167/19717
167/19717
72/19717
72/19717
73/19717
73/19717
76/17697
16/17697
43/17697
11/17697
132/17697 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05
 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000581514 0.000589485 0.0003979876 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.000450681
0.0001552276
0.0001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00230924
0.002217009
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.0033384871 | 2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
3.09675E-09
4.12596E-09
4.12596E-09
4.12596E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000263885
0.000263885
0.000263885
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000957338
0.0001760329
0.0001760329
0.00175512762
0.015512762
0.022562939
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL13/CCL19/CXCR4/PLA2G7/COR01A/ CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CXCR4/PLA2G7/COR01A/ CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CXCR01A/CD300A/MZB1/ SLAMFR/SAMSN1/IGLL5 ALX5/CD14/CTSC/CTSS/CYBA/DCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/ SLC2A5/VAMP8/CD300A CD14/CYSA/NDCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ YAMP8/CD300A CD14/CTSC/CTSS/CYBA/DCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ YAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ YAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ YAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ YAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ YAMP8/CD300A CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/CXCR4/FLA2G7/COR01A/SLAMF8 CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/CXCR4/TLR8/IGLL5 CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/SLC2A5/ CYBA/FGGR1B/HLA-DRA/HLA-DRA | 17 16 14 11 15 15 11 14 11 7 8 6 3 4 4 7 3 4 5 4 4 4 4 5 4 4 4 5 4 5 4 <li< td=""></li<> |
| BP BP BP BP BP BP BP BP CC MF
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:006909
GO:0050864
GO:0043312
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:0070820
GO:0070820
GO:0070820
GO:0042611
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042571
GO:0042613
GO:0042613
GO:0042571
GO:0042571
GO:0042571
GO:0042571
GO:0042571
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
mHC class II protein complex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
antigen binding
MHC class II protein complex binding
MHC protein complex binding
MHC protein complex binding
MHC protein complex binding
immunoglobulin receptor binding
CCR chemokine receptor binding
chemokine activity
IgG binding
integrin binding | Gene Ratio
17/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/63
7/63
7/63
8/63
7/63
8/63
3/63
3/63
3/63
3/63
3/63
3/63
3
 | BgRatio
499/18670
485/18670
369/18670
184/18670
485/18670
485/18670
488/18670
489/18670
224/18670
499/18670
393/19717
164/19717
164/19717
16/19717
16/19717
72/19717
72/19717
72/19717
73/19717
76/17697
16/17697
43/17697
43/17697
11/17697 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-10 1.45234E-10
 1.45234E-10 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000581514 0.00058748 0.000395083 0.000395083 0.00138748 0.00138748 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000186714
0.000450681
0.000450681
0.000450681
0.000450681
0.0001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.00230924
0.003384871 |
2.02205E-10
9.53674E-10
9.53674E-10
2.25249E-09
4.12596E-09
4.12596E-09
4.12596E-09
4.12596E-09
1.43634E-08
1.53429E-08
3.90875E-06
4.24541E-05
6.33699E-05
0.000109326
0.000109326
0.000263885
0.000263885
0.000263885
0.000263885
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.000908899
0.00090899
0.00090899
0.00090899
0.00090899
0.00090899
0.00090899
0.00090899
0.00090899
0.00090899
0.0009
0.0009089
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009
0.0009 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL13/CCL19/CXCR4/PLA2G7/COR01A/
CD300A/IGLV1-44/SLAMF8 CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5 ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A5/VAMP8/CD300A CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5 ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8 CD56/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8 CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CYBA/NCKAP1L/ITGB2/ | 17 16 14 11 15 15 11 14 11 7 8 3 4 4 7 3 4 4 7 5 6 7 7 8 6 7 8 8 9 10 11 11 15 11 14 14 14 15 15 16 17 18 19 10 10 10 11 11 14 14 14 14 14 14 15 15 16 16 17 18 16 16 16 16 17 18 14 14 14 14 14 14 14 15 16 16 16 16 16 16 16 |
| BP BP BP BP BP BP BP BP CC MF
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:0043312
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:00030670
GO:00101002
GO:00101002
GO:0042611
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:00050664
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
mHC class II protein complex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
mitigen binding
MHC class II protein complex binding
MHC class II protein complex binding
chemokine receptor binding
immunoglobulin receptor binding
chemokine activity
lgG binding
integrin binding
chemokine receptor binding | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
8/63
7/63
8/63
3/63
4/63
4/63
4/63
4/63
4/63
4/63
4
 | BgRatio
499/18670
485/18670
369/18670
369/18670
485/18670
485/18670
485/18670
499/18670
224/18670
224/18670
393/19717
164/19717
167/19717
167/19717
167/19717
167/19717
72/19717
72/19717
72/19717
72/19717
72/19717
160/17697
16/17697
16/17697
132/17697
132/17697
132/17697
17/17697 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100
 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.00010581514 0.000589485 0.000138748 0.00138748 0.001439003 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.00108227
0.000186714
0.000450681
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00230924
0.00230924
0.00230924
0.00230924
0.003384871
0.03384871
0.03384871 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.0001760329 0.001760329 0.0017512762 0.015512762 0.026507951 0.026507951 5.29626E-06
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL19/CXCR4/PLA2G7/COR01A/
CD300/IGL/1-44/SLAMF8 CD58/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/MZB1/
SLAMF8/SAMSN1/IGLL5 ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/
SLC2A6/VAMP8/CD300A CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/COR01A/CD300A/IGLV1-44/
SLL5 FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5 ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8 CD56/FCGR2B/IGLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8 CD14/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD300A NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8 CD56/FCGR2B/IGLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RCAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/
SLAMF8 CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/RCAC2/CCL19/VAMP8/CD300A CYBA/FCGR1B/HLA-DRA/HAC2/VAMP8/CD300A CYBA/FCGR2B/IGHM/IGKC/IGLC1/IGB2/PTPRC/SLC2A5/VAMP8/CD300A CYBA/FCGR1B/HLA-DRA/HAC2/VAMP8/CD300A CYBA/FCGR1B/HLA-DRA/HLA-DRA HLA-DMA/HLA-DMB/HLA-DRA HLA-DMA/HLA-DMB/HLA-DRA HLA-DMA/HLA-DMB/HLA-DRA< | 17 16 14 11 15 15 15 11 14 11 7 8 6 3 4 4 7 3 4 4 7 3 4 3 2 4 4 5 4 4 4 4 4 5 5 6 6 7 7 8 6 7 7 8 7 7 8 8 4 4 4 7 7 8 6 7 7 8 7 8 7 8 7 8 7 8 7 8 8 9 9 9 <l< td=""></l<> |
| BP BP BP BP BP BP BP BP CC MF
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:006909
GO:0050864
GO:0043312
GO:002283
GO:002283
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:00101002
GO:00101002
GO:0010807
GO:0042611
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:004602
GO:00050664
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
duftC class II protein complex
MHC protein complex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
antigen binding
MHC class II protein complex binding
MHC protein complex binding
CCR chemokine receptor binding
chemokine receptor binding
integrin binding
oxidoreductase activity, acting on NAD(P)H, oxygen as
acceptor | Gene Ratio
17/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
8/63
7/63
8/63
6/63
3/63
4/63
4/63
4/63
4/63
4/63
4
 | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 164/19717 167/19717 16/19717 16/19717 16/19717 16/17697 25/19717 76/19717 160/17697 43/17697 49/17697 132/17697 66/17697 152/8076 60/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100
 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000581514 0.000589485 0.00138748 0.001439003 6.13591E-08 5.55121E-07 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.0023384
0.0023384
0.0023384
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871
0.003384871 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.0001760329 0.0001760329 0.0001760329 0.0015512762 0.015512762 0.015512762 0.026507951 0.026507951 0.026507951 5.29626E-06 2.39578E-05
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL18/CCL18/CCL19/CXCR4/PLA2G7/COR01A/
CD500/GR2B/NCKAP1L/ILA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD500A/MZB1/
SLC2A6/AMB/B/CD500A CD46/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD500A/MZB1/
SLC2A6/AMB/B/CD500A CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/COR01A/CD500A/IGL/1-44/
ISL5 FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD500A/MZB1/SLAMF8/SAMSN1/IGLL5 ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD500A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD500A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD500A ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VAMP8/CD500A NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/COR01A/SLAMF8 CD56/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5 CTSS/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/SLC2000A ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A CD14/CV5BA/NCKAP1L/ITGB2/MIP9/SERPINA1/CD300A CD14/CV5BA/NCKAP1L/ITGB2/MIP9/SERPINA1/CD300A CYBA/FCGR1B/ILA-DRA ILA-DMA/HLA-DMB/ILA-DRA ILA-DMA/HLA-DMB/ILA-DRA IGM1/IGKC/IGLC1/IGLV1-44/IGLL5 ILA-DMA/HLA-DMB/HLA-DRA IGM1/IGKC/IGLC1/IGLV1-44/IGLL5 ILA-DMA | 17
16
14
11
15
15
15
11
14
11
7
8
6
3
4
4
4
7
3
4
4
4
7
3
4
3
4
3
4
3
4
3
2
4
3
2
9
6 |
| BP BP BP BP BP BP BP CC MF
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:006909
GO:0050864
GO:0043312
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:0009897
GO:0019807
GO:0019807
GO:0019807
GO:0042611
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:004203
GO:0005178
GO:0042379
GO:0050664
Hsa04145
hsa05416
hsa05416
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
granule membrane
endocytic vesicle membrane
granule membrane
differentiary granule membrane
grangocytic vesicle membrane
phagocytic vesicle membrane
antigen binding
MHC class II protein complex
immunoglobulin complex, circulating
tertiary granule membrane
grange binding
MHC protein complex binding
MHC class II protein complex binding
chemokine receptor binding
immunoglobulin receptor binding
chemokine activity
lgG binding
integrin binding
oxidoreductase activity, acting on NAD(P)H, oxygen as
acceptor
Phagosome
Viral myocarditis
Tuberculosis | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
11/60
14/60
11/63
7/63
8/63
3/63
3/63
3/63
3/63
3/63
3/63
3
 | BgRatio
499/18670
485/18670
369/18670
369/18670
488/18670
488/18670
488/18670
488/18670
499/18670
224/18670
393/19717
164/19717
164/19717
167/19717
167/19717
167/19717
72/19717
72/19717
72/19717
73/19717
76/17697
16/17697
16/17697
16/17697
11/17697
132/17697
132/17697
11/17697
152/8076
60/8076
180/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100
4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000581514 0.000589485 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00125417
0.000230924
0.00230924
0.001552276
0.001552276
0.001254217
0.000230924
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155525
0.0015555
0.0015555
0.001555
0.0015555
0.0015555
0.001555 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.000957338 0.001760329 0.001760329 0.0017512762 0.015512762 0.015512762 0.026507951 0.026507951 0.026507951 5.29626E-06 2.39578E-05 9.26229E-05 0.00102447
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL18/CCL19/CCR01A/CD300A/MZB1/
SLAMF8/SMMSN1/IGL15
CD88/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CCR01A/CD300A/MZB1/
SLAMF8/SMMSN1/IGL15
ALOXS/CD14/CTS2/CTS5/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/
SLC2A5/NAMP8/CD300A
CD14/CYBA/DCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5
ALOXS/CD14/CTS2/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMP8/CD300A
ALOXS/CD14/CTS2/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMP8/CD300A
ALOXS/CD14/CTS2/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMP8/CD300A
ALOXS/CD14/CTS2/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMP8/CD300A
ALOXS/CD14/CTS2/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMP8/CD300A
ALOXS/CD14/CTS2/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMP8/CD300A
ALOXS/CD14/CTS2/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMP8/CD300A
ALOXS/CD14/CTS2/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/PTPRC/RAC2/CCR1/IL8/GL19/CD300A/IGLY1-44/MZB1/
SLAMF8
CD14/CD86/FCGR2B/IGLM/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCR1/IL8/IGL15
CTS5/CYBA/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/SLC2A5/
VMP8/CD300A
CYBA/FCGR1B/ILA-DMA/HLA-DMA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA
HLA-DMA/HLA-DMB/HLA-DRA | 17
16
14
11
15
15
15
11
14
11
7
8
6
3
4
4
4
7
3
4
3
4
3
4
3
4
3
4
3
2
4
3
2
9
6
8
5 |
| BP BP BP BP BP BP BP BP CC MF MF MF MF MF MF KEGG KEGG KEGG KEGG
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:006909
GO:0050864
GO:0043312
GO:0002283
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:0070820
GO:0070820
GO:0070820
GO:0042611
GO:0042611
GO:0042611
GO:0042611
GO:004261
GO:004261
GO:004261
GO:0030660
GO:003802
GO:0023026
GO:0023026
GO:0023026
GO:0023026
GO:0023026
GO:0023026
GO:0023026
GO:0034987
GO:0034987
GO:0048020
GO:0019864
GO:0042379
GO:005178
GO:0042379
GO:0050644
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
dendocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
ghagocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
ghagocytic vesicle membrane
ghagosome
diremokine receptor binding
chemokine receptor binding
chemokine receptor binding
oxidoreductase activity, acting on NAD(P)H, oxygen as
acceptor
Phagosome
Viral myocarditis
Tuberculosis
Intestinal immune network for IgA production | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/63
7/63
7/63
7/63
7/63
8/63
6/63
3/63
4/63
3/63
4/63
4/63
4/63
4
 | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 489/18670 489/18670 489/18670 488/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 298/19717 16/19717 16/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/17697 11/17697 152/8076 60/8076 180/8076 49/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07
2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.00019581514 0.000589485 0.000138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.001439003 | 3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
2.45605E-08
0.000108227
0.000186714
0.000450681
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.003384871
0.003384871
0.033384871
0.033384871
0.033384871
0.003384871 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.000957338 0.0001760329 0.001760329 0.001760329 0.0017512762 0.02550386 0.015512762 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.000103447 0.000103447 0.000103447 0.000103447
 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/FAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CXR01A/ CD88/FCGR2B/MCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CXR01A/CD300A/M2B1/ SLAMP3/SAMSN1/IGLL5 ALCXX/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/G100A//GLV1-44/ IGLL5 FCGR2B/MCKAP1L/IGHM/IGKC/IGLC1/ITGB2/MPP/COR01A/CD300A/IGLV1-44/ IGLL5 FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/MPP/COR01A/CD300A/IGLV1-44/ IGLL5 FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALCXX/COL4/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALCXX/COL4/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXR4/PLA2G7/COR01A/SLAMF8 CD8#/CGR2B/IA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/CAMP8/CD300A/IGLV1-44/MZB1/ SLAMF8 CD14/CD88/FCGR2B/IAL-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/CXR4/ILB8/GLS CTS:/CYBA/NCKAP1L/ITGB2/MMP9/XBMP8/CD300A CD4/CD88/FCGR2B/IAL-DMA/HA/PMP/SERPINA1/CD300A CD14/CD88/FCGR2B/IAL-DMA/HA/PMP/SERPINA1/CD300A CV14/CFSC/CTSS/CVBA/PCG300A CVBA/FCGR1B/ILA-DRA IGLAS/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A </td <td>17
16
14
11
15
15
15
11
14
11
7
8
6
3
4
4
4
7
3
4
4
4
7
3
4
3
4
3
4
3
2
4
3
2
4
3
2
9
6
8
5
6</td> | 17
16
14
11
15
15
15
11
14
11
7
8
6
3
4
4
4
7
3
4
4
4
7
3
4
3
4
3
4
3
2
4
3
2
4
3
2
9
6
8
5
6 |
| BP BP BP BP BP BP BP BP CC MF MF MF MF MF MF KEGG KEGG KEGG KEGG KEGG
 | ID
GO:0050900
GO:0051249
GO:0042119
GO:0006909
GO:0050864
GO:002283
GO:0002446
GO:0002446
GO:0002697
GO:0002697
GO:0002697
GO:0070820
GO:0070820
GO:0070820
GO:0070820
GO:0030667
GO:0030667
GO:0042611
GO:0042611
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042571
GO:0042571
GO:0042571
GO:0042571
GO:0042571
GO:0042571
GO:0042571
GO:0042302
GO:0023026
GO:0023026
GO:0023026
GO:0023023
GO:0023026
GO:0042379
GO:0048020
GO:0042379
GO:0042379
GO:0042379
GO:0042379
GO:0042379
GO:0042379
GO:0050664
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
diffection complex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
antigen binding
MHC class II protein complex
immunoglobulin receptor binding
MHC protein complex binding
immunoglobulin receptor binding
cCR chemokine receptor binding
chemokine activity
lgG binding
integrin binding
oxidoreductase activity, acting on NAD(P)H, oxygen as
acceptor
Phagosome
Viral myocarditis
Tuberculosis
Intestinal immune network for IgA production
Hematopoietic cell lineage
Allograft rejection | Gene Ratio
17/60
16/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/63
7/63
7/63
8/63
7/63
8/63
3/63
3/63
3/63
3/63
3/63
3/63
3
 | BgRatio
499/18670
485/18670
498/18670
369/18670
184/18670
485/18670
485/18670
488/18670
489/18670
224/18670
393/19717
164/19717
164/19717
167/19717
167/19717
167/19717
167/19717
72/19717
72/19717
72/19717
73/19717
76/17697
16/17697
16/17697
132/17697
11/17697
132/17697
132/17697
152/8076
60/8076
180/8076
180/8076
 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-101 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.00019512 0.000395083 0.000195124 0.000395083 0.000138748 0.00138748 0.00138748 0.001439003 6.13591E-08 5.55121E-07 3.21921E-06 4.7939E-06 1.06974E-05 | 3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.000450681
0.0001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00230924
1.00025877
0.000771375
0.000129841 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.0001760329 0.001760329 0.001760329 0.00175512762
0.0015512762 0.02550386 0.015512762 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.000103447 0.000134471 0.000184671 0.000184671 0.000134471 | CD48/NCKAP1L/IGH/MGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CXR01A/ CD88/FCG782/MCKAP1L/HLA-DMB/IGH/MGKC/IGLC1/PTPRC/RAC2/CCL19/CXR01A/CD300A/M2B1/ ALCXS/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/G100A9/ SIC2AS/MAMP8/CX00000 CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGH//IGKC/IGLC1/ITGB2/PTPRC/CXR01A/CD300A/IGLV1-44/ IGL5 FCGR2B/NCKAP1L/IGH/MIGKC/IGLC1/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/ AMP8/CD300A ALCXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/ AMP8/CD300A ALCXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/ VAMP8/CD300A ALCXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/ VAMP8/CD300A ALCXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/ VAMP8/CD300A ALCXS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTRC/S100A9/SLC2AS/ VAMP8/CD300A ALCXS/CD3/SCARDAPIL/ITGB2/MP9/SERPINA1/PTRC/S100A9/SLC2AS/ ALCXS/CD3/CD4/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTRC/S100A9/SLC2AS/ CD4/CVB4/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/ ALCXS/CTSS/CVBA/POC/CD3/SLC2AS/ CD8/FCGR2B/HLA-DMB/MEX/GRC/IGL1/ITGB2/PTPRC/NCXCAR/TLR8/IGL5 | 17
16
14
11
15
15
15
11
14
11
7
8
6
3
4
4
4
7
3
4
4
7
3
4
3
4
4
7
3
4
3
2
4
3
2
4
3
2
4
3
2
4
3
2
4
3
2
4
3
2
4
3
2
4
3
2
4
3
2
4
3
2
4
3
2
4
3
2
4
5
6
4
5
6
6
7
6
7
7
7
7
8
6
7
7
7
8
7
7
8
7
7
8
7
8 |
| BP BP BP BP BP BP BP CC MF MF MF MF MF MF KEGG
 | ID GO:0050900 GO:0051249 GO:0042119 GO:0050864 GO:0012283 GO:0002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00030670 GO:00030661 GO:0030662 GO:0042613 GO:0030660 GO:0030670 GO:0030670 GO:0030670 GO:0030670 GO:0030823 GO:0030823 GO:0030873 GO:0030873 GO:0005178 GO:00050664 hsa0414
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
ghagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
ghagocytic vesicle membrane
phagocytic vesicle membrane
ghagocytic vesicle membrane
ghago | Gene Ratio
17/60
16/60
14/60
14/60
15/60
15/60
15/60
15/60
11/63
7/63
8/63
7/63
8/63
3/63
3/63
3/63
3/63
3/63
3/63
3
 | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 485/18670 488/18670 489/18670 489/18670 489/18670 489/18670 499/18670 224/18670 393/19717 164/19717 185/19717 167/19717 167/19717 167/19717 16/17697 16/17697 16/17697 16/17697 132/17697 132/17697 152/8076 60/8076 180/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 38/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000589485 0.000138748 0.000138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.001439003 6.13591E-08 5.55121E-07 3.21921E-06 <tr< td=""><td>3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.00108227
0.00186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.000258877
0.000771375
0.000771375
0.000771375</td><td> 2.02205E-10
9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.0001760329 0.001760329 0.001760329 0.00175512762 0.015512762 0.015512762 0.026507951 5.29626E-06 2.39578E-05 0.000103447 0.000184671 0.000184671 0.000550263 0.000184671 0.000550263 0.000645734 </td><td>CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL19/CCL19/CCR1/PLA2G7/COR01A/CD300A/NZB1/ CD58/FCG782P/NCKAP1L/ILA.DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/NZB1/ SLAMF8/SAMSN1/IGLL5 ALDX3/CD14/CTS/CCTS9/CV58/DOCK2/FCGR2B/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/TGH//IGKC/IGLC1/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/NZB1/SLAMF8/SAMSN1/IGLL5 ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A CD4/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/SCR04/TLB8/IGLL5 CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A</td><td>17
16
14
11
15
15
15
11
14
11
7
8
6
3
4
4
4
7
3
4
4
7
3
4
3
4
3
2
4
3
2
9
6
8
5
6
4
5
6
4
5
4</td></tr<> | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.00108227
0.00186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.000258877
0.000771375
0.000771375
0.000771375 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.0001760329 0.001760329 0.001760329 0.00175512762 0.015512762 0.015512762 0.026507951 5.29626E-06 2.39578E-05 0.000103447 0.000184671 0.000184671 0.000550263 0.000184671 0.000550263 0.000645734 | CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL19/CCL19/CCR1/PLA2G7/COR01A/CD300A/NZB1/ CD58/FCG782P/NCKAP1L/ILA.DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/COR01A/CD300A/NZB1/ SLAMF8/SAMSN1/IGLL5 ALDX3/CD14/CTS/CCTS9/CV58/DOCK2/FCGR2B/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/TGH//IGKC/IGLC1/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/NZB1/SLAMF8/SAMSN1/IGLL5
ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A ALDX3/CD14/CTS/CCTS9/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMMP8/CD300A CD4/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/SCR04/TLB8/IGLL5 CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A CD14/CVBA/NCKAP1L/TGB2/MMP9/SERPINA1/CD300A | 17
16
14
11
15
15
15
11
14
11
7
8
6
3
4
4
4
7
3
4
4
7
3
4
3
4
3
2
4
3
2
9
6
8
5
6
4
5
6
4
5
4 |
| BPBPBPBPBPBPBPCC <td>ID GO:0050900 GO:0051249 GO:0042119 GO:0050864 GO:0050864 GO:002283 GO:0002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00030670 GO:00030670 GO:0030667 GO:0030667 GO:0042613 GO:0030670 GO:0030670 GO:0030670 GO:0030670 GO:0030823 GO:0042613 GO:0030870 GO:0030870 GO:0042019 GO:00423026 GO:0050664 hsa04145 hsa05152 hsa04640 hsa05140 hsa05330 hsa05140 hsa05332 hsa05332</td> <td>leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
matigen binding
MHC class II protein complex
immunoglobulin receptor binding
MHC class II protein complex binding
MHC class II protein complex binding
cCR chemokine receptor binding
MHC class II protein complex binding
immunoglobulin receptor binding
cCR chemokine receptor binding
cCR chemokine receptor binding
integrin binding
integrin binding
integrin binding
integrin binding
chemokine receptor binding
chemokin</td> <td>Gene Ratio
17/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/63
7/63
7/63
7/63
8/63
7/63
8/63
3/63
3/63
3/63
3/63
3/63
3/63
3</td> <td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 499/18670 224/18670 458/18670 393/19717 164/19717 164/19717 167/19717 167/19717 16/17697 25/19717 76/19717 16/17697 16/17697 16/17697 132/17697 132/17697 152/8076 60/8076 180/8076 180/8076 38/8076 38/8076 38/8076 43/8076</td> <td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.27284E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000395083 0.000395083 0.000138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.001439003 6.13591E-08 5.55121E-07 3.21921E-06</td> <td>3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.0002509
0.0002500
0.000771375
0.000771375
0.000771375
0.000771375</td> <td> 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.0001034861 0.026507951 5.29626E-06 2.39578E-05 9.26229E-05 0.000103447 0.000184671 0.000550263 0.000550263 0.000550263 0.000550263 0.000550263 0.000645734 0.000645734 </td> <td>CD49/NCKAP1L/IGH/MIGKC/GLG1/ITGB2/RAC2/S100A9/CC13/CC119/CC19/CCR4/PL/2G7/CCR01A/
CD300A/IGL14/4/SLAMF8/ CD49/NCKAP1L/IGH/MIGKC/GLG1/PTPRC/RAC2/CC119/CCR01A/CD300A/IZB1/ SLAMF8/SAMSN1/GLL5 ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A CD3/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A CD14/CD8/RCGR2B/HLA-DMB/RCC/GLC1/ITGB2/PTPRC/XCCR4/TLR8/GLL5 CTS3/CYBA/NCKAP1L/ITGB2/MP9/SERPINA1/CD300A CD14/CD8/RCGAP1L/ITGB2/MP9/SERPINA1/CD300A CD14/CD8/RCGAP1L/ITGB2/MP9/SERPINA1/CD300A CD14/CD8/RCGAP1L/ITGB2/MP9/SERPINA1/CD300A CD14/CD8/RCGAP1L/ITGB2/MP9/SERPINA1/CD300A CD14/CD8/RCGAP1L/ITGB2/TPRC/XCGA/MP8/CD300A</td> <td> 17 16 14 11 15 15 11 14 11 7 8 6 3 4 4 7 3 4 4 7 3 4 4 7 3 4 3 2 4 4 7 5 6 4 5 4 4 4 </td>
 | ID GO:0050900 GO:0051249 GO:0042119 GO:0050864 GO:0050864 GO:002283 GO:0002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00030670 GO:00030670 GO:0030667 GO:0030667 GO:0042613 GO:0030670 GO:0030670 GO:0030670 GO:0030670 GO:0030823 GO:0042613 GO:0030870 GO:0030870 GO:0042019 GO:00423026 GO:0050664 hsa04145 hsa05152 hsa04640 hsa05140 hsa05330 hsa05140 hsa05332 hsa05332
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
matigen binding
MHC class II protein complex
immunoglobulin receptor binding
MHC class II protein complex binding
MHC class II protein complex binding
cCR chemokine receptor binding
MHC class II protein complex binding
immunoglobulin receptor binding
cCR chemokine receptor binding
cCR chemokine receptor binding
integrin binding
integrin binding
integrin binding
integrin binding
chemokine receptor binding
chemokin | Gene Ratio
17/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/63
7/63
7/63
7/63
8/63
7/63
8/63
3/63
3/63
3/63
3/63
3/63
3/63
3
 | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 499/18670 224/18670 458/18670 393/19717 164/19717 164/19717 167/19717 167/19717 16/17697 25/19717 76/19717 16/17697 16/17697 16/17697 132/17697 132/17697 152/8076 60/8076 180/8076 180/8076 38/8076 38/8076 38/8076 43/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.27284E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000395083 0.000395083 0.000138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.001439003 6.13591E-08 5.55121E-07 3.21921E-06
 | 3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.0002509
0.0002500
0.000771375
0.000771375
0.000771375
0.000771375 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.0001034861 0.026507951 5.29626E-06 2.39578E-05 9.26229E-05 0.000103447 0.000184671 0.000550263 0.000550263 0.000550263 0.000550263 0.000550263 0.000645734 0.000645734 | CD49/NCKAP1L/IGH/MIGKC/GLG1/ITGB2/RAC2/S100A9/CC13/CC119/CC19/CCR4/PL/2G7/CCR01A/
CD300A/IGL14/4/SLAMF8/ CD49/NCKAP1L/IGH/MIGKC/GLG1/PTPRC/RAC2/CC119/CCR01A/CD300A/IZB1/ SLAMF8/SAMSN1/GLL5 ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A ALCX5/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A CD3/CD14/CTS2/CTS3/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CO300A CD14/CD8/RCGR2B/HLA-DMB/RCC/GLC1/ITGB2/PTPRC/XCCR4/TLR8/GLL5 CTS3/CYBA/NCKAP1L/ITGB2/MP9/SERPINA1/CD300A CD14/CD8/RCGAP1L/ITGB2/MP9/SERPINA1/CD300A
 CD14/CD8/RCGAP1L/ITGB2/MP9/SERPINA1/CD300A CD14/CD8/RCGAP1L/ITGB2/MP9/SERPINA1/CD300A CD14/CD8/RCGAP1L/ITGB2/MP9/SERPINA1/CD300A CD14/CD8/RCGAP1L/ITGB2/TPRC/XCGA/MP8/CD300A | 17 16 14 11 15 15 11 14 11 7 8 6 3 4 4 7 3 4 4 7 3 4 4 7 3 4 3 2 4 4 7 5 6 4 5 4 4 4 |
| BP BP BP BP BP BP BP CC
 | ID GO:0050900 GO:0051249 GO:0042119 GO:0050864 GO:0050864 GO:002283 GO:0002283 GO:0002697 GO:00030666 GO:0030666 GO:0042611 GO:0030670 GO:0030809 GO:00423026 GO:00423026 GO:00423026 GO:00423026 GO:0042379 GO:0042302 Hsa041
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
complex binding
MHC class II protein complex
MHC protein complex binding
MHC class II protein complex binding
CCR chemokine receptor binding
CCR chemokine receptor binding
chemokine receptor binding
integrin binding
chemokine receptor binding
chemokine receptor binding
integrin binding
integrin binding
chemokine receptor binding
integrin binding
integrin binding
integrin binding
integrin binding
integrin binding
integrin binding
integrin binding
chemokine receptor binding
integrin bindin | Gene Ratio
17/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/63
7/63
7/63
7/63
8/63
6/63
3/63
3/63
3/63
3/63
3/63
3
 | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 499/18670 224/18670 499/18670 224/18670 393/19717 164/19717 165/19717 167/19717 16/19717 16/19717 16/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 60/8076 180/8076 99/8076 38/8076 7/8076 42/8076 93/8076 38/8076 93/8076 38/8076 93/8076 38/8076 93/8076 38/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 6.80025E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.00019581514 0.000395083 0.0001979876 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.0001439003
 | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.0002509
0.0002509
0.000905209
0.000905209
0.000905209
0.000905209
0.000905209 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.0001760329 0.001760329 0.001760329 0.0017512762 0.0015512762 0.015512762 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.000103447 0.000103447 0.0001846714 0.000550263 0.000103447 0.000550263 0.000103447 0.000645734 0.000645734 0.00086406
 | CD48/NCKAP1L/IGH/MIGKC/GLG1/ITGB2/RAC2/S100A9/CC13/CC119/CC19/CCR4/PLA2G7/CCR014/ CD58/FCG2R2B/CKAP1L/IL-D/BB//GH/MIGKC/GLG1/PTPRC/RAC2/CC119/CCR014/CD300A/M2B1/ SLAMFB/SAMSN1/GL5 ALOSS/CD14/CT5C/CT5S/CYBA/DOCK2/FCGR2B/NCKAP1L/TGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/GB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/TGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALOSS/CD14/CT5C/CT5S/CYBA/DOCK2/NCKAP1L/TGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALOSS/CD14/CT5C/CT5S/CYBA/DOCK2/NCKAP1L/TGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALOSS/CD14/CT5C/CT5S/CYBA/DOCK2/NCKAP1L/TGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALOSS/CD14/CT5C/CT5S/CYBA/DOCK2/NCKAP1L/TGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ AUMP8/CD300A ALOSS/CD14/CT5C/CT5S/CYBA/DOCK2/NCKAP1L/TGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ AUMP8/CD300A CD14/CT5C/CT5S/CYBA/DOCK2/NCKAP1L/TGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CD300A CD14/CT5C/CT5S/NCWBA/DOCK2/NCKAP1L/TGB2/MIP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VMAP8/CD300A CD14/CT5C/CTSS/NCWBA/PG/CD300A CD14/CT5C/CTSS/NCWAP1/CG2/CM4P8/CD300A CD14/CT5C/CTSS/NCWAP1/CG2/CM4P8/CD300A CD14/CT5S/NCKAP1L/TGB2/TPRC/CXCR4/TL88/GL1 G14/CT5S/NCWAP1/CG2/CM4P8/CC300A (TACTSS/NCKAP1L/TGB2/TPRC/CXCR4/TL88/ | 17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 7 8 9 6 3 4 7 8 9 6 13 2 9 6 5 6 4 7 8 16 17 18 19 11 12 13 14 15 16 17 |
| BPBPBPBPBPBPBPCC <td>ID GO:0050900 GO:001249 GO:0006909 GO:0050864 GO:002283 GO:0002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00070820 GO:0030667 GO:0030667 GO:0042611 GO:0030667 GO:0030667 GO:0030670 GO:0042611 GO:0030670 GO:0030823 GO:0042372 GO:0042372 GO:00423023 GO:0042379 GO:0042379 GO:0042379 GO:0042379 GO:0005178 Hsa04145 Hsa05416 Hsa05416 Hsa05416 Hsa04472 Hsa04472 Hsa04447 Hsa05332 Hsa045140 Hsa053323</td> <td>leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
endocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
granule
ficolin-1 ething manute
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
granule membrane
tertiary granule membrane
phagocytic vesicle membrane
granule membrane
chemokine activity
lgG binding
immunoglobulin receptor binding
CCR chemokine receptor binding
chemokine receptor binding
chemokine activity
lgG binding
integrin binding
circle binding
circle binding
circle binding
difference activity, acting on NAD(PH, oxygen as
acceptor
Phagosome
Viral myocarditis
Tuberculosis
Intestinal immune network for IgA production
Hematopoietic cell lineage
Allograft rejection
Leishmaniasis
Graft-versus-host disease
Type I diabetes mellitus
Cell adhesion molecules</td> <td>Gene Ratio
17/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/63
7/63
7/63
7/63
8/63
6/63
3/63
3/63
3/63
3/63
3/63
3</td> <td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 489/18670 488/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 167/19717 16/19717 25/19717 76/19717 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 60/8076 180/8076 49/8076 38/8076 77/8076 42/8076 38/8076 38/8076 38/8076 38/8076 39/8076 38/8076 39/8076 38/8076 38/8076 39/8076 38/8076 39/8076 39/8076 39/8076 <</td> <td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-05 6.80025E-05 6.80025E-05 6.80025E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.00019581514 0.000395083 0.0001979876 0.000138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.0001439003 6.13591E-08 5</td> <td>3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
2.29925E-08
2.45605E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.000450681
0.0001552276
0.0001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.000230924
1000000000000000000000000000000000000</td> <td> 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000957338 0.0001760329 0.0001760329 0.001760329 0.001750364 0.001550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.0000645734 0.000645734 0.000645734 0.000645734 0.000645734 0.000866406 0.000866406 0.000866406 0.000923419 </td> <td>CD48/NCKAP1L/IGH/MIGKC/GLC1/ITGB2/RAC2/S100A9/CC13/CC119/CCR4/PLA2G7/CORO1A/CD300A/M281/ CD48/PCG2RE9/CR54/PL/LA-DM8/IGH/MIGKC/GLC1/PTPRC/RAC2/CC119/CORO1A/CD300A/M281/ ALDXIC014/CT52/CTS3/CYBA/DOCK2/PCGR28/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD4/CYGBA/DOCK2/PCGR28/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD4/CYGBA/DOCK2/PCGR28/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALDXIC014/CT52/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC014/CT52/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC014/CT52/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC014/CT52/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CAC/TS7/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CAC/TS7/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTCTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTCTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CSTCR1/ITGB2/MP9/SERPINA1/DE/CXCR4/PL2G7/C</td> <td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 13 2 9 6 3 4 7 8 10 7 8 13 2 9 6 5 6 7 8 10 11 12 13 14 15 16 17 18 19 10 <</td>
 | ID GO:0050900 GO:001249 GO:0006909 GO:0050864 GO:002283 GO:0002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00070820 GO:0030667 GO:0030667 GO:0042611 GO:0030667 GO:0030667 GO:0030670 GO:0042611 GO:0030670 GO:0030823 GO:0042372 GO:0042372 GO:00423023 GO:0042379 GO:0042379 GO:0042379 GO:0042379 GO:0005178 Hsa04145 Hsa05416 Hsa05416 Hsa05416 Hsa04472 Hsa04472 Hsa04447 Hsa05332 Hsa045140 Hsa053323
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
endocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
granule
ficolin-1 ething manute
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
granule membrane
tertiary granule membrane
phagocytic vesicle membrane
granule membrane
chemokine activity
lgG binding
immunoglobulin receptor binding
CCR chemokine receptor binding
chemokine receptor binding
chemokine activity
lgG binding
integrin binding
circle binding
circle binding
circle binding
difference activity, acting on NAD(PH, oxygen as
acceptor
Phagosome
Viral myocarditis
Tuberculosis
Intestinal immune network for IgA production
Hematopoietic cell lineage
Allograft rejection
Leishmaniasis
Graft-versus-host disease
Type I diabetes mellitus
Cell adhesion molecules | Gene Ratio
17/60
16/60
14/60
11/60
15/60
15/60
15/60
15/60
11/63
7/63
7/63
7/63
8/63
6/63
3/63
3/63
3/63
3/63
3/63
3
 | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 489/18670 488/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 167/19717 16/19717 25/19717 76/19717 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 60/8076 180/8076 49/8076 38/8076 77/8076 42/8076 38/8076 38/8076 38/8076 38/8076 39/8076 38/8076 39/8076 38/8076 38/8076 39/8076 38/8076 39/8076 39/8076 39/8076 < | 1.85598E-13 1.75971E-12
 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-05 6.80025E-05 6.80025E-05 6.80025E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.00019581514 0.000395083 0.0001979876 0.000138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.0001439003 6.13591E-08 5 | 3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
2.29925E-08
2.45605E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.000450681
0.0001552276
0.0001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.000230924
1000000000000000000000000000000000000 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000957338 0.0001760329 0.0001760329 0.001760329 0.001750364 0.001550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447
0.000550263 0.000103447 0.000550263 0.0000645734 0.000645734 0.000645734 0.000645734 0.000645734 0.000866406 0.000866406 0.000866406 0.000923419 | CD48/NCKAP1L/IGH/MIGKC/GLC1/ITGB2/RAC2/S100A9/CC13/CC119/CCR4/PLA2G7/CORO1A/CD300A/M281/ CD48/PCG2RE9/CR54/PL/LA-DM8/IGH/MIGKC/GLC1/PTPRC/RAC2/CC119/CORO1A/CD300A/M281/ ALDXIC014/CT52/CTS3/CYBA/DOCK2/PCGR28/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD4/CYGBA/DOCK2/PCGR28/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ CD4/CYGBA/DOCK2/PCGR28/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALDXIC014/CT52/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC014/CT52/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC014/CT52/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC014/CT52/CTS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CAC/TS7/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CAC/TS7/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTCTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CTCTSC/TS5/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/ ALMXIC03/CSTCR1/ITGB2/MP9/SERPINA1/DE/CXCR4/PL2G7/C | 17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 13 2 9 6 3 4 7 8 10 7 8 13 2 9 6 5 6 7 8 10 11 12 13 14 15 16 17 18 19 10 < |
| BP BP BP BP BP BP BP BP CC BP BP BP BP BP BP BP BP GC CC CC GC
 | ID
GO:0050900
GO:0042119
GO:0042119
GO:0050864
GO:0050864
GO:002283
GO:0002446
GO:0002446
GO:0002697
GO:0002697
GO:00070820
GO:0070820
GO:0070820
GO:0070821
GO:0030667
GO:0030667
GO:0042611
GO:0042611
GO:0042611
GO:0042613
GO:0042613
GO:0042613
GO:0042613
GO:0042571
GO:0042613
GO:0042571
GO:0042571
GO:0030670
GO:0030670
GO:0030800
GO:0019864
GO:0023023
GO:0042379
GO:0019864
GO:0019864
GO:0019864
GO:0019864
GO:0019864
GO:0019864
GO:0042379
GO:0050664
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immune response
neutrophil mediated immune response
neutrophil mediated immune response
neutrophil mediated immune response
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
medicytic vesicel membrane
endocytic vesicel membrane
medicytic vesicel membrane
phagocytic vesicel membrane
phagocytic vesicel membrane
phagocytic vesicel membrane
catigen binding
MHC class II protein complex
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicel membrane
catigen binding
MHC class II protein complex binding
MHC protein complex binding
MHC protein complex binding
cCR chemokine activity
lgG binding
integrin binding
chemokine receptor binding
coxidoreductase activity, acting on NAD(P)H, oxygen as
acceptor
Phagosome
Viral myocarditis
Tuberculosis
Intestinal immune network for IgA production
Hematopoietic cell lineage
Allograft rejection
Leishmaniasis
Graft-versus-host disease
Type I diabetes meliitus
Cell adhesion molecules
Rheumatoid arthritis
Staphylococcus aureus infection
Autoimmune thyroid disease | Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 15/60 11/60 14/60 11/60 15/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 3/59 <td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 489/18670 489/18670 489/18670 489/18670 489/18670 224/18670 499/18670 393/19717 164/19717 185/19717 16/19717 25/19717 16/19717 25/19717 76/19717 160/17697 16/17697 16/17697 16/17697 16/17697 132/17697 66/17697 132/17697 152/8076 60/8076 38/8076 38/8076 38/8076 38/8076 39/8076 38/8076 39/8076 38/8076 38/8076 39/8076 39/8076 39/8076 39/8076 39/8076</td> <td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-05 0.6005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000138748 0.000138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.001439003 6.13591E-08 5.55121E-07 3.21921E-06 1.06974E-05 6.12967E-05 6.12967E-05 <t< td=""><td>3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.00186714
0.000450681
0.001450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155525
0.00155525
0.00155555
0.001555555
0.001555555
0.001555555</td><td> 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000957338 0.001760329 0.001760329 0.00175512762 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.000103447 0.000103447 0.000550263 0.000645734 0.000645734 0.00086406 0.00086406 0.000923419 0.000960106 2.0005 </td><td>CD48/NCKAP1L/IGH/MIGKC/IGLC1/TGB2/RAC2/S100A9/CCL19/CCL19/CCR14/PLA2G7/COR01A/
CD300/IGU144/SLA/RS
CD48/PCCR28/RCKAP1L/IL-D/MR/IGH/MIGKC/IGLC1/TFTR/C/RAC2/CCL19/COR01A/CD300A/MZ81/
SLA/RS/MIP/CD300A CD14/CYBA/DOCK2/PCGR28/NCKAP1L/IGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A CD14/CYBA/DOCK2/PCGR28/NCKAP1L/IGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A CD14/CYBA/DOCK2/PCGR28/NCKAP1L/IGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A CD3/CYCRAPIL/ITGB2/MP9/CD300A ALOS/CD14/CTSC/CTSS/WAPA/MAP/CD300A CD4/CVBA/NCKAP1L/ITGB2/MMP9/MAP/CC300A ALOS/CD14/CTSC/CTSS/WMR9/MMP3/CD300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB</td><td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 3 4 7 8 9 6 11 7 8 3 4 7 8 10 11 12 9 6 5 4 5 4 5 4 <</td></t<></td> | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 489/18670 489/18670 489/18670 489/18670 489/18670 224/18670 499/18670 393/19717 164/19717 185/19717 16/19717 25/19717 16/19717 25/19717 76/19717 160/17697 16/17697 16/17697 16/17697 16/17697 132/17697 66/17697 132/17697 152/8076 60/8076 38/8076 38/8076 38/8076 38/8076 39/8076 38/8076 39/8076 38/8076 38/8076 39/8076 39/8076 39/8076 39/8076 39/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-05
 0.6005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000138748 0.000138748 0.00138748 0.00138748 0.00138748 0.00138748 0.00138748 0.001439003 6.13591E-08 5.55121E-07 3.21921E-06 1.06974E-05 6.12967E-05 6.12967E-05 <t< td=""><td>3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.00186714
0.000450681
0.001450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155525
0.00155525
0.00155555
0.001555555
0.001555555
0.001555555</td><td> 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000957338 0.001760329 0.001760329 0.00175512762 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.000103447 0.000103447 0.000550263 0.000645734 0.000645734 0.00086406 0.00086406 0.000923419 0.000960106 2.0005 </td><td>CD48/NCKAP1L/IGH/MIGKC/IGLC1/TGB2/RAC2/S100A9/CCL19/CCL19/CCR14/PLA2G7/COR01A/
CD300/IGU144/SLA/RS CD48/PCCR28/RCKAP1L/IL-D/MR/IGH/MIGKC/IGLC1/TFTR/C/RAC2/CCL19/COR01A/CD300A/MZ81/
SLA/RS/MIP/CD300A CD14/CYBA/DOCK2/PCGR28/NCKAP1L/IGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A CD14/CYBA/DOCK2/PCGR28/NCKAP1L/IGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A CD14/CYBA/DOCK2/PCGR28/NCKAP1L/IGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A CD3/CYCRAPIL/ITGB2/MP9/CD300A ALOS/CD14/CTSC/CTSS/WAPA/MAP/CD300A CD4/CVBA/NCKAP1L/ITGB2/MMP9/MAP/CC300A ALOS/CD14/CTSC/CTSS/WMR9/MMP3/CD300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB</td><td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 3 4 7 8 9 6 11 7 8 3 4 7 8 10 11 12 9 6 5 4 5 4 5 4 <</td></t<> | 3.23684E-10
1.52661E-09
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.00186714
0.000450681
0.001450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155525
0.00155525
0.00155555
0.001555555
0.001555555
0.001555555 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000957338 0.001760329 0.001760329 0.00175512762 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.000103447 0.000103447 0.000550263 0.000645734 0.000645734 0.00086406 0.00086406 0.000923419 0.000960106 2.0005
 | CD48/NCKAP1L/IGH/MIGKC/IGLC1/TGB2/RAC2/S100A9/CCL19/CCL19/CCR14/PLA2G7/COR01A/
CD300/IGU144/SLA/RS CD48/PCCR28/RCKAP1L/IL-D/MR/IGH/MIGKC/IGLC1/TFTR/C/RAC2/CCL19/COR01A/CD300A/MZ81/
SLA/RS/MIP/CD300A CD14/CYBA/DOCK2/PCGR28/NCKAP1L/IGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A CD14/CYBA/DOCK2/PCGR28/NCKAP1L/IGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A CD14/CYBA/DOCK2/PCGR28/NCKAP1L/IGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A ALOS/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
VMR9/CD300A CD3/CYCRAPIL/ITGB2/MP9/CD300A ALOS/CD14/CTSC/CTSS/WAPA/MAP/CD300A CD4/CVBA/NCKAP1L/ITGB2/MMP9/MAP/CC300A ALOS/CD14/CTSC/CTSS/WMR9/MMP3/CD300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB2/MMP3/MAP/CC300A CD4/CVBA/NCKAP1L/ITGB | 17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 3 4 7 8 9 6 11 7 8 3 4 7 8 10 11 12 9 6 5 4 5 4 5 4 < |
| BP BP BP BP BP BP BP CC
 | ID GO:0050900 GO:0051249 GO:006909 GO:0050864 GO:002283 GO:0002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00030505 GO:00030670 GO:001002 GO:00306661 GO:0042613 GO:0042613 GO:0030666 GO:0030670 GO:0030823 GO:0042571 GO:0030823 GO:00423026 GO:00423026 GO:00423026 GO:0050664 hsa04145 hsa05152 hsa045140 hsa05330 hsa045140 hsa053140 hsa053140 hsa053140 hsa05320 hsa05320 hsa05320 hsa04670
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
ficoline activity
ficoline activity
ficoline activity
differentiary granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
ficoline activity
figa binding
MHC class II protein complex binding
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
antigen binding
dimmunoglobulin receptor binding
cCER chemokine receptor binding
chemokine activity
figa binding
timmunoglobulin receptor binding
chemokine activity
figa binding
timmunoglobulin receptor binding
chemokine activity
figa binding
chemokine activity
figa binding
chemokine activity
figa binding
chemokine activity
figa binding
chemokine activity
figa binding
chemokine activity
figa binding
chemokine receptor binding
chemokine receptor binding
chemokine receptor binding
chemokine receptor binding
chemokine receptor binding
chemokine receptor binding
coxidoreductase activity, acting on NAD(P)H, oxygen as
acceptor
Phagosome
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
firateritis
fi | Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 15/60 11/60 14/60 17/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 4/63 3/59 3/52 3/52 5/42
 | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 499/18670 224/18670 458/18670 393/19717 164/19717 164/19717 167/19717 167/19717 16/19717 16/19717 16/17697 25/19717 72/19717 72/19717 16/17697 16/17697 152/8076 60/8076 180/8076 99/8076 38/8076 77/8076 42/8076 93/8076 38/8076 73/8076 43/8076 93/8076 93/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076 <t< td=""><td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.0001979876 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.0001439003 6.13591E-08 5.55121E-07 3.21921E-06</td><td>3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.00108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155525
0.00155525
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.00155555
0.00155555
0.001555555
0.001555555
0.001555555
0.001555555
0.0015555</td><td>2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.0001760329 0.000183356 0.0001760329 0.0014555689 0.001550263 0.0026507951 5.29626E-06 2.39578E-05 9.26229E-05 0.000103447 0.000550263 0.0001846714 0.0001846714 0.000086406 0.000086406 0.000086406 0.000986406 0.000986406 0.000960106 0.000960106</td><td>CD49N0CKIP1L/GHM/GKC/GLC1/TGB2/PAC2/S100A9/CCL19/CCR19/CCR29/COL19/CCR300A/M2B1/ CD58FFCG2R58/CKAP1L/HCAMB/GKM/GKC/GLC1/TFRC/FAC2/CCL19/CCR01A/CD300A/M2B1/ SLAMS/GD1A/CTSC/CTSS/CVBA/DOCK2/FCGR28/NCKAP1L/TGB2/MP9/95ERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CVF0A/DOCK2/FCGR28/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CVF0A/DOCK2/FCGR28/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CD8/FCGR28/NCKAP1L/TGB2/MP9/ADOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CVSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CD8/FCGR28/NCKAP1L/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CD8/FCGR28/NCKAP1L/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CD8/FCGR28/NCKAP1L/TGB2/PTPRC/XCRATLR8/GLL5 CD14/CD8/FCGR28/NCKAP1L/TGB2/MP9/SERPINA1/E8/GLL5 CD14/CTSS/CVBA/FCGR020A</td><td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 3 4 7 8 9 6 13 2 9 6 5 4 5 4 5 14 15 16 17 18 19 14 15 16 17 18 </td></t<> | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100
 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.0001979876 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.0001439003 6.13591E-08 5.55121E-07 3.21921E-06 | 3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.00108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155525
0.00155525
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.00155555
0.00155555
0.001555555
0.001555555
0.001555555
0.001555555
0.0015555 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.0001760329 0.000183356 0.0001760329 0.0014555689 0.001550263 0.0026507951 5.29626E-06 2.39578E-05 9.26229E-05 0.000103447 0.000550263 0.0001846714 0.0001846714 0.000086406 0.000086406 0.000086406 0.000986406 0.000986406 0.000960106 0.000960106
 | CD49N0CKIP1L/GHM/GKC/GLC1/TGB2/PAC2/S100A9/CCL19/CCR19/CCR29/COL19/CCR300A/M2B1/ CD58FFCG2R58/CKAP1L/HCAMB/GKM/GKC/GLC1/TFRC/FAC2/CCL19/CCR01A/CD300A/M2B1/ SLAMS/GD1A/CTSC/CTSS/CVBA/DOCK2/FCGR28/NCKAP1L/TGB2/MP9/95ERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CVF0A/DOCK2/FCGR28/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CVF0A/DOCK2/FCGR28/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ ALXXS/CD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CD8/FCGR28/NCKAP1L/TGB2/MP9/ADOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CVSC/CTSS/CVBA/DOCK2/NCKAP1L/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CD8/FCGR28/NCKAP1L/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CD8/FCGR28/NCKAP1L/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A9/ CD14/CD8/FCGR28/NCKAP1L/TGB2/PTPRC/XCRATLR8/GLL5 CD14/CD8/FCGR28/NCKAP1L/TGB2/MP9/SERPINA1/E8/GLL5 CD14/CTSS/CVBA/FCGR020A | 17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 3 4 7 8 9 6 13 2 9 6 5 4 5 4 5 14 15 16 17 18 19 14 15 16 17 18 |
| BPBPBPBPBPBPBPCC <td>ID GO:0050900 GO:0051249 GO:0042119 GO:0050864 GO:0024312 GO:0002283 GO:0002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00030670 GO:0030667 GO:0030667 GO:0042611 GO:0030667 GO:0030670 GO:0042611 GO:0030670 GO:0030670 GO:0042611 GO:0030670 GO:0030670 GO:0042611 SO:00423023 GO:00423023 GO:0042379 GO:0050664 Nsa04145 Nsa04145 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140</td> <td>leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
grange binding
MHC class II protein complex
immunoglobulin receptor binding
tertiary granule membrane
phagocytic vesicle membrane
grange binding
MHC class II protein complex binding
cCRC chemokine receptor binding
chemokine receptor binding
chemok</td> <td>Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 11/60 11/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 3/59 3/52 3/42 5/42 6/42 5/42</td> <td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 489/18670 489/18670 499/18670 224/18670 499/18670 224/18670 499/18670 224/18670 393/19717 164/19717 185/19717 167/19717 16/19717 16/19717 16/19717 16/19717 16/17697 16/17697 16/17697 16/17697 132/17697 132/17697 132/17697 152/8076 60/8076 180/8076 99/8076 38/707 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076</td> <td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.00018131 0.00018131 <</td> <td>3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155525
0.00155525
0.00155525
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.00155555
0.00155555
0.00155555
0.00155555</td> <td> 2.02205E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.00090899 0.00090899 0.00090894 0.000908045734 0.000908045734 0.000960106 0.000960106 0.000960106 0.0002316483 </td> <td>CDBRNCKAP1L/LIGHMUGKC/GLC1/ITGB2/RAC2/S100A9/CCL19/CCR14/CD3000A/X2D1/ CDBRYGGREB/RACAP1L/LIGHMUGKC/GLC1/ITFRC/RAC2/CCL19/COR01A/CD300A/X2D1/ SLCAPS/MAMPA/CD300A SLCAPS/MAMPA/CD300A CDLV/CPAL/DOCK2/FCGREB/RACKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A CDLV/CPAL/DOCK2/FCGREB/RACKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A CDLV/CPAL/DOCK2/FCGREB/RACKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A CVS/FARD/CCRAP1L/TGB2/MP9/CR10/SCCAPA/MAP8/CD300A CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/CD30A CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/CD30A CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/CD30A CD14/CUBA/FACKAP1L/TGB2/MMP9/SERPINA1/PTPRC/RCC2/CCI 19/AMP8/CD30A CD14/CUBA/FACKAP1L/TGB2/MMP9/SERPINA1/PTPRC/RC2/CCI 19/CM2 CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/CD30A CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/PTPRC/RC2/CCI 19/CM2 <td< td=""><td>17 16 14 11 15 15 17 16 14 15 15 16 17 16 17 15 17 16 17 15 16 17 16 17 15 17 18 19 6 3 4 7 8 9 6 13 2 9 6 5 6 5 6 5 6 5 6 5 6 5 6 7 7 8 9 16</td></td<></td> | ID GO:0050900 GO:0051249 GO:0042119 GO:0050864 GO:0024312 GO:0002283
GO:0002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00030670 GO:0030667 GO:0030667 GO:0042611 GO:0030667 GO:0030670 GO:0042611 GO:0030670 GO:0030670 GO:0042611 GO:0030670 GO:0030670 GO:0042611 SO:00423023 GO:00423023 GO:0042379 GO:0050664 Nsa04145 Nsa04145 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140 Nsa045140 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector
process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
grange binding
MHC class II protein complex
immunoglobulin receptor binding
tertiary granule membrane
phagocytic vesicle membrane
grange binding
MHC class II protein complex binding
cCRC chemokine receptor binding
chemokine receptor binding
chemok | Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 11/60 11/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 3/59 3/52 3/42 5/42 6/42 5/42 | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 489/18670 489/18670 499/18670 224/18670 499/18670 224/18670 499/18670 224/18670 393/19717 164/19717 185/19717 167/19717 16/19717 16/19717 16/19717 16/19717 16/17697 16/17697 16/17697 16/17697 132/17697 132/17697 132/17697 152/8076 60/8076 180/8076 99/8076 38/707
149/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 1.45234E-100 1.45234E-100 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.00018131 0.00018131 <
 | 3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155525
0.00155525
0.00155525
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.0015555
0.00155555
0.00155555
0.00155555
0.00155555 | 2.02205E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.00090899 0.00090899 0.00090894 0.000908045734 0.000908045734 0.000960106 0.000960106 0.000960106 0.0002316483 | CDBRNCKAP1L/LIGHMUGKC/GLC1/ITGB2/RAC2/S100A9/CCL19/CCR14/CD3000A/X2D1/ CDBRYGGREB/RACAP1L/LIGHMUGKC/GLC1/ITFRC/RAC2/CCL19/COR01A/CD300A/X2D1/ SLCAPS/MAMPA/CD300A SLCAPS/MAMPA/CD300A CDLV/CPAL/DOCK2/FCGREB/RACKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A CDLV/CPAL/DOCK2/FCGREB/RACKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A CDLV/CPAL/DOCK2/FCGREB/RACKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A ALXXSCD14/CTSC/CTSS/CVBA/DOCK2/RCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AS/
MMP9/CD300A CVS/FARD/CCRAP1L/TGB2/MP9/CR10/SCCAPA/MAP8/CD300A CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/CD30A CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/CD30A CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/CD30A CD14/CUBA/FACKAP1L/TGB2/MMP9/SERPINA1/PTPRC/RCC2/CCI 19/AMP8/CD30A CD14/CUBA/FACKAP1L/TGB2/MMP9/SERPINA1/PTPRC/RC2/CCI 19/CM2 CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/CD30A CD14/CUBA/FACKAP1L/TGB2/MP9/SERPINA1/PTPRC/RC2/CCI 19/CM2 <td< td=""><td>17 16 14 11 15 15 17 16 14 15 15 16 17 16 17 15 17 16 17 15 16 17 16 17 15 17 18 19 6 3 4 7 8 9 6 13 2 9 6 5 6 5 6 5 6 5 6 5 6 5 6 7 7 8 9 16</td></td<> | 17 16 14 11 15 15 17 16 14 15 15 16 17 16 17 15 17 16 17 15 16 17 16 17 15 17 18 19 6 3 4 7 8 9 6 13 2 9 6 5 6 5 6 5 6 5 6 5 6
 5 6 7 7 8 9 16 |
| BP BP BP BP BP BP BP CC
 | ID GO:0050900 GO:001249 GO:0020804 GO:002283 GO:0002440 GO:0002697 GO:00030660 GO:00030661 GO:0030661 GO:0030661 GO:0030661 GO:0030670 GO:0030670 GO:0030670 GO:0030823 GO:0030823 GO:0030823 GO:0030823 GO:0030823 GO:0030823 GO:0030823 GO:0030823 GO:0030823 GO:0003823 GO:0003823 GO:0019864 GO:0005178 GO:0005178 SO304672 hsa04145 hsa053152 hsa04472 hsa05332 hsa05332 <
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
secretory granule membrane
tertiary granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
tertiary granule membrane
tertiary granule membrane
munoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
grange binding
MHC class II protein complex binding
tertiary granule membrane
phagocytic vesicle membrane
grange binding
tertiary granule membrane
tertiary granue membrane
tertiary granu | Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 15/60 11/60 14/60 11/60 14/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 3/59 3/59 3/59 3/59 3/59 3/59 3/59 2/59 4/42 6/42 8/42 5/42 6/42 5/42 6/42 5/42 6/42 5/42 6/42 6/42 6/42 6/42 6/42 6/42 6/42 6/42 6/42 6/42 6/42 6/42 6/42 6/42 <td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 499/18670 224/18670 393/19717 164/19717 185/19717 298/19717 167/19717 167/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 60/8076 180/8076 99/8076 38/8076 77/8076 42/8076 38/8076 19/8076 38/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076</td> <td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.0001102188 9.95363E-07 1.91121E-05 7.68384E-05 0.00019581514 0.000138748 0.000138748 0.00138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.0001439003 6.13591E-08 5.55121E-07 3.21921E-06 1.06974E-05 6.73296E-05 6.73296E-05 <td>3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155</td><td> 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.0001760329 0.000550386 0.001760329 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000645734 0.00086406 0.00086406 0.000960106 0.000960106 0.00032316483 0.002316483 0.002316483 </td><td>CDBNDCKAP1LUGHMURKC/GLC1/ITGB2/RAC2/S100AB/CC13/CCL19/CCR014/CD300A/M2B1/ CDBAFCGR2BR/CKAP1LURA/MIRKC/GLC1/ITFRC/RAC2/CCL19/CCR014/CD300A/M2B1/ SLAMSCD14/CTSC/CTSS/CVBA/DOCK2/FCGR2B/INCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ CD14/CVB2/ROCK2/FCGR2B/RACKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ FCGR2B/RCKAP1LUGH/MIRKC/GLC1/PTFRC/RAC2/CCL19/CCR014/CD300A/GL/1-44//SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ CMAPRC20300A CASK/CSPA/NCKAP1LITGB2/MP9/SERPINA1/PTPRC/SCORPIALSAMF8 CD14/CDBA/FLA/DMB/KLC0ACL1/TGB2/PTPRC/RC2CCL19/AMP8/CD300A CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA</td><td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8
 13 2 9 6 3 4 7 8 10 7 8 11 7 8 13 14 15 16 17 18 19 11 12 13 14 15 16 17 18 19</td></td> | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 499/18670 224/18670 393/19717 164/19717 185/19717 298/19717 167/19717 167/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 60/8076 180/8076 99/8076 38/8076 77/8076 42/8076 38/8076 19/8076 38/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.0001102188 9.95363E-07 1.91121E-05 7.68384E-05 0.00019581514 0.000138748 0.000138748 0.00138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.0001439003 6.13591E-08 5.55121E-07 3.21921E-06 1.06974E-05 6.73296E-05 6.73296E-05
<td>3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155</td> <td> 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.0001760329 0.000550386 0.001760329 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000645734 0.00086406 0.00086406 0.000960106 0.000960106 0.00032316483 0.002316483 0.002316483 </td> <td>CDBNDCKAP1LUGHMURKC/GLC1/ITGB2/RAC2/S100AB/CC13/CCL19/CCR014/CD300A/M2B1/ CDBAFCGR2BR/CKAP1LURA/MIRKC/GLC1/ITFRC/RAC2/CCL19/CCR014/CD300A/M2B1/ SLAMSCD14/CTSC/CTSS/CVBA/DOCK2/FCGR2B/INCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ CD14/CVB2/ROCK2/FCGR2B/RACKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ FCGR2B/RCKAP1LUGH/MIRKC/GLC1/PTFRC/RAC2/CCL19/CCR014/CD300A/GL/1-44//SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ CMAPRC20300A CASK/CSPA/NCKAP1LITGB2/MP9/SERPINA1/PTPRC/SCORPIALSAMF8 CD14/CDBA/FLA/DMB/KLC0ACL1/TGB2/PTPRC/RC2CCL19/AMP8/CD300A CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA</td> <td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 13 2 9 6 3 4 7 8 10 7 8 11 7 8 13 14 15 16 17 18 19 11 12 13 14 15 16 17 18 19</td> | 3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
6.67562E-06
7.25059E-05
0.000108227
0.000186714
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.0001760329 0.000550386 0.001760329 0.026507951 0.026507951 0.026507951 0.026507951 0.026507951 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000550263 0.000103447 0.000645734 0.00086406 0.00086406 0.000960106 0.000960106 0.00032316483 0.002316483 0.002316483
 | CDBNDCKAP1LUGHMURKC/GLC1/ITGB2/RAC2/S100AB/CC13/CCL19/CCR014/CD300A/M2B1/ CDBAFCGR2BR/CKAP1LURA/MIRKC/GLC1/ITFRC/RAC2/CCL19/CCR014/CD300A/M2B1/ SLAMSCD14/CTSC/CTSS/CVBA/DOCK2/FCGR2B/INCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ CD14/CVB2/ROCK2/FCGR2B/RACKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ FCGR2B/RCKAP1LUGH/MIRKC/GLC1/PTFRC/RAC2/CCL19/CCR014/CD300A/GL/1-44//SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ ALOXSCD14/CTSC/CTSS/CVBA/DOCK2/NCKAP1LITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2AF/ CMAPRC20300A CASK/CSPA/NCKAP1LITGB2/MP9/SERPINA1/PTPRC/SCORPIALSAMF8 CD14/CDBA/FLA/DMB/KLC0ACL1/TGB2/PTPRC/RC2CCL19/AMP8/CD300A CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA CD14/CDBA/FLA/DMB/KLA/DA | 17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 13 2 9 6 3 4 7 8 10 7 8 11 7 8 13 14 15 16 17 18 19 11 12 13 14 15 16 17 18 19 |
| BPBPBPBPBPBPBPCC <td>ID GO:0050900 GO:001249 GO:0020804 GO:0020804 GO:0002440 GO:0002440 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00070820 GO:00030667 GO:00190807 GO:0030667 GO:0030667 GO:0030667 GO:0030670 GO:0030670 GO:0030670 GO:0030670 GO:0030823 GO:0030803 GO:0042379 Hsa04145 hsa04472 hsa04472 hsa04472 hsa044940 hsa053320</td> <td>leukocyte migration
regulation of lymphocyte activation
neutrophil activation
neutrophil degranulation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
tertiary granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
tertiary granule membrane
endocytic vesicle membrane
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
antigen binding
MHC class II protein complex binding
GCR chemokine receptor binding
CCR chemokine receptor binding
immunoglobulin receptor binding
chemokine receptor b</td> <td>Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 15/60 11/60 14/60 11/60 14/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 4/63 3/59 3/51 3/52 5/42 6/42 5/42 6/42<td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 499/18670 224/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 167/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 60/8076 180/8076 938/8076 180/8076 93/8076 180/8076 93/8076 180/8076 93/8076 180/8076 180/8076 180/8076 180/8076 180/8076 180/8076 180/8076 180/8076</td><td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.0001979876 0.000395083 0.0001979876 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.0001439003 6.13591E-08 5.55121E-07 3.21921E-06 1.06974E-05 <td>3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155</td><td>2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.0001760329 0.0001760329 0.0001760329 0.001760329 0.001760329 0.001750386 0.001760329 0.001760329 0.002550386 0.001760329 0.0026507951 0.026507951 0.026507951 0.000550263 0.0000550263 0.0000645734 0.0000550263 0.0000645734 0.000086406 0.000086406 0.000096106 0.0002316483 0.002316483</td><td>CDBARCAGENUCAPILUIGHUNGKC/GLC1/TGB2/PAC2/S100A8/CCL19/CCL19/CCR04/AC29/COR01A/
CD88/FCGRI28/CAPIL/LA-SMB/GHM/GKC/GLC1/PTPC/FAC2/CCL19/CCR01A/CD300A/M281/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/PCGR28/NCKAPIL/TGB2/PTPRC/CCR01A/CD300A/M281/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/PCGR28/NCKAPIL/TGB2/PTPRC/CCR01A/CD300A/GL1-4/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CTS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD3/NCKAPIL/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD3/NCKAPIL/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CS3/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/
CD30A/CL3DA/CAPIL/TGB2/CCAPIL/TGB2/COR01A
CD30A/CL3DA/CL3DA/CL3DA
CD30A/CL3D</td><td>17 16 14 11 15 15 11 14 17 8 3 4 7 8
 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 3 4 7 8 9 6 11 7 8 3 4 7 8 10 11 12 13 14 15 16 17 18 17 18 </td></td></td> | ID GO:0050900 GO:001249 GO:0020804 GO:0020804 GO:0002440 GO:0002440 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00070820 GO:00030667 GO:00190807 GO:0030667 GO:0030667 GO:0030667 GO:0030670 GO:0030670 GO:0030670 GO:0030670 GO:0030823 GO:0030803 GO:0042379 Hsa04145 hsa04472 hsa04472 hsa04472 hsa044940 hsa053320
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
neutrophil degranulation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
tertiary granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
tertiary granule membrane
endocytic vesicle membrane
immunoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
antigen binding
MHC class II protein complex binding
GCR chemokine receptor binding
CCR chemokine receptor binding
immunoglobulin receptor binding
chemokine receptor b | Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 15/60 11/60 14/60 11/60 14/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 4/63 3/59 3/51 3/52 5/42 6/42 5/42 6/42 <td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 488/18670 499/18670 224/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 167/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 60/8076 180/8076 938/8076 180/8076 93/8076 180/8076 93/8076 180/8076 93/8076 180/8076 180/8076 180/8076 180/8076 180/8076 180/8076 180/8076 180/8076</td> <td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.0001979876 0.000395083 0.0001979876 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.0001439003 6.13591E-08 5.55121E-07 3.21921E-06 1.06974E-05 <td>3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155</td><td>2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.0001760329 0.0001760329 0.0001760329 0.001760329 0.001760329 0.001750386 0.001760329 0.001760329 0.002550386 0.001760329 0.0026507951 0.026507951 0.026507951 0.000550263 0.0000550263 0.0000645734 0.0000550263 0.0000645734 0.000086406 0.000086406 0.000096106 0.0002316483 0.002316483</td><td>CDBARCAGENUCAPILUIGHUNGKC/GLC1/TGB2/PAC2/S100A8/CCL19/CCL19/CCR04/AC29/COR01A/
CD88/FCGRI28/CAPIL/LA-SMB/GHM/GKC/GLC1/PTPC/FAC2/CCL19/CCR01A/CD300A/M281/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/PCGR28/NCKAPIL/TGB2/PTPRC/CCR01A/CD300A/M281/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/PCGR28/NCKAPIL/TGB2/PTPRC/CCR01A/CD300A/GL1-4/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CTS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD3/NCKAPIL/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD3/NCKAPIL/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CS3/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/
CD30A/CL3DA/CAPIL/TGB2/CCAPIL/TGB2/COR01A
CD30A/CL3DA/CL3DA/CL3DA
CD30A/CL3D</td><td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 3 4 7 8 9 6 11 7 8 3 4 7 8 10 11 12 13 14 15 16 17 18 17 18 </td></td> | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670
 488/18670 488/18670 499/18670 224/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 167/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 60/8076 180/8076 938/8076 180/8076 93/8076 180/8076 93/8076 180/8076 93/8076 180/8076 180/8076 180/8076 180/8076 180/8076 180/8076 180/8076 180/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.0001979876 0.000395083 0.0001979876 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.0001439003 6.13591E-08 5.55121E-07 3.21921E-06 1.06974E-05
<td>3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155</td> <td>2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.0001760329 0.0001760329 0.0001760329 0.001760329 0.001760329 0.001750386 0.001760329 0.001760329 0.002550386 0.001760329 0.0026507951 0.026507951 0.026507951 0.000550263 0.0000550263 0.0000645734 0.0000550263 0.0000645734 0.000086406 0.000086406 0.000096106 0.0002316483 0.002316483</td> <td>CDBARCAGENUCAPILUIGHUNGKC/GLC1/TGB2/PAC2/S100A8/CCL19/CCL19/CCR04/AC29/COR01A/
CD88/FCGRI28/CAPIL/LA-SMB/GHM/GKC/GLC1/PTPC/FAC2/CCL19/CCR01A/CD300A/M281/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/PCGR28/NCKAPIL/TGB2/PTPRC/CCR01A/CD300A/M281/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/PCGR28/NCKAPIL/TGB2/PTPRC/CCR01A/CD300A/GL1-4/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CTS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD3/NCKAPIL/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD3/NCKAPIL/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CS3/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/
CD30A/CL3DA/CAPIL/TGB2/CCAPIL/TGB2/COR01A
CD30A/CL3DA/CL3DA/CL3DA
CD30A/CL3D</td> <td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 3 4 7 8 9 6 11 7 8 3 4 7 8 10 11 12 13 14 15 16 17 18 17 18 </td> | 3.23684E-10
1.52661E-09
3.60573E-09
4.9572E-09
6.60473E-09
6.60473E-09
7.9094E-09
2.29925E-08
2.45605E-08
2.45605E-08
7.25059E-05
0.000108227
0.000186714
0.000450681
0.000450681
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.001552276
0.00155 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.000908899 0.0001760329 0.0001760329 0.0001760329 0.001760329 0.001760329 0.001750386 0.001760329 0.001760329 0.002550386 0.001760329 0.0026507951 0.026507951 0.026507951 0.000550263 0.0000550263 0.0000645734 0.0000550263 0.0000645734 0.000086406 0.000086406 0.000096106 0.0002316483 0.002316483
 | CDBARCAGENUCAPILUIGHUNGKC/GLC1/TGB2/PAC2/S100A8/CCL19/CCL19/CCR04/AC29/COR01A/
CD88/FCGRI28/CAPIL/LA-SMB/GHM/GKC/GLC1/PTPC/FAC2/CCL19/CCR01A/CD300A/M281/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/PCGR28/NCKAPIL/TGB2/PTPRC/CCR01A/CD300A/M281/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/PCGR28/NCKAPIL/TGB2/PTPRC/CCR01A/CD300A/GL1-4/
SLAXS/CD14/CSC/CS3/CSCMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CSC/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CTS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD14/CS3/CS3/CSMB/DOCK2/NCKAPIL/TGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD3/NCKAPIL/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CD3/NCKAPIL/TGB2/MP9/SERPINA1/PTPRC/S100A9/SLC2A5/
ALXXS/CS3/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CG98/NCKAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/MP9/SERPINA1/CD300A
CD14/CS4DA/CAPIL/TGB2/
CD30A/CL3DA/CAPIL/TGB2/CCAPIL/TGB2/COR01A
CD30A/CL3DA/CL3DA/CL3DA
CD30A/CL3D | 17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 3 4 7 8 9 6 11 7 8 3 4 7 8 10 11 12 13 14 15 16 17 18 17 18 |
|
 | ID GO:0050900 GO:0051249 GO:0042119 GO:0050864 GO:00243312 GO:002283 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00030670 GO:00030670 GO:00306661 GO:0042613 GO:0030667 GO:0030670 GO:0030670 GO:0030670 GO:0030670 GO:0030670 GO:0030873 GO:0030873 GO:0030873 GO:0030873 GO:0030873 GO:0042379 GO:0050664 hsa04145 hsa05150 hsa045140 hsa05320 hsa045140 hsa05320 hsa045320 hsa045310 hsa045310 hsa04670 hsa040402 hsa044620 <td>leukocyte migration
regulation of lymphocyte activation
neutrophil activation
neutrophil degranulation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
tertiary granule membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
grange binding
MHC class II protein complex binding
MHC protein complex binding
CCR chemokine receptor binding
CCR chemokine receptor binding
chemokine receptor processing
cortice cell lineage
type I diabetes mellitus
Cell adhesion molecules
phereumitus
terketop at the signaling pathway
toll-like receptor signaling pathway
toll-like receptor signaling pathway</td> <td>Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 11/60 15/60 11/60 14/60 11/60 14/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 4/63 4/63 3/59 3/52 5/42 6/42 4/42 4/42<td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 489/18670 488/18670 489/18670 489/18670 499/18670 224/18670 499/18670 393/19717 164/19717 185/19717 16/19717 25/19717 16/19717 25/19717 76/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 66/17697 152/8076 93/8076 38/8076 152/8076 152/8076 93/8076 93/8076 93/8076 149/8076 93/8076 16/17697 152/8076 16/17697 152/8076 16/149/8076 93/8076</td><td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.0001979876 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.00018131 0.00018131 0.00018131 0.00018131 0.000183130 0.000183130 0.000183130 0.000153725</td><td>3.23684E-101.52661E-091.52661E-093.60573E-094.9572E-096.60473E-097.9094E-092.29925E-082.45605E-082.45605E-086.67562E-067.25059E-050.0001082270.0001867140.0004506810.0015522760.0015522760.0015522760.0015522760.0015522760.0015522760.001330848710.005942170.005942170.005942170.005942170.005942170.00195372160.00195372160.00195372160.0012145530.0001298410.0001298416410.00033848710.00012145530.00012145530.00012145530.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.00134586230.00120685820.012068582<</td><td>2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.0001760329 0.000183356 0.000183356 0.000183356 0.0001760329 0.001550263 0.0015512762 0.015512762 0.026507951 5.29626E-06 2.39578E-05 9.26229E-05 0.000184671 0.000550263 0.000184671 0.000086406 0.000086406 0.000086406 0.000086406 0.000086406 0.000086406 0.000086406 0.0003271604 <t< td=""><td>Descrictors Constructors Constructors</td><td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 8 9 6 13 2 9 6 5 6 7 8 9 14 15 16 17 18 19 11 12 13 14 15 16 <!--</td--></td></t<></td></td>
 | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
neutrophil degranulation
neutrophil degranulation
neutrophil degranulation
neutrophil activation involved in immune response
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
tertiary granule membrane
endocytic vesicle membrane
munoglobulin complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
phagocytic vesicle membrane
grange binding
MHC class II protein complex binding
MHC protein complex binding
CCR chemokine receptor binding
CCR chemokine receptor binding
chemokine receptor processing
cortice cell lineage
type I diabetes mellitus
Cell adhesion molecules
phereumitus
terketop at the signaling pathway
toll-like receptor signaling pathway
toll-like receptor signaling pathway | Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 11/60 15/60 11/60 14/60 11/60 14/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 4/63 4/63 3/59 3/52 5/42 6/42 4/42 4/42 <td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 489/18670 488/18670 489/18670 489/18670 499/18670 224/18670 499/18670 393/19717 164/19717 185/19717 16/19717 25/19717 16/19717 25/19717 76/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 66/17697 152/8076 93/8076 38/8076 152/8076 152/8076 93/8076 93/8076 93/8076 149/8076 93/8076 16/17697 152/8076 16/17697 152/8076 16/149/8076 93/8076</td> <td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.0001979876 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.00018131 0.00018131 0.00018131 0.00018131 0.000183130 0.000183130 0.000183130 0.000153725</td> <td>3.23684E-101.52661E-091.52661E-093.60573E-094.9572E-096.60473E-097.9094E-092.29925E-082.45605E-082.45605E-086.67562E-067.25059E-050.0001082270.0001867140.0004506810.0015522760.0015522760.0015522760.0015522760.0015522760.0015522760.001330848710.005942170.005942170.005942170.005942170.005942170.00195372160.00195372160.00195372160.0012145530.0001298410.0001298416410.00033848710.00012145530.00012145530.00012145530.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.00134586230.00120685820.012068582<</td> <td>2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.0001760329 0.000183356 0.000183356 0.000183356 0.0001760329 0.001550263 0.0015512762 0.015512762 0.026507951 5.29626E-06 2.39578E-05 9.26229E-05 0.000184671 0.000550263 0.000184671 0.000086406 0.000086406 0.000086406 0.000086406 0.000086406 0.000086406 0.000086406 0.0003271604 <t< td=""><td>Descrictors Constructors Constructors</td><td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 8 9 6 13 2 9 6 5 6 7 8 9 14 15 16 17 18 19 11 12 13 14 15 16 <!--</td--></td></t<></td> | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 489/18670 488/18670 489/18670 489/18670 499/18670 224/18670 499/18670 393/19717 164/19717 185/19717 16/19717 25/19717 16/19717 25/19717 76/19717 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 16/17697 152/8076 66/17697 152/8076 93/8076 38/8076 152/8076 152/8076 93/8076 93/8076 93/8076 149/8076 93/8076
16/17697 152/8076 16/17697 152/8076 16/149/8076 93/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-111 2.65098E-111 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-100 1.45234E-101 1.45234E-102 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.73155E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.0001979876 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.00018131 0.00018131 0.00018131 0.00018131 0.000183130 0.000183130 0.000183130 0.000153725
 | 3.23684E-101.52661E-091.52661E-093.60573E-094.9572E-096.60473E-097.9094E-092.29925E-082.45605E-082.45605E-086.67562E-067.25059E-050.0001082270.0001867140.0004506810.0015522760.0015522760.0015522760.0015522760.0015522760.0015522760.001330848710.005942170.005942170.005942170.005942170.005942170.00195372160.00195372160.00195372160.0012145530.0001298410.0001298416410.00033848710.00012145530.00012145530.00012145530.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.00134586230.00120685820.012068582< | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.0001760329 0.000183356 0.000183356 0.000183356 0.0001760329 0.001550263 0.0015512762 0.015512762 0.026507951 5.29626E-06 2.39578E-05 9.26229E-05 0.000184671 0.000550263 0.000184671 0.000086406 0.000086406 0.000086406 0.000086406 0.000086406 0.000086406 0.000086406 0.0003271604 <t< td=""><td>Descrictors Constructors Constructors</td><td>17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 8 9 6 13 2 9 6 5 6 7 8 9 14 15 16 17 18 19 11 12 13 14 15 16 <!--</td--></td></t<> | Descrictors Constructors | 17 16 14 11 15 15 11 14 17 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 3 4 7 8 9 6 8 9 6 13 2 9 6 5 6 7 8 9 14 15 16 17 18 19 11 12 13 14 15 16 </td
 |
| BPBPBPBPBPBPBPCC <td>ID GO:0050900 GO:001249 GO:0050864 GO:002383 GO:002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00030670 GO:0019807 GO:0030666 GO:0030670 GO:0030803 GO:0042302 GO:0042379 GO:0050664 hsa04145 hsa05310 hsa045140 hsa045140 hsa045320 hsa045310 hsa040670 hsa040401 <!--</td--><td>leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
fulleC class II protein complex
MHC protein complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
grangetytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
fulleC protein complex binding
tertiary granule membrane
grangetytic vesicle membrane
chemokine receptor binding
cCR chemokine receptor binding
cCR chemokine receptor binding
chemokine receptor disease
type I diabetes mellitus
Cell adhesion molecules
Type I diabetes mellitus
Cell adhesion molecules
traper traper dispanaling pathway
toxipa pathway</td><td>Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 11/60 11/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 3/59 3/52 6/42 6/42 5/42 6/42 3/42 4/42 4/42 4/42 4/42</td><td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 499/18670 224/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 167/19717 16/19717 16/19717 16/19717 16/19717 16/19717 16/19717 16/17697 16/17697 16/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/3076 99/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076</td><td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-101 1.45234E-101 1.45234E-102 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.0001979876 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.00018131 0.00018131 0.00018131 0.00018131 0.0001831305 0.000155725 0.00028782 0.0001531305 0.0001531305</td><td>3.23684E-101.52661E-091.52661E-093.60573E-094.9572E-096.60473E-097.9094E-092.29925E-082.45605E-082.45605E-082.45605E-080.0001082270.0001082270.00010822760.00015522760.0015522760.0015522760.0015522760.0015522760.0015522760.0016350050.002309240.002309240.002372160.005942170.005942170.005942170.005942170.005942170.005942170.0002588770.0012309240.00125372160.00129416410.0333848710.0002588770.00012944160.00012944160.0012145530.0012145530.0012145530.00122470190.001244760.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.00134586230.0120685820.0120685820.0150665270.0150665270.0150665270.016514642</td><td>2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.0001033366 0.001760329 0.000183356 0.001760329 0.001760329 0.0015512762 0.026507951 5.29626E-06 0.0015512762 0.026507951 0.026507951 5.29626E-06 0.000184671 0.000550263 0.0001846714 0.000550263 0.0000550263 0.0000645734 0.0000866406 0.000096106 0.000096106 0.0002697645 0.0002697645 0.0003271648</td><td>CDBARCACHILAGHUNGKORLCINTGED/INACE/SIGMARCE/INACE</td><td>17 16 14 11 15 15 11 14 17 18 19 6 3 4 7 8 3 4 7 8 7 8 7 8 9 6 3 4 7 8 9 6 11 12 9 6 13 2 9 6 14 15 16 17 18 19 11 11 12 13 14 15 16 17 18 <tr td=""></tr></td></td>
 | ID GO:0050900 GO:001249 GO:0050864 GO:002383 GO:002446 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:0002697 GO:00030670 GO:0019807 GO:0030666 GO:0030670 GO:0030803 GO:0042302 GO:0042379 GO:0050664 hsa04145 hsa05310 hsa045140 hsa045140 hsa045320 hsa045310 hsa040670 hsa040401 </td <td>leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
fulleC class II protein complex
MHC protein complex, circulating
tertiary granule membrane
phagocytic vesicle membrane
grangetytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
fulleC protein complex binding
tertiary granule membrane
grangetytic vesicle membrane
chemokine receptor binding
cCR chemokine receptor binding
cCR chemokine receptor binding
chemokine receptor disease
type I diabetes mellitus
Cell adhesion molecules
Type I diabetes mellitus
Cell adhesion molecules
traper traper dispanaling pathway
toxipa pathway</td> <td>Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 11/60 11/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 3/59 3/52 6/42 6/42 5/42 6/42 3/42 4/42 4/42 4/42 4/42</td> <td>BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 499/18670 224/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 167/19717 16/19717 16/19717 16/19717 16/19717 16/19717 16/19717 16/17697 16/17697 16/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/3076 99/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076 93/8076</td> <td>1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-101 1.45234E-101 1.45234E-102 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.0001979876 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.00018131 0.00018131 0.00018131 0.00018131 0.0001831305 0.000155725 0.00028782 0.0001531305 0.0001531305</td> <td>3.23684E-101.52661E-091.52661E-093.60573E-094.9572E-096.60473E-097.9094E-092.29925E-082.45605E-082.45605E-082.45605E-080.0001082270.0001082270.00010822760.00015522760.0015522760.0015522760.0015522760.0015522760.0015522760.0016350050.002309240.002309240.002372160.005942170.005942170.005942170.005942170.005942170.005942170.0002588770.0012309240.00125372160.00129416410.0333848710.0002588770.00012944160.00012944160.0012145530.0012145530.0012145530.00122470190.001244760.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.00134586230.0120685820.0120685820.0150665270.0150665270.0150665270.016514642</td> <td>2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.0001033366 0.001760329 0.000183356 0.001760329 0.001760329 0.0015512762 0.026507951 5.29626E-06 0.0015512762 0.026507951 0.026507951 5.29626E-06 0.000184671 0.000550263 0.0001846714 0.000550263 0.0000550263 0.0000645734 0.0000866406 0.000096106 0.000096106 0.0002697645 0.0002697645 0.0003271648</td> <td>CDBARCACHILAGHUNGKORLCINTGED/INACE/SIGMARCE/INACE</td> <td>17 16 14 11 15 15 11 14 17 18 19 6 3 4 7 8 3 4 7 8 7 8 7 8 9 6 3 4 7 8 9 6 11 12 9 6 13 2 9 6 14 15 16 17 18 19 11 11 12 13 14 15 16 17 18 <tr td=""></tr></td> | leukocyte migration
regulation of lymphocyte activation
neutrophil activation
phagocytosis
regulation of B cell activation
neutrophil degranulation
neutrophil degranulation
neutrophil degranulation
neutrophil mediated immunity
leukocyte chemotaxis
regulation of immune effector process
external side of plasma membrane
tertiary granule
ficolin-1-rich granule
ficolin-1-rich granule
secretory granule membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
fulleC class II protein complex
MHC protein complex, circulating
tertiary granule membrane
phagocytic vesicle
membrane
grangetytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
endocytic vesicle membrane
fulleC protein complex binding
tertiary granule membrane
grangetytic vesicle membrane
chemokine receptor binding
cCR chemokine receptor binding
cCR chemokine receptor binding
chemokine receptor disease
type I diabetes mellitus
Cell adhesion molecules
Type I diabetes mellitus
Cell adhesion molecules
traper traper dispanaling pathway
toxipa pathway | Gene Ratio 17/60 16/60 16/60 14/60 11/60 15/60 11/60 11/60 11/63 7/63 8/63 6/63 3/63 4/63 4/63 4/63 3/59 3/52 6/42 6/42 5/42 6/42 3/42 4/42 4/42 4/42 4/42 | BgRatio 499/18670 485/18670 498/18670 369/18670 184/18670 485/18670 488/18670 499/18670 224/18670 499/18670 224/18670 458/18670 393/19717 164/19717 185/19717 167/19717 16/19717 16/19717 16/19717 16/19717 16/19717 16/19717 16/17697 16/17697 16/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/17697 132/3076 99/8076 93/8076 149/8076 93/8076 149/8076 93/8076 149/8076
 93/8076 | 1.85598E-13 1.75971E-12 2.62606E-12 8.27003E-12 1.42121E-11 2.43026E-11 2.65098E-111 2.65098E-111 2.65098E-111 3.62817E-111 1.18654E-100 1.45234E-101 1.45234E-101 1.45234E-102 4.17226E-08 9.06323E-07 2.02926E-06 4.66784E-06 1.5378E-05 1.69005E-05 6.80025E-05 8.27284E-05 8.27284E-05 0.000102188 9.95363E-07 1.91121E-05 7.68384E-05 0.000395083 0.0001979876 0.000395083 0.000138748 0.000138748 0.000138748 0.000138748 0.000138748 0.00018131 0.00018131 0.00018131 0.00018131 0.0001831305 0.000155725 0.00028782 0.0001531305 0.0001531305
 | 3.23684E-101.52661E-091.52661E-093.60573E-094.9572E-096.60473E-097.9094E-092.29925E-082.45605E-082.45605E-082.45605E-080.0001082270.0001082270.00010822760.00015522760.0015522760.0015522760.0015522760.0015522760.0015522760.0016350050.002309240.002309240.002372160.005942170.005942170.005942170.005942170.005942170.005942170.0002588770.0012309240.00125372160.00129416410.0333848710.0002588770.00012944160.00012944160.0012145530.0012145530.0012145530.00122470190.001244760.0013459050.0013459050.0013459050.0013459050.0013459050.0013459050.00134586230.0120685820.0120685820.0150665270.0150665270.0150665270.016514642 | 2.02205E-10 9.53674E-10 9.53674E-10 2.25249E-09 3.09675E-09 4.12596E-09 4.12596E-09 4.12596E-09 4.94099E-09 1.43634E-08 1.53429E-08 3.90875E-06 4.24541E-05 6.33699E-05 0.000109326 0.000263885 0.000263885 0.000908899 0.000908899 0.000908899 0.0001033366 0.001760329 0.000183356 0.001760329 0.001760329 0.0015512762 0.026507951 5.29626E-06 0.0015512762 0.026507951 0.026507951 5.29626E-06 0.000184671 0.000550263 0.0001846714 0.000550263 0.0000550263 0.0000645734 0.0000866406 0.000096106 0.000096106 0.0002697645 0.0002697645 0.0003271648 |
CDBARCACHILAGHUNGKORLCINTGED/INACE/SIGMARCE/INACE | 17 16 14 11 15 15 11 14 17 18 19 6 3 4 7 8 3 4 7 8 7 8 7 8 9 6 3 4 7 8 9 6 11 12 9 6 13 2 9 6 14 15 16 17 18 19 11 11 12 13 14 15 16 17 18 <tr td=""></tr> |
|
 |
 | |
 |
 | | |
 | | |

Table S1 (continued)

Table S1 (contin	nued)								
ONTOLOGY KEGG	ID hsa05321	Description Inflammatory bowel disease	Gene Ratio	65/8076	P value 0.004567287	p.adjust 0.023026738	qvalue 0.016426207	genelD HLA-DMA/HLA-DMB/HLA-DRA	Count 3
KEGG	hsa05221	Acute myeloid leukemia	3/42	67/8076	0.004973176	0.023513674	0.016773565	BCL2A1/CD14/CSF1R	3
KEGG	hsa04210	Apoptosis	4/42	136/8076	0.005246853	0.023513674	0.016773565	BCL2A1/CTSC/CSF2RB/CTSS	4
KEGG	hsa05322	Systemic lupus erythematosus	4/42	136/8076	0.005246853	0.023513674	0.016773565	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04662	B cell receptor signaling pathway	3/42	82/8076	0.008711718	0.037647067	0.026855672	CD72/FCGR2B/RAC2	3
KEGG	hsa04658	Th1 and Th2 cell differentiation	3/42	92/8076	0.011918685	0.049729685	0.035474852	HLA-DMA/HLA-DMB/HLA-DRA	3
ONTOLOGY			Gene Ratio	BgRatio	P value	p.adjust	qvalue		Count
Ы	40.0000000		17/00	433/100/0	1.000002 10	0.2000+2 10	2.022002 10	CD300A/IGLV1-44/SLAMF8	17
BP	GO:0051249	regulation of lymphocyte activation	16/60	485/18670	1.75971E-12	1.52661E-09	9.53674E-10	CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/	16
BP	GO:0042119	neutrophil activation	16/60	498/18670	2.62606E-12	1.52661E-09	9.53674E-10	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/	16
Di	GO.0042110		10/00	400/100/0		1.020012 00	0.000142 10	SLC2A5/VAMP8/CD300A	10
BP	GO:0006909	phagocytosis	14/60	369/18670	8.27003E-12	3.60573E-09	2.25249E-09	CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/	14
BP	GO:0050864	regulation of B cell activation	11/60	184/18670	1.42121E-11	4.9572E-09	3.09675E-09	IGLES FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	11
BP	GO:0043312	neutrophil degranulation	15/60	485/18670	2.43026E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/	15
								VAMP8/CD300A	
BP	GO:0002283	neutrophil activation involved in immune response	15/60	488/18670	2.65098E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VAMP8/CD300A	15
BP	GO:0002446	neutrophil mediated immunity	15/60	499/18670	3.62817E-11	7.9094E-09	4.94099E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/	15
								VAMP8/CD300A	
BP	GO:0030595	leukocyte chemotaxis	11/60	224/18670	1.18654E-10	2.29925E-08	1.43634E-08	NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8	11
BP	GO:0002697	regulation of immune effector process	14/60	458/18670	1.45234E-10	2.45605E-08	1.53429E-08	CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/ SLAMF8	14
CC	GO:0009897	external side of plasma membrane	11/63	393/19717	4.17226E-08	6.67562E-06	3.90875E-06	CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5	11
CC	GO:0070820	tertiary granule	7/63	164/19717	9.06323E-07	7.25059E-05	4.24541E-05	CTSS/CYBA/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A	7
CC	GO:0101002	ficolin-1-rich granule	7/63	185/19717	2.02926E-06	0.000108227	6.33699E-05	ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A	7
CC	GO:0030667	secretory granule membrane	8/63	298/19717	4.66784E-06	0.000186714	0.000109326	CD14/CYBA/NCKAP1L/ITGB2/PTPRC/SLC2A5/VAMP8/CD300A	8
00	GO:0030666	MHC class II protein complex	3/63	16/19717	1.69005F-05	0.000450681	0.000263885	HI A-DMA/HI A-DMB/HI A-DBA	3
CC	GO:0042611	MHC protein complex	3/63	25/19717	6.80025E-05	0.001552276	0.000908899	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042571	immunoglobulin complex, circulating	4/63	72/19717	8.27284E-05	0.001552276	0.000908899	IGHM/IGKC/IGLC1/IGLL5	4
CC	GO:0070821	tertiary granule membrane	4/63	73/19717	8.73155E-05	0.001552276	0.000908899	CYBA/ITGB2/VAMP8/CD300A	4
CC	GO:0030670	phagocytic vesicle membrane	4/63	76/19717	0.000102188	0.001635005	0.000957338	CYBA/RAC2/VAMP8/CORO1A	4
MF	GO:0003823	antigen binding	7/59	160/17697	9.95363E-07	0.000230924	0.000183356	CD48/HLA-DRA/IGHM/IGKC/IGLC1/IGLV1-44/IGLL5	7
MF	GO:0023026	MHC class II protein complex binding	3/59	16/17697	1.91121E-05	0.002217009	0.001760329	HLA-DMA/HLA-DMB/HLA-DRA	3
MF	GO:0023023		3/59 1/50	∠ə/1/697 76/17697	0.000119510	0.006931710	0.00550296	ובא-טואריו ובא-טואס חבא-טאא IGHM/IGKC/IGLC1/IGLI 5	კ ⊿
MF	GO:0048020	CCR chemokine receptor binding	-, 59 3/59	43/17697	0.000395083	0.018331851	0.014555689	CCL13/CCL18/CCL19	+ 3
MF	GO:0008009	chemokine activity	3/59	49/17697	0.000581514	0.019537216	0.015512762	CCL13/CCL18/CCL19	3
MF	GO:0019864	IgG binding	2/59	11/17697	0.000589485	0.019537216	0.015512762	FCGR1B/FCGR2B	2
MF	GO:0005178	integrin binding	4/59	132/17697	0.000979876	0.02841641	0.022562939	ITGB2/LCP1/SPP1/ITGBL1	4
MF	GO:0042379	chemokine receptor binding	3/59	66/17697	0.00138748	0.033384871	0.026507951	CCL13/CCL18/CCL19	3
MF	GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	2/59	17/17697	0.001439003	0.033384871	0.026507951	CYBA/KMO	2
KEGG	hsa04145	Phaoosome	9/42	152/8076	6.13591F-08	7.42445F-06	5.29626F-06	CD14/CTSS/CYBA/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGR2/CORO1A	9
KEGG	hsa05416	Viral myocarditis	6/42	60/8076	5.55121E-07	3.35848E-05	2.39578E-05	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/RAC2	6
KEGG	hsa05152	Tuberculosis	8/42	180/8076	3.21921E-06	0.000129841	9.26229E-05	CD14/CTSS/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/CORO1A	8
KEGG	hsa04672	Intestinal immune network for IgA production	5/42	49/8076	4.7939E-06	0.000145016	0.000103447	CD86/HLA-DMA/HLA-DMB/HLA-DRA/CXCR4	5
KEGG	hsa04640	Hematopoietic cell lineage	6/42	99/8076	1.06974E-05	0.000258877	0.000184671	CD14/CD37/CSF1R/HLA-DMA/HLA-DMB/HLA-DRA	6
KEGG	hsa05330	Allograft rejection	4/42	38/8076	4.10371E-05	0.000771375	0.000550263	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa05140	Leishmaniasis	5/42	77/8076	4.4625E-05	0.000771375	0.000550263	CYBA/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05332	Graft-versus-host disease	4/42	42/8076	6.12967E-05	0.000905209	0.000645734		4
KEGG	hsa04514	Cell adhesion molecules	6/42	149/8076	0.000108131	0.001214553	0.000866406	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/PTPRC	4 6
KEGG	hsa05323	Rheumatoid arthritis	5/42	93/8076	0.000110414	0.001214553	0.000866406	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05150	Staphylococcus aureus infection	5/42	96/8076	0.000128378	0.001294476	0.000923419	FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05320	Autoimmune thyroid disease	4/42	53/8076	0.000153857	0.001345905	0.000960106	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04061	Viral protein interaction with cytokine and cytokine receptor	5/42	100/8076	0.000155725	0.001345905	0.000960106	CSF1R/CCL13/CCL18/CCL19/CXCR4	5
KEGG	hsa04670	Leukocyte transendothelial migration	5/42	114/8076	0.00028782	0.002321749	0.001656228	CYBA/ITGB2/MMP9/RAC2/CXCR4	5
KEGG	hsa04062	Chemokine signaling pathway	6/42	192/8076	0.000429397	0.003247314	0.002316483	DOCK2/RAC2/CCL13/CCL18/CCL19/CXCR4	6
KEGG	hsa04612	Astrima	3/42	78/8076	0.000531305	0.003781638	0.002697645		3
KEGG	hsa04012	NF-kappa B signaling pathway	4/42	104/8076	0.001994807	0.012068582	0.008609167	BCL2A1/CD14/CCL13/CCL19	4
KEGG	hsa04620	Toll-like receptor signaling pathway	4/42	104/8076	0.001994807	0.012068582	0.008609167	CD14/CD86/SPP1/TLR8	4
KEGG	hsa05145	Toxoplasmosis	4/42	112/8076	0.002614852	0.015066527	0.010747762	ALOX5/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa05202	Transcriptional misregulation in cancer	5/42	192/8076	0.003002662	0.016514642	0.01178078	BCL2A1/CD14/CD86/CSF1R/MMP9	5
KEGG	hsa04060	Cytokine-cytokine receptor interaction	6/42	295/8076	0.00390778	0.02055832	0.014665353	CSF1R/CSF2RB/CCL13/CCL18/CCL19/CXCR4	6
KEGG	hsa05321	Inflammatory bowel disease	3/42	65/8076	0.004567287	0.023026738	0.016426207	HLA-DMA/HLA-DMB/HLA-DRA	3
KEGG	hsa05221	Acute myeloid leukemia	3/42	67/8076	0.004973176	0.023513674	0.016773565	BCL2A1/CD14/CSF1R	3
KEGG	hsa04210	Apoptosis	4/42	136/8076	0.005246853	0.023513674	0.016773565	BCL2A1/CTSC/CSF2RB/CTSS	4
KEGG	nsa05322	Systemic lupus erytnematosus	3/42	136/8076	0.005246853	0.023513674	0.016773565	CD86/HLA-DMA/HLA-DMB/HLA-DKA	4
KEGG	hsa04658	Th1 and Th2 cell differentiation	3/42	92/8076	0.011918685	0.049729685	0.035474852	HLA-DMA/HLA-DMB/HLA-DRA	3
ONTOLOGY	ID	Description	Gene Ratio	BgRatio	P value	p.adjust	qvalue	genelD	Count
BP	GO:0050900	leukocyte migration	17/60	499/18670	1.85598E-13	3.23684E-10	2.02205E-10	CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/	17
PD	00.0051040		10/00	405/10070			0 500745 10		10
ВР	GO:0051249	regulation of lymphocyte activation	16/60	485/18670	1.75971E-12	1.52661E-09	9.53674E-10	CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/P1PRC/RAC2/CCL19/CORO1A/CD300A/M2B1/ SLAMF8/SAMSN1/IGLL5	16
BP	GO:0042119	neutrophil activation	16/60	498/18670	2.62606E-12	1.52661E-09	9.53674E-10	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/	16
PD	CO:0006000	phagooutosis	14/60	260/18670	8 27002E 12	2 605725 00	2 25240E 00		14
DF	GO.0000909	phagocytosis	14/00	309/10070	0.27003E-12	3.00573E-09	2.23249E-09	IGLL5	14
BP	GO:0050864	regulation of B cell activation	11/60	184/18670	1.42121E-11	4.9572E-09	3.09675E-09	FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	11
BP	GO:0043312	neutrophil degranulation	15/60	485/18670	2.43026E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/ VAMP8/CD300A	15
BP	GO:0002283	neutrophil activation involved in immune response	15/60	488/18670	2.65098E-11	6.60473E-09	4.12596F-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/	15
								VAMP8/CD300A	
BP	GO:0002446	neutrophil mediated immunity	15/60	499/18670	3.62817E-11	7.9094E-09	4.94099E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/	15
BP	GO:0030595	leukocyte chemotaxis	11/60	224/18670	1.18654E-10	2.29925E-08	1.43634E-08	NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8	11
BP	GO:0002697	regulation of immune effector process	14/60	458/18670	1.45234E-10	2.45605E-08	1.53429E-08	CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/	14
00	00.000	and an and a state of the state		000/115	A 47005-	6.07505-	0.000=		
	GO:0009897	external side of plasma membrane	11/63	393/19717	4.1/226E-08	6.67562E-06	3.90875E-06	CD14/CD80/FCGH2B/IGHM/IGKC/IGLC1/IIGB2/PTPRC/CXCR4/TLR8/IGLL5	11 7
CC	GO:01010020	teruary granule	7/63	יטי/ וש/1 <i>ו</i> 185/19717	2.02926F-06	0.000108227	4.24041E-05	ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A	(7
CC	GO:0030667	secretory granule membrane	8/63	298/19717	4.66784E-06	0.000186714	0.000109326	CD14/CYBA/NCKAP1L/ITGB2/PTPRC/SLC2A5/VAMP8/CD300A	, 8
CC	GO:0030666	endocytic vesicle membrane	6/63	167/19717	1.5378E-05	0.000450681	0.000263885	CYBA/FCGR1B/HLA-DRA/RAC2/VAMP8/CORO1A	6
СС	GO:0042613	MHC class II protein complex	3/63	16/19717	1.69005E-05	0.000450681	0.000263885	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042611	MHC protein complex	3/63	25/19717	6.80025E-05	0.001552276	0.000908899	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042571	immunoglobulin complex, circulating	4/63	72/19717	8.27284E-05	0.001552276	0.000908899	IGHM/IGKC/IGLC1/IGLL5	4
CC	GO:0070821	tertiary granule membrane	4/63	73/19717	8.73155E-05	0.001552276	0.000908899	CYBA/ITGB2/VAMP8/CD300A	4
CC	GO:0030670	phagocytic vesicle membrane	4/63	76/19717	0.000102188	0.001635005	0.000957338		4
₩F	GO:0003823	Antigen binding	7/59 3/50	160/17697	9.95363E-07	0.002217000	0.001760200		۲ د
MF	GO:0023020	MHC protein complex binding	3/59	25/17697	7.68384F-05	0.00594217	0.004718148	HLA-DMA/HLA-DMB/HLA-DRA	з 3
MF	GO:0034987	immunoglobulin receptor binding	4/59	76/17697	0.000119512	0.006931719	0.00550386	IGHM/IGKC/IGLC1/IGLL5	4
MF	GO:0048020	CCR chemokine receptor binding	3/59	43/17697	0.000395083	0.018331851	0.014555689	CCL13/CCL18/CCL19	3
MF	GO:0008009	chemokine activity	3/59	49/17697	0.000581514	0.019537216	0.015512762	CCL13/CCL18/CCL19	3
MF	GO:0019864	IgG binding	2/59	11/17697	0.000589485	0.019537216	0.015512762	FCGR1B/FCGR2B	2
MF	GO:0005178	integrin binding	4/59	132/17697	0.000979876	0.02841641	0.022562939	ITGB2/LCP1/SPP1/ITGBL1	4
MF	GO:0042379	chemokine receptor binding	3/59	66/17697	0.00138748	0.033384871	0.026507951	CCL13/CCL18/CCL19	3
MÉ	GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	2/59	17/17697	0.001439003	0.033384871	0.026507951	GYBA/KMU	2
KEGG	hsa04145	Phagosome	9/42	152/8076	6.13591E-08	7.42445E-06	5.29626E-06	CD14/CTSS/CYBA/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/CORO1A	9
KEGG	hsa05416	Viral myocarditis	6/42	60/8076	5.55121E-07	3.35848E-05	2.39578E-05	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/RAC2	6
KEGG	hsa05152	Tuberculosis	8/42	180/8076	3.21921E-06	0.000129841	9.26229E-05	CD14/CTSS/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/CORO1A	8
KEGG	hsa04672	Intestinal immune network for IgA production	5/42	49/8076	4.7939E-06	0.000145016	0.000103447	CD86/HLA-DMA/HLA-DMB/HLA-DRA/CXCR4	5
KEGG	hsa04640	Hematopoietic cell lineage	6/42	99/8076	1.06974E-05	0.000258877	0.000184671	CD14/CD37/CSF1R/HLA-DMA/HLA-DMB/HLA-DRA	6
KEGG	hsa05330	Allograft rejection	4/42	38/8076	4.10371E-05	0.000771375	0.000550263		4 F
KEGG	hsa05332	Leisimaniasis Graft-versus-host disease	5/42 4/42	42/8076	+.40∠2E-U5 6.12967F-05	0.000905200	0.000645734	CD86/HLA-DMA/HLA-DMB/HLA-DRA	ວ 4
KEGG	hsa04940	Type I diabetes mellitus	4/42	43/8076	6.73296E-05	0.000905209	0.000645734	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04514	Cell adhesion molecules	6/42	149/8076	0.000108131	0.001214553	0.000866406	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/PTPRC	6
KEGG	hsa05323	Rheumatoid arthritis	5/42	93/8076	0.000110414	0.001214553	0.000866406	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05150	Staphylococcus aureus infection	5/42	96/8076	0.000128378	0.001294476	0.000923419	FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05320	Autoimmune thyroid disease	4/42	53/8076	0.000153857	0.001345905	0.000960106	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04061	Viral protein interaction with cytokine and cytokine receptor	5/42	100/8076	0.000155725	0.001345905	0.000960106	CXRA/ITGR2/MMP9/RAC2/CXCR4	5
	115aU407U		5/42	192/8076	0.00028782	0.002321749	0.00100228		5 6
KE(-i(-i	11.36.00		· ·· — ·	1.12.11.11.11.11	0.00.000	0.000	0.000		U

Cluster	Score	Nodes	Edges	Node IDs
Module 1	6.571	15	46	DOCK2, TLR8, CD52, HLA-DRA, CSF1R, CD300A, EVI2B, MMP9, CD86, LCP1, NCKAP1L, CD14, CTSS, RAC2, S100A9
Module 2	5.429	8	19	CD48, FCGR2B, CYTIP, CSF2RB, ITGB2, PTPRC, CCL19, CORO1A

Table S2 Detail information of two key functional modules.

Table S3 Gene Ontology and Kyoto	Encyclopedia of Genes and	Genomes pathway enrichment	analyses of hub genes.
----------------------------------	---------------------------	----------------------------	------------------------

ONTOLOGY	ID	Description	P value	p.adjust	geneID	Count
BP	GO:0070661	leukocyte proliferation	2.48847E-09	2.22718E-06	CD86/CSF1R/DOCK2/NCKAP1L/PTPRC/RAC2/CD300A	7
BP	GO:0007159	leukocyte cell-cell adhesion	5.83685E-09	2.61199E-06	CD86/NCKAP1L/ITGB2/PTPRC/RAC2/S100A9/CD300A	7
BP	GO:0042110	T cell activation	5.27508E-08	7.60517E-06	CD86/DOCK2/NCKAP1L/LCP1/PTPRC/RAC2/CD300A	7
BP	GO:0046651	lymphocyte proliferation	6.41178E-08	7.60517E-06	CD86/DOCK2/NCKAP1L/PTPRC/RAC2/CD300A	6
BP	GO:0032943	mononuclear cell proliferation	6.69642E-08	7.60517E-06	CD86/DOCK2/NCKAP1L/PTPRC/RAC2/CD300A	6
BP	GO:0043312	neutrophil degranulation	7.14053E-08	7.60517E-06	DOCK2/NCKAP1L/ITGB2/MMP9/PTPRC/S100A9/CD300A	7
BP	GO:0002283	neutrophil activation involved in immune response	7.44788E-08	7.60517E-06	DOCK2/NCKAP1L/ITGB2/MMP9/PTPRC/S100A9/CD300A	7
BP	GO:0046631	alpha-beta T cell activation	8.39338E-08	7.60517E-06	CD86/DOCK2/NCKAP1L/PTPRC/CD300A	5
BP	GO:0042119	neutrophil activation	8.55476E-08	7.60517E-06	DOCK2/NCKAP1L/ITGB2/MMP9/PTPRC/S100A9/CD300A	7
BP	GO:0002446	neutrophil mediated immunity	8.67274E-08	7.60517E-06	DOCK2/NCKAP1L/ITGB2/MMP9/PTPRC/S100A9/CD300A	7
CC	GO:0070820	tertiary granule	7.76795E-06	0.000419077	NCKAP1L/ITGB2/MMP9/CD300A	4
CC	GO:0101002	ficolin-1-rich granule	1.25022E-05	0.000419077	NCKAP1L/ITGB2/MMP9/CD300A	4
CC	GO:0101003	ficolin-1-rich granule membrane	1.53321E-05	0.000419077	NCKAP1L/ITGB2/CD300A	3
CC	GO:0030667	secretory granule membrane	8.06369E-05	0.001653057	NCKAP1L/ITGB2/PTPRC/CD300A	4
CC	GO:0009897	external side of plasma membrane	0.00023395	0.002871573	CD86/ITGB2/PTPRC/TLR8	4
CC	GO:0005925	focal adhesion	0.000262428	0.002871573	ITGB2/LCP1/PTPRC/RAC2	4
CC	GO:0005924	cell-substrate adherens junction	0.000269922	0.002871573	ITGB2/LCP1/PTPRC/RAC2	4
CC	GO:0030055	cell-substrate junction	0.000280154	0.002871573	ITGB2/LCP1/PTPRC/RAC2	4
CC	GO:0070821	tertiary granule membrane	0.00156887	0.014294145	ITGB2/CD300A	2
CC	GO:0005884	actin filament	0.003579709	0.029353613	LCP1/RAC2	2
MF	GO:0048365	Rac GTPase binding	0.001322735	0.074331524	DOCK2/NCKAP1L	2
MF	GO:0005178	integrin binding	0.004738111	0.074331524	ITGB2/LCP1	2
MF	GO:0032395	MHC class II receptor activity	0.00788484	0.074331524	HLA-DRA	1
MF	GO:0017048	Rho GTPase binding	0.008364282	0.074331524	DOCK2/NCKAP1L	2
MF	GO:0019887	protein kinase regulator activity	0.008639343	0.074331524	NCKAP1L/RAC2	2
MF	GO:0008429	phosphatidylethanolamine binding	0.008670141	0.074331524	CD300A	1
MF	GO:0050786	RAGE receptor binding	0.008670141	0.074331524	S100A9	1
MF	GO:0035325	Toll-like receptor binding	0.009454864	0.074331524	S100A9	1
MF	GO:0036041	long-chain fatty acid binding	0.011022581	0.074331524	S100A9	1
MF	GO:0019207	kinase regulator activity	0.011295508	0.074331524	NCKAP1L/RAC2	2
KEGG	hsa05416	Viral myocarditis	1.30353E-06	0.000102979	CD86/HLA-DRA/ITGB2/RAC2	4
KEGG	hsa04514	Cell adhesion molecules	4.90976E-05	0.001939354	CD86/HLA-DRA/ITGB2/PTPRC	4
KEGG	hsa05323	Rheumatoid arthritis	0.000301683	0.00794431	CD86/HLA-DRA/ITGB2	3
KEGG	hsa04670	Leukocyte transendothelial migration	0.00054926	0.010847895		3
KEGG	hsa05330	Allograft rejection	0.001381269	0.019940988		2
KEGG	nsa05332	Gran-versus-nost disease	0.001686132	0.019940988		2
KEGG	nsa04940	lype i diabetes mellitus	0.001766923	0.001106160		2
KEGG	hsa04072	Transprintional misure vertice in concer	0.002289738	0.021120102		2
KEGG	hsa05202		0.002484004	0.021120102		Э
KEGG	hsa05320	Autoinmune inyroid disease	0.002074198	0.021120102		2
KEGG	hsa04015	Rapi signaling partway	0.003205535	0.023021509		о О
KEGG	hsa04810		0.005566022	0.023401300		о О
KEGG	hsa03140	Leisnmaniasis	0.005566922	0.033629756		2
KEGO	115aU4057	Stophylococcup ouroup infection	0.00020029	0.04211/000		2
KEGG	hea04666	Staphylococcus aureus Infection	0.000040762	0.04211/000		2
KEGG	hea04640		0.0001 13313	0.042117050		2
KEGG	115aU404U	Toll-like receptor signaling pathway	0.0030003300	0.04211/000		2
NEGG	115804020	ion-ince receptor signaling patriway	0.009903037	0.043730101		۷